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An Actor-Oriented Dynamic Network Approach

The Case of Interorganizational Network Evolution

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There is a growing interest in intra- and interorganizational network dynamics. The central question in the latter domain is, "How do firms choose collaborative partners given their present network configuration, their goals, and characteristics to get a strategic network position?" We introduce actor-oriented network models as a method to describe and explain the development of interorganizational collaboration networks. The models are applied to longitudinal data about collaborative agreements within the genomics industry.

Keywords: *actor-oriented models; interfirm network dynamics; empirical test*

As demonstrated by three special issues in *Journal of Mathematical Sociology* (Doreian & Stokman, 1996, 2003; Stokman & Doreian, 2001), the study of network dynamics is of growing importance among sociologists, social psychologists, and network statisticians. All three issues were devoted to the underlying mechanisms that induce the evolution of social networks: which micro mechanisms (i.e., individual choices) lead to which macro outcomes (i.e., network structures), and how and why do these structures change over time? More recently, research on networks and their dynamics is also flourishing in the strategy and organization literature; see, for instance, review articles by Borgatti and Foster (2003) and Brass, Galaskiewicz, Greve, and Tsai (2004). One emerging and particularly important topic is the ongoing dynamics of networks that result from collaborative choices (among others, Ahuja, 2000; Chung, Singh, & Lee, 2000; Ebers, 1999; Gulati, 1995, 1999; Gulati & Gargiulo, 1999; Hagedoorn, 2006; Powell, 1998; Powell, Koput, Smith-Doer, & Owen-Smith, 1999); today's choice of an alliance partner affects tomorrow's options as it changes the network structure and thereby the future alternatives and strategies of all fellow network members. For advancements in the latter topic, new statistical techniques are required that can analyze these complex longitudinal network data structures (e.g., Hagedoorn, 2006). Most techniques, however, are not able to deal with these data structures in a satisfactorily and statistically sound way. Snijders (1995, 1996, 2001, 2005) and Snijders & Van Duijn (1997) introduced actor-oriented modeling that does not assume statistical independence between observations and combines continuous time Markov analysis and random utility models. Originally these models were designed to model the

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evolution of expressive networks consisting of individuals (see van de Bunt, 1999; van de Bunt, Van Duijn, & Snijders, 1999; van de Bunt, Wittek, & De Klepper, 2005; Van Duijn, Zeggelink, Huisman, Stokman, & Wasseur, 2003). However, actor-oriented modeling is also particularly adequate to capture the manner in which interfirm networks evolve as a consequence of interaction between network structure and alliance partner choice. Actor-oriented modeling is also an answer to a call for the application of agent-based modeling to solve the puzzle of the interaction between network (i.e., macro) outcomes and a firm's (i.e., micro) choices (Macy & Willer, 2002). This is warranted because actor-oriented modeling allows for assessing of the relevant mechanisms based on individual (i.e., firm) choices. These choices are modeled under the assumption that firms are driven by the expected amount of utility derived from the selection of specific partners, taking the present network configuration and the theoretically desired outcome explicitly into account.

The main purpose of this article is to introduce the use of actor-oriented statistical network models in the field of interorganizational networks to, firstly, demonstrate the richness of the models in general and, secondly, show that these models are suited for describing and explaining the development of interorganizational networks. We restrict ourselves to several appealing, though theoretically straightforward, causes of interfirm network evolution.

Overview

This article first discusses arguments that form the base of actor-oriented statistical modeling and then details the functions we applied to the problem of interfirm cooperation. Subsequently, we analyze the collaboration within the field of genomics with these tools. Lastly, we show some new issues that emerge from this approach, including new developments in actor-oriented modeling, and some drawbacks.

The remainder of this article uses the following notation. The focal actor is called ego, always referred to as (actor) i. Ego is the organization on which the perspective of an argument is based. All other organizations are called alters, most of the time referred to as (actors) j, k, and so on. A relation between ego and alter is either absent (i.e., two organizations do not collaborate) or present (i.e., two organizations do collaborate).[1]

An Actor-Oriented Statistical Network Approach

Existing Dynamic Network Models

The network literature does not provide many stochastic network models that express the dynamic aspects of the development of social networks. We distinguish two main approaches: the loglinear approach and the Markov approach.

The first set of dynamic stochastic network models is based on the loglinear approach. These models are generalizations of Holland and Leinhardt's (1981) well-known p_1-model, extended by Wasserman (1987); Wasserman and Iacobucci (1988); Anderson, Wasserman, and Crouch (1999); Snijders and Van Duijn (2002); Van Duijn, Snijders, and Zijlstra (2004); and Zijlstra, Van Duijn, and Snijders (2006). The original p_1-model includes three sets of

parameters, referred to as expansiveness (i.e., the tendency to choose others), popularity (i.e., the tendency to be chosen by others), and reciprocity effects (i.e., the tendency to establish reciprocated relationships). The loglinear approach offers the opportunity to add individual attributes (also called actor covariates) to the analysis, but these attributes are used only to define nonoverlapping and exhaustive subgroups, each group member having identical parameters. If continuous covariates are included, the model requires a large amount of parameters. The random effects–oriented p_2-model overcomes the latter problem (see, for instance, Van Duijn et al., 2004). For an extensive discussion of the loglinear model in general and the p_1-model in particular, we refer to Wasserman and Faust (1994) and Van Duijn et al.

The second, more elaborated, set of stochastic dynamic network models is based on Markov processes. Because the models that we apply are Markov-based models, we explain them in more detail. For additional information, we refer to Holland and Leinhardt (1977), Wasserman (1980), and especially Leenders (1995, 1996). Markov analysis is a statistical technique suitable for the analysis of time-dependent stochastic processes. Suppose that at several points in time, the state of some system (i.e., the network) is observed. It is assumed that the underlying time parameter t is continuous, whereas the network is only observed at two or more points in time. The process is a Markov process if for any point in time, the conditional distribution of the future given the present and the past is a function only of the present. All relevant information is therefore assumed to be part of the present state. Although this seems a strong assumption, it can in principle be met by incorporating relevant information from the past in the present state. Several meaningful matrices are defined. The probability matrix contains the conditional probabilities of making the transition from one state at $time = t$ into another state at $time = t + \Delta$ (i.e., from no collaboration to collaboration). Markov analysis, however, does not concentrate on the probability of going from one state into another, but uses this information to calculate so-called transition rates (i.e., the rate at which some state changes into another). The relation between the probability matrix and the transition rates matrix is called the intensity matrix. Given some conditions (i.e., time stationarity and time and population homogeneity; see Leenders, 1995, 1996), the entries of the intensity matrix can be interpreted as change intensities that are expressed by so-called change rate functions. In our case, they would refer to the rate at which a collaboration between ego (e.g., firm x) and alter (e.g., firm y) will change. Three parameters based on the intensity matrix have an appealing interpretation. The first one defines the probability that within a very small interval of time state x is left, the second one defines the probability that a system shifts from state x to state y given that a transition occurs, and finally, the third parameter is an estimation of the expected length of time that a system remains in state x. Wasserman (1980) and Leenders (1995, 1996) elaborated Markov models for social networks.

Several limitations of Markov modeling and loglinear analysis reduce the strength of the two approaches. The loglinear approach produces an abundance of parameters and treats changes between the state of a network at $time = t$ and $time = t + 1$ as discrete steps, such that the interpretation of the loglinear parameters depends on the length of the interval between the observations. Continuous time Markov analysis, however, is explicitly based on processes in continuous time. Therefore the interpretation of the change rate parameters does not depend on the length of the intervals. Structural effects, such as the tendency toward transitivity or structural balance, are difficult to represent, especially in

loglinear analysis. Markov models are somewhat more flexible. Transitivity, for instance, can be modeled, although not in a completely satisfactory way, because of the implied violation of dyad independence. It seems that the Markov approach, compared to loglinear analysis, has many advantages. Moreover, because the strong assumptions that had to be made when applying Markov models have been convincingly relaxed by Leenders (1995, 1996), Markov modeling has become a very powerful approach. However, there are still some restrictions. Whether these are disadvantages depends on the research goal. First, it is impossible to simultaneously model actor behavior and the network structure as dependent variables. In the present study, this is not our focus. More importantly, however, Markov analysis does not overcome the problems of statistical dependencies caused by the relational and longitudinal aspects of the empirical data structure. As is the case for all multivariate statistical methods, Markov analysis is restricted by the assumption of independence between cases (in our case, firms in a collaboration network). Finally, although Markov analysis comes close, there is a limited connection between theory and data analysis. Preferably, we need a model that integrates mathematical deductions of the implications of a network theory with a statistical model, such that it can be used for a direct empirical test of the applied theory. Actor-oriented statistical network models are especially designed to do so.

Actor-Oriented Statistical Network Models[2]

This section introduces the actor-oriented statistical network model, which is developed to describe and explain the development of closed networks over time (Snijders, 1995, 1996, 2001, 2005; Snijders & Van Duijn, 1997), and overcomes the aforementioned problems. The model describes the development of a social network through time as a result of the rational actions of individual actors. Given the restrictions determined by the structure of the network and the distribution of actor and dyadic attributes, it is assumed that each individual actor maximizes his utility. The models combine random utility models (see below); continuous time Markov models, as explained in the former section; and simulation, which makes them especially suited for rational choice theory-based dynamic network models (Snijders, 1995). We assume that strategic partner choice of companies can be modeled along these lines.

We have as data a number of adjacency matrices, called $C_{ij(t)}$ (from Collaboration), in which cell *(ij)* stands for the existence of the collaboration between ego *i* and alter *j*; ego and alter either have a collaborative relationship or they have not, and (*t*) denotes the moment in time the collaboration network is observed (at least two and, in our case, three). Actors *i* and *j* are in a range from 1 to *n* (in our case, $n = 48$ genomic firms that are involved in collaborative relationships with each other). As said, the relation network should be time dependent. The dyadic covariates (e.g., mutual group membership) and individual attributes (i.e., organizational attributes, such as size, financial well-being, and status), on the other hand, may be either constant over time or time dependent.

For each actor, a utility function is defined. This function, which is what is actually maximized by the actors, is based on substantive arguments and constructed such that it represents the costs and rewards for an actor to be in a specific state at a certain moment

in time. This is the core of the model, and as such, it determines its success or failure because it is a direct representation of the theory at hand. Because the individual utility functions include elements that are not represented in the model by measured variables, this is modeled as a random component. Therefore, the utility function contains statistical parameters that have to be estimated from real observed data. The utility function may differ between actors. For instance, the meaning of organizational collaboration may depend on the status of the alter firm, its capabilities, or its resources.

For each actor, a set of admissible actions is defined. These actions may refer to relations with the others in the network. In our case, firms may start, consolidate, or dissolve a collaborative relationship with all potential partners. The actors choose their actions according to a heuristic that determines which action in which situation is most likely to be chosen in view of optimizing expected utility. The heuristic actors use once they have the opportunity to act is modeled as a random utility model in which the actor chooses among the possible actions with probabilities that are an increasing function of the expected utility as calculated from the variables in the model. These types of models are called discrete choice models.

Discrete choice models are models for situations in which the dependent variable is a discrete set of choices. This set of choices can relate to a whole range of topics: which political party to vote for, which brand of coffee to buy, which study to start, which bank to trust, and which organizations to collaborate with. In general, the choice of action for actor i at *time* $= t$, a_{it}, from a set of allowed actions A, is based on a number of independent variables. If an action can be described as a function of one or more substantive utility arguments, it is assumed that the actor is able to foresee (i.e., calculate) the expected effects of future actions. This yields that each action ego can take (i.e., start or dissolve a partnership) is associated with a change in utility $\Delta U_{it}(a)$. Because the choice of action can also be based on utility arguments that are not explicitly modeled in the utility function and because of measurement and/or specification errors, it is assumed that ego chooses the action that maximizes $\Delta U_{it}(a) + E_{it}(a)$, in which $E_{it}(a)$ is random disturbance. Under certain conditions on the distribution of $E_{it}(a)$, this leads to the multinomial logit model (Agresti, 2002; Maddala, 1983; McFadden, 1973):

$$p_{it}(a) = \frac{\exp(\Delta U_{it}(a)/\sigma)}{\sum\limits_{a=1}^{A} \exp(\Delta U_{it}(a)/\sigma)}.$$

This model states that, in case the expected change in utility is approximately the same for all actions, ego's choice is more or less entirely based on pure chance. However, if, compared to other actions, one action is associated with a relatively large increase of expected utility, the probability that ego chooses this specific action is also relatively large. Let us apply this to the collaboration process. If firm i (ego) has no collaboration partners, this firm has the opportunity to choose a suitable partner from a closed set of alters (i.e., all other firms). Each firm is evaluated in terms of expected utility, based on which this firm decides (with a certain probability) to start a partnership with one of the other firms or consolidate the present situation. Note that because of the random

component $E_{it}(a)$, ego does not necessarily choose the action that is associated with the largest expected increase of utility.

The actor-oriented model, when elaborated for a practical application, contains unknown parameters that have to be estimated from observed data by a statistical procedure. Because the proposed stochastic models are too complex for the application of classical maximum likelihood estimation procedures and testing methods, Snijders (1996) proposed the method of moments and computer simulation. The procedure to analyze and to approximate expected values of relevant statistics, called theta (θ), is based on the recursive Robbins-Monro stochastic approximation method (see, e.g., Chen, 2002) and adapted by Snijders (2001). Because this procedure provides the researcher with estimates of these statistics and its covariance matrix, a test can be applied using

$$t = \frac{\hat{\theta}_j}{S.E.(\hat{\theta}_j)},$$

in which the standard error ($S.E.$) can directly be obtained from the covariance matrix of the thetas. Snijders (1996, 2005) proposed to use an approximate standard normal distribution.

In summary, we observe at several points in time the collaboration network of a closed group of genomic firms and collect information regarding a number of fixed and changeable individual and dyadic attributes. However, because we have no information about what happens in between the measurement points, this is simulated using the random utility model. The organizational actions that make the network develop from one structure into another are the core of the simulation procedure. By maximizing utility, actors decide with certain probabilities which actions to take (in our case, which partnerships to start, maintain, or dissolve). The probabilities for action and the exact formulation of the utility components are based on substantive arguments derived from the literature. The software that is used for the estimation is called SIENA (Simulation Investigation for Empirical Network Analysis), which is part of the network software package STOCNET and can be downloaded for free from Snijders' home page.[3]

Before we explain the main determinants of collaboration and their translation into components of the utility function, we present the data.

Data Collection

Information on collaborative agreements mentioned in the trade press on the genomic industry was collected. The set of original genomic companies was chosen on the basis of trade press, scientific press, and commercial sources (see, e.g., Jones, 2000; Reed, 2000; Wickelgren, 1999). For the current study, the collaborations amongst the most often portrayed genomic companies and large mainly pharmaceutical companies have been collected.

The occurrence of collaborative agreements of any sort focused on joint R&D, technology collaboration was obtained from information contained in the electronic newsletter *Bioinform*[4] from 1998 to 2000. We constructed networks for 1998, 1999, and 2000 separately, and treated 1998 plus mentioned prior relations as the baseline network. Because this article is intended to show some the of finesses of actor-oriented modeling, we have

Figure 1
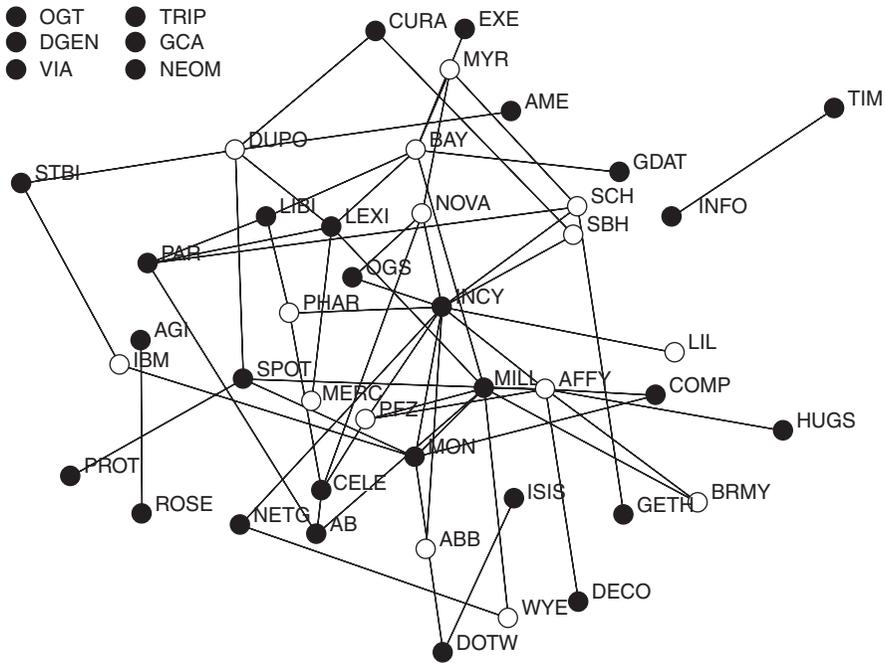**The Genomic Collaboration Network at *Time* = 1 (1998)**
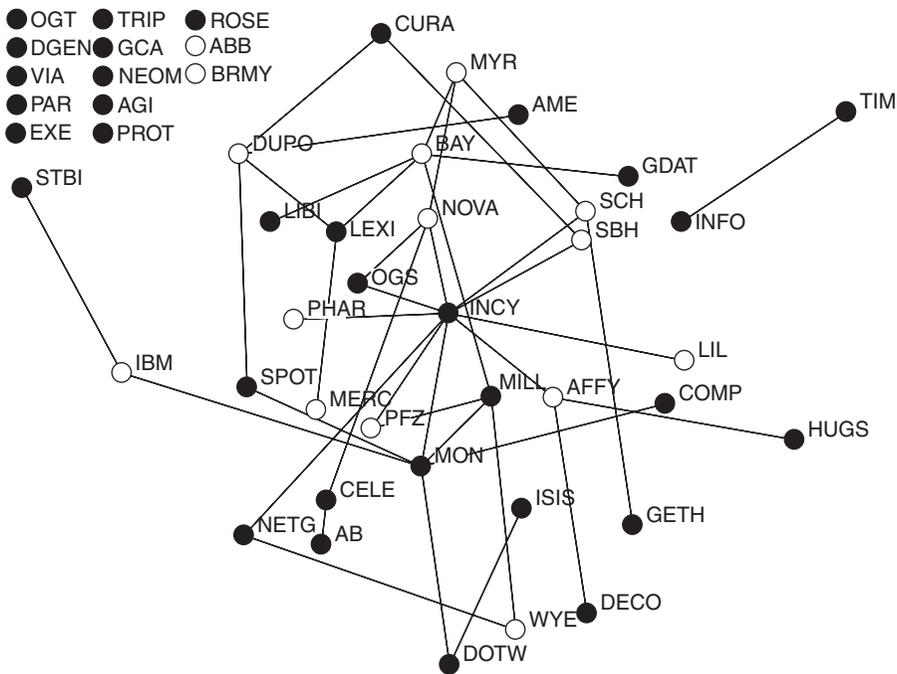
Note: White circles represent large genomic organizations; black circles represent small genomic organizations.

chosen only one data source. For most players, in addition to their Web sites, and for a couple key players, the SEC filings were used to corroborate whether we covered the significant events. There are no missing data for the period from 1998 to 2000.

Below we present several descriptive statistics of the genomic collaboration networks. Before doing so, we provide graphical representations of the genomic collaboration networks. Figure 1 , Figure 2, and Figure 3 show graphical representations of three consecutive "snapshots" of the genomic collaboration networks (1998, 1999, and 2000). They show that the structure of the network changes rapidly. In terms of the number of partners, the figures show that in 1998, there are some key players, especially INCY, which has 10 partners, MON (6 partners), and BAY (5 partners). Between 1998 and 1999, AFFY (from 3 to 6 partners) and MILL (from 4 to 7 partners) are highly active in the collaborative activity; INCY still has the largest number of partners (11). From 1999, almost all organizations are subject to change. Besides OGT (a private genomic firm), all organizations are engaged in one or more collaborations. The most central organization remains INCY, which initiated many new collaborations (from 11 to 19).

The dynamics regarding the above figures are summarized in Table 1, which shows the number of changes between subsequent observations of the three collaboration networks: $0 \rightarrow 0$ stands for the number of firms that do not collaborate at two consecutive time

Figure 2
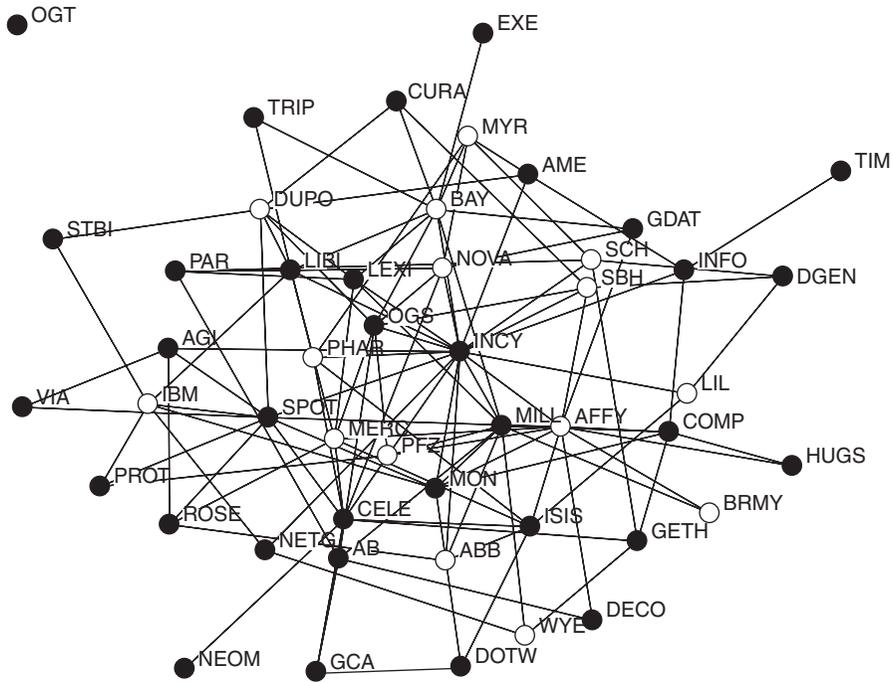**The Genomic Collaboration Network at *Time* = 2 (1999)**

Note: White circles represent large genomic organizations; black circles represent small genomic organizations.

points, whereas $1 \rightarrow 1$ is the number of firms that do collaborate at two consecutive time points. The final two transitions ($0 \rightarrow 1$ and $1 \rightarrow 0$) are the number of new partnerships and the number of dissolved partnerships over two consecutive time points, respectively. Over the period from 1998 to 2000, 82 (20 + 62) new partnerships emerged. No partnerships dissolved during this period.[5]

Table 2 shows several key network descriptives of the genomic collaboration networks. Density is the number of collaborations divided by the total number of dyads. The mean degree is the mean number of collaborative partners over all organizations. The degree of transitivity is defined as the ratio between the number of transitive triads and the total number of triads (for more details, see Zeggelink, 1993). The degree of segmentation is developed by Baerveldt & Snijders (1994); the higher its value, the more segmented the network. Table 2 shows that since 1998, the collaboration network has become denser (from 0.045 to 0.109), more transitive (from 0.014 to 0.080), and consequently less segmented (0.907 to 0.575).

The data shows that in the period from 1998 to 2000, the network changes rapidly. What we do not know, however, is what happens in between the three observations. This is where actor-oriented modeling comes in. We already gave an outline of this type of modeling. In the next section, we implement the model in the specific field under study, namely partnership choice in the genomic industry.

Figure 3
The Genomic Collaboration Network at *Time* = 3 (2000)

Note: White circles represent large genomic organizations; black circles represent small genomic organizations.

The Actor-Oriented Model Applied to Partnership Choice

As said, in this article, we restrict ourselves to the main determinants of collaboration and stress that for now, we merely want to demonstrate the usefulness of the actor-oriented approach. Our main goal is to construct a time-dependent individual utility function of the following form:

$$EU^i = \sum_{d=1}^{D} \alpha_d EU^i_{(d)},$$

in which EU^i stands for the utility ego expects given the network, and actor and dyadic attributes. Ego's expected utility consists of D substantive components (comparable to the exploratory variables in a regression analysis) of which the relative importance is indicated by α_d (comparable to β in a regression analysis). These utility components are defined as

$$EU^i_{(d)} = \sum_{j=1, j \neq i}^{g} EU^{ij}_{(d)},$$

Table 1
Number of Changes Between Subsequent Observations

Observed Period	$0 \rightarrow 0$	$0 \rightarrow 1$	$1 \rightarrow 0$	$1 \rightarrow 1$	Missing	Total
1998–1999	1,068	20	0	40	0	1,128
1999–2000	1,006	62	0	60	0	1,128

Note: The total number of transitions (1,128) equals g ($g = 48$) times $g - 1$ divided by 2.

Table 2
Network Characteristics of the Genomic Collaboration Networks

Year	Density	Mean Degree (Standard Deviation)	Degree of Transitivity	Degree of Segmentation
1998	0.035	1.67 (1.86)	0.014	0.907
1999	0.053	2.50 (2.32)	0.035	0.837
2000	0.109	5.10 (3.50)	0.080	0.575

in which $EU^{ij}_{(d)}$ stands for i's expected utility regarding a partnership with j. These utility components are explicated in the remainder of this section. We describe the following causes of the development of interorganizational networks: reputation (reflected in the tendency to form transitive triads), status (reflected in the tendency to form relationships with organizations that are engaged in many collaborations), familiarity (modeled by means of a dyadic attribute, namely 2-clique comembership), and covariate related similarity (in this case, size). Each feature is explained verbally, mathematically (i.e., as a component of the utility function), and graphically.

Network-Related Reputation: Transitivity

Structural embeddedness of two organizations refers to the number of common partners of these two organizations. If alter j collaborates with alter k and ego collaborates with alter k, alter k is a reliable source of information about the trustworthiness and reputation of alter j. The number of organizations both ego and alter j collaborate with equals $\sum_{k=1,k\neq i\neq j}^{n} C_{ik}C_{jk}$. Remember that C_{ij} is the adjacency matrix: Ego and alter either have a collaborative relationship ($C_{ij} = 1$) or they have not ($C_{ij} = 0$). The transitivity component of ego's utility function is then defined as $EU^{ij}_{(trs)} = C_{ij} \sum_{k=1,k\neq i\neq j}^{n} C_{ik}C_{jk}$. It states that the more collaborative partners ego and alter have in common, the larger the increase of ego's amount of expected utility when initiating a collaboration with alter. The reputation effect is shown in Figure 4. Suppose actor i can choose between actor j (which does not lead to a transitive triad) and actor k (which makes the triad ikl transitive). The reputation effect suggests that actor i prefers actor k (shown by a straight arrow) over actor j (shown by a dotted arrow): $EU^{ij}_{(trs)} < EU^{ik}_{(trs)}$.

Figure 4
Representation of the Reputation Effect (i.e., Transitivity Effect)
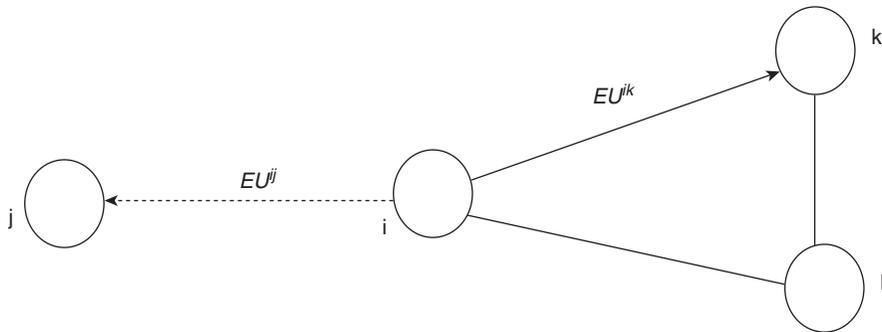

Network-Related Status

We assume that the larger the number of genomic organizations that show their interest in ego, the more status ego possesses with regard to a relative ranking of genomic organizations. Less privileged organizations (i.e., organizations with a relatively low amount of status) can benefit from organizations high on the status ladder. This so-called indirect status can be reached by trying to become a partner with high-status organizations. This component of the utility function is defined as $EU^{ij}_{(sts)} = C_{ij} \sum_{k=1, k \neq i,j}^{n} C_{kj}$. Thus $EU^{ij}_{(sts)}$ expresses that starting a collaboration with high-status alters (i.e., alters with a relatively high indegree) will increase ego's amount of expected utility to a larger extent than it would were ego to initiate a collaboration with low-status alters (i.e., alters with a relatively small indegree). The status effect is shown in Figure 5: Actor i can choose between actor j (with no partners) and actor k (with three partners). If the status effect is correct, actor i prefers actor k over actor j: $EU^{ij}_{(sts)} < EU^{ik}_{(sts)}$.

Familiarity: 2-Clique Comembership

During the process of establishing collaborations, ego may, either on purpose or not, become part of some informal "conglomerate" or "strategic group" of collaborating genomic organizations. Within this group, institutional rules, norms, and so on may arise that foster collaboration (Kogut, 2000). For example, it might be that as long as it is still possible to collaborate with potential partners that are "members" of the own group, this is favored by the other group members, above collaborating with "nonmembers." Furthermore, ego likely has more reliable information about the credibility and integrity of group members than it has about nongroup members.[6] A promising network operationalization is 2-clique comembership (emphasizing the closeness of a group).[7] A 2-clique is a group of actors of which all members can reach each other in maximal two steps. Now let V_{ij} be the dyadic

Figure 5
Representation of the Status Effect (i.e., Popularity Effect)
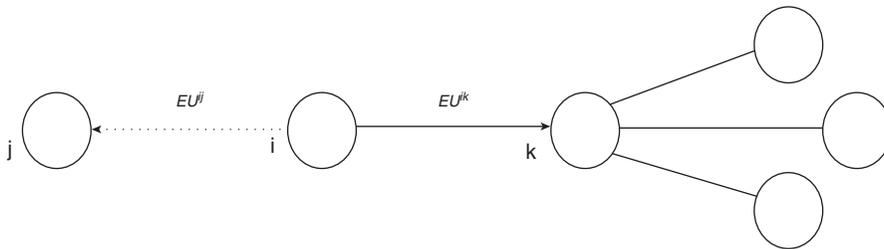
covariate matrix, in which cell *(ij)* stands for the number of 2-clique comemberships. The familiarity component of ego's utility function is then defined as $EU^{ij}_{(grp)} = C_{ij}(V_{ij} - \bar{d}_V)$, in which $\bar{d}_V$ is the mean of all cells *(ij)* of V_{ij}. It states that initiating a collaboration with alters that belong to the same groups ego does will increase ego's amount of expected utility to a larger extent than initiating a collaboration with alters that do not belong to the same groups ego does (see Figure 6): $EU^{ij}_{(grp)} < EU^{ik}_{(grp)}$. The line between actor *i* and actor *k* stands for an extra link between the two actors (in this case, the number of 2-cliques both actors belong to together).

Actor Attribute Similarity

The preference for similar and, under specific conditions, complementary organizations (for instance, in terms of resources) is an important determinant for the establishment of collaboration. Similarity is defined as $S_{ij(v)} = |v_i - v_j| - \bar{d}$, in which *v* is some attribute (either dichotomous or continuous) and $\bar{d}$ is the mean of all $|v_i - v_j|$. In case two organizations are similar with respect to *v*, $S_{ij(v)} = 0$; if dissimilar, $S_{ij(v)} > 0$. The similarity component of ego's utility function regarding organizational characteristics is then defined as $EU^{ij}_{(sim)} = -C_{ij} S_{ij(v)}$. For interpretation purposes, the minus sign is added. It now states that starting a partnership with an alter to whom ego is similar with respect to a certain attribute *v* will increase ego's amount of expected utility to a larger extent than initiating a partnership with an alter to which ego is less similar. This effect is shown in Figure 7, in which circles and squares represent some attribute: $EU^{ij}_{(sim)} < EU^{ik}_{(sim)}$, thus actor *i* prefers actor *k* who is similar (both actors are circles) over actor *j* who is not similar (a square vs. a circle).

Together, the above-mentioned components define the total utility function.

Directed Versus Nondirected Networks

A final distinction that we make is between directed and nondirected networks. Directed networks consist of relations that might be asymmetric (e.g., advice relations), whereas undirected networks consist of relations that by nature cannot be asymmetric, such as the

Figure 6
Representation of the Familiarity Effect (i.e., a Dyadic Covariate Effect)

Figure 7
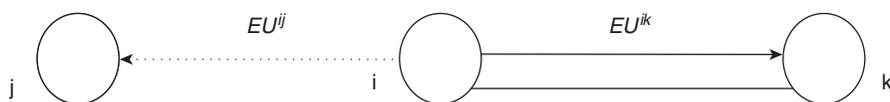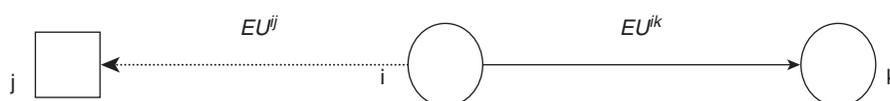**Representation of the Similarity Effect (i.e., an Actor Attribute Effect)**

collaboration network this study addresses. Actor-oriented modeling has originally been designed to describe directed affective networks. Only recently have the models been adapted to deal with undirected networks. Snijders, Steglich, Schweinberger, and Huisman (2005) proposed five undirected network models. The first two are actor oriented (i.e., in the simulation process, individual actors are randomly chosen), and the other three are dyad oriented (i.e., dyads are randomly chosen).

The first actor-oriented model is the forcing model in which ego decides one-sidedly to create or dissolve a tie; this decision only depends on ego's expected utility. The second actor-oriented model, the so-called unilateral initiative and reciprocal confirmation model, looks likes the forcing model. However, alter has to confirm to the proposal made by ego; therefore, the decision depends on, first, ego's and, second, alter's expected utility. The three dyad-oriented models consider *pairs of actors*. In the pairwise conjunctive model, a new tie is created or an existing tie is dissolved if both actors agree or, phrased differently, if both actors choose the same action based on their expected utility. In the pairwise disjunctive model, a new tie is created or an existing tie is dissolved if either ego or alter wishes this (again based on expected utility). Finally, in the pairwise compensatory model, the decision is made based on the sum of their utilities for the creation or dissolution of the tie.

In this article, we follow the actor-oriented unilateral initiative and reciprocal confirmation model. One firm is chosen and, based on the expected amount of utility, "decides" whether to initiate a collaboration. If so, the chosen partner firm also "decides," based on the expected amount of utility, whether it wishes to collaborate. This comes close to a real situation, in which one firm takes the initiative for collaboration and the other firm then either agrees or refuses.

We have introduced the data and showed several components of the utility function that may explain the network changes shown in Figures 1 through 3. In the next section, we present some preliminary results provided by the proposed actor-oriented model.

Table 3
Results Period 1998–2000

Parameters	Rate Model	Model 1a	Model 1b	Model 2	Final Model
Rate $\lambda_{1998-1999}$	0.84***	0.81***	0.74***	0.73***	0.76***
Rate $\lambda_{1999-2000}$	3.05***	2.46***	2.23***	2.32***	2.56***
Trust: transitivity		0.41***	−0.09		
Status: popularity			7.97***	3.95**	4.07**
Size				−0.24	
2-clique comembership					0.23***

Note: Standard error between brackets; estimations are based on 2000 simulation runs.
*$p < 0.10$; **$p < 0.05$; ***$p < 0.01$.

Results

The results are presented in four consecutive steps. First we present a model that only includes the rate parameters λ. It indicates the expected, though estimated, number of changes of relations with another actor per time period per organization. Following this, we add two structural parameters: first, network-related reputation (i.e., transitivity) and second, network-related status (i.e., popularity). Then we add one individual covariate, namely size operationalized as a dummy (relatively small versus relatively large), and one dyadic attribute, namely 2-clique comembership. Each time an effect is not significant, it is at first included in the next model. If, however, the effect remains not significant, it is left out in the remaining analyses. These in-between results are not presented. All other results are summarized in Table 3.

Table 3 shows that the general rate parameter for 1998 to 1999 is smaller ($\lambda = 0.84$) than for 1999 to 2000 ($\lambda = 3.05$). This is in line with the results shown in Table 1 and the trend that is shown in Figures 5 through 7. It means that between 1998 and 1999, on average, the expected number of changes is 0.84 per firm, and between 1998 and 2000, on average, 3.05. Note that these numbers are expected changes, based on the simulation process. This implies that they may differ from the actual number of changes, because during the simulation process (between two measurement points), a relationship between two firms could appear and disappear, which increases the number of changes by two although no changes have been observed.

Model 1a and model 1b show the results of two network-related effects: the former includes only the reputation effect (i.e., transitivity); the latter also includes the status effect (i.e., popularity). At first, the reputation effect is positive and significant at the 1% level (0.41, $p < 0.01$). This suggests that organizations prefer to start partnerships with organizations that are already partners of partners. Hence, make the triad transitive. However, if the status parameter is added to the model (see model 1b), the reputation effect disappears and even becomes negative though not significant. In other words, what at first sight seemed to be a preference for transitivity is actually a preference for collaboration with high-status others (7.97, $p < 0.01$).

Figure 8
Representation of the Network-Related Status
Effect and the 2-Clique Comembership Effect
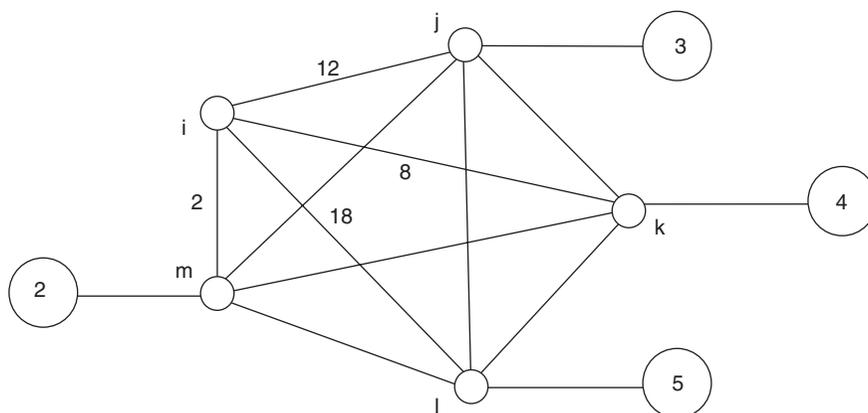
Model 2 includes the size similarity effect. The result, although not significant (0.24, $p > 0.10$), shows that organizations have a slight preference to initiate a partnership with organizations of a different size, which is not strange because most small organizations are genomic organizations, whereas most large organizations are customers of services and technology of the genomic companies. They simply are resource dependent on each other. Finally, we added the dyadic covariate 2-clique comembership. This effect is positive and fairly strong (0.23, $p < 0.01$).[8] There is a tendency for ego to start partnerships with firms that belong to the same groups of organizations, but with whom ego had not yet started collaborations. Except for the status effect, the other effects are not significant.

Summarized, firms start partnerships with firms that have high network status and that are familiar because of the many groups of firms both partners belong to without being partners themselves (yet). These results are depicted in Figure 8.

Figure 8 should be read as follows. As always, the focal actor ego is i. Suppose ego is not partner of actors j, k, l, and m. The line between ego and these four actors is valued by the number of 2-cliques to which they belong.[9] For instance, ego and actor k are both members of the same eight 2-cliques. The lines between ego and the other three actors are valued accordingly. All actors also have partners outside the plotted network. The numbers are printed in the large circles. For instance, actor k is partner of four other firms. Suppose that ego has the opportunity to start a partnership with any of the four other actors. What would the results predict? This depends on the values shown in Figure 8, and the estimates of the sizes of network-related status effect and the 2-clique comembership effect. Both are positive. Without calculating the precise numbers, it is easy to see that starting a partnership with actor l promises the highest amount of expected utility, whereas starting a partnership with actor m leads to the lowest amount of expected utility. Given that the probability of making a choice is an increasing function of the amount of expected utility, the model would predict that actor i chooses actor l with the highest probability and actor m with the lowest probability.

Discussion

Summary

Actor-oriented models provide important insights in interfirm network dynamics. Although at first, actor-oriented models were designed to describe the evolution of expressive networks through time (Van de Bunt, 1999; Van de Bunt et al., 1999, 2005; Van Duijn et al., 2003), the models can be applied to all possible fields of interest, as long as changing networks are the main focus. Because theories of network evolution are increasingly getting more attention in interfirm and partner choice literature (Ahuja, 2000; Ebers, 1999; Gulati, 1995, 1999; Gulati & Gargiulo, 1999; R. Hagedoorn, 2006; Powell, 1998; Powell et al., 1999), this is the right time and place to introduce these types of models.

In short, actor-oriented statistical models combine random utility models and continuous time Markov models (Snijders, 1995, 1996, 2001, 2005; Van Duijn & Snijders, 1997). They describe the development of a social network through time as a result of the rational actions of individual actors. Given the structure of the network and the distribution of actor and dyadic attributes, it is assumed that each individual actor maximizes his utility. The only assumption one must be willing to take is that strategic partner choice can be modeled along these lines, meaning to accept that organizations can be modeled as if they are rational actors. With the methodological purpose of this study in mind, we focused on a limited though widely accepted set of potential interfirm network effects in the genomic industry. On the actor level, we restricted ourselves to the exogenous effect of size and the endogenous effects of reputation (in the models, also referred to as transitivity) and status (also referred to as popularity). On the dyadic level, we included the effect of 2-clique comembership on network formation.

Substantively, we can conclude that organizations have a preference for high-status partners and do not rely on reputation mechanisms, which we operationalized on a triadic level. Although the effect of reputation (i.e., transitivity) seemed to matter, this effect completely disappeared after entering the status effect into the equation. Furthermore, being part of a ''group'' of genomic organizations (in terms of cliques) has considerable consequences for the search for new partners. Firms have a preference for partners that belong to the same groups of organizations they also belong to in terms of partnerships, but with whom they do not collaborate yet.

Conclusion

We hope to have shown that the models are rich, appropriate, theoretically appealing, easy to use, and worth exploring. In the near future, we extend the models by, for instance, the effect of investments put into the collaboration (modeled by means of a so-called endowment function), the effect of the history of a given pair of collaborating organizations, and a more elaborated version of the reputation effect. Furthermore, we will make a distinction between the several transitions from no collaboration to full collaboration and introduce the reciprocity effect by viewing collaboration as initially an asymmetric relationship. This latter extension depends on the level of detail of the data we have at our disposal. Moreover, additional rate of change functions can be introduced assuming that some players are more eager (e.g.,

as a result of their financial status) to establish collaborations than others. Also, differentiation between the establishment and the dissolution of interorganizational collaborations and its relation to, for instance, firm performance can be introduced. This type of model is introduced in Snijders, Steglich, and Schweinberger (2006). Finally, we will introduce the effect of multiplexity, so that differentiation between weak and strong ties can be modeled.

Momentarily, the actor-oriented models, however, have some drawbacks. Depending on the research question, these are either small or large. First, the models are restricted to binary network data. Second, although some first efforts are made to come up with goodness-of-fit tests and measures for explained variation in actor-oriented models (Schweinberger, 2005; Snijders, 2004), the models still lack easy-to-understand and easy-to-use procedures to calculate or approximate these tests and measures. Third, actors can only change their network choices with respect to one kind of network. This makes it impossible to model, say, friendship choices and advice choices simultaneously. For now the only option is to model either of the two networks as a changing dyadic covariate.[10]

Regardless of the drawbacks that are on the agenda of Snijders and his colleagues, we hope to have demonstrated that researchers interested in network dynamics in general and interorganizational in particular can and should benefit from these state-of-the-art actor-oriented models.

Notes

1. Most network research is interpersonal network research. In this type of research, a relationship can also be labeled *asymmetric*, meaning either ego chooses alter, but alter does not choose ego, or vice versa.

2. This article is not intended as a mathematical introduction to actor-oriented modeling. This is the expertise of Snijders (1995, 1996, 2001, 2005) and colleagues. Here we present an outline of this type of modeling to show its excellent applicability for the investigation of interorganizational network dynamics.

3. http://stat.gamma.rug.nl/snijders.

4. http://www.bioinform.com.

5. For the industry under study, genomics, it is assumed that the average lifespan of collaboration is continuing beyond the three years studied.

6. We are aware that our familiarity argument is only one among several. Given the aim of this article, this is not an issue we want to raise.

7. For more details on *n*-cliques, we refer to textbooks on social network analysis, such as Wasserman and Faust (1994), Degenne and Forsé (1999), or Scott (2000).

8. The effect of 2-clique comembership is probably underestimated, because ego and alter can already be partners and at the same time be comembers of a number of 2-cliques.

9. The cliques themselves are not shown in Figure 8. This would lead to a chaotic visual representation.

10. Because the models are mathematically complex, a minor drawback is that the estimation of a complex model takes a considerable amount of time. The time needed is proportional to the number of parameters, the number of actors, and the amount of change between time points. In extreme cases, the analyses might take several hours on a fast personal computer but usually it takes much less time.

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