

Review

Sexual networks: implications for the transmission of sexually transmitted infections

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Abstract

The structures of sexual networks are essential for understanding the dynamics of sexually transmitted infections. Standard epidemiological models largely disregard the complex patterns of intimate contacts. Social network analysis offers important insight into how to conceptualize and model social interaction and has the potential to greatly enhance the understanding of disease epidemics.

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1. Introduction

Standard epidemiological models largely disregard the complex patterns and structures of intimate contacts. In this article we review contemporary literature on social networks that has furthered our understanding of the social aspects of sexual disease transmission. Sociologists, statisticians, and mathematicians have been studying social networks since the middle of the last century, and they have generated a large and wide-ranging literature covering many different aspects of social networks; empirically as well as conceptually and methodologically [1]. And the network perspective has proven to have wide-ranging implications for the study of nature and many areas of modern society [2]. Lately, social scientists have been accompanied in their interest in social networks by physicists, who bring to the field novel models and methods from statistical physics [3,4]. Social network analysis (SNA) offers important insight into how to conceptualize and model social interaction. By offering the present review of the research literature, we suggest that network analysis provides important implications also for the epidemiology of sexually transmitted infections (STI). The review's focus is on sexual contact networks and their implications for disease transmission (Sections 4–6). To provide

some background understanding, we start by briefly presenting the basics of traditional epidemiological modeling (Sections 2 and 3). And we finish with some concluding remarks (Section 7).

2. The standard epidemiological model

In standard epidemiological models, persons are assumed to be in either one of three states. According to these states the population can be classified into three fractions of susceptible (*S*), infected (*I*), or resistant (*R*) persons. It is conventional to distinguish between SI, SIS, and SIR models, and in all these, interaction between persons is assumed to be random [5]. The problem with this last assumption is the core of this review. For most sexually transmitted diseases, the SIS model makes most sense, since few sexually transmitted diseases confer any immunity after infection. An important exception is of course HIV, which is still appropriately described, at least in the Western world, with the SI model.

The random interaction assumption is expelled by Eq. (1), which gives the SIS model as a continuous model in its simplest form, consisting of a system of two differential equations,

$$\begin{aligned} \frac{dS}{dt} &= \frac{-c\beta S(t)I(t)}{N} + \frac{I(t)}{D}, \\ \frac{dI}{dt} &= \frac{c\beta S(t)I(t)}{N} - \frac{I(t)}{D}. \end{aligned} \quad (1)$$

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There are two dependent variables in Eq. (1): the number of susceptible persons, S , and the number of infected persons, I . At each point in time $S(t) + I(t) = N$, where N is the population size. Parameter c is the number of potentially infectious contacts per person, parameter β is the probability of infection per contact between susceptible and infected, and D is the mean duration of the infection [6]. Evidently, this model is homogeneous across persons, as each person is assumed to have the same number of contacts, c . This is what we refer to as the assumption of random interaction. Of course, in the case of STI, this simple model could also take into account gender differences, etc., by adding more equations to the system of equations [7,8].

For many diseases, like measles or flu, diffused through droplets from the breath of infected persons, random interaction is a reasonable assumption and probably a good approximation. That is, there is an abundance of everyday situations where a person is exposed to such infections, for instance on public transportation, in the workplace, and in shops. A significant advantage of the random interaction assumption is that it can easily be modeled with differential equations, and these models can be studied analytically [9]. If the rate of interaction and the transmission probability of the disease between an infected and a susceptible person are known, it is possible to estimate important variables. For example, these models can be used to predict whether an epidemic will occur, how big it will be, and the proportion of the population that has to be vaccinated to prevent an epidemic.

A critical notion in disease epidemiology is the basic reproduction number, R_0 . In the homogeneous deterministic model (Eq. (1)) this number tells us how many uninfected persons an infected person will transmit his or her infection to on the average in a totally susceptible population [5]:

$$R_0 = c\beta D. \quad (2)$$

R_0 has received special attention because in the homogeneous model it is quite intuitive. If R_0 is less than one, then the disease will go extinct. With R_0 equaling exactly one, we have an unstable equilibrium with no change in the number of infected or susceptible, i.e., the disease is endemic. A value larger than one upsets the replacement situation, which means that if $R_0 > 1$ the outcome is an epidemic.

From this simple model we clearly see that practitioners will want to reduce R_0 , which can be done by reducing at least one of the parameters c , β , or D . However, once we start modeling stochastic processes, or heterogeneous populations, there is less consensus on the interpretation of R_0 and, as we will see, modeling implications are less straightforward. It should be noted that models based on Eq. 1 are only suitable for the analysis of large populations. Stochastic models are called for to analyze epidemics in smaller populations [9,10].

3. Heterogeneity in the standard model

The random interaction assumption, however, is not well suited for modeling the diffusion of a STI. Sex is simply not random [11]. As is the case in most social interaction, societal dimensions structure sexual contacts. An early approach to this non-randomness problem in the diffusion of STIs has been to divide the population into subpopulations defined by gender and the level of sexual activity and then to model the diffusion within subpopulations and between subpopulations as systems of differential equations. The rationale is that a small group of sexually very active persons can be modeled by conceptualizing them as one of the subpopulations, usually referred to as a core group [12–16]. These types of models have been used to study the difference between two particular scenarios.

In the first scenario, known as assortative interaction, most contacts take place within the different groups, i.e., sexually active persons have sex with other sexually active persons, while sexually low-active persons have sex with other sexually low-active persons. In the second scenario, known as disassortative interaction, most contacts take place between the groups, i.e., sexually active persons have sex with sexually low-active persons. Theoretical analyses have demonstrated that assortative interaction generates a faster initial spread of the STI, but a smaller size total epidemic. A disassortative interaction pattern on the other hand, generates a slow initial spread, but a large-size epidemic. The mixed scenario, where interaction takes place both within and between the subgroups, known as symmetric association, generates a spreading pattern somewhere between the two extremes.

Most empirical studies indicate that assortative interaction is the closest match to empirical reality [17,18]. One interesting exception is the results from a study of a male homosexual population in Iceland that displays a disassortative pattern [19]. The distinction between assortative and disassortative interaction has also been used for other variables besides gender and sexual activity, such as socio-economic status [20], age, and ethnicity [21] and has been found to be related to STI transmission. These studies demonstrate that assortative interaction is structured across sociological variables, i.e., people are more likely to sexually interact with people from the same social class, age group, and ethnic group. An apparent exception is contact between prostitutes and their clients [22], which can then act as bridges between subgroups [23–25].

A further step away from the standard model, and the assumption of a homogeneous c -parameter, is to study the distribution of the number of contacts that persons have. Several empirical studies have demonstrated that the variation in number of sexual partners is very large [11,26–28]. While most people report 1–4 sexual partners during their lifetimes, some report several hundred or more. This has extremely interesting implications that will be discussed later in this article. Anderson and May [5] have shown that the

variation in number of sexual partners has to be taken into consideration when estimating R_0 . In a heterogeneous population, R_0 is no longer equal to the average number of infections produced by an infected person in an uninfected population. Rather,

$$R_0 = \rho_0 \left(1 + \frac{\sigma^2}{\mu} \right), \quad (3)$$

where ρ_0 is the average number of infections produced by an infected person in an uninfected population, σ^2 is the variance of the number of contacts, and μ is the mean number of contacts in the population. From this equation, it is clear that the larger the variance in number of partners in the population for a given μ , the less infectious an infection needs to be in order to still be able to reproduce itself, i.e. to generate an epidemic.

Even though modeling groups of persons with different levels of sexual activity is more realistic than assuming random interaction in the whole population, such models do not take into account important factors such as partnership formation, duration of partnership, and concurrency [29]. It is theoretically possible to incorporate these factors in a deterministic model by letting each unique combination be represented by an equation in a system of differential equations. However, adding factors soon gives the system too many dimensions to be analytically solvable [30,31].

4. Network models

It is evident that modeling structured interaction by means of flow equations quickly becomes fairly cumbersome. More seriously, however, random interaction between humans is at odds with everyday intuition and experience as well as empirical reports on human sexual behavior [11]. Still, to bring leverage to intuitive ideas, analytical tools are needed to conceptualize interaction structure at the level of persons. A cross-disciplinary field known as SNA provides these tools. An utterly simple depiction of social life starts with conceptualizing each human person as a dot, or node (or vertex). Social, and physical, relations between persons are conceptualized as links between dots, or edges between nodes (or arcs between vertices). This idea was first used some 70 years ago when Jacob Moreno began to draw up “sociograms” of relationships within social groups [32]. Mathematically, the set of all nodes and edges in a social system define a graph, and the analytical treatment of such graphs is known as graph theory. Graph theory goes back at least to Leonard Euler’s “solution” of the so-called Königsberg bridge problem in 1736¹, but was not firmly established until the 1950s [33]. Together with anthropological studies stemming out of

Manchester, also in the 1950s, graph theory was the catalyst in the development of SNA that now provides the basic tools for analyzing sociograms [1,34].

The key to SNA is that the focus of study shifts from persons only to relations between them, as well as overall patterns of relationships in a population. These relations can connect persons to form dyads, triads, or, in the present context, larger networks. Several issues have to be considered when shifting the unit of observation from persons to interrelated persons. We can here only mention the most relevant in passing, but extensive discussions of core concepts and measures for network analysis can be found elsewhere [1,35–37]. From the perspective of statistical inference for example, we have to move beyond the assumption of independent observations, as we deal with interrelated persons. This also means that the problem of boundary specification becomes acute when deciding on the boundaries of populations of interest on social network studies. Boundary specification is also problematic when deciding on sample selection when studying ego networks [38].

An ego network begins from one particular person, for whom relations to other persons are mapped. Thus, the collection of data for an ego network of sexual contacts would start with an identified person (possibly infected) and one would re-construct all distinct sexual contacts for him or her, as well as contacts between other persons in that ego network. In contrast, the collection of data for a complete sexual network could start with all (possibly infected) persons identified in a community, and then one would attempt to re-construct all distinct sexual connections between them. Of course, both types of data collection prevent informants from being anonymous to the investigator [39]. There are advantages and disadvantages in all strategies for data collection, and both ego network and complete network data collection can be affected by sampling and measurement errors if not properly designed.

Some key concepts and ideas will be of relevance for the continued discussion. First, a network consists of the set of edges between a set of identified nodes; this is also referred to as a graph. This implies that a node can be part of the network (group or population), while not being connected to any other node. Such a node is called an isolate. Second, the number of edges that a node has defines the degree of a node; so that a degree of four means that a node has four edges. In the present context, persons with a high degree are of highest interest, since these are the persons with many sexual contacts. Third, degree centrality measures the degree of a node relative to the degree of other nodes in the network. Nodes with the highest centrality have the largest number of edges. Fourth, the network density is given by the observed number of edges in the network relative to the number of possible number of edges in the network. Fifth, a set of nodes in a network that are connected by a set of edges is called a

¹ Königsberg consisted of four regions of land connected by seven bridges. The problem is posed as a question: Is it possible to start a walk anywhere in the city of Königsberg, cross each bridge once and only once, and return to the starting point? What Euler actually proved, by treating the problem in network form, was that this could not be done. (The proof

demonstrates that for the walk to be possible the nodes have to have an even degree, and the graph needs to be connected.)

network component (sometimes a cluster or, if forming a completely connected subgraph, a clique). Think of components as isolated subsets within the network. Epidemics can only take place within components. Note that a component is different from the idea of a cluster as used in epidemiology. In epidemiology, a cluster is defined by the set of infected persons believed to be related by a common etiologic process regardless of their personal interrelationship.

Social scientists have studied social diffusion along lines very similar to the SIS models previously mentioned for quite some time, but it is only recently that the details of interaction structure have been seriously considered [40]. Classical sociological studies include the spread of drug prescription among medical practitioners and the diffusion of new techniques in agriculture. Early mathematical analyses of disease transmission in so-called random networks are found in [41,42]. However, it was not until the outbreak of the HIV/AIDS epidemic that one came to fully realize that a network perspective was crucial for understanding disease dynamics [43], and it was then that serious empirical studies began to show up [23,24].

5. The empirical study of sexual networks

Knowledge on the actual structure of sexual networks that goes beyond ego-network data, such as number of partners and relationship duration, is based on clinical contact tracing and volunteered information associated with contact tracing. Contact tracing means that a person diagnosed with an STI is asked to list all of his or her sexual partners. These in turn are contacted, tested, and asked to reveal the same information. The frequency and procedure for contact tracing differs between different countries [44–46], but studies of contact tracing have found a similar pattern. They reveal that sexual networks consist of many relatively small sexual clusters (components) [47,48]. This has a number of possible explanations. With regards to data collection, contact tracing is sometimes a blunt tool, as it relies on the memory and willingness of clients to reveal information, not to mention the difficulties in tracing people that might be known only on a first-name basis, at best! There is also the possible complication of different strains of the same type of disease being active in the same population.

The contact tracing system used in Manitoba, Canada is especially well suited for studying sexual networks because all persons that are found to have an STI, and their partners, are registered in a centralized information system. In studying a 6-month period (November 1997–May 1998), researchers were able to identify a network of 4544 individuals, which consisted of 1503 connected components with sizes varying from 2 to 82 persons [46]. The component distribution was very skewed, with only 23 components having 19 or more persons. In a study of gonorrhoea transmission in these 23 components, two distinct types of components were identified. One “linear component”, characterized by assortative mixing with a degree of the individual nodes ranging from

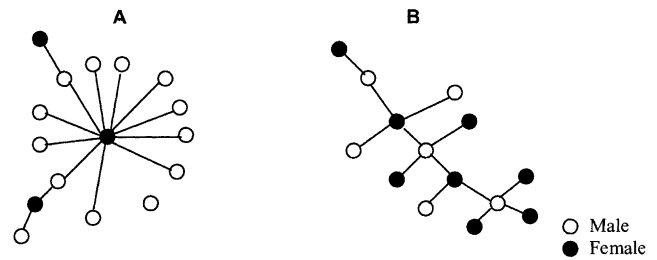


Fig. 1. Example of a radial component, A, and a linear component, B, as identified by Wylie and Jolly [46]. Infection dynamics have been found to differ between the two components.

one to four, and one “radial component”, characterized by disassortative mixing with respect to number of partners, having one highly centralized node, and many nodes with a degree of 1–2. Examples of these two components are presented in Fig. 1. Interestingly they found no gonorrhoea in the radial components, but they did find gonorrhoea in the majority of the linear components.

A disadvantage with using contact tracing data is that it limits generalizations about the structure of sexual interaction in general, because it involves selection on the dependent variable, i.e. being infected. The components of the sexual contact network found in contact tracing are very likely the subsets that exhibit those structural properties that are optimal for the transmission of STIs. Careful statistical research will hopefully propose future solutions to problems like this. A second drawback of contact tracing data is that it focuses solely on sexual contacts. Anthropological field study suggests that in addition to sexual contacts, non-sexual contacts can be good indicators for an increased risk of catching syphilis [49]. Thus, depending on the context, contact tracing should perhaps be systematically complemented with the collection of other types of social network data, to reveal structures of multiple and only partly overlapping networks that foster disease transmission.

Few networks are static, and sexual networks are most certainly not. The emergence and dissolution of sexual partnerships needs to be considered, because STIs are only transmitted as long as there is an ongoing sexual relation between two persons [50]. Therefore an alternative approach to studying the network of sexual contacts between persons is to study the network of concurrent sexual relationships [51,52]. This approach gives rise to another type of graph, called a line graph [53], where the contacts between the persons are seen as nodes in the network. When we let a contact between two persons define a node in the graph, an edge is present whenever a person has more than one contact. Two graphical examples of sexual contacts and their corresponding line graphs are shown in Fig. 2.

Both contact networks displayed in Fig. 2a and b have the same level of network density, $d = 4/10^2$. Despite this fact, it is much easier for an STI to propagate in network a (left) than

² Network density, d , is measured by calculating the ratio $\frac{l}{n(n-1)/2}$, where l is the number of edges and n is the number of nodes.

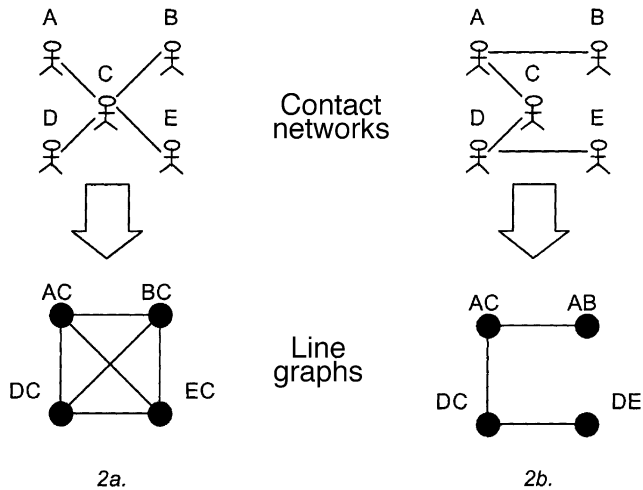


Fig. 2. Two contact networks, and corresponding line graphs following Morris and Kretzschmar [51]. In the line graph, every edge in the contact network is translated into a node, e.g., edge A–C in 2a becomes the node AC. Nodes with degree >1 in the contact network will contribute to new edges in the line graph, e.g., in 2b there is an edge between D and C and D and E in the contact network (C has a degree of 2), thus there will be an edge between DC and DE in the line graph.

in network b. This is due to the fact that the level of concurrent sexual relations is much higher in network a than in network b, as can be seen by considering the corresponding line graphs.

A measure for assessing the level of concurrency in a line graph has been suggested by Morris and Kretzschmar. The concurrency, κ_2 , is given by the following equation.

$$\kappa_2 = L_2 \left(\frac{N_2(N_2 - 1)}{2} \right)^{-1} \tag{4}$$

$$= \begin{cases} 1 & \text{all_pairs_adjacent} \\ 0 < \kappa_2 < 1 & \text{some_pairs_adjacent} \\ 0 & \text{no_pairs_adjacent_ (monogamy)} \end{cases}$$

L_2 is the number of links and N_2 is the number of nodes in the line graph (i.e. κ_2 is the density of the line graph). By further calculating the mean number of concurrent relationships per relationship, the index of concurrency κ_3 , it has been proven that concurrency is a function of the mean and the standard deviation of the degree distribution [52]. Since these properties can be calculated solely on the basis of ego-network data (i.e. local information), it is possible to estimate concurrency by using random samples of the population [51,52], which is very difficult for several other network measures such as e.g., density and component size [54].

The idea of using line graphs [51,52] has been developed even further by taking into consideration that an STI can propagate between two non-concurrent sexual relationships that occur relatively closely in time [55]. To handle this possibility in defining the line graph, it has been suggested that a sexual relation should be seen as active for some period, depending on the type of disease, after the sexual partnership ended.

6. New approaches to the study of epidemics in networks

In the late 1990s physicists became interested in the study of complex networks [2], and in that they have introduced a new angle of approach to the study of social networks. The catalyst was a revisit to the small world problem, initially explored by psychologist Stanley Milgram [56]. From a famous experiment that he conducted in the mid 1960s, Milgram drew the conclusion that any two randomly selected persons in the US are on average separated by six steps. Milgram’s finding suggests that the world of social acquaintances has a peculiar structure in which people are not as locally embedded as we might think. Mathematically, no one was able to make good sense of this finding until it was recently demonstrated that for all types of large connected graphs, only a few edges need to be rewired at random in order to decrease the average distance between the nodes dramatically [57]. Put more formally, by randomly rewiring any connected graph, it will have the same average distance as a random graph with similar density. This work has been applied to various types of networks, e.g., the Internet, metabolic networks and food webs [3,58].

In contrast to much of traditional SNA that has focused on the relationship between single nodes and their relation to the network, this new line of research has very much been focused on identifying classes of networks and their properties. The classification is based on studying the degree distribution, i.e., the number of links, k , connecting to a node. This relates back to our previous discussion on the number of contacts in Section 3. So far, three types of networks have been identified based on their degree distributions, $P(k)$. These are single-scale, broad-scale and scale-free networks [4]. There are indications that sexual networks belong to the group of scale-free networks [27]. A scale-free network is a network where nodes do not have a typical number of edges. Most nodes have only a small number of edges, but a significant number of nodes have a large number of edges, and all frequencies of edges in between these two extremes are represented. This means that the standard deviation around the mean is extremely large, and growing with added observations. Consider the following comparison with a well-known single-scale parameter (with a Gaussian distribution) to see what this implies: if the height distribution of humans were scale-free there would be men and women 100 m tall walking around among us. The mathematical form of a scale-free degree distribution has the form of a power-law, $P(k) \sim k^{-\alpha}$. The typical way to identify a power-law distribution is to plot the frequency distribution of connectivities in a graph with logarithmic axes. In such a graph, the power-law will take the form of a straight line, as shown in Fig. 3 below.

As can be seen in Fig. 3, the tail of the power-law distribution has a much slower decay than other probability distributions, such as the Poisson distribution depicted here. The probability that an extreme number will occur from a random sample cannot be neglected if we are dealing with power-law

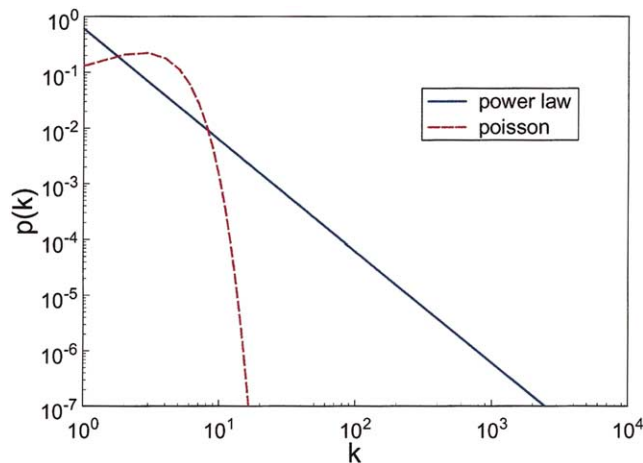


Fig. 3. Comparison of the functional form of a Poisson distribution and a power-law distribution for connectivity, k , with logged axes. Studies suggest that the connectivity distribution for sexual contacts might follow a power-law, thus indicating a scale-free network structure.

phenomena. The proposal that the network of sexual contacts is scale free, with a degree distribution following a power-law, helps explain why we observe such a wide spread in the number of sexual contacts [27]. The skew of the distribution might also help explain the large discrepancy in the number of partners that males and females report [59].

It is interesting to note that a slope $\alpha < 3$ means that the standard deviation becomes infinite in populations of infinite size. The human population is certainly not infinite, but this also has implications for finite populations. It has recently been demonstrated that in a scale-free network contagiousness needs only to be very low for an epidemic process to develop [60]. This result was foreseen already by Anderson and May [5] as can easily be seen by reflecting on Eq. (3) in Section 3 [61]. Another property of scale-free networks is that despite their high susceptibility they are very sensitive to strategic removal of nodes. This turns out to be of importance for the prevention of the spread of STIs because if only a few very active persons are removed (or change their behavior), the network very soon falls apart in separated components [62,63], thus preventing the emergence of epidemics. Recent refined analysis, however, points out that this does not hold true under the assumption of assortative mixing [64]. It is also worth noting that in a scale-free network, epidemics can reproduce with a considerably lower number of infected persons at each point in time, than in a random network [60]. The study of scale-free networks and of epidemics in scale-free networks is still in its infancy, but it holds much promise for the future³. Very recent work includes the analysis of spread dynamics [65–67] and immunization strategies [68,69] in scale-free networks. An exciting next step will be to consider the fact that sexual contacts differ in their duration, and to incorporate this into epidemic models in scale-free networks.

³ See, e.g., <<http://arxiv.org/archive/cond-mat>> for work in progress.

7. Discussion

The research literature convincingly demonstrates that a full understanding of the transmission of STIs has to take into account the structure of sexual networks [70]. Social network analysis provides the essential tool for analyzing social structures, including sexual networks. Classic SNA offers a powerful way to conceptualize static networks, but because sexual interaction is not static, advances in the study of network dynamics are highly relevant for the study of sexual networks. Work in this direction is growing [37], and is, at least partly, driven by the application of SNA to disease transmission [51,55,71,72].

Some of the work reported here utilizes a new analytical approach, namely computer simulation models [73]. In some respects, computer simulation is a more flexible tool than mathematical modeling. For instance, all sorts of heterogeneity of persons and networks are easily built into the model. However, this also means that these models often contain a very large parameter space, and thus are much harder to thoroughly analyze than an analytical mathematical model. Computer simulations have recently been used to build large dedicated dynamic models of disease transmission in networks [74]. This particular type of policy modeling is quite new, but given previously successful attempts to model complex phenomena of modern societies, such as traffic systems and consumer behavior, it is a potentially useful tool for epidemiologists. Other less grand examples of the use of simulation models include the evaluation of centrality measures [75] ([76] for an evaluation using real data) and the already mentioned models of concurrency [52] and mixing [55]. Simulation models can also be used for data interpolation. For example, if one has knowledge about the micro-mechanisms of social interaction, this information could be used to generate the network structure in the population through computer simulations. Such structures can subsequently be used in modeling the epidemic [77].

Lastly, we wish to underscore the importance of intensified data collection. If we are to learn more about how social interaction and social structure mediate disease transmission, more empirical work is crucial. And to conduct successful empirical analysis, data on the interpersonal spread of diseases is urgently needed. Recordings by physicians and other practitioners who handle patients with sexual diseases are important sources of data, as demonstrated by the use of contact-tracing data in the Manitoba study [46]. Where routines for contact tracing are not worked out, they should be developed, preferably in a supra-national spirit, with this purpose in mind. An increased awareness about the importance of interpersonal relationships should also be more widely incorporated when collecting large-scale survey data. Combined with surveys and field studies of groups with high-risk behavior, contact tracing can help paint an approximate picture of the complexity of sexual networks [78].

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