

# Determinants and Consequences of Sexual Networks as They Affect the Spread of Sexually Transmitted Infections

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Because pathogens spread only within the unique context of a sexual union between people when one person is infectious, the other is susceptible to new infection, and condoms are not used to prevent transmission, the epidemiological study of sexually transmitted infections (STIs) is particularly challenging. Social network analysis entails the study of ties among people and how the structure and quality of such ties affect individuals and overall group dynamics. Although ascertaining complete sexual networks is difficult, application of this approach has provided unique insights into the spread of STIs that traditional individual-based epidemiological methods do not capture. This article provides a brief background on the design and assessments of studies of social networks, to illustrate how these methods have been applied to understanding the distribution of STIs, to inform the development of interventions for STI control.

Sexually transmitted infections (STIs) pose challenges to epidemiological study, because the pathogens causing them to spread are transmitted within the unique context of a sexual union between people when one person is infectious, the other is susceptible to new infection, and condoms are not used to prevent transmission. The degree to which disease disseminates depends on the extent to which infected persons have additional sex partners. Thus, the epidemiological study of STIs involves research into the determinants of sexual networks (figure 1) resulting from sexual linkages. The process of ascertaining such relational links, to investigate theories of network and group behavior, has been applied widely in fields ranging from anthropology to computer science and is useful for the study of communicable diseases like STIs, for which links among

people have direct consequences for population morbidity and mortality.

The goal of this article is to describe the determinants and consequences of sexual networks and their implications for STI epidemiology. We provide a brief overview of the determinants of sexual networks; include background on research principles, study designs, and assessments used in the study of social and sexual networks; and present a summary of research that illustrates the consequences of sexual networks and their structure for the spread of STIs. Furthermore, we discuss other network-related phenomena that address network behavior, including mixing and concurrency, and the relatively new discovery of the formation of scale-free networks, since all these factors have important implications for the spread and control of STIs.

## DETERMINANTS OF SEXUAL NETWORKS

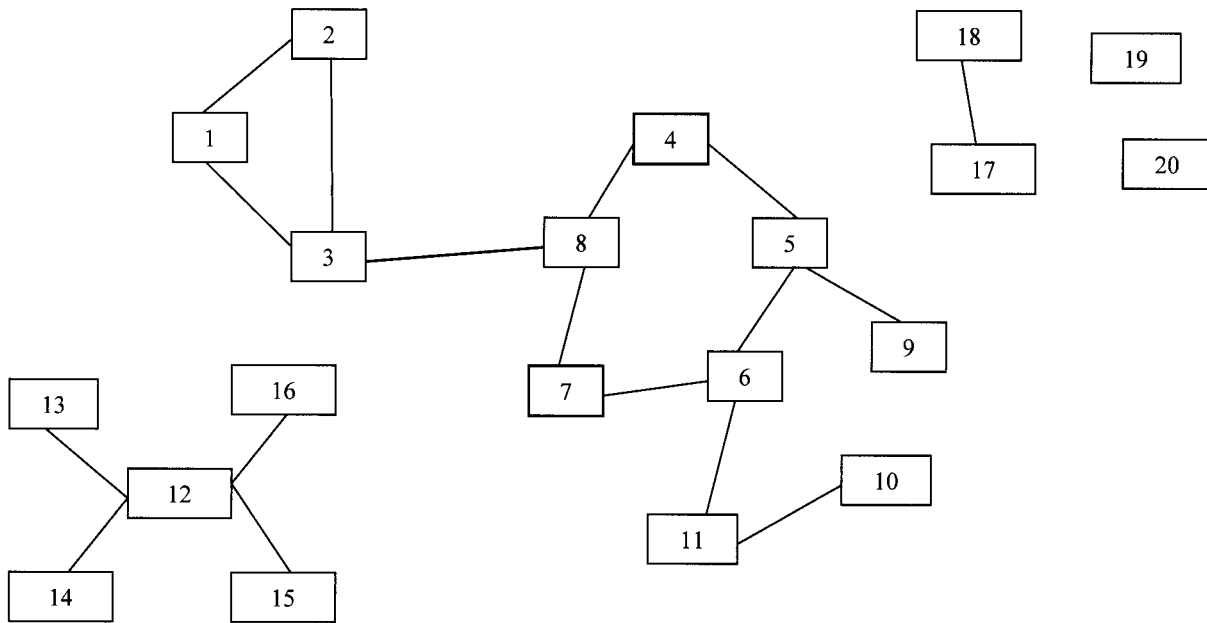
Societal determinants of sexual networks pertain to the underlying social, economic, cultural, and political forces, as well as the technological advances, in a country, region, or even smaller community that have macro effects on network formation. These types of factors may be difficult to quantify and/or study formally [1]; yet, they warrant examination because they affect the

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**Figure 1.** Network graph. A  $k$ -core is a set of people connected to at least  $k$  other people, to form a closed loop. Nodes 1–3 and nodes 4–8 each form a 2-core.

availability of sex partners and influence partnership choices. The political changes in and economic collapse of the Soviet Union, for example, have led to large changes in the composition of populations in cities that have enhanced the spread of sex work and, thus, linkages from sex workers to others, thereby increasing the incidence of STIs [2].

Two other determinants of sexual networks are social norms and the physical spaces in which networks form. Social norms are shaped by cultural factors at the societal level and continue to develop within the networks themselves, to influence individual and partnership behaviors that affect network structure, density, and proliferation over time. Engaging in sex work in the former Soviet Union, for instance, has evolved into an acceptable form of income for many, which is a clear change in social norms.

The physical places where networks form is another critical determinant of sexual networks. The Centers for Disease Control and Prevention (CDC; Atlanta) recommends that disease-investigation specialists (DISs) working in public health departments collect information about where people meet their partners and where they live as a way to trace and treat partners and prevent additional infections [3]. This practice has been implemented throughout the United States and incorporated into network-based research. The majority of gonorrhea cases in Colorado Springs, for example, were diagnosed among people living within 4 census tracts of a large military institution, who met their partners at a limited number of bars, clubs, and social gathering places [4]. On the basis of this premise, a more detailed methodology [5] for identifying places (rather than

people) where high-risk sexual dyads meet was developed and used in South Africa, where the incidence of HIV infection continues to increase at astonishing rates. Field staff conducted anonymous interviews of >3000 men and >1500 women, in 200 venues distributed over 4 townships or business districts. This approach allowed them to estimate the number of new partnerships, identify areas where commercial sex work took place, note differences in partnership dynamics between townships and business areas, and learn that condom distribution in many of the venues was inadequate for the volume of partnership acquisition. This paradigm shift of moving from individuals to high-risk meeting places also was recently incorporated into an intervention to curb transmission of syphilis in Baltimore [6]. After identifying certain streets where sex work occurs, outreach workers were able to locate at least 2 new individuals with cases of infection who were not found through standard DIS practices. Importantly, the places where networks form can serve as a springboard for other types of interventions, such as the distribution of condoms and the dissemination of public health messages regarding safer sex practices and STI education.

The experience of HIV infection and STIs among men who have sex with men (MSM) in San Francisco and other large US cities illustrates how specific subcultures interact to influence the formation and growth of sexual networks. Visiting bathhouses to find anonymous sex partners, an established social norm within the gay culture during the 1980s, created networks in which the first AIDS cases were traced and graphed [7, 8]. Over the past decade, technological advances have en-

abled MSM (and others) to easily meet [9, 10] through chat rooms on the Internet. This macro-level effect has given rise to a new set of social norms and unique “places” and mechanisms that people can use to find sex partners, thus creating novel ways in which sexual networks form and influence the incidence of HIV infection and STIs.

## ORIGINS OF SEXUAL NETWORK EPIDEMIOLOGY

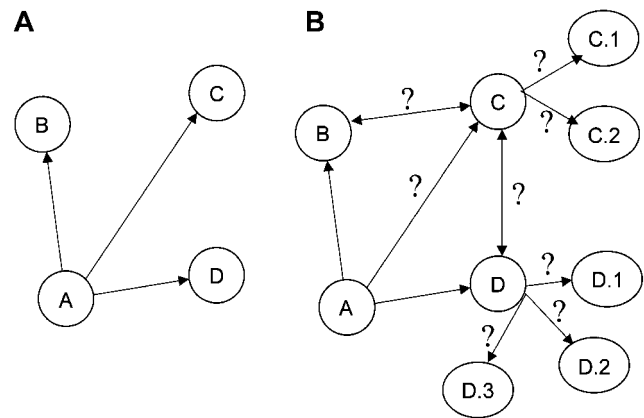
The formal study of social relationships among people has its earliest roots in sociology, during the 1930s. Moreno [11] is credited with conceiving the idea of visually depicting ties within small groups of people. The specification of such ties allows for the study of group structure, an individual’s position within that structure, the interplay between an individual’s position and behavior, and overall group dynamics. This subfield of study was called sociometry [11, 12], from which 2 primary study designs, known as “egocentric” and “sociometric” (described below), have evolved.

In part, the concept of sexual networks grew from the work of local public health departments that traced the partners of patients with syphilis, as early as the 1930s, for purposes of treatment and prevention. Patients who sought care at publicly funded clinics were interviewed about their sex partners, by trained nurses or social workers, to discover the source and break the chain of infection [13, 14]. Modern individual-based epidemiological methods evolved to address sexual networks when investigators began to ask subjects about their partners in, for example, studies of serodiscordant couples, to assess both infectiousness and susceptibility, particularly with regard to HIV infection (e.g., [15, 16]). In recognition of the fact that people may have >1 sex partner, investigators now ask subjects detailed information about all their partners (rather than recruiting a couple), which reflects an egocentric network study design (described below).

## SOCIAL NETWORK ANALYSIS

Networks are typically represented as graphs, in which nodes denote people and links indicate a sexual tie between 2 people (figure 1). Networks also may include smaller subgraphs, called “components,” that are not necessarily connected, as well as unconnected singleton nodes [12].

**Network study designs.** Two basic approaches to conducting network-based research have evolved. In an egocentric study design, the index subject (person A) names his or her sex partners (persons B, C, and D) and describes them [12] (figure 2A). In this study design, the index subject (A) provides information about his or her sex partners, thus characterizing subject A’s personal network. Information ascertained from the index subject about each partnership includes the duration of the relationship, the type of partner (e.g., steady, casual, or



**Figure 2.** Distinction between network study designs. *A*, Egocentric design. *B*, Sociometric design. The egocentric design entails ascertainment of the social ties of only the index subject, whereas all ties among all subjects are determined in the sociometric design.

anonymous), the frequency and types of sexual activity, and the frequency of condom use, as well as other risk and demographic data about each partner (e.g., race/ethnicity, age, and drug-using habits). Although no data are collected from the partners themselves, the egocentric approach signifies an important conceptual advancement beyond traditional, strictly individual-based epidemiological methods of addressing partnership linkages.

Because egocentric studies are based solely on self-reported data from the index subject, the actual structure of the entire network cannot be directly determined. In contrast, the sociometric study design entails theoretical specification and compilation of all ties among people and recruitment of as many of the identified partners as possible [12]. In figure 2*B*, person A represents the index subject, who names persons B, C, and D. The sociometric approach entails an iterative process in which persons B, C, and D are traced, recruited, and then asked to name their contacts, to assess whether they are linked to each other and to identify other contacts in the network. These data are used to create graphs, called “sociograms,” of the topology of relationships among people [11] (figures 1 and 2*B*).

Data collected in an egocentric study can be used to indirectly approximate a sociogram of the links among persons A, B, C, and D; however, the resulting graph is inevitably biased, because index subject A may not be able to or may not want to correctly report the names of person B’s other sex partners. In an egocentric study, persons B, C, and D are never contacted directly; thus, the source for data on the other links in the network is only person A. Hence, egocentric approaches are usually applied to obtain an in-depth characterization of the nature of individual personal networks in specific populations. On the other hand, participants theoretically may be more likely to report high-risk behavior and more of their contacts (especially

if they can use nicknames or initials) than they might be in a sociometric study, in which they would be required to provide specific locating information for tracing, recruiting, and enrolling their contacts.

Ascertaining the sexual contacts of all subjects, to compile the actual network, allows for direct examination of the relationship between network structure and distribution of STI. However, this design suffers from incomplete-network bias when partners cannot be traced or recruited for a variety reasons. For example, to date, most studies of sexual networks have been conducted with public health clinic-based samples of patients with STIs, who served as index subjects. Within public health departments, additional tracing of sexual contacts is restricted to partners (of the index patients with STIs) who also have positive test results. Follow-up of uninfected partners usually is not done (and is prohibited by law in some jurisdictions). Because STI-positive persons may have positions within the network that are systematically different from those who remain uninfected, incomplete and biased networks may result when only the STI-positive partners are traced. Population-based network studies can avoid such bias if both infected and uninfected people serve as index subjects and *all* sex partners are contacted, regardless of infection status. The incomplete ascertainment of sociometric networks is inevitable in both clinical and research settings, because (1) people may be reluctant to name all sex partners; (2) they may be unable to provide information about anonymous partners or partners with whom sex was exchanged for money, drugs, or shelter; (3) they may be unable or unwilling to provide adequate contact information for locating partners; or (4) partners may be locatable but difficult to reach.

Despite the limitations of these study designs, both sociometric and egocentric studies have illustrated important processes and factors that affect the spread of STIs and that would not have been identified through standard individual-based epidemiological techniques. In the next section, we present some of the basic measures developed to assess sexual networks and illustrate their application to STI epidemiology.

**Measures and assessments.** Network density provides an assessment of the overall network connectedness and is defined as the proportion of actual ties among people, from all possible links, if every node (i.e., person) is tied to every other node [12]. Denser sexual networks are an indication of higher contact rates among people, which create more opportunities for transmission and, thus, are more risky.

Microstructural network descriptions include quantities such as the number of components, the size of the largest component, and the number of dyads, triads, and other substructures, such as “*k*-cores” (defined in figure 1 legend). A network characterized with many unconnected dyads, for example, will theoretically have a lower incidence of STIs than a network with

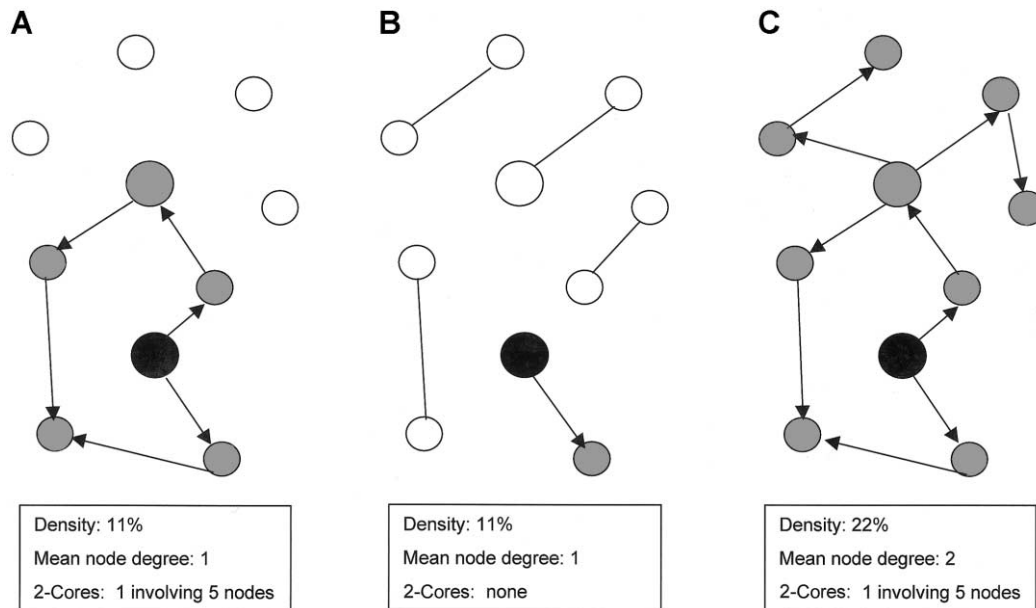
many closed loops of multiple persons, configured into 2-core or 3-core formations.

The most straightforward individual-level assessment is node degree, which is simply the number of links that a node has to other nodes. Node degree is an especially useful measure, since it can be easily assessed within the context of an egocentric study, by asking index persons to report total number of sex partners. Node degree also can be extracted from the graph produced in a sociometric study, by counting the number of links per node, which is considerably more expensive to implement [17]. There are other network measures that classify individual node position as either central or peripheral. However, the association between individual node position and STI transmission and acquisition is still being explored through simulation [18, 19] and empirical study [20].

Overall, these sociometric assessments characterize the structure of the network. These measures describe overall network connectedness within the population, microstructural details of network configuration, and individual position and prominence within the network [12] and, when considered together, can provide insights into the potential of STI transmission, as illustrated in figure 3. The density and average node degree of the networks in panels *A* and *B* are equal; however, greater disease transmission could occur in the network in panel *A*, owing to the existence of a 2-core involving 5 nodes. Furthermore, both networks in panels *A* and *C* contain a single 2-core of 5 nodes; yet, the density and average node degree are higher in the network in panel *C*, which expedites transmission.

Other measures directly relevant to STIs have been developed that relate individual position to network connectedness. Specifically, “cut points” and “bridges” represent properties of nodes and links, respectively, that describe specific positions within a network for STI transmission. Cut points refer to singleton *nodes* or a *set of nodes* that keep a network connected but, if removed, would break up the graph into smaller, disconnected components [12]. In figure 1, node 8 represents a cut point, because removal of that person would break the largest component into 2 smaller components, thus prohibiting STI transmission from one part of the population to another. In social network analysis, the term “bridge” refers to the *links* (rather than the nodes) connecting subcomponents [12], such as the line between nodes 3 and 8 in figure 1. In epidemiological research on STIs, the word “bridge” has been used interchangeably for both nodes and links that connect components (e.g., [21, 22]). Although this may create some confusion, clearly identifying key connections among nodes is critical to network-level interventions.

The application of egocentric and sociometric study designs and the various assessments attributed to networks and subjects appear in many epidemiological studies of STIs and HIV infection. In the next section, we review selected research that



**Figure 3.** Relevance of network assessments. These measures describe individual, microstructural, and overall structural network characteristics to be considered simultaneously, to obtain a more complete assessment of the potential of disease transmission. *Black circle*, infected individual; *gray circle*, partner with potential for infection.

exemplifies how these approaches have contributed to our understanding of the consequences of network structure and the dissemination of STIs. Then, we focus on the qualities of network ties (in contrast to the structure of the ties), in a discussion of mixing, concurrency, and self-organizing properties.

### CONSEQUENCES OF NETWORKS IN STI EPIDEMIOLOGY

**Patient 0 and the earliest cases of AIDS.** Although traditional theories of network formation assumed that ties were created randomly [23, 24], network data compiled by the CDC when AIDS cases were first reported during the 1980s support the assertion that partner choice is intentional [8]. To demonstrate that an infectious disease existed in a single network that linked MSM in New York City, Los Angeles, and San Francisco, Klov Dahl [8] applied graph and probability theory to show that the connections between case patients were not random. Because thousands of sex partners were reported [7, 8], the infamous “Patient 0,” a Canadian airline attendant with AIDS, clearly was a cut point in this network. Patient 0’s sexual linkages formed the key bridges between epidemics in these places, substantially expanding the geographic boundaries of the network [8]. The eventual death of Patient 0 and his removal from the network slowed the AIDS outbreak within each metropolitan area. Because Patient 0’s sexual network was extremely large, it also was extremely sparse, since his contacts were spread over a large geographic area. This observation contradicts the assumption that all sexual networks must be dense in order for

transmission to occur: Patient 0’s links acted as bridges between many otherwise-disconnected components.

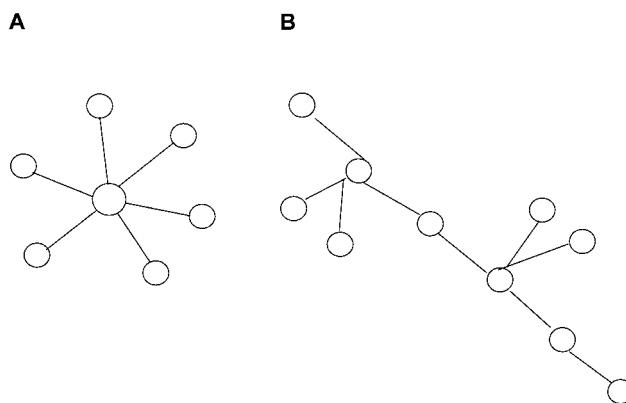
**HIV in the Bushwick injection drug user (IDU) community.** When variables that characterize a subject’s network position and partnership risks are included in analyses, individual factors often associated with STIs have been shown to lose statistical significance. For example, statistical models that simultaneously included sociometric position, egocentric partner data, and individual characteristics and behaviors have demonstrated the key role of network factors in identifying the risks associated with HIV infection among IDUs in the Bushwick neighborhood of Brooklyn, New York [25, 26]. In one analysis, the authors showed that being a member of a 2-core, a sociometric centrality measure (as defined in figure 1), was a significant risk factor for HIV infection, in traditional epidemiological multivariate logistic regression, whereas the number of other people with whom the subjects injected drugs and race/ethnicity both lost their significance [26]. Another analysis indicated that other individual-based variables, such as frequency of injection drug use, backloading, and number of IDU partners, were not significant predictors of HIV infection, whereas network-type variables were significant, including being part of a connected component (sociometric) and whether one of the subjects’ contacts was an older African American IDU (egocentric) [25]. Individual risk factors that remained significant in both analyses were the number of years of injection drug use and whether men reported having sex with other men. Traditional individual-based analysis with individual-based variables, augmented

with network-based variables, contributed to explaining HIV acquisition.

**Syphilis outbreak in Atlanta.** Microstructural network measures were used to describe a syphilis outbreak in a suburb of Atlanta that required treatment of at least 10 minors and prophylaxes for an additional 200 youths aged 12–20 years who were potentially exposed [27]. Note that, although the incidence of syphilis in this portion of the United States is higher than in other areas, syphilis usually was not seen among youths [28]. Through the process of contact tracing, public health officials learned of sex parties among teens in this community. They created a sociogram, which showed that the network grew from 7 people in 3-cores in the early phase to 15 people embedded within 8-core microstructures during the later period of the outbreak [27], which prompted spread of the disease over a 2-year time period. The study illuminated interesting data describing the consequences of sexual networks and *how* the outbreak occurred. However, the determinants that would explain *why* the network started and proliferated remain unknown.

**Differences in the spread of gonorrhea in London and Sheffield, United Kingdom.** In an effort to identify differences in partnership dynamics and network structures, researchers in the United Kingdom pursued a combination egocentric and sociometric study of patients with gonorrhea, from 2 distinctly different public health clinics, that included a large diverse population in London and a smaller, contained group in the town of Sheffield [29]. Direct comparisons of the network structures from each population were not feasible because of significant differences in network ascertainment. Only 52% of the contacts in London were identified, compared with 63% in Sheffield, because the patient load in London included more MSM who had numerous anonymous partners and more partners from out of town, whereas most of the incomplete network ascertainment in Sheffield could be attributed to a core of 13 sex workers (SWs). Despite the deficits in contact tracing, indirect comparisons of networks did indeed illuminate differences in transmission patterns between these 2 populations, by identifying the differences in the probable primary sources of infection (i.e., anonymous partners and SWs). These findings indicate the need for different approaches to intervention and control that could be implemented in the places where networks form.

**Gonorrhea and chlamydia in Manitoba, Canada.** The networks formed during a 6-month period in 1997–1998 when case patients with chlamydia and/or gonorrhea and their contacts were identified (tracked centrally by the public health department) in the province of Manitoba and were mapped both sociometrically and geographically [30]. Visual review of the network components revealed 2 types of microstructures (shown in figure 4), described as either “radial” (figure 4A) or “linear” (figure 4B). When the components were imposed onto geographic maps, the radial-type components spanned fewer



**Figure 4.** Types of components found in a study of sexual networks of patients with sexually transmitted infections and their contacts, in Manitoba, Canada. Two types of components, with different characteristics, were found (adapted from [30]). A, “Radial” components (only chlamydia cases were detected). B, “Linear” components (both chlamydia and gonorrhea cases were detected).

geographic locations than did the linear-type components [30]. In a similar study of cases in Manitoba that were diagnosed during 1990–1992, several individuals who were in cut point positions caused the networks to span significant distances and to include people living in various communities throughout this large region, some of which are only accessible by airplane or boat [21]. Thus, efforts to control STIs cannot necessarily be limited to specific areas where prevalence is known to be high.

**Pathogen considerations.** The unique properties and transmission dynamics of each STI pathogen (infectivity or transmission probability per sex act and duration of infectiousness) also play an important role in the spread of STIs through networks. For outcomes such as HIV infection, the synergistic effect of infections themselves, in which susceptibility to and infectiousness from 1 pathogen is influenced by coinfection with other pathogens [31], also must be considered in addition to the structure of the network. Within 2 identical networks with the same determinants and configuration, the epidemiology could vary considerably, depending on the pathogen. In the networks formed during 1997–1998 in Manitoba, only chlamydia was found among the radial-type components, whereas the linear-type components harbored both gonorrhea and chlamydia. Because the findings originated from a biased sample of infected case patients and their infected contacts, the significance of this finding remains unclear. Nevertheless, continued work comparing network structures and the pathogens within them may provide new insights into transmission.

## OTHER NETWORK-RELATED PHENOMENA

Because the process of analyzing sexual networks typically happens after the time of transmission, it tends to be a descriptive task. However, the identification of particular network behav-

iors could eventually lead to the establishment of network-related risk factors that can be used in a predictive manner, creating opportunities for intervention. One way to accomplish the goal of identifying predictors of high-risk networks is to examine the qualities and characteristics of the linkages among people in the network, instead of simply focusing on network topology. Are some partnerships more risky for STI transmission than others, despite the underlying network structure? Indeed, investigations related to sexual mixing, concurrency, and self-organizing networks have shown potential to serve as new risk factors and as proxies for high-risk networks.

**Sexual mixing.** One topic particularly pertinent to the spread of STIs is sexual mixing. Sexual mixing provides an assessment of the types of contact patterns within and across risk groups [32]. Assortative (like with like) mixing occurs when individuals classified with respect to an attribute related to risk of acquiring STI, such as age, typically have sex with each other more often than with others outside their group. Conversely, disassortative mixing (like with unlike) occurs when people with differential risk form partnerships. Random mixing refers to contact patterns that are completely independent from the risk attribute and that arise proportionately to the number of people in each risk category.

Statistics that quantify the extent to which mixing occurs within a population can be estimated from a study sample, ideally by using sociometric data, but they also have been constructed from egocentric data (e.g., [33–36]). A mixing matrix is compiled by creating a table of the types of partnerships within and across predefined risk groups, as shown in table 1, which lists both the number and proportion of each type of linkage among the 3 age groups. The first of these measures (referred to as “Q”) [37] is computed from eigenvalues. Although the measure is a continuous value, it often is applied as a categorical assessment, for which any values  $>0$  indicate assortative mixing and all negative values indicate disassortative patterns (e.g., [33]). More recently, Newman [38, 39] derived a similar statistic from the mixing matrix that is based on the total number of links in each cell (instead of the percentages) and that is mathematically more robust because (1) it weights the linkages by the frequency with which they occur and (2) it does not change values when the rows and columns of a nonsymmetric matrix are transposed.

In addition to quantifying mixing within populations, both sociometric and egocentric data can be used to classify individuals as either assortative or disassortative mixers. By use of self-reported egocentric data about sex partners, a direct indication of mixing can be obtained by comparisons between the characteristics (e.g., age, race/ethnicity, or drug use) of the index subject and those of his or her partners. Once a sociogram has been constructed, individuals can be classified as mixers

**Table 1. Hypothetical sexual mixing matrix within and across 3 age groups.**

Age group, years	No. (%) of partnerships, by age group		
	<15 Years	15–19 Years	20–30 Years
<15	95 (95)	5 (5)	0 (0)
15–19	5 (1)	195 (39)	300 (60)
20–30	0 (0)	300 (50)	300 (50)

on the basis of whether their positions or node degrees are similar to those of their contacts in the network.

Epidemiological findings suggest that most sexual networks conform to assortative mixing, when assessed by use of node degree to represent different levels of sexual activity (and risk) [24, 33], with a clear exception. The original Q statistic was applied to a small population of MSM in an isolated community in Iceland [34]. Investigators constructed a network from 22 of the 35 known case patients with HIV infection and their sexual contacts, for the years 1980–1987. From these linkages, they created a mixing matrix based on the number of sex partners. The network was actually quite disassortative ( $Q = -0.102$ ), indicating that the people with fewer partners tended to link with those with multiple partners.

Disassortative mixing also has been shown repeatedly to increase the odds of infection, in individual-based logistic regression or generalized estimating equations. In strictly egocentric studies of adolescents, for example, the age of the participants’ partner(s) can be ascertained and included in statistical models. One study of African American teens recruited from sexually transmitted disease (STD) and adolescent clinics showed that the young women whose partners were at least 2 years older also were less likely to have used a condom during their last sexual episode [40]. Not surprisingly, adolescent females who have sex with older men have been shown to be at increased risk for STIs [41] and HIV infection [42]. Thus, although populations tend to exhibit assortative sexual mixing overall, the degree to which some individuals choose partners unlike themselves appears to increase their individual risk. These small amounts of disassortative mixing also may have population-level effects, as has been shown both in mathematical models and by empirical study.

In early models of communicable diseases, random contact among people was assumed and, thus, usually was expressed as 1 rate [24]. Hethcote and Yorke [43] incorporated mixing into a population model of gonorrhea transmission, by adding multiple contact rates across groups with different levels of sexual activity, including a more active core group. They demonstrated that the greater the rates of crossover between core members and noncore members (disassortative mixing), the greater the degree to which gonorrhea was transmitted.

Empirical research has been conducted in both a high-risk

population and the general population, to explore the effect of dissortative mixing among some individuals in populations that, overall, were characterized by assortative mixing.  $Q$  statistics were computed from egocentric data for (high-risk) men and women, from among ~600 patients with STIs who attended 2 clinics in the Seattle area [33] between 1992 and 1994, and were compared with egocentric data from a national study of the (low-risk) general population of US adults [44], conducted during the same decade. Mixing was assortative for men and women in each clinic population, with respect to the number of sex partners in the previous 3 months (the  $Q$  statistic ranged between 0.10 and 0.23), as well as for those in the national study ( $Q = 0.35$ ). Despite overall assortative mixing in both the high- and low-risk populations, enough linkages between a high-risk core group and lower-risk subgroups must have occurred (described below), since gonorrhea and chlamydia remained endemic.

Subsequent analyses using population-level and individual-level characteristics of the clinic attendees were conducted to identify dissortative-mixing patterns based on different types of risk categories (other than node degree) and to identify the pockets of the population in the clinic study that may have mixed dissortatively [36]. The investigators computed  $Q$  statistics with respect to age, race/ethnicity, and education, and, in all instances, they found assortative mixing. However, stratified individual-based analysis showed that those who mixed with partners unlike themselves, with respect to age and race/ethnicity, were more likely to be infected with chlamydia or gonorrhea. Every group-level assessment revealed assortative mixing; yet, various types of individual-level dissortative mixing increased the risk of infection, which explains, in part, why these bacterial STIs persist. The epidemiological consequences of mixing are basically understood, but public health interventions designed to alter mixing patterns have yet to be conceived, with perhaps the exception of finding ways to discourage young people from having sex with older people, which is now being evaluated in some developing countries.

Newman [39] has conducted simulations addressing the effect of mixing on STI control. In his model, mixing was based on levels of node connectivity (i.e., number of sexual links per person). The mathematical relationship that he derived between mixing and the growth and size of components served as the basis from which the simulations were constructed. He determined that assortatively mixed networks are highly robust to the removal of high-degree nodes (as a type of intervention). In a population with assortative mixing, highly connected nodes tend to link to other high-degree nodes to create large, densely connected components that compose a core group. Furthermore, the less-connected nodes also link to low-degree nodes to form small, dispersed, unconnected components. The removal of *some* of these high-degree nodes will not eradicate

disease within the densest part of the network, and their removal will not curb spread to other portions of the network. In assortative networks, many other highly connected nodes will remain in these dense substructures, a small proportion of which are linked to less-dense portions of the network, to allow continued small amounts of dissemination of disease. Conversely, dissortative networks are likely to have many more linkages between highly connected and less-connected nodes (or, people with high risk and low risk) distributed more widely across the population, to create several subcomponents that are loosely connected to each other. In theory, removal of the high-degree nodes in these dissortative networks has a greater effect on the reduction of incidence, because their elimination from the network would break the components into smaller, disconnected components and would decrease the number of transmission pathways in the bulk of the population. Newman [39] suggests that the degree of mixing determines the extent to which disease is contained within the core group or disseminates to more of the population.

Mixing is a characteristic of partnerships that manifests within networks to affect their structure. Both assortative and dissortative mixing can occur simultaneously in a population and can influence individual risk for infection and overall incidence in the population. Continued development of interventions that focus on disaggregating core and noncore groups and dissuading individuals from entering into high-risk partnerships will inevitably help lower the prevalence of persistent STIs.

**Concurrency.** The concept of concurrent partners has achieved increasingly more attention in epidemiological studies of HIV and other STIs [45, 46]. Although having multiple sex partners has been clearly established as a risk factor for acquiring an STI, the pattern and the duration and timing of partnerships merits exploration, because concurrency may be an indicator of sexual network structure.

In most studies published to date (e.g., [47–51]), concurrency has been defined as partnerships overlapping in time, when one partnership begins before another terminates. Other descriptions have been used that can lead to confusion, such as “multiple sex partners at one time,” which may refer to group sexual situations or a series of 1-time sexual encounters during a short period [52, 53] (which also has been studied through the examination of the length of the gap in time between partners [54]). In a study in San Francisco of adolescents recruited from the city’s public STD clinic, the investigators defined concurrency as having at least 1 casual partner during the same 2-week period as another, main partner [55].

Regardless of the precise definition of concurrency, people engage in simultaneous sexual partnerships for a variety of reasons [56], and its occurrence is widespread. A telephone survey of persons aged 18–39 years who were recruited through random-digit dialing in Seattle indicated that men (27%) are more like-

ly than women (18%) to report concurrent partners. Stratified analyses by gender have revealed different predictors for concurrency, such as having been in jail, for men, and early coital debut, for women. Similarly among women aged 15–44 participating in the 1995 National Survey of Family Growth [57], another population-based survey, 12% had concurrent partners, and concurrency was more frequent (35%) among women whose coital debut was as early as age 12 or 13 years [51]. Given the prevalence of concurrency, its effects on acquisition and transmission of STIs have been investigated in a host of mathematical models and empirical epidemiological studies.

Watts and May [58] developed a deterministic model to represent concurrency, which assumed that old partnerships did not dissolve before new partnerships formed. The model also accommodated differential rates of HIV transmission from new partners, versus that for previous partnerships. The patterns of disease growth revealed an initial high incidence rate, followed by a slower rate. Furthermore, the greater the proportion of concurrent partnerships included in the model, the faster the initial incidence rate increased among those initially uninfected.

Morris and Kretzschmar [52] designed, from graph theory, a creative model to measure concurrency that could hold constant the total number of partnerships in the population (i.e., network density), while altering the configuration of links to represent various amounts of concurrency. In theory, larger proportions of people in concurrent sexual partnerships create denser networks with more transmission pathways, which elevates incidence. However, by manipulating graphs, the model controlled overall network density, to isolate the effect of concurrency. In 1000 simulations, the prevalence of HIV disease was shown to increase as the level of concurrency increased. The prevalence variance in the simulations also widened as concurrency levels increased, suggesting that incidence and prevalence become less predictable in populations characterized by high levels of concurrency, which is an important consideration for disease control.

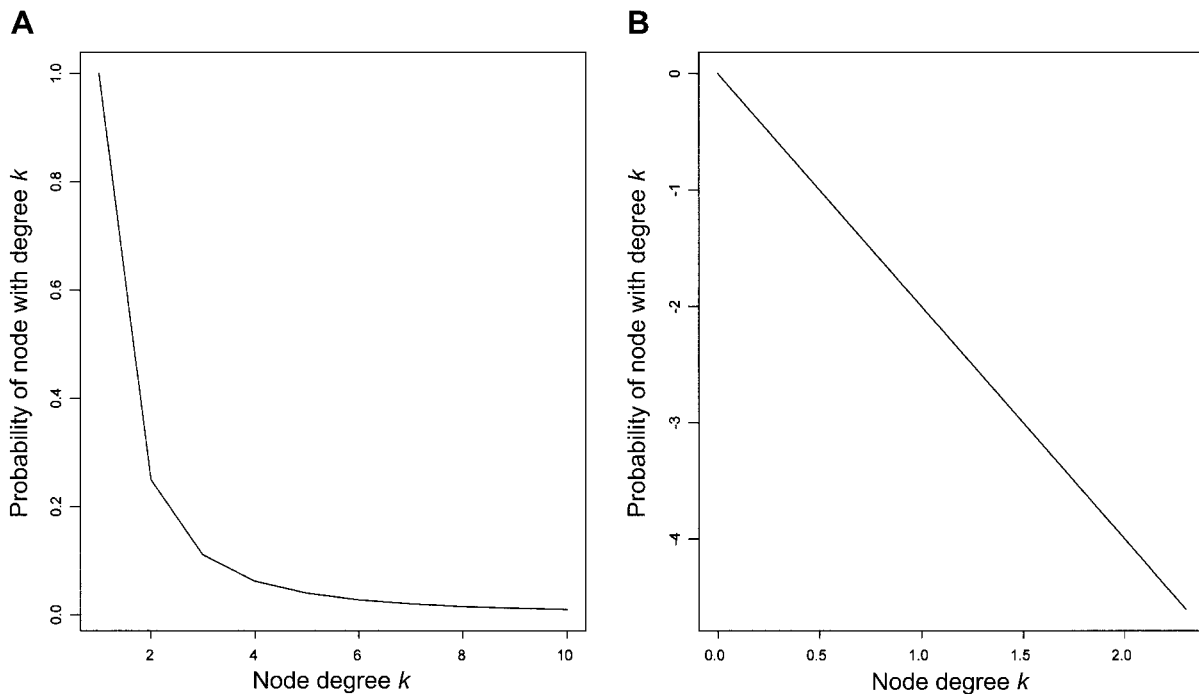
Analogous approaches have been pursued in individual-based epidemiological studies designed to determine whether concurrency poses additional risk for infection, by controlling for the number of sex partners. In the study of adolescents from San Francisco mentioned above, multivariate regression showed that concurrent partnerships were a statistically significant risk for gonorrhea, chlamydia, or nongonococcal urethritis (odds ratio [OR], 1.6; 95% confidence interval [CI], 1.1–2.5), whereas the number of sex partners (in the previous 6 months) failed to reach significance (OR, 0.9; 95% CI, 0.6–1.3) [55]. An analysis of the National Survey of Sexual Attitudes and Lifestyles (Natsal 2000), a population-based cross-sectional probability sample of >11,000 subjects, aged 16–44 years, across

Great Britain [50], funded by several agencies in Great Britain, found positive associations between number of partners and concurrency and chlamydial infections, in a multivariate logistic regression analysis [59]. Unlike in the analysis of the adolescents [55], the number of partners in the previous year was categorized as 0–1 (reference group), 2–4 (OR, 3.57; 95% CI, 1.6–7.96), and  $\geq 5$  (OR, 8.89; 95% CI, 2.89–27.33). Furthermore, concurrency was defined as “overlapping partnerships” (OR, 2.84; 95% CI, 1.20–6.76).

These divergent results pertaining to the role of the number of partners, when concurrency is included in the model, suggest that controversy around the role of concurrency in the spread of STIs may still exist. In later simulation experiments, Kretzschmar [60] examined the issue of the number of sex partners versus concurrent partners using the graph theory–based model referenced above [52]. Imposing greater levels of concurrency while holding average number of partners per subject constant elevated prevalence substantially, because the average size of the largest component in the networks increased [60]. Conversely, keeping concurrency levels constant while increasing the average number of partners did not alter component size enough to substantially affect prevalence of disease. In the epidemiological studies in which concurrency remained a risk factor, controlling for number of partners supported the results of these simulations, suggesting that concurrency represents changes in the underlying network structure and configuration that the number of partners and network density do not capture.

In the epidemiological studies, the relative risks associated with concurrency may be biased, owing to differential misclassification, which can either over- or underestimate the true risk ratio [61]. Systematic misclassification of “exposure to concurrency” is difficult to avoid for subjects with 1 partner when that partner has other concurrent partners who are unknown to the subject. The example of monogamous women with male partners who have concurrent partners, described by Morris [46], illustrates the effects of misclassification of concurrency, when concurrency is treated as a predictor for *acquiring* an STI. As Morris explains, “a traditional logistic regression would not attribute the monogamous women’s infection to concurrency, however, because these women do not themselves have concurrent partners....[T]he basic point is that concurrency creates a risk for the partner, not the index case” [46, page 505]. Thus, the role of concurrency at the individual level should be studied as a predictor of *transmitting* infection (rather than of *acquiring* infection). In fact, 2 epidemiological investigations of sexual networks have attributed transmission to some form of concurrency [48, 62].

Potterat et al. [48] developed and applied a measure to quantify the potential to transmit chlamydia, as part of a study of sexual networks among case patients recruited from STD clinics



**Figure 5.** Power-law distribution for scale-free networks. *A*, Example of a power-law distribution. *B*, Power law plotted on a log-log scale. The equation for a power-law curve is  $P(k) \sim k^{-\alpha}$ , where  $P(k)$  is the probability that a node has degree  $k$  and  $\alpha$  is the slope of the line when the distribution is plotted on a log-log scale.

in Colorado Springs between July 1996 and June 1997. Both the number of sex partners (OR, 1.6;  $P < .001$ ) and overlapping partnerships were associated with transmission, but concurrency was a stronger predictor (OR, 3.2;  $P < .001$ ).

A multicenter epidemiological study in the southeastern United States, where endemic syphilis persists, also found an association between concurrency and syphilis transmission [62]. Among 743 index case patients, 63 were classified as transmitters, on the basis of whether their partners, who were traced and tested, had a diagnosis of an earlier disease stage. Participants with at least 2 concurrent partners were 3 times more likely to be transmitters, but the finding was marginally significant (OR, 3.1; 95% CI, 0.9–11), whereas the number of sex partners in the previous 2 months was not significant (OR, 0.8; 95% CI, 0.2–2.8). The article does not report the proportion of sexual contacts who were unable to be located and tested, which possibly could have resulted in an underestimate of the number of transmitters. These studies also suffer from other implementation obstacles, because they rely on accurate, self-reported information from patients on the timing of sexual contact, relative to the onset of symptoms, to correctly classify subjects and partners as being susceptible or infectious. Furthermore, as in other network studies, successful recruitment of sex partners was critical. If the investigators were unable to trace and test all partners, then the number of transmitters may

have been underestimated, which can bias the results toward null findings.

**Scale-free networks.** A new theory of self-organizing networks has been gaining momentum in the past few years, on the basis of empirical observations in a number of different disciplines. Looking specifically at the distribution of node degree, physicists have discovered that many real-world networks do not conform to a Poisson distribution, as predicted by a graph that is randomly constructed. Instead, many self-organized networks follow the form shown in figure 5A, with a disproportionately large number of nodes having very few connections, while a very small group of nodes is extremely connected. These distributions are called “power laws” because they follow the form  $P(k) \sim k^{-\alpha}$ , where  $P(k)$  is the probability that a node has degree  $k$  and  $\alpha$  is the slope of the line when the distribution is plotted on a log-log scale (figure 5B).

The shape of this curve implies that nodes possess different capacities to acquire links—that is, a few nodes, termed “hubs,” have many links, whereas most nodes are linked to very few others. Hubs are extremely rare: the chance of being a hub or even of having 10 links to other nodes is  $<1\%$ , whereas  $>80\%$  of nodes are linked to only 1 other node in this example (figure 5A). Although the distinction between a cut point and a hub has not been explicitly made in the literature on network analysis, important differences between the 2 types of nodes exist.

Cut points can consist of either 1 node or several nodes and may only have 1 or 2 key bridges joining components. In contrast, hubs refer to unique nodes in the network that have substantially more links than other nodes, which, if removed, could break down the network.

Power-law networks became the center of attention when physicists researching the World Wide Web discovered the distribution after constructing a partial graph of the linkages between Web sites [23, 63]. They also suggested that this network was formed through a process called “preferential attachment,” in which the more connected nodes in a network tend to acquire links at a more rapid rate than nodes with fewer connections, a process that they also referred to as “the rich get richer” [23]. Networks with this property of preferential attachment are termed “scale-free networks,” because the distribution appears to be the same as the network grows. Barabasi, the primary author of much of this work, claims that hubs “offer convincing proof” that *all* types of networks, including a broad range of social networks (from film actors to those in molecular biology and computers), are scale-free networks exhibiting preferential attachment behavior [64]. In light of this claim, research pertaining to the extent to which sexual networks actually model scale-free networks is currently under way and is somewhat controversial, given the implications for public health (explained below).

Estimating parameter values for the exponent  $\alpha$  in the equation for the power-law curve is at the crux of this technical debate, because  $\alpha$  determines the variance of the distribution of node degree (or contact rate). Moreover, the contact-rate variance affects the value of the reproductive number ( $R_0$ ; i.e., the no. of secondary infections transmitted in an entirely susceptible population, when 1 subject is infected [65]). When the contact variance is infinite,  $R_0$  exceeds the epidemic threshold level, and disease remains endemic and cannot be arrested [65]. Conversely, a bounded or finite contact variance keeps  $R_0$  below the epidemic threshold level, allowing for infectious diseases to die out in the population. Hence, the values for  $\alpha$  may have implications for control of STIs.

In a national study of adults in Sweden [66], the distribution of the number of lifetime partners fit a power-law curve indicating preferential attachment, when first scrutinized. Liljeros et al. [67] thus concluded that efforts to control STIs would need to “radically change,” without offering suggestions for alternative public health measures. Dezsó and Barabasi [68] also have suggested that the scale-free nature of sexual contacts could be the key to implementing cost-effective immunizations for STIs. They propose use of contact tracing to identify those individuals who are likely to be hubs in the network and suggest that, by immunizing these highly connected individuals, overall connectivity can be reduced to the point that the disease can no longer remain endemic. Jones and Handcock [69–71] used

a maximum-likelihood estimate to evaluate the results reported by Liljeros et al. in 3 study populations, including the Swedish study population [66], a national survey of US adults [44], and a heterosexual network in Uganda [72]. They concluded that the node distributions in these populations were actually more distinctly L-shaped than is the gradual slope of the curve depicted in figure 5A, suggesting that sexual networks do not exert strong patterns of preferential attachment [69].

Liljeros et al. [67] claimed that the data in the Swedish study conform very closely to the parameterization of curves discovered from their earlier findings, which results in infinite variance for the node-degree distribution, whereas the results reported by Jones and Handcock [69–71] refute this conclusion. However, both sets of investigators question each other’s statistical methods [70, 73]. Further scrutiny and development of the best statistical method for approximation of the curves of node distributions are merited. Furthermore, continued research in other populations, particularly high-risk or highly active groups such as adolescents or MSM, could help answer the question of whether all sexual networks do indeed emulate the preferential attachment behavior of other types of networks.

## CONCLUSION

Network analysis has been applied in a broad range of fields to explain how the structure and nature of ties among individuals affect individuals and larger-group dynamics. Much of the sexual network–based research that has been published to date has applied methods of social network analysis to the reporting of descriptive information about the dissemination of STIs after the networks formed and people became infected. If perfect collection of sexual network data were possible—with complete ascertainment of data from all sex partners, accurate timing of all sexual episodes, and exact transmission information for each pathogen—in theory, the information could be used in a more predictive way. Although implementation of sexual network–based research falls short of this ideal, it nevertheless has proved to be a useful extension in explaining STI epidemiology, as described here. Unlike other traditional and current epidemiological methods that focus strictly on either individuals or populations, the principles of sexual networks are based on the dynamics of sexual partnerships and the topology of the linkages in a group. Continued development and research into network-related concepts, such as preferential attachment, and those areas specifically relevant to STIs, such as mixing and concurrency, will help reach the goal of being able to use network-based data to anticipate how STIs may spread. As a result, many new efforts to control STIs have begun to evolve from an individual base to a network base [74], which inevitably should be more successful.

## References

1. Aral SO. Determinants of STD epidemics: implications for phase appropriate intervention strategies. *Sex Transm Infect* **2002**; 78(Suppl 1): i3–13.
2. Aral SO, St. Lawrence JS. The ecology of sex work and drug use in Saratov Oblast, Russia. *Sex Transm Dis* **2002**; 29:798–805.
3. Wasserheit JN. Program operations guidelines for STD prevention partner services. In: Wasserheit JN, ed. Atlanta: Division of STD Prevention, National Center for HIV, STD, and TB Prevention, Centers for Disease Control and Prevention, **2003**:PS1–4.
4. Potterat JJ, Rothenberg RB, Woodhouse DE, Muth JB, Pratts CI, Fogle JS. Gonorrhoea as a social disease. *Sex Transm Dis* **1985**; 12:25–32.
5. Weir SS, Pailman C, Mahlalela X, Coetzee N, Meidany F, Boerma J. From people to places: focusing AIDS prevention efforts where it matters most. *AIDS* **2003**; 17:895–903.
6. Michaud J, Ellen J, Johnson S, Rompalo A. Responding to a community outbreak of syphilis by targeting sex partner meeting location: an example of a risk-space intervention. *Sex Transm Dis* **2003**; 30:533–8.
7. Shilts R. And the band played on: politics, people and the AIDS epidemic. New York: Penguin Group, **1987**.
8. Klodahl AS. Social networks and the spread of infectious diseases: the AIDS example. *Soc Sci Med* **1985**; 21:1203–16.
9. Elford J, Bolding G, Sherr L. Seeking sex on the Internet and sexual risk behaviour among gay men using London gyms. *AIDS* **2001**; 15:1409–15.
10. Kim AA, Kent C, McFarland W, Klausner JD. Cruising on the Internet highway. *J Acquir Immune Defic Syndr* **2001**; 28:89–93.
11. Moreno JL, Jennings HH. Who shall survive? A new approach to the problem of human interrelations. Washington, DC: Nervous and Mental Disease Pub. Co., **1934**.
12. Wasserman S, Faust K. Social network analysis: methods and applications. New York: Cambridge University Press, **1994**.
13. Parran T. Shadow on the land: syphilis. New York: Reynal & Hitchcock, **1937**.
14. Parran T, Vonderlehr RA. Plain words about venereal disease. New York: Reynal & Hitchcock, **1941**.
15. Padian N, Shiboski S, Jewell N. Male-to-female transmission of human immunodeficiency virus. *JAMA* **1987**; 258:788–90.
16. Padian NS, Shiboski S, Vittinghoff E, Glass S. Heterosexual transmission of HIV: results from a ten year study. *Am J Epidemiol* **1997**; 146: 350–7.
17. Friedman SR, Aral S. Social networks, risk-potential networks, health, and disease. *J Urban Health* **2001**; 78:411–8.
18. Ghani A, Garnett G. Risks of acquiring and transmitting sexually transmitted diseases in sexual partner networks. *Sex Transm Dis* **2000**; 27: 579–87.
19. Bell DC, Atkinson JS, Carlson JW. Centrality measures for disease transmission networks. *Soc Networks* **1999**; 21:1–21.
20. Rothenberg RB, Potterat JJ, Woodhouse DE, et al. Choosing a centrality measure: epidemiologic correlates in the Colorado Springs study of social networks. *Soc Networks* **1995**; 17:273–97.
21. Jolly AM, Wylie JL. Gonorrhoea and chlamydia core groups and sexual networks in Manitoba. *Sex Transm Infect* **2002**; 78(Suppl 1):i145–51.
22. Morris M, Podhistita C, Wawer M, Handcock M. Bridge populations in the spread of HIV/AIDS in Thailand. *AIDS* **1996**; 10:1265–71.
23. Barabasi A-L. Linked: the new science of networks. Cambridge, MA: Perseus Publishing, **2002**.
24. Liljeros F, Edling CR, Nunes Amaral LA. Sexual networks: implications for the transmission of sexually transmitted infections. *Microbes Infect* **2003**; 5:189–96.
25. Kottiri BJ, Friedman SR, Neaigus A, Curtis R, Desjarlais DC. Risk networks and racial/ethnic differences in the prevalence of HIV infection among injection drug users. *J Acquir Immune Defic Syndr* **2002**; 30:95–104.
26. Friedman SR, Neaigus A, Jose B, et al. Sociometric risk networks and risk for HIV infection. *Am J Public Health* **1997**; 87:1289–96.
27. Rothenberg RB, Sterk C, Toomey KE, et al. Using social network and ethnographic tools to evaluate syphilis transmission. *Sex Transm Dis* **1998**; 25:154–60.
28. Centers for Disease Control and Prevention. Primary and secondary syphilis in the United States 1999. *MMWR Morb Mortal Wkly Rep* **2001**; 50:113–7.
29. Day S, Ward H, Ghani AC, et al. Sexual histories, partnerships and networks associated with the transmission of gonorrhoea. *Int J STD AIDS* **1998**; 9:666–71.
30. Wylie JL, Jolly A. Patterns of chlamydia and gonorrhoea infection in sexual networks in Manitoba, Canada. *Sex Transm Dis* **2001**; 28:14–24.
31. Wasserheit JN. Epidemiological synergy: interrelationships between human immunodeficiency virus infection and other sexually transmitted diseases. *Sex Transm Dis* **1992**; 19:61–77.
32. Boily M-C, Poulin R, Benoit M. Some methodological issues in the study of sexual networks from model to data to model. *Sex Transm Dis* **2000**; 27:558–71.
33. Garnett GP, Hughes JB, Anderson RM, et al. Sexual mixing patterns of patients attending sexually transmitted diseases clinics. *Sex Transm Dis* **1996**; 23:248–57.
34. Haraldsdottir S, Gupta S, Anderson R. Preliminary studies of sexual network in a male homosexual community in Iceland. *J Acquir Immune Defic Syndr* **1992**; 5:374–81.
35. Laumann EO, Youm Y. Racial/ethnic group differences in the prevalence of sexually transmitted diseases in the United States: a network explanation. *Sex Transm Dis* **1999**; 26:250–61.
36. Aral SO, Hughes JB, Stoner BP, et al. Sexual mixing patterns in the spread of gonococcal and chlamydial infections. *Am J Public Health* **1999**; 89:825–33.
37. Gupta S, Anderson R, May R. Networks of sexual contacts: implications for the pattern of spread of HIV. *AIDS* **1989**; 3:807–17.
38. Newman M. Assortative mixing in networks. *Phys Rev Lett* **2002**; 89: 208701.
39. Newman M. Mixing patterns in networks. *Phys Rev E Stat Nonlin Soft Matter Phys* **2003**; 67:026126.
40. DiClemente R, Wingood G, Crosby R, et al. Sexual risk behaviors associated with having older sex partners: a study of black adolescent females. *Sex Transm Dis* **2002**; 29:20–4.
41. Catania JA, Binson D, Stone V. Relationship of sexual mixing across age and ethnic groups to herpes simplex virus–2 among unmarried heterosexual adults with multiple sexual partners. *Health Psychol* **1996**; 15:362–70.
42. Gregson S, Nyamukapa CA, Garnett GP, et al. Sexual mixing patterns and sex-differentials in teenage exposure to HIV infection in rural Zimbabwe. *Lancet* **2002**; 359:1896–903.
43. Hethcote H, Yorke J. Gonorrhoea: transmission dynamics and control. In: Levin S, ed. Lecture notes in biomathematics. Berlin: Springer-Verlag, **1984**:32–45.
44. Laumann EO, Gagnon JH, Michael RT, Michaels S. The social organization of sexuality: sexual practices in the United States. Chicago: University of Chicago Press, **1994**.
45. Garnett GP, Johnson AM. Coining a new term in epidemiology: concurrency and HIV. *AIDS* **1997**; 11:681–3.
46. Morris M. Concurrent partnerships and syphilis persistence: new thoughts on an old puzzle. *Sex Transm Dis* **2001**; 28:504–7.
47. Ford K, Woosung S, Lepkowski J. American adolescents: sexual mixing patterns, bridge partners, and concurrency. *Sex Transm Dis* **2002**; 29: 13–9.
48. Potterat J, Zimmerman-Rogers H, Muth S, et al. Chlamydia transmission: concurrency, reproduction number, and the epidemic trajectory. *Am J Epidemiol* **1999**; 150:1331–9.
49. Manhardt L, Aral S, Holmes K, Foxman B. Sex partner concurrency measurement, prevalence, and correlates among urban 18–39-year-olds. *Sex Transm Dis* **2002**; 29:133–43.
50. Johnson AM, Mercer C, Erens B, et al. Sexual behavior in Britain: partnerships, practices, and HIV risk behaviors. *Lancet* **2001**; 358:1835–42.
51. Adimora A, Schoenbach V, Bonas D, Martinson F, Donaldson K, Stancil

- T. Concurrent sexual partnerships among women in the United States. *Epidemiology* **2002**; 13:320–7.
52. Morris M, Kretzschmar M. Concurrent partnerships and the spread of HIV. *AIDS* **1997**; 11:641–8.
  53. Morris M, Kretzschmar M. Concurrent partnerships and the transmission dynamics in networks. *Soc Networks* **1995**; 17:299–18.
  54. Kraut-Becher J, Aral SO. Gap length: an important factor in sexually transmitted disease transmission. *Sex Transm Dis* **2003**; 30:221–5.
  55. Rosenberg M, Gurvey J, Adler N, Dunlop M, Ellen J. Concurrent sex partners and risk for sexually transmitted diseases among adolescents. *Sex Transm Dis* **1999**; 26:208–12.
  56. Gorbach PM, Stoner BP, Aral S, Whittington WL, Holmes K. “It takes a village”: understanding concurrent sexual partnerships in Seattle, Washington. *Sex Transm Dis* **2002**; 29:453–62.
  57. Potter F, Iannachione V. Sample design, sampling weights, imputation, and variance estimation in the National Survey of Family Growth. *Vital Health Stat* **1998**; 2:1–63.
  58. Watts C, May R. The influence of concurrent partnerships on the dynamics of HIV/AIDS. *Math Biosci* **1992**; 108:89–104.
  59. Fenton KA, Korovessis C, Johnson AM, et al. Sexual behavior in Britain: reported sexually transmitted infections and prevalent genital *Chlamydia trachomatis* infection. *Lancet* **2001**; 358:1851–4.
  60. Kretzschmar M. Sexual network structure and sexually transmitted disease prevention: a modeling perspective. *Sex Transm Dis* **2000**; 27: 627–35.
  61. Kleinbaum DG, Kupper LL, Morgenstern H. *Epidemiologic research principals and quantitative methods*. New York: Van Nostrand Reinhold, **1982**.
  62. Koumans E, Farley T, Gibson J, et al. Characteristics of persons with syphilis in areas of persisting syphilis in the United States: sustained transmission associated with concurrent partnerships. *Sex Transm Dis* **2001**; 28:497–503.
  63. Barabasi A-L, Albert R. Emergence of scaling random networks. *Science* **1999**; 286:509–12.
  64. Barabasi A-L, Bonabeau E. Scale-free networks. *Sci Am* **2003**; 288:60–9.
  65. Anderson RM, May RM. *Infectious diseases of humans: dynamics and control*. Oxford: Oxford University Press, **1991**.
  66. Lewin B, ed. *Sex in Sweden: on the sexual life in Sweden*. Stockholm: National Institute of Public Health, **1996**.
  67. Liljeros F, Edling CR, Nunes Amaral LA, Stanley HE, Aberg Y. The web of human sexual contacts. *Nature* **2001**; 411:907–8.
  68. Dezso Z, Barabasi A-L. Halting viruses in scale-free networks. *Phys Rev E Stat Nonlin Soft Matter Phys* **2002**; 65:1–4.
  69. Jones J, Handcock MS. An assessment of preferential attachment as a mechanism for human sexual network formation. *Proc R Soc Lond B Biol Sci* **2003**; 270:1123–8.
  70. Jones J, Handcock M. Sexual contacts and epidemic thresholds. *Nature* **2003**; 423:605–6.
  71. Jones J, Handcock M. An assessment of preferential attachment as a mechanism for human sexual network formation [working paper 23]. Seattle: Center for Statistics and the Social Sciences, University of Washington, **2002**.
  72. Serwadda D, Gray RH, Wawer MJ, et al. The social dynamics of HIV transmission as reflected through discordant couples in rural Uganda. *AIDS* **1995**; 9:745–50.
  73. Liljeros F, Edling CR, Stanley HE, et al. (Reply to) sexual contacts and epidemic thresholds [letter]. *Nature* **2003**; 423:606.
  74. Rothenberg R. How a net works: implications of network structure for the persistence and control of sexually transmitted diseases and HIV. *Sex Transm Dis* **2001**; 28:63–8.