Using sexual affiliation networks to describe the sexual structure of a population

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Accepted 7 May 2007

The structure of sexual networks has a central role in the dynamics of transmission of sexually transmitted infections (STIs). Unfortunately, it is extremely difficult to obtain reliable data on sexual contacts between individuals. However, the venues where people recruit sexual partners may provide valuable information on sexual networks. This article reviews how data on ''sexual affiliations'' between people and venues may be collected, analysed, and used for surveillance and prevention of STIs.

Both empirical[1] and modelling studies[2–4] support the notion that sexual network structure has a central role in transmission dynamics of STIs. Unfortunately, obtaining information on sexual networks directly is extremely difficult, and common sampling methods which trace the direct contacts of an individual may be subject to serious sampling biases.[5][6]

Rather than trying to identify networks of sexual contacts, the network of people and the venues where they recruit partners may provide a rich, albeit indirect, source of data on sexual networks. The observation that individuals may congregate at particular venues (eg, commercial sex workers in brothels or street corners in ''red light'' districts, men who have sex with men (MSM) in gay bars and clubs) is the rationale for time-location sampling to obtain a representative sample of individuals from ''hidden'' populations. The term ''venues'' is used to mean: a physical place, such as a bar; a ''virtual'' place, such as an internet site; an event, such as a party; or some combination of the above, such as a theme night at a club. The networks of individuals and their sex partner meeting venues can be described as ''sexual affiliation networks'', to distinguish them from sexual networks of direct contacts. This review describes how data on sexual affiliations may provide valuable information relating to the sexual structure of a population, and the transmission of STIs. I focus on approaches that maintain the duality of individuals and venues.[7]

EMPIRICAL DATA SUPPORTING THE ROLE OF SEXUAL AFFILIATIONS IN THE SPREAD OF STIs

There is an increasing body of literature showing that venues where people meet may have an important role in the spread of STIs. Most of the gonorrhoea cases in a well-documented outbreak in Colorado Springs were found among individuals who met their partners in a limited number of bars, clubs and social meeting places.[8] More recently, De et al[9] showed the importance of a motel bar in a gonorrhoea outbreak in Alberta. In rural Zimbabwe, Lewis et al[10] reported higher levels of sexual behaviour and stronger associations with commercial sex among those who had been to a beer hall than those who had not. During the early stages of the HIV epidemic in the USA, high rates of unprotected anal intercourse among MSM in bathhouses fuelled the early spread of HIV,[11] and bathhouses and ''cruising'' areas continue to be associated with high-risk sexual activity.[12] The internet is rapidly becoming an important venue for sexual partner recruitment,[13] and internet sites can act as foci of STI transmission.[14] In a study of recently HIV-infected MSM, 70% reported using the internet to meet sex partners.[15] The structure of these internet dating networks seems to be quite different from in-person networks.[16] Development of a common theoretical background to study sexual affiliation networks would allow us to compare and contrast the structure of these networks in detail.

The apparent importance of venues in structuring sexual networks has led to surveillance efforts being targeted at places where people meet their partners to access populations at risk of STIs. The Centers for Disease Control and Prevention's Young Men's Health Study successfully recruited a large number of young MSM from 263 venues that included dance clubs, street locations within ''gay neighbourhoods'', bars, health clubs, cafes, shops, gay youth organisations, parks, adult bookstores, bathhouses and Pride events, and found that many young MSM were unaware of their HIV status.[17–19] By targeting sex partner meeting places, individuals at risk of syphilis infection have been identified, who may have been missed through standard field investigations.[20][21] In San Francisco, the possibility of HIV testing within gay sex clubs has been evaluated,[22] and sex clubs and bookstores have been surveyed for self-reported frequency of HIV and syphilis testing.[23] Weir and colleagues have developed methods to identify sex partner meeting places in South Africa; this provided useful information on networks containing individuals with high rates of partner acquisition, who are at high risk of STIs.[24][25] This and similar approaches have been applied in Mexico,[26] Kazakhstan,[27] Burkina Faso,[28] Jamaica[29] and London, England.[30]

Access to populations through the venues where they meet or recruit sex partners also offers opportunities for prevention. Interventions may concentrate on increasing condom usage at venues that act as foci for STI transmission. In Managua, Nicaragua, condom distribution in motels, where both commercial and non-commercial sex occurs, markedly increased levels of condom usage.[31] The internet is being used for STI/HIV prevention, through banner advertising, online outreach, online partner notification, online laboratory slips for syphilis testing, and ''chat-rooms'' focused on distributing information relating to STIs.[32] Other interventions may involve disrupting the sexual network so as to reduce contact between HIV positive and HIV negative individuals.[33] ''POZ parties'', a sexual environment organised to facilitate sex partner recruitment between HIV-positive MSM, may act to reduce the number of new HIV

Abbreviations: ERGM, exponential random graph model; MSM, men who have sex with men; STI, sexually transmitted infection

infections, but high rates of unprotected sex may facilitate the spread of other STIs and the risk of HIV superinfection.[34]

COLLECTING DATA ON SEXUAL AFFILIATIONS

Compared with other forms of sexual network data,[35] information on sexual affiliations is much easier to obtain, especially for large networks, and tends to be more robust to biases in the sampling process than other forms of network data. However, affiliation data have limitations. Although the probability of contact may be higher among individuals who use the same venues for sexual partner recruitment, contact between these individuals is by no means certain. This is a particular problem when venues are lumped together into broad classes (eg, "public sex venues"). To increase the accuracy of information regarding sexual mixing, the specific venue visited, the times at which the venue was visited, and information about how people recruit partners within a given venue should be collected.

A similar problem can arise when comparing sexual affiliations of individuals infected with an STI; two individuals with the same STI who recruit partners from the same venue may not be epidemiologically linked. To help overcome this problem, genetic variation of pathogens can be exploited.[36] HIV exhibits extensive genetic variation, and epidemiologically linked individuals carry similar viruses.[37] Bacteria associated with STIs, such as *Neisseria gonorrhoeae*, also exhibit strain structure, and this information can be used to test whether individuals infected with the same strain are closer in the network than individuals infected with different strains.[38–41]

In addition to affecting the probability of contact between individuals, the individuals and the nature of the contacts between them may depend on the structure of the affiliation network. A given individual may behave differently with a partner recruited from a particular venue and demographics of attendees may vary across venues. Hence egocentric information on demographics and partnership-level information are also needed to assess the impact of the structure of the affiliation network on STI transmission. Collecting data on social affiliations may also be useful, to control for the number of visits to a venue and to assess the extent of overlap between the social network and the sexual network.[42]
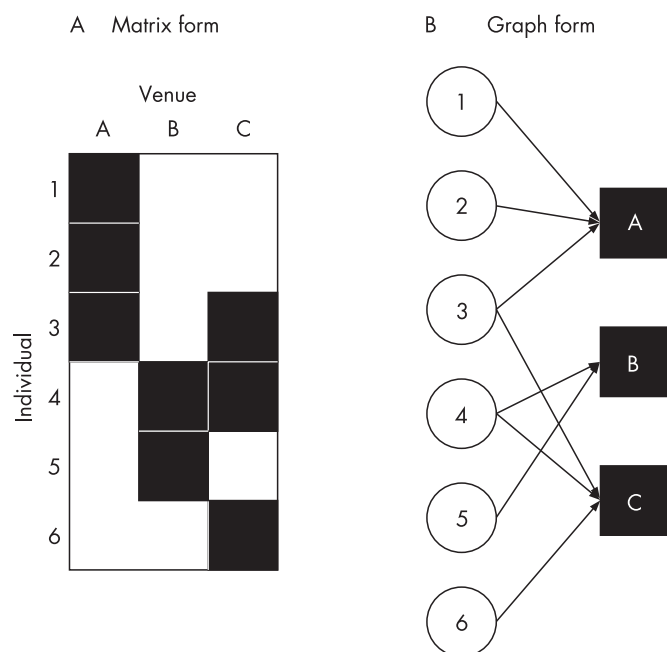
Figure 1   Representations of an affiliation network as a matrix (A) or a graph (B).

REPRESENTING SEXUAL AFFILIATION NETWORKS

In contrast with a sexual network, which consists of direct links between individuals (also known as "one-mode"), a sexual affiliation network consists of links from people to places ("two-mode"). One way to represent a network is as a matrix, with N rows corresponding to individuals and M columns corresponding to venues (fig 1A). Alternatively, a network can be represented as a graph, in which vertices represent the individuals and venues in the network, and edges represent links between individuals and venues (fig 1B). Ideally, the network should be laid out such that individuals are plotted close together if they recruited partners from mostly the same venues, and venues are plotted close together if partners were recruited there by mostly the same individuals.[43]

MODELLING SEXUAL AFFILIATIONS

Mathematical and simulation models are useful tools to study the structure of networks and the implications of network structure on STI transmission. An important parameter underlying the structure of networks is the degree, which is simply the number of connections either to or from an entity in a network. For affiliation networks, there are two kinds of degree, one for individuals, and one for venues, both of which affect the connectivity of the network.[44] For example, if the number of venues visited per person is Poisson distributed with mean μ, and the number of individuals per venue is Poisson distributed with mean v, then the average number of first and second neighbours of an individual is μv and $(\mu v)^2$, respectively. When $\mu v < 1$, the network is disconnected (ie, there are a number of separate subnetworks of people to venues); when $\mu v \geq 1$, a "giant component" of linked people and venues emerges.

An affiliation network can be reduced to a network of people to people who are linked by visiting the same venue, and hence the degree distribution of both individuals and venues can affect the clustering of individuals imposed by the venues. Watts and Strogatz[45] defined clustering on a (one-mode) network as three times the number of "triangles" on the graph (three people connected to each other), divided by the number of connected triples (two people connected to a person in common). For the above example, clustering between individuals is greater when the mean number of venues visited per individual μ is greater, although in general, the clustering may also depend on the degree distribution of the venue. For example, if the number of individuals per venue follows a negative binomial distribution with mean v and variance $v+v^2/\omega$, the clustering coefficient is $1/\{1+\mu\,[(\omega+1)/(\omega+2)]\}$—that is, when the variance in degree distribution of the venues is higher, the clustering coefficient between individuals is greater. Similar methods could be used to explore models in which the degrees of individuals and venues are correlated (eg, if people who visit more venues, visit more popular venues).[46]

Models of affiliation networks can be used to perform statistical tests of network structure, and determine the impact of this structure on the transmission of STIs. Although many studies have modelled the effect of one-mode network structure on the transmission of infectious diseases, especially STIs (reviewed in Newman,[2] Liljeros *et al*[3] and Keeling and Eames[4]), relatively few studies have combined an affiliation network with a model of disease transmission. A notable exception is a study of the spread of *Mycoplasma pneumoniae* in an institution with multiple wards.[47]

ANALYSING SEXUAL AFFILIATION NETWORKS

In order to place models of network structure in context, the structure of real sexual affiliation networks should be known. I briefly review two broad approaches to analyse such data:
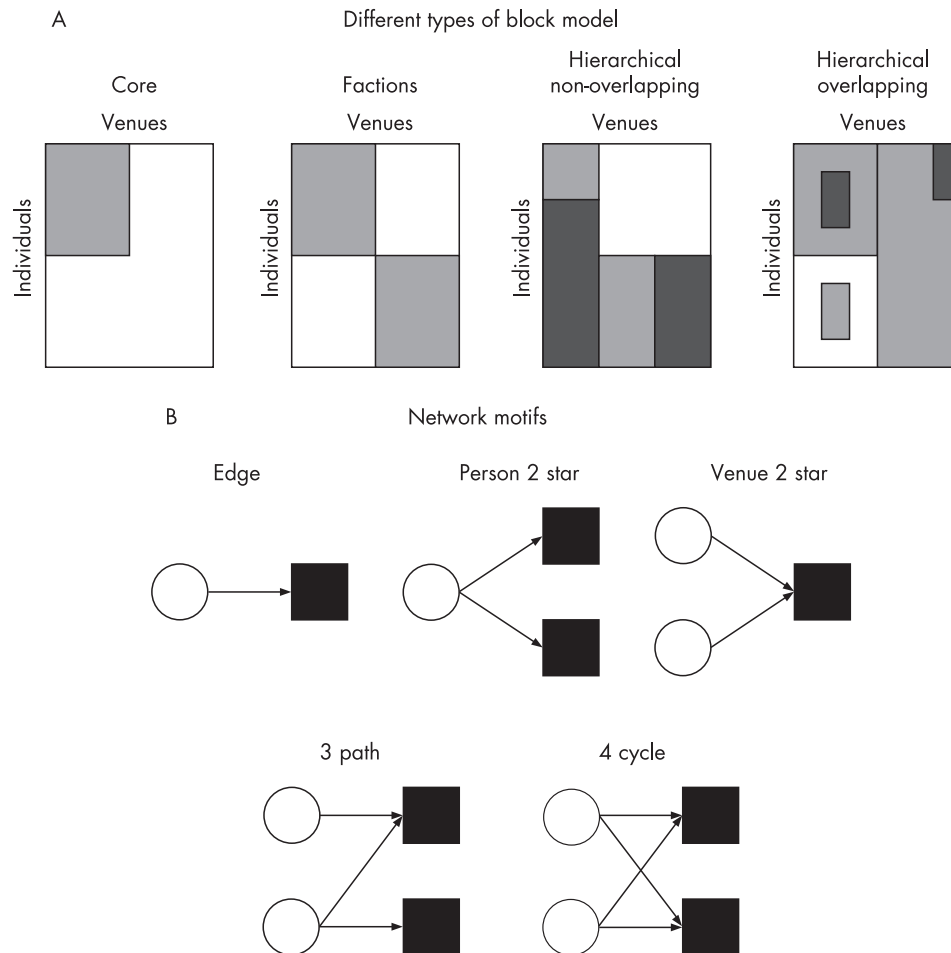
Figure 2 (A) Various blockmodels for affiliation networks and (B) different motifs that can be used to describe an affiliation network.

- blockmodels, which aim to place individuals and venues into interlocking blocks;
- tests for the significance of summary statistics calculated from the observed network.

Blockmodels

An active area of research involves devising ways to detect ''blocks'' within affiliation networks.[48 49] Figure 2A illustrates some idealised block structures. The core-periphery structure is an ideal typical pattern that divides both the rows and the columns into two classes. One of the blocks on the main diagonal (the core) is a high-density block consisting of closely connected individuals and venues; the other block on the main diagonal (the periphery) is a low-density block (fig 2A), consisting of individuals who do not visit the same venues, and venues that are disjoint because they are not visited by a common set of individuals. An alternative blockmodel is that of ''factions'', groupings that have high density of ties within the group, and low density of ties between groups, such there are joint groupings of individuals and venues that are as mutually exclusive as possible (fig 2A).

However, the patterns of visits by individual probably will not fall into neat discrete blocks. One approach is to extend the notion of blocks beyond high-density and low-density blocks as described by Doreian *et al*.[49] Another approach involves performing hierarchical clustering on individuals and venues separately, which offers greater flexibility in describing blocks.[50] Figure 2A gives examples of blocks under a hierarchical model. However, real sexual affiliation data may show more complex structure than can be captured with these models. In addition, these approaches are more descriptive than statistical in nature[51]; they provide a goodness of fit in terms of the number of discrepant observations, but without a p value or a posterior probability attached to the model. A number of statistical approaches for blockmodelling have been suggested for one-mode networks, that could be extended to consider affiliation networks.[52 53] Recently, statistical methods have been proposed that allow deterministic methods to be adapted to statistical inference (Gelman A, Leenen I, Van Mechelen I, *et al*. Bridges between deterministic and probabilistic classification models. Department of Statistics, Columbia University, USA, 2003; Leenen I, Van Mechelen I, Gelman A, *et al*. Bayesian hierarchical classes analysis. IAP Statistics Network, 2004; unpublished works), which show great promise for performing tests of core-group or faction structure in affiliation data.

Testing the significance of summary statistics

Another approach to test for structure in an affiliation network is to calculate descriptive statistics from an observed network, and compare these statistics to those from simulated networks. For example, we can think of a network as being made up of a number of smaller building blocks (subnetworks or network motifs). Figure 2B illustrates some motifs that may be found in an affiliation network[54]: edges (a link between an individual and a venue), person 2 star (a person linked to two venues), venue 2 star (a venue connected to two people), 3 path (two people connected to two venues, with one venue in common) and 4 cycle (two people connected to two venues, with both venues in common). In contrast with blockmodels, which

attempt to find discrete blocks, characterising a network in terms of a number of summary statistics can consider more continuous, perhaps overlapping, patterns.

One approach to testing the significance of these statistics is to compute summary statistics from randomised networks, and compare them with those from the observed network. By preserving the row and column sums of the affiliation matrix,[55] we can test for structure that is not simply attributable to the degree distributions of individuals and venues. The number of each motif in fig 2 for the network depicted in fig 1 are: edges = 8; person 2 star = 2; venue 2 star = 7; 3 path = 7; and 4 cycle = 0. Based on 1000 randomisations, 77% of randomised networks had the same number of 3 path and 4 cycle, and the remaining 23% of randomised networks had six 3 path and 1 4 cycle—that is, the structure of the network was not markedly different from a network in which individuals and venues are linked at random (although this network is too small to make robust inferences). Different networks can be compared using standardised values of these parameters.[54][56]

A recently developed class of models that is becoming increasingly popular in network analysis is exponential random graph models (ERGMs), also known as p* (p star) models.[57] In an ERGM, the probability of observing a network (represented as a matrix), y, $P_\theta(Y = y)$ is given $P_\theta(Y = y) = \exp[\theta'u(y) - \psi(\theta)]$, where $u(y)$ is a vector of summary statistics, θ is a vector of parameters and $\psi(\theta)$ is a normalising constant. ERGMs provide a means to test the significance of a wide variety of summary statistics, and could be applied, for example, to test whether infected and uninfected individuals are located in different parts of the sexual affiliation network.

A common approach to fit an ERGM is using a pseudolikelihood criterion.[57] Essentially, the model can be reformulated as a logistic regression in which the outcome is a tie in the network, and the predictors include changes in the summary statistics induced by changing the tie from presence to absence. This is an attractive approach, which circumvents the difficult problem of calculating the normalising constant $\psi(\theta)$, and can be implemented in standard statistical software. Pseudolikelihood models for affiliation networks have been developed,[58–60] although none have been applied to sexual affiliation data. The changes in the number of motifs for the network depicted in fig 1 are shown in table 1. Note that the presence of a link between person 4 and venue A would greatly increase the

connectivity of the network (more 3 path); the absence of this link in the observed network implies a tendency against connectivity.

However, pseudolikelihood parameter estimates and associated errors may be misleading due to the interdependence between observations, and model fits should be treated as exploratory.[61–63] To fit these models using maximum likelihood, it is necessary to calculate the normalising constant, $\psi(\theta)$, by simulating networks under the model, and optimising the parameters to provide the best match between the summary statistics of the observed data and those of the simulated data. Despite the apparent simplicity of this idea, it is remarkably difficult to obtain simulated networks that look like real-life networks using these models,[64] and maximum likelihood estimation of ERGMs is a topic of current research.

DISCUSSION

Sexual affiliation data may provide important information on sexual networks and the spread of STIs. Analysis of an affiliation network may provide information on how to target venues to maximise coverage of the population for the purposes of surveillance and prevention.

There are a number of needs for future research. First, we need to develop methods to gather affiliation data. An increasing number of studies are employing the PLACE methodology,[24–29] which is certainly a promising start, although further research is needed to adapt PLACE for different settings. It is important for study participants to identify individual venues, rather than lumping venues together into broad categories (such as "beer halls"[10]). The sexual affiliation network is only one part of the risk environment for acquisition and transmission of STIs, and should be analysed along with factors such as substance use, the physical context of the actual sexual act (in a bathroom, at home, rest stop, etc.), the times at which the venue is visited and the duration of the visit, and how partners are chosen at a given venue. In addition, information on multiple, possibly overlapping, memberships may help to focus outreach efforts, for example sex partner recruitment and needle sharing patterns in injection drug users.

Second, methodology in the analysis of such data is needed. Missing data are a common problem in many surveys,[65] and affiliation data are no exception, although a model-based assessment of affiliation networks is still required to determine the impact of failing to recruit particular individuals, or failing to identify all the venues; in the latter case, capture-recapture type methods could be to estimate the total number of venues used for sex partner recruitment. Sexual affiliations may

Table 1 Changes in the number of motifs for the network depicted in fig 1 as a result of toggling the tie from 1 to 0

Tie	Person	Venue	Edge	Person 2 star	Venue 2 star	3 path	4 cycle
1	1	A	1	0	2	1	0
0	1	B	1	1	2	5	0
0	1	C	1	1	3	7	1
1	2	A	1	0	2	1	0
0	2	B	1	1	2	5	0
0	2	C	1	1	3	7	1
1	3	A	1	1	2	4	0
0	3	B	1	2	2	9	1
1	3	C	1	1	2	5	0
0	4	A	1	2	3	10	1
1	4	B	1	1	1	3	0
1	4	C	1	1	2	4	0
0	5	A	1	1	3	5	0
1	5	B	1	0	1	1	0
0	5	C	1	1	3	6	1
0	6	A	1	1	3	6	1
0	6	B	1	1	2	5	1
1	6	C	1	0	2	2	0

Key messages

- There is an increasing body of literature showing that venues where people meet may have an important role in the spread of STIs, and these are an increasingly important focus of STI surveillance and prevention.
- The venues where people meet sexual partners, which I denote "sexual affiliations", may provide valuable information on the structure of sexual networks. Compared with other forms of sexual network data, information on sexual affiliations is much easier to obtain, especially for large networks, and tends to be more robust to biases in the sampling process than other forms of network data.
- Mathematical and statistical models of sexual affiliations are needed to help interpret and analyse such data.

change over time, necessitating the development of dynamic network models.[66] This also requires us to understand the rules by which an individual chooses a particular venue. Accumulation of sexual affiliation data may help encourage the development of appropriate statistical methods.

Third, we need to understand the relationship between sexual networks, sexual affiliation networks and the transmission networks of STIs. Mathematical and simulation models will be needed to help interpret the multiplex nature of the sexual structure of a population, and its implications for the spread and persistence of STIs.

ACKNOWLEDGEMENTS

AUTHOR'S CONTRIBUTION

SF is the sole author of this paper and was responsible for the review, analysis and writing of this paper.

Competing interests: None.

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