Estimating individual action dispositions using binary and frequency egocentric sexual network data

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The degree distribution of nodes in a sexual network has been under thorough investigation, as has its implications for the spread of sexually transmitted infections. However, not only the structure of the network is of importance in regulating the propagation of an infection. Two nodes connected by an edge may take actions that reduce the transmission probability through that edge. Condom use is one such action. In this article, we derive models for individual action dispositions, and how they together generate an outcome on the edge connecting two nodes. We derive two main models: One where two connected nodes generate one outcome together (suitable for casual sex partners), and one where they generate several outcomes together (suitable for steady sex partners). We model different disposition distributions and different rules on how the dispositions generate outcomes, using an egocentric network dataset on condom use behavior.

KEYWORDS
egocentric network analysis, sexual behavior, sexually transmitted infections, social networks
1 | INTRODUCTION

The aim when gathering a sample of individuals is to infer some specific quantity, such as the prevalence of a disease, the distribution of political views, or the distribution of the number of sex partners. When sampling a set of individuals we are in fact taking a sample from an underlying social network. For some quantities, the network structure has less impact, while others are highly dependent on the network. For example, the spread of an infectious disease will greatly depend on the social network of friends, colleagues, and acquaintances, since infection takes place between individuals in close proximity to each other, while the occurrence of a noncommunicable diseases will depend less on this network.

In social and sexual networks individuals are represented by nodes and relationships between individuals are represented by edges. The number of edges a node has is the degree of that node. The literature on sexual networks, their properties and connections to the spread of sexually transmitted infections (STIs), are extensive. Focus has previously been on the degree distribution of sexual networks, including conclusions concerning the distribution of the number of sex partners being extremely right-skewed, similar to a power-law distribution (Liljeros, Edling, Amaral, Stanley, & Åberg, 2001); how to estimate the magnitude of the scaling parameter in a power-law distribution from data on individuals' degrees (Jones & Handcock, 2003); and how to statistically test the assumption of a power-law degree distribution against alternatives (Hamilton, Handcock, & Morris, 2008). Several studies conclude that the heterogeneity in the number of sex partners could help maintain an STI in a population (Hansson, Strömdahl, Leung, & Britton, 2020; Hethcote & Yorke, 1986; Jones & Handcock, 2003; Liljeros et al., 2001). The literature also includes how to measure concurrency (Morris & Kretzschmar, 1995), theoretical (Watts & May, 1992), and simulated (Morris & Kretzschmar, 1997) effects of concurrency on the spread of an STI, followed by a wide discussion on the effect concurrent sex partners has on the spread of HIV (Boily, Alary, & Baggaley, 2012; Goodreau, 2011; Halperin & Epstein, 2004; Leung & Kretzschmar, 2015; Sawers & Stillwaggon, 2010).

When taking a sample from the true underlying social network we lose information. Nonetheless, we can from the sampled nodes gain additional information on the nodes connected to the sampled ones. This is called egocentric network data, where a sampled node is named an ego and its neighbors alters (Hanneman & Riddle, 2005). We show an example of how the sampling procedure breaks the true network into an egocentric network in Figure 1.

FIGURE 1 Illustration of a complete network (a), the sampling of node 3 and 6 (b), and the egocentric network arising from this sampling (c)
Data on sexual behavior are an example of egocentric network data: sampled individuals (the egos) give information on the number of partners (the alters), and possibly additional information on the partners and the relationships (the edges connecting the ego and its alters). Examples of additional information are age and gender of the partner (Mercer et al., 2008); length of the relationship (Foxman, Newman, Percha, Holmes, & Aral, 2006; Hansson, Leung, Britton, & Strömdahl, 2019; Nguyen et al., 2015); type of sex (Fridlund, Stenqvist, & Nordvik, 2014); condom use behavior with the partners (Fridlund et al., 2014; Hansson et al., 2019; Mercer et al., 2008); and partnership type, for example, casual one-off and steady long-term (Fridlund et al., 2014; Hansson et al., 2019; Mercer et al., 2008). Some of these behaviors, such as whether a condom is used or which type of sex occurs in a relationship, are actions based on a joint decision between the two involved actors. In sexual behavioral data, the outcomes of these decisions are observed, not the individual dispositions giving rise to the outcomes. How we choose to define the mechanisms, the model, resulting in the observed outcome will have an effect on how we look at the outcome itself. In ignoring the network aspect of the data, one would simply look at the outcome as an observation from the sampled individual. When taking the network structure into account one would need to incorporate that the observed outcome depends on the action disposition of both the sampled individual and the partner (both the ego and alter).

As mentioned, the structure of the network is of importance for the spread of a disease. In addition, so is the dispositions of connected nodes generating outcomes that affect the transmission probability via the edges. If a node (person) with a large degree (many sex partners) gets infected, it could infect many of its neighbors (partners). This is indeed true, but imagine that this node use condom with all its neighbors, is this node then really a potential risk of spreading the disease? There are in fact outcomes determined by two connecting nodes that could greatly reduce the risk of transmission.

In this article, the focus lies on outcomes generated by two connected nodes, and specifically on outcomes that control the spread of a disease. We develop and extend models that are able to estimate action dispositions from egocentric network data, these action dispositions do in turn affect the outcome between connected nodes. Before this is explained in detail, we will go through the background and motivation behind the specific action disposition studied in this article.

### 1.1 Motivation and aim

Sexually transmitted infections (STIs) are a problem worldwide (WHO, 2016). The bacterial STI chlamydia is the most common; in the EU/EEA over 400,000 chlamydia cases were reported in 2017 (ECDC, 2019a). In the same year almost 90,000 new gonorrhea cases and 25,000 new HIV cases were reported (ECDC, 2019b, 2019c). Mathematical and statistical models are strong tools to assess effects of a potential intervention (Li et al., 2018; Punyacharoensin et al., 2016; Rönn et al., 2019; Xiridou, Geskus, de Wit, Coutinho, & Kretzschmar, 2003) and are therefore a means to guide public health authorities.

One aspect that greatly affects the spread of any disease throughout a population is the transmission probability. This is why consistent condom use is such a successful preventive measure against STIs: It directly decreases the transmission probability. In most models developed to study the spread of STIs, condom use is incorporated in such a way that it neglects the network aspect—they neglect that it is a decision made by two individuals in a relationship. Instead, it is incorporated as a fixed factor that decreases the probability of infection or as a factor that decreases the number of sex acts, and furthermore, that this factor is the same for all individuals.
This simplified approach has two implications: It assumes all individuals behave the same, and that the mean condom use, from some data, is used as an estimate for the proportion condom use in all sex acts. This second implication means that, even with a steady sexual partner, you will with this estimated probability use a condom in each sex act, where the condom outcomes in different sex acts are independent. Think of the two different scenarios where the number of partnerships and the number of sex acts are the same in the two: (a) with a probability .3, a condom is never used within a steady partnership and with a probability .7, a condom is always used within a steady partnership and (b) each time a couple have sex they use condom with a probability .7 independently of previous occasions. This is two very different behaviors but in both the mean condom use will be 70%. The spread of a disease will most likely be different in these two scenarios.

For the special case where only one outcome (binary data) is observed between the ego and its alters, for example, condom use with casual sex partners, the models derived in Hansson, Fridlund, Stenqvist, Britton, and Liljeros (2018) make it possible to test this homogeneous condom use assumption against nonhomogeneous condom use. With these models, it is possible to analyze both a same-sex population and a heterosexual population. However, in a population of men who have sex with men (MSM) it is possible that condom dispositions could be different depending on if an individual has receptive anal intercourse (RAI) or insertive anal intercourse (IAI). In this article, we modify and extend the models from Hansson et al. (2018) in two ways. First, we modify the binary data case to allow for different dispositions depending on what position you take: the insertive or receptive part. Second, we extend the models to allow for several outcomes with the same partner, that is, condom dispositions with steady sex partners.

1.2 Outline

In Section 2, we begin by describing the basics of the disposition models utilizing egocentric network data. Then, the two different extensions will be introduced, incorporating different positions to the binary case (Section 2.1) and allowing a couple to generate several outcomes with each other (Section 2.2). The Analysis section, Section 3, is divided into two subsections: A description of the dataset used to illustrate our models in Section 3.1, an MSM network; and the results when applying the derived models to the data in Section 3.2. We end by, in Section 4, summarizing the obtained results, discussing their possible implications, and giving suggestions for further research.

2 ACTION DISPOSITION MODELS

We will now briefly describe the core of the disposition models. A person who never wants to use a condom is coded as “1” and a person who always wants to use a condom is coded as “0.” Each node $i$ has a non-condom disposition $x_i$, $0 \leq x_i \leq 1$, for $i = 1, \ldots, n$, where $n$ is the sample size. The first part of the modeling is to decide on a distribution for the dispositions. The second part of the modeling is to create a translation of a couple’s two dispositions into a probability of condom
use. For this second part, we will need to specify the probability of not using a condom given the two dispositions of two connected nodes:

\[ P(\text{No condom}|x_i,x_j). \]

The homogeneous disposition model, that each individual has the same probability of using a condom in each sexual act, is described by

\[ P(\text{No condom}|x_i,x_j) = P(\text{No condom}) = q. \]

The disposition models in Hansson et al. (2018) allow genders to have different disposition distributions, but only for one type of disposition for each individual. However, they do not allow for different dispositions depending on, for example, the position at anal sex the sampled individuals take. Moreover, the models only consider a decision in which the result is observed once (binary outcomes). For details on the case of binary outcomes generated by two individuals we refer to Hansson et al. (2018) and its supporting information.

Consider a sexual network of men who have sex with men, the first extension is to create a model that could find possible asymmetries in dispositions when being the receiver and when being the giver at anal sex (Section 2.1). Next, when gathering data on sexual behavior, questions concerning behaviors both with casual partners and with steady partners are usually asked. The second extension is to allow several outcomes within one relationship, that is, creating a model that takes steady partnerships, frequency data, into account (Section 2.2). Note that we will model the mechanisms giving rise to the observed number of non-condom sex partners among a known number of sex partners. We will not model how individuals choose their partners.

### 2.1 Two types of dispositions for binary outcomes

The aim of the extension in this section is to create a model where nodes have two types of dispositions, type \( g \) and type \( r \), depending on which type/position it takes in an action together with a connected node. For a heterosexual network, the types would be fixed as the positions at anal sex are defined. In a same-sex MSM network, the type an individual has may change. If the sampled node is of type \( g \) at a certain point, its neighbor will be of type \( r \), then if the sampled node change to type \( r \) its neighbor change to type \( g \). The data considered consists of, for each sampled node, the following: the number of partners it had as type \( g \), and for each of these partners if a condom was used; and the number of partners it had as type \( r \), and for each of these partners if a condom was used.

We aim at testing a null model where the dispositions for type \( g \) and type \( r \) come from two distributions that are the same, against an alternative where the two distributions are different. In terms of application, we specifically aim at testing whether the condom dispositions when being the receptive actor (receiver) and the insertive actor (giver) come from the same or different distributions. Assume that a participant has a disposition for non-condom use when being type \( g \) and a disposition for non-condom use when being type \( r \). These two dispositions come from two independent random variables \( X_g \sim F(\theta_g) \) (when being the giver) and \( X_r \sim F(\theta_r) \) (when being the receiver). The distributions \( F_g \) and \( F_r \) can be fixed to have the same parameters or allowed to be different. As a consequence, even if the distributions are the same an individual will not have exactly the same dispositions when being type \( g \) and type \( r \).
In assuming independence of the dispositions of type \( g \) and of type \( r \), we circumvent the problem of the possibility of a sex-act to include that the sampled node is first type \( g \) and then later type \( r \). Due to this assumption, both the sampled node and its partner’s dispositions will be independent in both actions since they switch position. In addition, the number of sex acts a sampled node has being type \( g \) is assumed independent of the number of sex acts the sampled node has being type \( r \). We further assume that the event that a sampled individual uses condom with one of its partners is independent of the event that another sampled individual uses condom with one of its partners. The validity of this assumption requires that the sample is relatively small in comparison to the whole sexual network and that no contact tracing was utilized in gathering the sample. This assumption, of independence of sampled nodes, implies that the likelihood will be given by the product of the probabilities of observing each node’s number of non-condom acts as type \( g \) (among its number of acts as type \( g \)) and of observing each node’s number of non-condom acts as type \( r \) (among its number of acts as type \( r \)).

The number of times a sampled node was type \( g \) and type \( r \) are denoted \( d_g \) and \( d_r \), respectively, and the number of these that was without a condom are denoted \( m_g \) and \( m_r \), respectively. Denote the random variable of the number of type-\( g \) non-condom contacts among \( d_g \) type-\( g \) acts in total by \( Z_{dg}^g \), and similarly denote the random variable of the number of type-\( r \) non-condom contacts among \( d_r \) type-\( r \) acts by \( Z_{dr}^r \). Due to independence of nodes, the likelihood will be given by the product of the probabilities of observing each node’s number of type-\( g \) and type-\( r \) non-condom contacts

\[
P\left(Z_{dg}^g = m_g, Z_{dr}^r = m_r \right) := P\left(Z_{dg}^g = m_g, Z_{dr}^r = m_r \mid \theta_g, \theta_r \right).
\]

This probability will depend on the distribution assumed for the dispositions. By stating this now, we drop the notation with the conditioning on \( \theta_g, \theta_r \). Furthermore, by assuming independence of the number of acts that are of type \( g \) and the number of acts that are of type \( r \) of a sampled node, and the independence of the dispositions, this probability simplifies to

\[
P\left(Z_{dg}^g = m_g \right) P\left(Z_{dr}^r = m_r \right)
\]

Now consider one sampled node, even if the dispositions of different partners are independent, the events of non-condom use between different partners will be dependent through the sampled node’s own disposition. To find the probability of observing \( m_g \) non-condom acts among \( d_g \) partners and observing \( m_r \) non-condom acts among \( d_r \) partners, condition on the dispositions \( x_g \) and \( x_r \) of the sampled node, that is,

\[
P\left(Z_{dg}^g = m_g \right) P\left(Z_{dr}^r = m_r \right) = E \left[P\left(Z_{dg}^g = m_g \mid X_g \right) \right] \times E \left[P\left(Z_{dr}^r = m_r \mid X_r \right) \right]. \quad (1)
\]

In doing this, the number of non-condom acts among different partners will be independent. Equation (1) is the key to find the likelihood in order to make inference. To find an expression for Equation (1) we need to specify the disposition distributions and the rule from two connected nodes dispositions into a non-condom probability. This will be the content of the following two subsections. Before we go into these details, we want to stress that in setting up the extension in this manner we can use many of the results found in Hansson et al. (2018). The difference here is that a node is allowed to be two types, both receptive and insertive, while in Hansson et al. (2018) a node is fixed to female or male. Therefore, when we deviate from previously shown results we will point this out.
2.1.1 Continuous beta dispositions

A suitable continuous choice for the disposition distribution is the Beta distribution, since it is quite flexible and has its support on [0, 1], and we therefore assume Beta distributions with parameters \( \theta_g = (\alpha_g, \beta_g) \) and \( \theta_r = (\alpha_r, \beta_r) \). Given a sex act between two individuals, where one is the insertive actor with disposition \( x_g \) and one is the receptive actor with disposition \( x_r \), use the following rule for the non-condom probability

\[
P(\text{No condom}|x_g, x_r) = x_g^{\gamma} x_r^{1-\gamma},
\]

where \( 0 \leq \gamma \leq 1 \). If \( \gamma = 0.5 \) the non-condom probability is given by the geometric mean of the two dispositions, leading to that the two individuals' dispositions have equal weight. If \( \gamma = 1 \) the insertive actor decides whether a condom is used and if \( \gamma = 0 \) the receptive actor decides. If \( \gamma > 0.5 \), the insertive actor will have a larger influence and if \( \gamma < 0.5 \), the receptive actor will have a larger influence. For the continuous model, we will use the geometric mean rule as a default. Note that the geometric mean rule with Beta distributed dispositions is a generalization of the homogeneous disposition model. If \( \alpha = \alpha_g = \alpha_r, \beta = \beta_g = \beta_r \), and if \( \alpha \) and \( \beta \) are set to very large values, then the disposition distribution would essentially be a one-point distribution and all individuals would use this value as their disposition. This yields the same mechanisms as the homogeneous disposition model.

Let \( a \in \{r, g\} \), with continuous dispositions the two probabilities in Equation (1) can be expressed by

\[
P(Z_a^a = m_a) = \int_0^1 P(Z_a^a = m_a|x_a) f_X(x_a) \, dx_a.
\]

By conditioning on the dispositions of the \( d_g \) and the \( d_r \) partners we have that

\[
P(Z_g^{d_g} = m_g) = \int_0^1 \left( \frac{d_g}{m_g} \right) \left( \frac{x_g^{\gamma} E[X_r^{1-\gamma}]^{m_g}}{1 - x_g^{\gamma} E[X_r^{1-\gamma}]} \right)^{d_g - m_g} f_X(x_g) \, dx_g,
\]

\[
P(Z_r^{d_r} = m_r) = \int_0^1 \left( \frac{d_r}{m_r} \right) \left( \frac{x_r^{1-\gamma} E[X_g^{\gamma}]}{1 - x_r^{1-\gamma} E[X_g^{\gamma}]} \right)^{d_r - m_r} f_X(x_r) \, dx_r.
\]

And by expanding the powers \( (1 - x_g^{\gamma} E[X_r^{1-\gamma}])^{d_g - m_g} \) and \( (1 - x_r^{1-\gamma} E[X_g^{\gamma}])^{d_r - m_r} \) using the binomial theorem, the two integrals can be written as

\[
P(Z_g^{d_g} = m_g) = \sum_{i=0}^{d_g - m_g} \binom{d_g - m_g}{i} E[X_g^{\gamma(m_g+i)}] E[X_r^{1-\gamma}]^{m_g+i}
\]

\[
P(Z_r^{d_r} = m_r) = \sum_{j=0}^{d_r - m_r} \binom{d_r - m_r}{j} E[X_r^{1-\gamma(m_r+j)}] E[X_g^{\gamma}]^{m_r+j}.
\]

2.1.2 Pro-con-neutral model

With the pro-con-neutral model, we create a model that captures the hypothesis that people with strong opinions, either for or against the action at hand, are more influential than individuals with
weaker opinions. This is a discrete distribution where a node can have one of three dispositions \{C, I, N\}, either for condom C, against (non-condom) N, or neutral (easily influenced) I. An I type individual will do as any of the other two types prefer. In addition, to capture that I types are neutral, the non-condom probability when two I types meet is set to .5. Let \( \mathbf{P} \) denote the matrix where the \( k \)th element is given by the probability \( \epsilon_{kl} = P(\text{No condom}|x_i = k, x_j = l) \), where \( k, l = \{C, I, N\} \). \( \mathbf{P} \) is then given by

\[
\mathbf{P} = \begin{pmatrix}
C & I \\
I & N \\
N & N
\end{pmatrix}
\begin{pmatrix}
\epsilon_{CC} & \epsilon_{CI} & \epsilon_{CN} \\
\epsilon_{IC} & \epsilon_{II} & \epsilon_{IN} \\
\epsilon_{NC} & \epsilon_{NI} & \epsilon_{NN}
\end{pmatrix}
= \begin{pmatrix}
0 & 0 & \epsilon_{CN} \\
0 & 0.5 & 1 \\
\epsilon_{CN} & 1 & 1
\end{pmatrix}.
\]

(2)

The probability of having disposition \( U = C, I, N \) when being type \( a \in \{r, g\} \) is denoted \( p_a \), where \( p_C + p_I + p_N = 1 \). The parameters to estimate are \( \theta_g = (p_C^g, p_I^g, p_N^g) \) and \( \theta_r = (p_C^r, p_I^r, p_N^r) \). The two parts of Equation (1) will with the pro-con-neutral model become

\[
P(Z_{d_a}^a = m_a) = P(Z_{d_a}^a = m_a|X_a = C)p_C^a + P(Z_{d_a}^a = m_a|X_a = I)p_I^a + P(Z_{d_a}^a = m_a|X_a = N)p_N^a.
\]

(3)

These different probabilities \( P(Z_d = m|X = C) \), \( P(Z_d = m|X = I) \) and \( P(Z_d = m|X = N) \) are given in appendix S1.2 in Hansson et al. (2018); however, they are not given in compact form and we simplify these further in the Supplementary Material S2. For acts as type \( a \in \{r, g\} \) of a sampled node, we have for \( b \neq a \) that

\[
P(m_a \text{ non-condom contacts} | X_I = U) = (\epsilon_{UC}p_C^b + \epsilon_{UI}p_I^b + \epsilon_{UN}p_N^b)^{m_a},
\]

and

\[
P(d_a - m_a \text{ condom contacts}|X_I = U) = (p_C(1 - \epsilon_{UC}) + p_I(1 - \epsilon_{UI}) + p_N(1 - \epsilon_{UN}))^{d_a - m_a}.
\]

Using the non-condom probabilities, \( \epsilon_{kl} \), given in Equation (2) for different combinations of meeting individuals, for example, \( \epsilon_{CC} = \epsilon_{CI} = 0 \) and \( \epsilon_{IN} = \epsilon_{NN} = 1 \), Equation (3) is for \( a \) and \( b \in \{r, g\} \) and \( a \neq b \) given by

\[
P(Z_{d_a}^a = m_a) = \binom{d_a}{m_a} p_{C}^{a} (p_{N}^{b} \epsilon_{CN})^{m_a} (p_{C}^{b} + p_{I}^{b} + p_{N}^{b}(1 - \epsilon_{CN}))^{d_a - m_a}
\]

\[
+ \binom{d_a}{m_a} p_{I}^{a} (0.5p_{I}^{b} + p_{N}^{b})^{m_a} (p_{C}^{b} + 0.5p_{I}^{b})^{d_a - m_a}
\]

\[
+ \binom{d_a}{m_a} p_{N}^{a} (p_{C}^{b} + p_{I}^{b})^{m_a} (p_{C}^{b}(1 - \epsilon_{CN}) + p_{N}^{b})^{d_a - m_a}.
\]

We have now specified the two parts of Equation (1) in order to be able to make inference.

The special case when no one is neutral (\( p_I = 0 \)) is referred to as the pro-con model. It is also possible to let the non-condom probability when a condom person meets a non-condom person, \( \epsilon_{CN} \), further depend on who is the giver and who is the receiver: \( \epsilon_{CN}^{gr} \) when the giver is the condom person and when the receiver is the non-condom person, and \( \epsilon_{CN}^{rg} \) when the reverse order holds.
2.2 Several outcomes generated by two connected nodes

We will now describe the second extension where we instead use the frequency of sex acts between two individuals and how often condom was used. In Section 2.2.1, we describe the case where position is not yet taken into account, while in Section 2.2.2, we allow for two types of disposition distributions depending on position.

Some of the basis from the models for binary outcomes will hold here as well. As before, assume that each individual independently of each other draw a disposition from a random variable \( X \sim F(\theta) \). However, we will in this section exclusively use a Beta distribution for this \( F \). We also denote the disposition of a node \( i \) by \( x_i \in [0, 1] \) and the disposition of a node \( j \) by \( x_j \in [0, 1] \). If node \( i \) and node \( j \) are connected by an edge the probability that they will not use a condom is given by \( \sqrt{x_i x_j} \). The difference from before is that the couple \( i,j \) will be allowed to generate several outcomes with each other. Let \( y_{ij} \) denote the probability of non-condom use between nodes \( i \) and \( j \), then \( y_{ij} = \sqrt{x_i x_j} \). Moreover, let \( K_{ij} \) be the random variable of the number of non-condom acts among a known number of sexual acts \( s_{ij} \) between \( i \) and \( j \). An observed outcome of \( K_{ij} \) is denoted \( k_{ij} \). Note that, if we knew the values \( x_i, x_j \), and consequently \( y_{ij} \), then \( K_{ij} \sim \text{Bin}(s_{ij}, y_{ij}) \).

2.2.1 One type of disposition for frequency data

With a sample of \( n \) nodes where the degree of node \( i \) is denoted \( d_i \), let \( \vec{d} = (d_1, \ldots, d_n) \) be the vector of degrees. From a sampled node \( i \) and its \( j \)th partner (\( j = 1, \ldots, d_i \)), the data consist of the number of condomless sex acts \( k_{ij} \) among the number of sex acts \( s_{ij} \). Let \( \vec{s} = (s_1, \ldots, s_n) \) be the number of sex acts with each partner for each sampled node, that is, each element of \( \vec{s} \) is in turn a vector: \( \vec{s}_i = (s_{i1}, \ldots, s_{id_i}) \). Also, the observed data are of the form \( (\vec{k}_1, \ldots, \vec{k}_n) \), where \( \vec{k}_i = (k_{i1}, \ldots, k_{id_i}) \). Note that, the degrees \( d_i \) and the number of sex acts \( s_{ij} \) are considered known quantities. As in Section 2.1, the numbers of non-condom acts of the sampled nodes are assumed to be independent, and consequently the likelihood of observing the frequencies \( \vec{k}_1, \ldots, \vec{k}_n \) will be given by

\[
L \left( \vec{k}_1, \ldots, \vec{k}_n | \theta, \vec{d}, \vec{s} \right) = \prod_{i=1}^{n} L \left( \vec{k}_i | \theta, d_i, \vec{s}_i \right) = \prod_{i=1}^{n} P \left( K_{i1} = k_{i1}, \ldots, K_{id_i} = k_{id_i} | \theta, d_i, \vec{s}_i \right). \tag{4}
\]

By assuming a Beta disposition distribution we have that \( \theta = (\alpha, \beta) \). From here on we drop the conditioning on \( \theta \). In what follows we will focus on \( P \left( K_{i1} = k_{i1}, \ldots, K_{id_i} = k_{id_i} | d_i, \vec{s}_i \right) \). If the probabilities of non-condom use with each partner were independent and observed \( (y_1, \ldots, y_{d_i}) \) the sought probability would be

\[
\prod_{j=1}^{d_i} \left( \frac{s_{ij}}{k_{ij}} \right)^{y_{ij}} (1 - y_{ij})^{s_{ij} - k_{ij}}.
\]

The even more simplified assumption that all acts would have the same probability, \( p \) say, of being without condom, that is, the homogeneous case, would give

\[
\prod_{j=1}^{d_i} \left( \frac{s_{ij}}{k_{ij}} \right)^{p k_{ij}} (1 - p)^{s_{ij} - k_{ij}}.
\]
However, the number of acts without condom with different partners depend on the disposition of the sampled node $i$. Therefore, we first need to condition on the disposition of node $i$, denoted $x_i$, to rid us these dependencies. Knowing the disposition $x_i$ of the sampled node, the number of non-condom acts with the $d_i$ partners will be independent. Hence

$$P\left(K_{i1} = k_{i1}, \ldots, K_{id_i} = k_{id_i} \mid s_i, x_i\right) = \int_0^1 f_{X_i}(x_i) \prod_{j=1}^{d_i} P\left(K_{ij} = k_{ij} \mid s_{ij}, x_i\right) \, dx_i. \quad (5)$$

The density of $f_{X_i}(x_i)$ is known (Beta distributed). To find the probability $P\left(K_{ij} = k_{ij} \mid s_{ij}, x_i\right)$ we use Lemma 1.

**Lemma 1.** Given a random variable $Y = \sqrt{X_iX_j}$, where $X_i$ and $X_j$ are two independent Beta distributed random variables with parameters $\left(\alpha_i, \beta_i\right)$ and $\left(\alpha_j, \beta_j\right)$,

(i) then the distribution of $Y \mid X_i$ is given by

$$f_{Y \mid X_i}(y) = \frac{2y}{x_iB(\alpha_i, \beta_j)} \left(\frac{y^2}{x_i}\right)^{\alpha_j-1} \left(1 - \frac{y^2}{x_i}\right)^{\beta_j-1},$$

for $0 < y < \sqrt{x_i}$.

(ii) Given a random variable $K \mid Y = y \sim \text{Bin}(m, y)$, but where only $X_i = x_i$ of $Y = \sqrt{X_iX_j}$ is observed, then

$$P(K = k \mid X_i = x_i) = \left(\frac{m}{k}\right) B(\alpha_j, \beta_j) \int_0^1 \sqrt{tx_i}^k \left(1 - \sqrt{tx_i}\right)^{m-k} t^{\alpha_j-1}(1 - t)^{\beta_j-1} \, dt. \quad (6)$$

We can express the probability of observing $k$ non-condom acts among $m$ acts, given your own disposition $x_i$, in terms of the integral in Lemma 1(ii). This integral can be further expressed with the generalized hypergeometric function as follows

$$P(K = k \mid m, x_i) = \left(\frac{m}{k}\right) B(\alpha_j, \beta_j) \int_0^1 \sqrt{tx_i}^k \left(1 - \sqrt{tx_i}\right)^{m-k} t^{\alpha_j-1}(1 - t)^{\beta_j-1} \, dt$$

$$= \left(\frac{m}{k}\right)^{x_i^{k/2}} B(\alpha_j, \beta_j) \left(\alpha_j + k \beta_j\right)_{3F_2} (\frac{k}{2}, \frac{m-k}{2}, \frac{1}{2} - \frac{m-k}{2}, \alpha_j + \beta_j + \frac{k}{2} x_i)$$

$$+ \left(\frac{m}{k}\right)^{x_i^{k/2}} B(\alpha_j, \beta_j) \sqrt{x_i(k-m)} B(\alpha_j + k + \frac{1}{2} \beta_j)_{3F_2} (\frac{k}{2}, \frac{1}{2} + \frac{1}{2}, \frac{1}{2} - \frac{m-k}{2}, 1 - \frac{m-k}{2}, \alpha_j + \beta_j + \frac{k}{2} x_i)$$

$$- \frac{m-k}{2} \frac{1}{2} + \alpha_j + \beta_j + \frac{k}{2} x_i. \quad (6)$$

The definition of the series $3F_2$ can be found in the Supplementary Material S1. The proofs of Lemma 1 and Equation (6) can be found in the Supplementary Material S2.
We therefore have two expressions for the likelihood,
\[
L\left(\vec{k}_1, \ldots, \vec{k}_n | \vec{d}, \vec{s}\right) = \prod_{i=1}^{n} \int_{0}^{1} \frac{1}{B(\alpha_i, \beta_i)} x_i^{\alpha_i-1} (1-x_i)^{\beta_i-1} \prod_{j=1}^{d_i} P\left(K_{ij} = k_{ij} | s_{ij}, x_i\right) \, dx_i
\]
\[
= \prod_{i=1}^{n} \int_{0}^{1} \frac{1}{B(\alpha_i, \beta_i)} x_i^{\alpha_i-1} (1-x_i)^{\beta_i-1} \prod_{j=1}^{d_i} P\left(K_{ij} = k_{ij} | s_{ij}, x_i\right) \, dx_i
\]
depending on the form chosen for \( P(K = k | s, x_i) \): the integral form or the form with the series \( _3F_2 \). Note that, in the likelihood \( L(\vec{k}_1, \ldots, \vec{k}_n | \vec{d}, \vec{s}) \), the parameters \((a_j, \beta_j)\) only comes in the probability \( P(K_{ij} = k_{ij} | s_{ij}, x_i) \) and \((a_t, \beta_t)\) in \( f_X(x_i) \).

### 2.2.2 Two types of dispositions for frequency data

We now consider the case with two different disposition distributions depending on position. In Section 2.2.1, we kept the indices for the sampled node, index \( i \), and its partners, index \( j \), to be able to assume different disposition distributions for the two positions.

Let \( n_g \) denote the number of sampled nodes who was of type \( g \) (giver) and let \( n_r \) denote the number who was of type \( r \) (receiver). Note that a sampled node can have been of both types. The \( n_r \) nodes had \( \vec{d}_r = (d_{r1}^i, \ldots, d_{r n_r}^i) \) number of partners with whom they were type \( r \). From a sampled node \( i \in \{1, \ldots, n_r\} \) and its partner number \( j \in \{1, \ldots, d_i^r\} \), the data consist of the number of condomless sex acts \( k_{ij}^r \) among their number of sex acts \( s_{ij}^r \) (where \( i \) is the receiver and \( j \) the giver). In the same manner as before, let \( \vec{s}^r = (s_{r1}^i, \ldots, s_{rn_r}^i) \), where \( s_{ri}^i = (s_{r1}^i, \ldots, s_{r d_i^r}^i) \). In addition, let \( \vec{t}_i = (k_{i1}^r, \ldots, k_{id_i^r}^r) \) for \( i = 1, \ldots, n_r \). Let the quantities for the \( n_g \) sampled nodes who were of type \( g \) be defined similarly, with the differences that we have \( g \) as superscript and that we denote the vector of the number of condomless sex acts by \( \vec{t}_i = (t_{i1}^g, \ldots, t_{id_i^g}^g) \) for \( i = 1, \ldots, n_g \).

By assuming independent dispositions in the two positions, the likelihood can be split into two parts
\[
L\left(\vec{k}_1, \ldots, \vec{k}_n, \vec{t}_1, \ldots, \vec{t}_{n_g} | \vec{d}_r, \vec{s}^r, \vec{d}_g, \vec{s}^g\right) = L_r\left(\vec{k}_1, \ldots, \vec{k}_n, \vec{t}_1, \ldots, \vec{t}_{n_g} | \vec{d}_r, \vec{s}^r\right) L_g\left(\vec{t}_1, \ldots, \vec{t}_{n_g} | \vec{d}_g, \vec{s}^g\right).
\] (7)

With different disposition distributions for type \( g \) and for type \( r \), a Beta distribution with parameters \((a_g, \beta_g)\) for type \( g \) and a Beta distribution with parameters \((a_r, \beta_r)\) for type \( r \), we have that
\[
L_r\left(\vec{k}_1, \ldots, \vec{k}_n, \vec{t}_1, \ldots, \vec{t}_{n_g} | \vec{d}_r, \vec{s}^r\right) = \prod_{i=1}^{n_r} \int_{0}^{1} \frac{1}{B(a_r, \beta_r)} x_r^{\alpha_r-1} (1-x_r)^{\beta_r-1} \prod_{j=1}^{d_i} P\left(K_{ij}^r = k_{ij}^r | s_{ij}^r, x_r\right) \, dx_r,
\] (8)
where \( P\left(K_{ij}^r = k_{ij}^r | s_{ij}^r, x_r\right) \) is equal to \( P\left(K_{ij} = k_{ij}^r | s_{ij}^r, x_r\right) \) with \((a_g, \beta_g)\) instead of \((a_j, \beta_j)\). And similarly,
\[
L_g\left(\vec{t}_1, \ldots, \vec{t}_{n_g} | \vec{d}_g, \vec{s}^g\right) = \prod_{i=1}^{n_g} \int_{0}^{1} \frac{1}{B(a_g, \beta_g)} x_g^{\alpha_g-1} (1-x_g)^{\beta_g-1} \prod_{j=1}^{d_i^g} P\left(K_{ij}^g = k_{ij}^g | s_{ij}^g, x_g\right) \, dx_g
\] (9)
where \( P \left( K_{ij}^g = \ell_{ij}^g | s_{ij}^g, x_g \right) \) is equal to \( P \left( K_{ij} = \ell_{ij}^g | s_{ij}^g, x_g \right) \) with \((\alpha_r, \beta_r)\) instead of \((\alpha_j, \beta_j)\).

For action dispositions in casual contact we created a model allowing one of the dispositions to weigh higher in the joint decision (Section 2.1.1) by defining

\[
P(\text{No condom}|x_g, x_r) = x_g^\gamma x_r^{1-\gamma}.
\]

This can also be implemented for frequency data by using the same kind of steps as in Lemma 1, but with the random variable \( Y = X_g^\gamma X_r^{1-\gamma} \).

3 | ANALYSIS

The models were implemented in R statistical software to find the maximum likelihood for each model. The models will be compared using likelihood-ratio tests when possible. Otherwise, we compare the models using AIC values (Akaike, 1974), where the model with the lowest AIC value fit the data best.

3.1 | Data

The MSM dataset used to demonstrate the developed models is originally from Sidebottom et al. (2019). This data were gathered at a gay-friendly STI/HIV-testing clinic in Stockholm, Sweden. Since the data were collected among a convenience sample of MSM visiting the clinic, it is not representative of all MSM in Sweden. The data consist of 403 MSM who visited the clinic between February 2 and December 15, 2015. Participants answered several demography questions concerning themselves, as well as details on their sexual history. The details on participants sexual history were gathered using a timeline follow-back (TLFB) method, which means that participants mark the timings of sexual partners on a timeline. Participants gave detailed information on their sexual partnerships the 12 months preceding their participation in the study. A casual sex partner was marked with a cross (at the date of sex) and a steady sex partner by the starting and ending times of the relationship.

To be included in this analysis, a participant must have reported having anal intercourse (AI) and additionally answered the questions concerning condom use. Two hundred and twenty-seven participants reported condom use behavior during AI with 692 casual sex partners and 190 participants reported condom use behavior during AI with 452 steady sex partners.

For casual sex partners, participants reported if they had receptive or insertive AI and whether or not a condom was used. Hence, for each casual sex partner, a participant could report two values. When not distinguishing between RAI and IAI (when considering AI aggregated), we define a non-condom sex partner as someone with whom you did not have consistent condom use with. For example, in a casual sex encounter when you were both the insertive and the receptive part sometime during the act, but a condom was only used when you were the receptive part, then this will be considered an unprotected casual sex encounter. Among all 692 casual sex partners with whom participants had AI, both RAI and IAI occurred with 87 of the partners.

The MSM data additionally include the number of sex acts with a steady sex partner. For each steady sex partner, participants reported the following: the number of receptive anal intercourses during a month and how often condom was used and the number of insertive anal intercourses
during a month and how often condom was used. Condom use was reported on a five-degree scale: always (100%), often (75%), half of the times (50%), seldom (25%), and never (0%). Therefore, we know (roughly) the number of acts during a month that were with and without a condom.

### 3.2 Results

The results of analyzing the MSM data are divided into two subsections. In Section 3.2.1, we focus on the binary disposition models suitable for casual sex partners and in Section 3.2.2, we focus on the frequency disposition models suitable for steady sex partners. For both types of relationships, we first test the homogeneous condom use assumption by using the aggregated AI data and comparing the homogeneous disposition model against the best fitted model not assuming homogeneous dispositions. Then we test if MSM have the same or different disposition distributions based on position at AI, for this test the data separating RAI and IAI are used and we compare the best fitted model assuming MSM have the same disposition distributions against the best fitted model assuming MSM have different disposition distributions. The results can be found in Table 1, where we show the maximum likelihood estimates, log-likelihoods, and corresponding AIC values at the MLEs.

#### 3.2.1 Binary outcome

We begin by testing our claim from the introduction, that condom use should not simply be modeled by assuming a fixed probability of condom use in each act. In Part 1 of Table 1, it is easily spotted that moving away from the homogeneous condom use greatly improves the model fit (either by comparing likelihoods or AIC values). Hence, the homogeneous assumption is not a good description of condom use behavior among this MSM population. The pro-con-neutral model fit the MSM casual data best, with roughly 40% being for condom use, 18% against, and 42% being neutral. The non-condom probability when two individuals of opposite dispositions meet is estimated to $\hat{\epsilon}_{CN} = 0.737$; therefore, if a couple consists of one individual for the use of condom and one against they will likely not use a condom.

In Part 2 of Table 1, we show the results for the disposition models where the positions the sampled individuals have with their partners are taken into account. The best fitted model assuming the disposition distributions are equal is shown in a and the best fitted model allowing for the non-condom disposition distributions to be different is shown in b. In doing a likelihood-ratio test between these models, we can reject model a in favor of model b ($p$-value .026). Hence, we make the conclusion that the non-condom disposition distributions are different when being the receiver and when being the giver during casual sex. When being the giver, 65% are for the use of condom, this in comparison to when being the receiver, then 85% are for the use of condom. Moreover, if two individuals with opposite dispositions meet and the receiver is against the use of condom, then no condom will be used with probability .95. This value can be compared with if the giver is against the use of condom, then no condom will be used with probability .73.

#### 3.2.2 Frequency outcome

The results for the models allowing for several outcomes generated by two connected nodes will be presented similar to the results for the binary case. First, we use the aggregated AI data and test
### TABLE 1  Fitted condom disposition models for the MSM casual relationship data when separating between insertive and receptive acts

#### Casual data

| Model                        | LogL  | AIC   | Parameter estimates |
|------------------------------|------|------|---------------------|
| 1. AI aggregated            |      |      |                     |
| a. Homogeneous              | $-340.72$ | 683.43 | 0.39 (0.019)         |
| $q$                          |      |      |                     |
| $\hat{p}_C$                  |      |      |                     |
| $\hat{p}_N$                  |      |      |                     |
| $\hat{p}_I$                  |      |      |                     |
| $\hat{\varepsilon}_{\text{CN}}$ |      |      |                     |
| b. Pro-con-neutral          | $-279.93$ | 565.85 | 0.40 (0.081) 0.18 (0.053) 0.42 (−) 0.74 (0.136) |
| 2. AI separated             |      |      |                     |
| Same dispositions            |      |      |                     |
| a. Pro-con                  | $-341.19$ | 686.37 | 0.75 (0.022) 0.25 (−) 0.81 (0.056) |
| $\hat{p}_C$                  |      |      |                     |
| $\hat{p}_N$                  |      |      |                     |
| $\hat{p}_I$                  |      |      |                     |
| $\hat{\varepsilon}_{\text{CN}}$ |      |      |                     |
| Different dispositions       |      |      |                     |
| b. Pro-con $\varepsilon_{\text{CN}}^{ab}$ | $-337.54$ | 683.08 | 0.65 (0.051) 0.85 (0.033) 0.35 (−) 0.15 (−) 0.95 (0.058) 0.73 (0.067) |
| Give                        |      |      |                     |
| Rec                         |      |      |                     |
| $\hat{\varepsilon}_{\text{CN}}^{gr}$ |      |      |                     |
| $\hat{\varepsilon}_{\text{CN}}^{rg}$ |      |      |                     |

#### Steady data

| Model                        | LogL  | AIC   | Parameter estimates |
|------------------------------|------|------|---------------------|
| 3. AI aggregated            |      |      |                     |
| a. Homogeneous              | $-954.72$ | 1911.44 | 0.52 (0.012)         |
| $q$                          |      |      |                     |
| $\hat{\alpha}$              |      |      |                     |
| $\hat{\beta}$               |      |      |                     |
| b. Beta geometric mean       | $-500.68$ | 1005.36 | 0.17 (0.003) 0.11 (0.004) |
| 4. AI separated             |      |      |                     |
| Same dispositions            |      |      |                     |
| a. Beta geometric mean       | $-574.46$ | 1152.92 | 0.22 (0.003) 0.14 (0.003) |
| $\hat{\alpha}$              |      |      |                     |
| $\hat{\beta}$               |      |      |                     |
| Different dispositions       |      |      |                     |
| b. Beta geometric mean       | $-574.15$ | 1156.19 | 0.21 (0.0077) 0.24 (0.0217) 0.14 (0.007) 0.13 (0.017) |
| $\hat{\alpha}_r$            |      |      |                     |
| $\hat{\alpha}_g$            |      |      |                     |
| $\hat{\beta}_r$             |      |      |                     |
| $\hat{\beta}_g$             |      |      |                     |

**Note:** The parameters for the two disposition distributions, for givers and receivers, are allowed to be different. The estimated standard errors are given in parenthesis below the point estimates. For the pro-con model we have that $p_C + p_N = 1$, and for the pro-con-neutral model that $p_C + p_N + p_I = 1$. Therefore, one less parameter needs to be estimated for these models and instead of the standard error for these parameters we have a parenthesis with a dash in it, (−).

**Abbreviations:** AIC, Akaike information criterion; LogL, log-likelihood; $\varepsilon_{\text{CN}}$, non-condom probability when a condom person meets a non-condom person; $\varepsilon_{\text{CN}}^{ab}$, non-condom probability when a type $i$ condom person meets a type $j$ non-condom person, where $a$ and $b \in \{g, r\}$; $p_C$, proportion of individuals for condom use; $p_N$, proportion against condom; $p_I$, proportion being neutral/indifferent; $q$, P(No condom).
the homogeneous disposition model against a nonhomogeneous disposition model. Then we use the data that separate insertive and receptive acts and compare the best fitted model assuming the disposition distributions to be the same in the two positions against the best fitted model assuming the disposition distributions to be different.

From Part 3 of Table 1 we see that, as in the case for the binary data, the homogeneous condom use model does not give a good fit in comparison to the alternative.

When we take into account the position of the sampled individuals and their partners (Part 4 of Table 1), in contrast to the casual binary outcomes, we cannot reject the null model that there is no difference in dispositions based on position (p-value .73).

4 | DISCUSSION AND CONCLUSIONS

The spread of an STI in a sexual network is regulated by both the infectious agent and sexual behaviors of individuals. When it comes to sexual behaviors, not only the structure of the network (such as the degree distribution) is of importance to understand the spread of an infection but also behaviors that could slow or stop transmission between two connected nodes. The focus of this article has been on (a) the action disposition distribution of nodes in a sexual network and (b) how the dispositions of two nodes connected by an edge generate a specific outcome; an outcome that could reduce the transmission probability through that edge. We have used different disposition distributions, created different models for how the dispositions of two connected nodes generate different outcomes, and have tested these models against each other using a dataset on sexual behavior of MSM.

The observed outcome in this article has been whether a condom was used in a sexual relationship. Two main models have been studied: One model where two sexual partners generate one binary outcome together (casual partners) and one model where two sexual partners generate several outcomes together (steady partners). In summary, for the binary outcome model we find that for MSM in Stockholm (a) we can reject the homogeneous condom use model; (b) there is a difference in condom dispositions depending on position with casual sex partners; and (c) a non-condom person's disposition seems to weigh higher in the decision on whether a condom is used. The MSM data additionally include details on the number of sex acts with steady sex partners, and therefore, the model for several outcomes by two connected nodes could be applied to this dataset. We find that the homogeneous condom use assumption can be rejected with steady sex partners, but we find no difference in disposition distribution between the two possible positions receiver and giver.

A heterosexual network consists of two types of nodes where different types connect to each other. In Hansson et al. (2018) the disposition distributions in a heterosexual network were studied. A same-sex network where individuals can take different positions is similar to a heterosexual network. The difference is that an individual is not fixed to either type but can change type. Here, we have expressed the problem in such a way that we allow individuals to change disposition depending on the type it is currently acting as.

For the MSM binary outcome data, we conclude that the non-condom disposition distributions are different when being the receiver and when being the giver. With a p-value of .026, we reject the model assuming the disposition distributions are the same in favor of the model allowing the disposition distributions to be different. When taking the position giver 65% are for the use of condom and 35% against. When taking the position receiver 85% are for the use of condom and 15% against. Hence, when taking the riskier position receiver, individuals have a tendency to
prefer the use of condom. These results suggest that, with casual sex partners, Swedish MSM engage in strategic positioning in combination with condom use. Strategic positioning is one behavioral intervention observed among MSM (Sullivan et al., 2012). In addition, when two individuals of opposite dispositions meet, where the receiver is against the use of condom, no condom will be used with a probability .95. On the other hand, if the giver is the one against the use of condom, no condom will be used with a probability .73. Thereby, there is a higher probability of no condom use when this is the preference of one of the sex partners. This finding may partly explain the rather low condom use levels reported by many studies among MSM (40%–60%) (Strömdahl et al., 2015). Condom use interventions targeting MSM would then need to aim for that both individuals in a sexual relationship are motivated to use condoms. Otherwise, if only one is motivated, this may not lead to the STI protective behavior of condom use at anal sex. Among heterosexual youth and penetrative vaginal sex, the trend was the opposite; there was a higher probability of condom use when this was the preference of one of the sex partners (Hansson et al., 2018). However, the estimated fraction of young heterosexuals being for the use of condom was much lower—only 3%.

For the MSM frequency data, the steady sex partner data, we found no difference in disposition distribution for the two positions. One possible explanation for this result is that within a steady partnership, the two actors may discuss past and future behaviors together and reach an agreement. This could lead to a joint convergence toward almost always using condom or almost never using condom. The parameter estimates for the disposition distribution support this possible explanation, a Beta distribution with shape parameters $\alpha = .24$ and $\beta = .14$ is pushed toward the limits 0 and 1.

The models were constructed to ease interpretation of both individual disposition and how to go from two dispositions to a probability of the action studied. A person completely for the action was coded as 0 and its opposite, someone completely against, as 1. One could have chosen the scale for the dispositions to be something else (e.g., $[0, \infty)$), but then it would be harder to interpret what opposite dispositions are. The simplest model used is the pro-con model (special case of the pro-con-neutral model with no one being neutral), where persons for the action always get their way ($\varepsilon_{CN} = 0$). Then the translation from disposition to probability of the action really is the product (or geometric mean) of the two possible dispositions 0 and 1. Therefore, with dispositions on $[0, 1]$, the geometric mean model is a continuous extension of the pro-con model. In the continuous extension we include, in contrast to the pro-con model, that both parties contribute to the probability of the action at hand.

There are several possible improvements that could be made to our models. First, we use the reported degree from participants as a known quantity, and we do not assume any model for how individuals choose their sexual partners. In creating a model for how individuals choose their partners, one could incorporate that individuals with a certain disposition behave differently in the number of sex partners they have or who they choose as a partner. Second, we use independent disposition distributions for when being the receiver and when being the giver. This is a simplification likely to be invalid in the real world, for example, given that an individual is for the use of condom as a receiver, this could likely increase the possibility that this individual is for the use of condom as a giver. Even though we assume this independence, we are able to test if the parameter values of the disposition distributions are the same or different, and finding them to be different for the binary data case. Future work could extend the models to include more dependencies between the dispositions. Third, for the model with several outcomes between two nodes, one could imagine that the probability of condom use likely would converge to either 0 or 1. That is, within a steady partnership, it could be that the couple comes to some agreement. One
way to incorporate this would be to let the probability of condom use depend on how long two individuals have been in a relationship with each other.

One future direction will in the following get particular attention. In the introduction, we argued that the way condom use is incorporated in models developed to study the spread of STIs, the homogeneous condom use, is too much of a simplification. We have here verified this statement for the Stockholm MSM data. To study the spread of an infectious disease, individuals are divided into different compartments representing infectious status (e.g., Hansson et al., 2019; Rönn et al., 2019; van Wees et al., 2018; Xiridou et al., 2003). Then a system of differential equations is set up, to symbolize in-flow and out-flow from the different compartments. This system is solved to obtain a steady-state prevalence. To incorporate the results from this study, one could divide individuals further according to condom disposition as well. In doing this, one could verify the effect of making the homogeneous condom use assumption on the spread of an STI.

Our study suggests that homogeneous condom use is not a good approximation of individuals condom use behavior. Models of the spread of STIs should instead incorporate condom use more similar to the pro-con model. Our findings additionally highlight that condom use interventions targeting MSM need to aim for both individuals in a sexual relationship. Finally, even though there is a high probability of a condom not being used when this is the preference of one of the sex partners, we find that MSM in Sweden visiting STI-clinics seem to prefer condom when taking the risker position receiver.

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**SUPPORTING INFORMATION**

Additional supporting information may be found online in the Supporting Information section at the end of this article.

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