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Methods and Measures for the Description of Epidemiologic Contact Networks

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ABSTRACT *This article describes new methods to characterize epidemiologic contact networks that involve links that are being dynamically formed and dissolved. The new social network measures are designed with an epidemiologic interpretation in mind. These methods are intended to capture dynamic aspects of networks related to their potential to spread infection. This differs from many social network measures that are based on static networks. The networks are formulated as transmission graphs (TGs), in which nodes represent relationships between two individuals and directed edges (links) represent the potential of an individual in one relationship to carry infection to an individual in another relationship. Network measures derived from transmission graphs include "source counts," which are defined as the number of prior relationships that could potentially transmit infection to a particular node or individual.*

KEYWORDS *Contact network, Mathematical models, Network measures.*

INTRODUCTION

Most of the literature in epidemiology that analyzes contact network data employs concepts from social network analysis based on static graphs.[1–7] This paper presents new methods for constructing dynamic graphs designed to reflect the potential of a network to transmit infection. These methods construct what we call *transmission graphs* (TGs). In TGs, the nodes represent a pair of individuals who are associated in a fashion that permits the transmission of infection between them. The directed edges of the graph represent the potential for one individual in a nodal pair to carry infection to another nodal pair in which the individual is involved.

We propose the use of "source counts" derived from TGs as elements for network measures at the individual and population levels. Source counts summarize the potential for the transmission of infection from prior or concurrent relationships and individuals to a particular relationship or individual. Aspects of individual source counts have the potential to provide summary measures of the overall network or characteristic neighborhoods of the network that reflect the potential for epidemic transmission or to sustain endemic infection.

The article is organized as follows: In the first section, we discuss the effect of contact patterns on epidemiologic population effects and the need to develop network measures that reflect the influence of contact patterns on infection transmission. In the second section, we lay out the formulation of two specific types of TGs:

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cumulative transmission graphs (CTGs) and interval transmission graphs (ITGs). The third section demonstrates the methods used to calculate source counts from TGs. In the fourth section, we present an example and discussion of the use of source counts using data generated from GERMS software. GERMS simulates the stochastic spread of infection in populations of discrete individuals that have heterogeneous mixing patterns and potentially different susceptibility to infection and contagiousness.[8] We also discuss directions for future work.

BACKGROUND AND RATIONALE

From a social network analysis perspective, the "distance" between two individuals is not merely a function of the physical distance between them, but also of the "social distance."[9] These social factors are important determinants of the structure of contact networks. The importance of patterns of contact networks in epidemiology has been shown by a number of authors.[4–7,10–16] The epidemiologic modeling literature indicates that the specific structure of the network of concurrent relationships is related to the magnitude of the spread of an infectious agent.[4–7,14,17] There are a number of papers that suggest that network-oriented survey design is essential to designing effective intervention strategies for some infectious diseases, especially sexually transmitted diseases.[18,19] There may be many infectious and chronic disease processes for which a social network approach will lead to insights regarding causality and intervention. Most authors who integrate social network analysis and epidemiology have done so in the context of sexual relationships among individuals when investigating sexually transmitted diseases and have applied social network analysis measures to these epidemiologic networks.[20–22] Despite the potential of social network analysis in the study of infectious disease transmission, little theoretical work was undertaken until the acquired immunodeficiency syndrome (AIDS) epidemic in the 1980s.[23]

In the last 10 years, there have been a number of investigators who have attempted to adapt social network measures to epidemiologic investigations.[5,24,25] These sociometric network measures capture strong determinants of population infection levels that are missed by individual risk factor measurements.[4,26] Contact tracing to define individual networks has been performed,[20,27,28] as have population surveys and the estimation of partnership rates for different types of individuals.[29]

Morris and Kretzschmar[5,6] have made a major advance by defining network measures related to partnership concurrency; some of these measures can be calculated using egocentric data. Because these measures do not consider relationships of current links to past links and because important determinants of population infection occur at the sociometric level that are not captured by the ego-centered data, these measures will still miss many determinants of infection. Much remains unknown regarding the influence that the conformation of a transmission network has on epidemic dynamics, specifically the relationship between contact patterns at different levels and their effect on the rate of change of epidemiologic outcome variables such as the endemic level of the infection and initial rate of epidemic rise. Contact networks are not static; they change through time. To capture important aspects of these continually changing networks, this article presents methods to describe dynamic networks and suggests summary measures for the description of these networks. To study transmission networks, it is important that measures of network conformation be developed that are epidemiologically interpretable and therefore relevant to epidemiologic theory.

We are developing sociometric network measures in which relationships between individuals, rather than individuals themselves, constitute the nodes of the network graph.[5] Directed links between these partnership nodes are defined when one individual is common to two nodes (partnerships) and the timing of formation and dissolution of those two relationships meet specified criteria chosen to reflect the potential for infection transmission.

TRANSMISSION GRAPH FORMULATION

The TGs are intended to represent epidemiologically meaningful paths through a network of contacts through time. TGs are constructed from individual contact data using a set of timing rules. Relationships between two individuals constitute the nodes of the TG. TGs are directed node graphs, also called *digraphs*, that have a specific epidemiologic interpretation. The essential properties of TG are that they consider temporal properties of disease transmission. TG incorporates some of the dynamic aspects of contact networks relevant to infection transmission. In this section, we discuss two specific TG formulations. The first is an ITG, and the second is the CTG.

Cumulative Transmission Graphs

The sociometric data needed for the formulation of a CTG includes (1) when a relationship began and ended, (2) which members constitute the relationship, and (3) the length of time corresponding to the sum of the incubation period and the duration of contiguousness. For example, in the case of gonorrhea, the first two data elements could be obtained either from contact histories obtained from an entire population or from contact tracing beginning with a representative sample of the population of interest. The incubation period would have to be obtained from the literature.[30] The major use of the work presented in this paper, however, is in advancing theory rather than in advancing the analysis of such data. Specifically, we plan to use our methods to understand better the behavior of infection transmission systems, utilizing simulations such as the one presented below. The algorithm for constructing the TG from the data is as follows:

> Define Tb_i as the beginning time of a relationship i, Te_i as the ending time of a relationship i, and δ as a fixed period with a length equal to the combined incubation period and duration of contagiousness.
>
> Given (1) the two relationships i and j share at least one member, (2) $Tb_j < \{Te_i + \delta\}$, and (3) $Tb_i < Te_j$.
>
> Then, relationship i has a directed link to relationship j.

All TG are "dynamic" in the sense that they capture something of the dynamics of the formation and dissolution of relationships of a population of individuals over time, resulting in a directed network of contacts. If we reduce δ to 0, then we are left only with bidirectional arrows representing temporally concurrent relationships identical to the graphs defined by Morris and Kretzschmar.[5]

To illustrate, the data might appear as follows in Table 1. The data are outlined in the table such that relationship 1 has individuals A and B as members, and the relationship starts at time 1 and ends at time 10. Relationship 6 has members A and E and a start time of 20 and ends at time 40. Compare the graphs in Fig. 1; as time increases, the cumulative graph becomes larger (or, in some cases, remains the same). The CTG represents all infection transmission potential up to a specified

TABLE 1. Data needed for a cumulative transmission graph

Relationship#	Members	Time 1111111111222222222233333333334444444444 5 1234567890123456789012345678901234567890123456789 0
1	A, B	|----------|
2	A, C	|--------|
3	B, C	|----------|
4	C, F	|--|
5	A, B	|----------
6	A, E	|----------|
7	D, G	|---|
8	D, E	|----------|
9	E, G	|-|

This table represents data where the relationship ID is listed in the first column. The IDs of the constituent member individuals are listed in the second column. The times that the relationsips are active are represented in the last column; time runs from 1 to 50 units.

time T. The *in-degree* of a node is the number of links that end at (point toward) the node. Similarly, the *out-degree* of a node is the number of links that start at (emanate from) the node. The sum of the in-degree and out-degree is the degree of the node.

The selection of δ for the formulation of a TG is essential to the interpretation of the graph and measures derived from the graph. The δ parameter represents a time interval equal to the combined incubation and duration of contagiousness of a particular disease. As defined above, the δ parameter overestimates infection transmission potential. The length and definition of this parameter could be modified, and this should be considered when interpreting measures extracted from TGs.

CTGs have some strengths and limitations. The major strength is also one of the main limitations: CTGs represent a continuous record of potential infection transmission. The number of links increases over time in CTGs. This tendency results from the fact that links are added and never removed. This means that the longer the time span represented by the cumulative graph, the greater the computational problem, and the harder it is to interpret measures derived from the graph. There is also a scaling problem when computing source counts on CTGs. Nodal source counts represent the number of nodes in the graph that could potentially

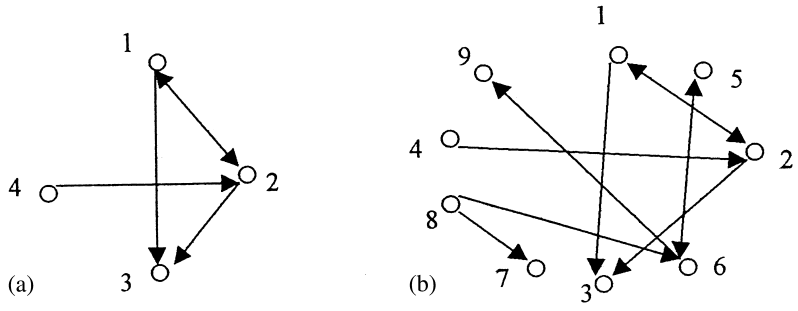

FIGURE 1. Graph 1a is a CTG representation of the data in Table 1 at time $T = 14$ with $\delta = 5$. Graph 1b is a CTG representation of the data in Table 1 at time $T = 50$ with $\delta = 5$.

transmit infection to a particular node, and an individual source count is the number of nodes that could potentially transmit infection to a particular individual. This means that CTGs that represent a long span of time will tend to have larger nodal and individual source counts than cumulative graphs that represent shorter time spans given the network conformation characteristics. In addition, relationships (nodes) that are "closer" to a particular relationship (node) are more likely to transmit infection forward to that relationship than relationships that are farther away. One way to address this issue is to weight the links to reflect this probability gradient. Alternatively, we can remove or "drop" links that are less relevant in terms of infection transmission. The dropping of links can also be used to address the scaling problem with cumulative graphs.

Interval Transmission Graphs

The difference between CTGs and ITGs is that cumulative graphs add nodes and links that are never removed, while interval graphs both add and remove nodes and links. The computation of the ITG allows comparisons to be made between two different networks, as well as the same network at different times.

The algorithm for the construction of an ITG is identical to that for the CTG outlined above with the addition of a rule for removing links and nodes. There is an additional parameter ω, which regulates the dissolution of links and nodes in the dynamic graph. In this article, we used $\delta = \omega$, although in general, it may be useful to consider different values of ω. The additional rule for the formation of an ITG is as follows: The in-degree links to a node n_k are dissolved at time $Te_k + \omega$. All links must be removed from the in-degree node. Nodes are removed from the ITG when all links (in-degree and out-degree) are removed.

Using this new rule, let us examine two examples of the formation of ITGs using the interval timing rule for the data in Table 1. Graphs 1a and 2a represent the CTG and the ITG representation at time 14, respectively. A comparison of graphs 2a and 2b in Fig. 2 reflects that there is more relationship activity at time 14 than at time 50 and reflects the dynamic nature of these TGs. The difference in the node and link density between the cumulative and interval graphs at time 50 is demonstrated in graphs 1b and 2b. The ITG more accurately reflects the infection transmission potential than the cumulative graph at time 50.

Consider a node k, which is far "down chain" from a node of interest, and a node j, which is only a few links down chain from the node of interest. Node k has

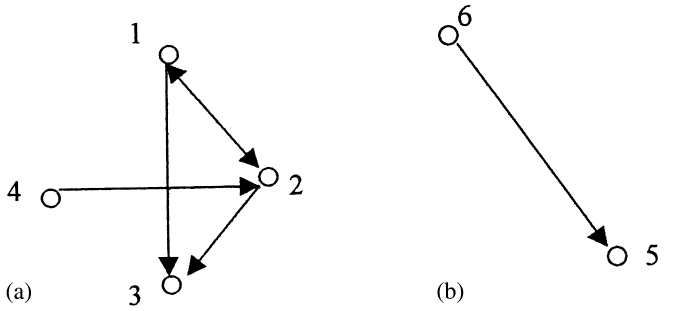

FIGURE 2. Graph 2a is the ITG representation at time $T = 14$ derived with $\delta = \omega$. Graph 2b is the ITG representation at time $T = 50$ derived with $\delta = \omega$ of 5.

a much smaller probability of actually infecting the node of interest compared to node *j*, which is closer. There are many weighting schemes possible, but the elimination of distant, less-relevant nodes and links has the advantage that it solves the scaling problem produced when CTGs representing time intervals of different lengths are examined.

CALCULATION OF SOURCE COUNTS FROM TRANSMISSION GRAPHS

From the TG, it is possible to construct a source count for each relationship, as well as for individuals who comprise these relationships. The *source count* is the number of previous partnerships that could have originated a chain of infection that could reach the partnership of concern. The method used to calculate the source counts depends on the data structure used to represent the TG.

Computing Relationship Source Counts

An adjacency matrix is a representation of a TG of size n and is an $n \times n$ matrix $\mathbf{X}$. A 1 appearing in the ith column and the jth row of an adjacency matrix signifies that node i can be reached by node j using one link (note that $\mathbf{X}^1 = \mathbf{X}$). Therefore, the two nodes are adjacent. The in-degree of node n_i can be found by computing the sum of the ith column (and the out-degree is found by computing the sum of the ith row) of an adjacency matrix $\mathbf{X}$.

To determine the nodes that are reachable using two links, the matrix $\mathbf{X}^2$ is examined similarly. The nodes that are reachable in m links are represented by the product matrix $\mathbf{X}^m$. The summation matrix $\mathbf{P}$ is the sum of these product matrices, $\mathbf{P} = \sum_{k=1}^{m} \mathbf{X}^k$ represents all of the possible paths between any two nodes. The integer m is the number of terms in the sum above that forms the matrix $\mathbf{P}$ and is never larger than 1 less than the order of the adjacency matrix $\mathbf{X}$. Note that the order of an adjacency matrix $\mathbf{X}$ is the number of nodes in the TG. Since we do not want to allow any node to have the potential to infect itself, there should be only zero elements on the diagonal of $\mathbf{P}$. Therefore, transform $\mathbf{P}$ by replacing all nonzero elements in the diagonal with 0. In addition, when calculating source counts, we are only interested in the number of *distinct* nodes that can reach a particular node. Both the number of nodes (relationships) that can potentially transmit infection forward to a particular node and the number of paths of potential infection transmission influence the risk of infection to a particular relationship. We feel that the number of paths of potential infection transmission is a measure of the "robustness" of the risk of infection to a relationship (node). If we do not wish to consider the number of paths that exist, only that there exists a path, we must transform the summation matrix such that the matrix $\mathbf{P}$ has no entries greater than 1. The transformations described above are combined below and summarized as a single transformation T.

Define a transformation T on a matrix $\mathbf{P}$: For $x_{ij} \in \mathbf{P}$ and $y_{ij} \in T(\mathbf{P})$, where $i \neq j$, $y_{ij} = 1$, if $x_{ij} \geq 1$, $y_{ij} = 0$ otherwise, where $i = j$, $y_{ij} = 0$.

Now, to define the reachability matrix $\mathbf{R}$ in terms of the summation matrix $\mathbf{P}$, apply the transformation described above, $\mathbf{R} = T(\mathbf{P})$. The reachability matrix $\mathbf{R}$ is an $n \times n$ matrix for which, if there is a 1 in the r_{ij} entry of the reachability matrix, then there is at least one path from the n_i node to the n_j node. Likewise, if there is a 0 in the r_{ij} entry of the reachability matrix $\mathbf{R}$, then there is no path from the n_i

node to the n_j node. Therefore, the source count of node i is exactly the sum of the ith column of the reachability matrix **R**. Consider the adjacency matrix representation of the digraph 1a in Fig. 1:

$$\mathbf{X} = \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix} \Rightarrow \mathbf{X}^2 = \begin{pmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 \end{pmatrix} \Rightarrow \mathbf{X}^3 = \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \end{pmatrix}$$

$$\therefore \mathbf{P} = \mathbf{X} + \mathbf{X}^2 + \mathbf{X}^3 = \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix} + \begin{pmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 \end{pmatrix} + \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \end{pmatrix} = \begin{pmatrix} 1 & 2 & 3 & 0 \\ 2 & 1 & 3 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 2 & 2 & 0 \end{pmatrix}$$

Now, transform **P** to **R** using the transformation $T(\mathbf{P})$, defined above,

$$\mathbf{R} = \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 1 & 1 & 0 \end{pmatrix}$$

The column sums (source counts) of the reachability matrix **R** are

$n_1 = 0 + 1 + 0 + 1 = 2$, $n_2 = 1 + 0 + 0 + 1 = 2$, $n_3 = 1 + 1 + 0 + 1 = 3$, $n_4 = 0 + 0 + 0 + 0 = 0$

Note that the matrix **P** reflects the number of paths between specified nodes, and the column sums represent the number of paths from the ancestors of a node to the particular node. While the column sums of the transformed matrix **R** specifies the number of distinct ancestors. This method works with any matrix representation of a graph whether the relation is directional or nondirectional. With slight modification, it also works for disconnected graphs. There are other efficient methods for the calculation of source counts, such as the Floyd-Warshall algorithm.[31]. The computer code for the construction of the CTG and ITG from the individual contact data (GERMS output) and the extraction of the node source counts was written in the C programming language and is available via the internet.[32]

Any partnership or individual characteristic can be used to specify source counts. For example, the source counts for sexual partnerships formed in one setting that may transmit gonorrhea could be specified. This would help establish the risk of partnerships formed in different settings. Alternatively, the number of source partnerships involving a specific type of individual could be used to derive the source partnerships for a class of individuals. For example, in any attempt to perceive immunity effects for gonorrhea, source counts for individuals with different past histories of infection could be used to control for exposure effects.

Computing Individual Source Counts

To compute the individual source counts, the nodal source count is added for each of the nodes that have the particular individual as a member. In this case, individual source counts are interpreted as the number of prior relationships that have the potential to transmit infection forward to a specified individual. Other statistics such as the mean, maximum, or other distribution information of the nodal source counts in some circumstances may prove to be more informative when computing individual counts.

Nodal progenitor counts represent the number of relationships that a particular node could potentially infect. Progenitor counts are defined analogous to source counts, but temporally reversed. Interactions between nonadjacent nodes (relationships) can be influenced by individuals in relationships that lie in the path between other nodes. The shortest path between two nodes is called a *geodesic*. A relationship (node) that lies on the geodesic between many other nodes has a large "betweenness" centrality.[9] Betweenness measures can be calculated for both nodes and individuals involved in ITGs using both source and progenitor counts.

EXAMPLE OF SOURCE COUNT USE AND CONCLUSIONS

The network data used in this work were generated by GERMS,[8] a microsimulation of individuals that enter into population contact processes. GERMS tracks and maintains the infection history, personal attributes, and relationships between individuals during which infection can be transmitted. This allows the reconstruction of the contact network and the transmission of infection through the population.[33]

In this section, we present data from GERMS based on gonorrhea transmission; we use it to demonstrate some early applications of source counts on data that illustrates the effect of mixing pattern on infection transmission at the population level. The results of a simulation are shown in Fig. 3. The parameter settings used to represent the differences between high-risk and low-risk groups are presented in Table 2. There are 10 individuals in the high-risk group and 50 individuals in the low-risk group.

The only difference between the runs is the mixing pattern. The prevalence is plotted versus time in days for three different mixing patterns: assortative, proportional, and disassortative. With proportional mixing, the high-risk individuals are equally available to mix with other high-risk individuals and the low risk individuals. Under assortative mixing, the high-risk individuals are almost exclusively available to form relationships with other high-risk individuals. Under disassortative mixing, high-risk individuals are almost exclusively available to form relationships with low-risk individuals and vice versa.

The individual source counts calculated on an ITG at times 180, 360, and 720

TABLE 2. Difference between parameter settings of high- and low-risk individuals

Parameter	High risk	Low risk
Contact rate	1 per 2 days	1 per 7 days
Relationship duration	7 days	90 days
Concurrency	High degree of concurrency	Monogamous

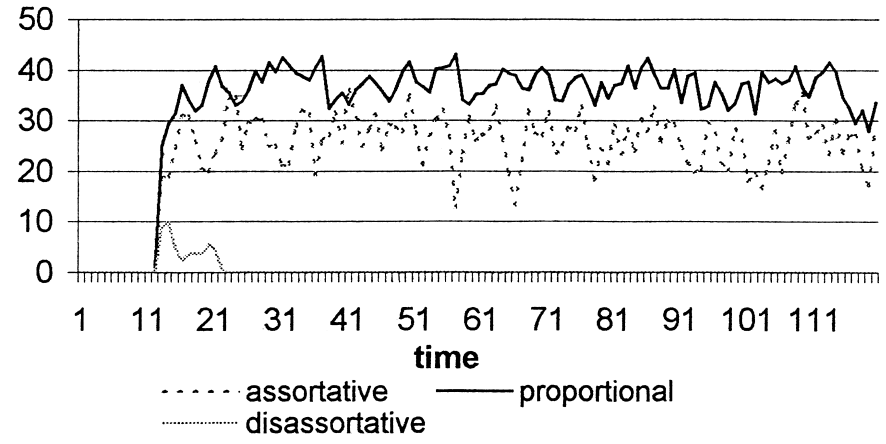

FIGURE 3. The effect of mixing on prevalence. Proportional mixing results in the highest endemic level, followed by assortative and disassortative mixing in descending order.

days for the proportional mixing example from Fig. 3 are shown in Fig. 4. Individual source counts represent the number of prior relationships that have the potential to transmit infection forward to the relationships that contain the specific individual as a constituent member. That is, individual source counts are the number of prior relationships that have the potential to transmit infection forward to the specific individual. Figure 4 shows that, while the source count for each individual changes over time, the overall qualitative structure of the plot remains constant over time. The fact that the plots remain qualitatively constant demonstrates that the simulation that generated the network data was at equilibrium before time 180. The differences between these plots in Fig. 4 are due to stochastic variation of the simulation.

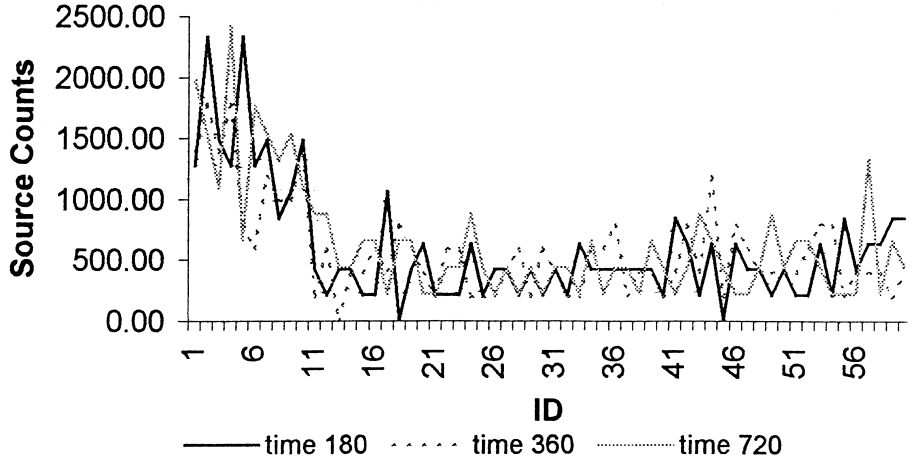

FIGURE 4. Individual source counts for a dynamic graph calculated at times 180, 360, and 720 days for the proportional mixing data. Individual source counts are shown on the *y* axis, and the individual IDs are on the *x* axis. IDs 1–10 correspond to the high-risk individuals, and IDs 11–60 correspond to the low-risk individuals.

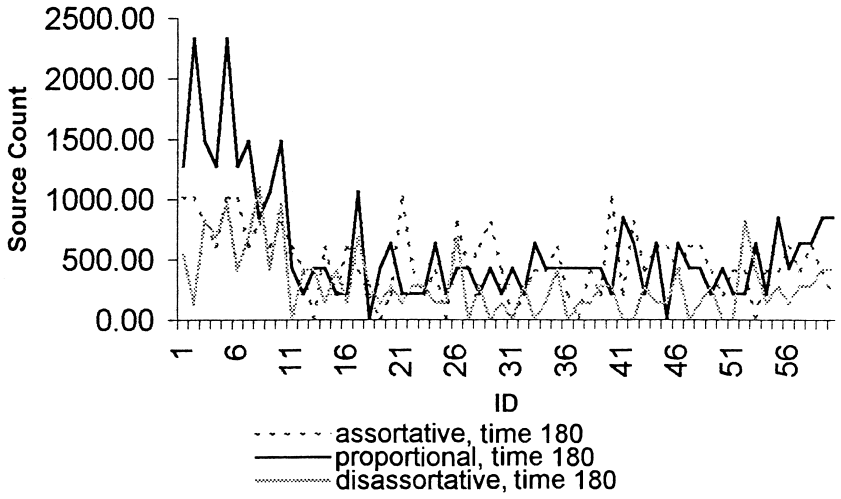

FIGURE 5. Individual source counts for the three different mixing patterns calculated at time 180. The individual IDs are plotted on the *x* axis and the source counts on the *y* axis. IDs 1–10 are the high-risk individuals, and IDs 11–60 are the low-risk individuals.

The individual source counts were calculated at time 180 for each of the mixing patterns and are plotted in Fig. 5. These plots show that the individual source counts for the high-risk individuals vary substantially for the different mixing patterns. Notice that for the assortative mixing case, many low-risk individuals have source counts similar to those of the high-risk individuals. More information is needed regarding the network conformation to explain this feature of the graph. For example, are the source counts for the low-risk individuals derived from long chains of transmission? Are the high-risk individual source counts derived from high-density clusters, some of which may be loosely connected? We are working on network measures that reflect aspects of network conformation such as betweenness, other aspects of centrality, and component number and size. In addition, the fact that so many individuals under disassortative mixing have source counts of 0 in Fig. 5 may account for the fact that infection dies out under this mixing pattern.

CONCLUSIONS

This article is an introduction to methods for modeling epidemiologic contact networks. We feel that these methods will be useful in modeling many infectious processes. These transmission graphs can be modified to represent different modes of transmission of infections. For example, in the case of waterborne Cryptosporidia, there could be two types of links. The first, links that represent transmission potential between individuals, could transmit infection in either direction. The second type of link could only transmit infection in one direction, from the water contaminator to the water consumer. Graph formulations are also possible that would involve relationships between an individual and an epidemiologic vector.

This work lays foundations for future work. Future work related to sampling techniques such as "snowball" sampling and missing data analysis may enable the estimation of these networks in real-world situations. Our plans for future work include the development of additional network measures based on TGs, such as

centrality and betweenness measures. We plan to use these measures to elucidate the relationship between model parameters and epidemiologic outcome measures. We also plan to use these measures to demonstrate the relationship between local or neighborhood network structure and the overall population dynamics. We feel that dynamic transmission graphs that have an epidemiologic interpretation and the measures derived from them will be useful to understand the effect of contact relationships on infection transmission dynamics.

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