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A stochastic agent-based model of pathogen propagation in dynamic multi-relational social networks

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Abstract

We describe a general framework for modeling and stochastic simulation of epidemics in realistic dynamic social networks, which incorporates heterogeneity in the types of individuals, types of interconnecting risk-bearing relationships, and types of pathogens transmitted across them. Dynamism is supported through arrival and departure processes, continuous restructuring of risk relationships, and changes to pathogen infectiousness, as mandated by natural history; dynamism is regulated through constraints on the *local agency* of individual nodes and their risk behaviors, while simulation trajectories are validated using system-wide metrics. To illustrate its utility, we present a case study that applies the proposed framework towards a simulation of HIV in artificial networks of intravenous drug users (IDUs) modeled using data collected in the Social Factors for HIV Risk survey.

Keywords

Agent-based systems, system dynamics, modeling and simulation environments, Social Factors for HIV Risk, risk network, network-based simulation

1 Introduction

Modeling the propagation of pathogens through risk-bearing interactions of actors in a social network is an emerging perspective in epidemiology, particularly in HIV research.[1–3] Approaches such as these shift our view of risk away from individuals to collective social bodies as the carriers and transmitters of infection. The subject of study here then is ''risk networks'', comprised of populations whose social interconnections signify particular ''risk behaviors'' that bear a potential for pathogen transmission. In the context of HIV, some examples of risk behaviors include social relationships which result in drug injection equipment sharing, and sexual relationships in the context of drug use. Although HIV will be used as a case study, the model presented in this paper is general enough to be applied towards the simulation of any epidemiological scenario in which disease transmission is driven by pairwise risk behaviors across a specifiable set of relationship types. Risk networks are now widely recognized as critical factors in understanding infection patterns, as they define the natural environment in which risk behaviors occur, and through which the propagation of infection proceeds.[4,5] The value of network-based simulation then, is that it can make the dynamic structures of risk visible and compelling,[6] and help further a change in perspective to one that sees collectivities (and their respective forms and dynamics) as health actors with specific and identifiable structures of risk.

For reasons of cost, most risk network studies are relatively small in scale compared to the size of the overall communities they seek to understand. Even large-scale network studies manage to interview only a small portion of the ambient risk network; e.g. the study of Social Factors for HIV Risk (SFHR) conducted in Brooklyn, New York, in the early 1990s involved interviews with several hundred people[7] out of the 30,000–80,000 intravenous drug users (IDUs) in Brooklyn at the time. In contrast, simulation allows researchers to operate at the scale of the phenomenon of interest. While simulation is necessarily far from perfect and not a substitute for direct research, when based on detailed data and constructed to conform closely to known,

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Table 17. DegreeBinned bivariate $\bar{\bar{\chi}}$.

$\bar{\bar{\chi}}$	[0–2)	[2–4)	[4–10)	[10–20)
[0–2)	77/158	37/158	29/158	15/158
[2–4)	57/203	77/203	40/203	29/203
[4–10)	42/195	50/195	64/195	39/195
[10–20)	15/100	23/100	31/100	31/100

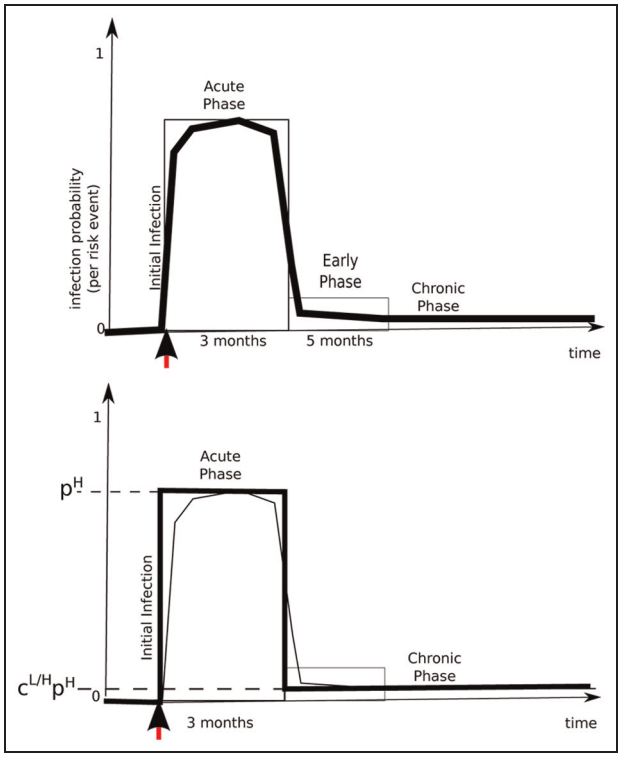

Figure 4. (*Top*) Infectiousness of HIV as a function of age of infection; (*bottom*) a simplified two-parameter representation.

reflect a network wherein risk partners are held as such for an average of 5 years. Justification for this includes the fact that 53 percent of the network noted that they had known *all* of their network for at least a year, and 43 percent of the network felt ''very close'' to some or all of their network.[7:p.130] Ethnographic reports from the SFHR network note considerable longevity to risk partnerships (see also Friedman, Chapter 3).[7,52] Here again, where wide variation in individual characteristics were obtained, we set the **churn interval standard deviation** $\sigma_C = 3.0$ years to ensure that actors chose their individual churn behavior from a distribution that allowed for rapid turn overs of less than 2 years (for their entire personal network) to long-term partnerships (of 8 years or more). It was later discovered that the changes to μ_C and σ_C had little effect on the simulation outcomes with respect to asymptotic HIV rates.

The **degree stability bias** w_S determined how closely individual nodes maintained their degree over the course of their participation in the network. On the whole, the justification for a fixed degree comes from prior work on drug scene ''roles''. [51,52] While, obviously, no direct parameter settings can be drawn from the data described by Friedman et al. and Curtis et al., the function used to determine the effects of the parameter, and the original parameter setting of 2.9 was designed such that variations from initial degree by roughly 30% were very likely to be corrected. It was discovered that the changes to w_S had little effect on the simulation outcomes with respect to asymptotic HIV rates.

The macroscopic population process **growth rate** $r_P = 0$ was set thereby specifying a constant population size, although certainly individuals were leaving and entering throughout (see below).

While a number of individuals in the SFHR study had few partners, or would be considered marginal members of the network itself, there is also a wealth of ethnographic reports on very short-term visitors to the network.[51,52] As far as we know, no solid estimates of the proportion of these transient participants is given, nor would we expect the number to be uniform across sub-networks in New York City. A ''drug market'' zone like that studied by the SFHR project is likely to have a greater proportion of transient members than a smaller, less public network. We took the **fraction of individuals that are ''transient''** $f_{tr} = 0$, as a base-line in the simulations here.

As with network churn, a dearth of diachronic data meant that we relied heavily for these parameter settings on ethnographic observation and the experience of project co-authors in the SFHR network. While many of the SFHR network members had been injectors for longer than 9 years, this does not mean that they participated in the same IDU network for that entire time. For this reason, the settings were made identical to the churn settings above, **mean duration of steadies' lifetimes** $\mu_{st} = 5.0$ years, and **standard deviation of steadies' lifetimes** $\sigma_{st} = 3.0$ years, so that participation varied widely from 2–8 years for ''steady'' participants.