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Modeling a dynamic bi-layer contact network of injection drug users and the spread of blood-borne infections

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ABSTRACT

Injection drug users (IDUs) are at high risk of acquiring and spreading various blood-borne infections including human immunodeficiency virus (HIV), hepatitis C virus (HCV), hepatitis B virus (HBV) and a number of sexually transmitted infections. These infections can spread among IDUs via risky sexual and needle-sharing contacts. To accurately model the spread of such contagions among IDUs, we build a bi-layer network that captures both types of risky contacts. We present methodology for inferring important model parameters, such as those governing network structure and dynamics, from readily available data sources (e.g., epidemiological surveys). Such a model can be used to evaluate the efficacy of various programs that aim to combat drug addiction and contain blood-borne diseases among IDUs. The model is especially useful for evaluating interventions that exploit the structure of the contact network. To illustrate, we instantiate a network model with data collected by a needle and syringe program in Chicago. We model sexual and needle-sharing contacts and the consequent spread of HIV and HCV. We use the model to evaluate the potential effects of a peer education (PE) program under different targeting strategies. We show that a targeted PE program would avert significantly more HIV and HCV infections than an untargeted program, highlighting the importance of reaching individuals who are centrally located in contact networks when instituting prevention programs.

1. Introduction

Many injecting drug using populations experience high prevalence of communicable diseases that are spread via risky injection practices and risky sexual contacts [1,2]. These include human immunodeficiency virus (HIV), hepatitis C virus (HCV), hepatitis B virus (HBV) and a number of sexually transmitted infections (STIs). Such diseases lead to significant morbidity and mortality – and subsequent health care costs – among injection drug users (IDUs). Controlling these diseases among IDUs is a key public health priority [3,4].

A variety of harm reduction measures aim to limit the spread of blood-borne diseases among IDUs [5]. These measures include infection screening and treatment, needle exchange programs, opioid replacement therapy and peer education programs. However, funds for such programs are limited. Thus, it is important to evaluate the effectiveness and cost-effectiveness of these interventions so as to maximize the health impact of available resources.

Compartmental models are frequently used to evaluate the cost-effectiveness of disease control interventions (e.g., [6]). Such models divide the population into compartments corresponding to various combinations of infection status, awareness and treatment status. A key limitation of compartmental models is the assumption of homogeneous mixing, which is not likely to be the case for an IDU population [7].

Individual-based models such as network models do not require the assumption of homogeneous mixing. Such models simulate the transmission and progression of communicable diseases on an individual basis, and thus can capture features of the underlying contact network as well as biological and behavioral heterogeneity. Individual-based models are thus well suited for assessing the effects of disease control efforts that exploit the underlying contact network. For example, efforts to curb the spread of HIV by reducing risky injection practices may have the greatest impact on reducing HIV spread if they are targeted to drug injectors who are centrally located in needle-sharing networks [8–10].

However, determining the underlying contact networks in even the smallest populations can be complicated by a variety of factors. First, determination of actual network structure requires knowledge of every relationship between individuals – a time-consuming

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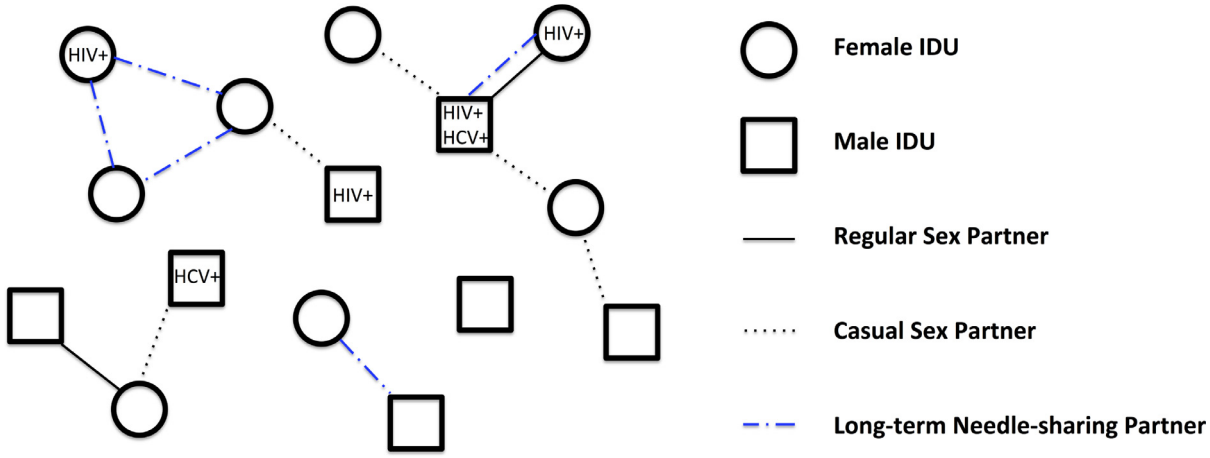

Fig. 1. Model schematic. We consider a population of male and female IDUs. At each time step $t = 1, 2, \ldots$ individuals can join or leave the population through initiating or abstaining from injection drug use. Each IDU can be associated with a number of characteristics including gender, age, disease status, disease awareness and treatment status, and drug abuse treatment status. We consider heterosexual and needle-sharing relationships, and one or more diseases (e.g., HIV, HCV) being spread via risky sexual and/or needle-sharing contacts. We distinguish two types of sexual partnerships: regular and casual partnerships. We distinguish two types of needle-sharing relationships: long-term needle-sharing and one-time needle-sharing (not represented in the risk network). We allow relationships to dissolve and form dynamically; thus the disease(s) can spread to any individuals who ever engage in risky behaviors.

task. Second, individuals may not recall all of their contacts and, even if they do, may not want to report them. Third, relationships do not remain steady: contact networks are constantly reshaping and it is impractical to monitor their dynamics over time. For these reasons, researchers typically simulate the structure and evolution of contact networks [11,12].

A number of network models have been introduced to model epidemics among IDUs (e.g., [13–16]). For example, one study developed a model based on an empirical network of 258 IDUs in Melbourne, Australia [16]. The sample size was small due to the difficulty in contact tracing. The authors employed a static network, and thus only reported numerical results over one simulated year. These and other published network models of IDU populations consider only needle-sharing as the route of disease transmission, and do not consider sexual transmission of disease. However, sexual transmission of diseases among IDUs may be significant, so existing models may inaccurately estimate the effects of programs that aim to control blood-borne disease among IDUs.

In this paper we introduce a bi-layer network model that captures both sexual and needle-sharing contacts (Fig. 1). We present methodology for inferring important parameters, such as those governing network structure and dynamics, from readily available data. Using this model, we can simulate the spread of one or more diseases among IDUs and evaluate the efficacy of different drug abuse and disease control interventions. We provide an illustrative example of HIV and HCV transmission among IDUs in a representative US urban center, and we estimate the relative effectiveness of peer education programs under different targeting strategies.

2. Methods

Our objective is to generate networks that capture important properties of real IDU networks. IDU behavioral surveillance systems often collect data on the total number of IDUs in a respondent's social network, whether the respondent shares needles with each of these individuals and, if so, at what frequency. From this data, one can infer a population-level degree distribution describing the proportion of individuals who have 0, 1, 2, or more needle-sharing partners during the survey period. Higher-order network features are usually not inferable from the data gathered by such surveys. Take clustering coefficient as an example: to compute this value for a needle-sharing network, each respondent has to identify the number of needle-sharing partnerships among his/her needle-sharing partners, yet many respondents may not possess such information. To avoid the difficulty in obtaining certain data, we create a needle-sharing network (and similarly a sexual contact network) that matches the empirical degree distributions of needle-sharing partnerships, while imposing no requirements on their higher-order properties.

Sexual partnerships may vary in many respects, such as duration, frequency, commercial or not, vaginal or anal, and consistency of condom use. Therefore it is reasonable to divide partnerships into subtypes based on differential characteristics. Here, we distinguish between regular versus casual sexual partnerships. A regular sex partner is defined as an individual's main partner (spouse or girlfriend/boyfriend) with whom one has sex at regular intervals. We assume that individuals can have at most one regular sex partner at any point in time. Casual sex partners are those who fall outside the definition of regular partner, with whom one has casual sex (possibly more than once).

Similarly, we distinguish two types of needle-sharing partnerships: long-term and one-time sharing. The term 'long-term sharing' describes sharing needles on a regular basis; such sharing typically occurs between friends, family and sex partners. 'One-time sharing' is non-repeating and is not restricted to intimate relationships.

Sex partners may share needles; thus the sexual contact network and needle-sharing network in our model are not independent. Many studies suggest that a significant proportion of regular sex partners are also injecting partners, due in part to greater trust and lower perceived risks of infection [9,17–19]. To incorporate this correlation in our model, we further divide long-term needle-sharing relationships into two classes: sharing between regular sex partners and between other social dyads (e.g., casual partners, friends and family). We will use the term 'steady needle-sharing partnership' to refer to a long-term sharing relationship between other social dyads exclusively.

Sexual and needle-sharing relationships may form and dissolve over time. To capture these dynamics we need to determine appropriate rules for updating the network at every time step. We assume that the degree distributions of the sexual contact network and needle-sharing network remain steady over time, and we model the number of sexual/needle-sharing partners of each IDU with a Markov chain whose steady state distribution corresponds