

On a Graph-Based Model for Simulating Sexually Transmitted Diseases

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Abstract: *The objective of this study is to develop a complex graph-based model and determine how epidemics of sexually transmitted infections play out on it. We constructed the graph, wherein node-degrees follow a power-law distribution, the partnership durations and formation patterns follow Weibull and uniform distributions respectively. The working of epidemics on this graph is investigated by simulating a basic model of HIV. The result shows that the epidemic outcome is higher compared to either a scenario of static partnerships or a scenario of a random graph regenerated in each time step for the epidemic time scale. The partnership network over time is neither completely static nor is it completely changing at every time step. Therefore, this graph-based model is realistic and can be adopted for simulating the epidemics of sexually transmitted infections.*

Keywords: *Dynamic sexual networks, stable partnerships, casual partnerships, partnership dissolution and formation.*

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I. Introduction

Sexually transmitted diseases (STDs) are defined as a group of communicable diseases that are transmitted predominantly by sexual contact heterosexually, homosexually and bisexually. The number of agents now known to be sexually transmitted include some 20 pathogens. Some of these agents (such as Chlamydia trachomatis, herpes simplex virus, human papilloma virus, hepatitis B virus, human immunodeficiency virus) tend to replace the classical venereal diseases both in importance and frequency as these agents are often more difficult to detect, treat, and control. Sexually transmitted diseases are a major public health problem in the world, especially in most African countries on account of their frequency, their associated morbidity and mortality, their impact on maternal and infant health, as well as their economic costs in terms of health expenditure and lost productivity, and, last but not least, because of their social consequences [De Schryver and Mmeheus (1990)]. More than a million people acquire a sexually transmitted infection (STI) every day. An estimated 499 million new cases of curable STIs (gonorrhoea, chlamydia, syphilis and trichomoniasis) occur every year. In addition, 536 million people are estimated to be living with incurable herpes simplex virus type 2 (HSV-2) infection. Approximately 291 million women have a human papillomavirus (HPV) infection at any given point in time. The burden of STIs is greatest in low income countries. The consequences of STIs have a profound impact on sexual and reproductive health: fetal and neonatal deaths. Syphilis in pregnancy leads to 305000 fetal and neonatal deaths each year, and leaves an additional 215000 infants at increased risk of dying from prematurity, low birth weight or congenital disease cervical cancer. HPV infection causes an estimated 530000 cases of cervical cancer and 275000 cervical cancer deaths each year. STIs such as gonorrhoea and chlamydia are an important cause of infertility; in sub-Saharan Africa, untreated genital infection may be the cause of up to 85% of infertility among women seeking infertility care. An STI such as syphilis or HSV-2 infection increases the chances of acquiring HIV infection by three-fold or more. In addition, the direct physical, psychological and social consequences of STIs have a major impact on quality of life and are a prime indicator of the quality of global sexual and reproductive health care [WHO (2012); WHO (2016)]. The menace of STIs has been attacked from medical and public health angles. There are interventions like treatment, condom use, vaccination, counseling and others. But social factors also contribute to the spread of STIs because they are social diseases. Of primary importance are the people and the sexual links along which diseases may spread. This leads us to the study of social networks. To check against the spread, the sexual interactions that prepare a fertile ground need to be investigated. More so, the playing out of epidemics of sexually transmitted infections on these sexual network structures need to be examined. Among the social aspects of networks investigated are concurrent partnerships, serial or sequential monogamy [Kretzchmar *et al* (1996)]. In our own case we investigate the aspect of partnership durations as they affect the spread of STIs. The plan of this article is as follows. Section 2 is devoted to graphs and modeling. Simulation is presented in section 3. Results, discussion and conclusive remarks are passed in sections 4, 6 and 6 respectively.

II. Graphs And Modeling

Classical epidemiological models ignore the importance of the complex patterns and structures of social interactions on the spread of diseases. So, most of the earlier epidemiological models trivialize the social aspects of disease transmission. However, since the middle of the twentieth century, sociologists, mathematicians have been studying social networks and have come up with a large literature spanning many different aspects of social networks from empirical, conceptual and methodological points of view [Liljeros (2003)].

Graphs used in the literature can be classified on the properties of interest. From the dynamism point of view, graphs or networks can be classified as static or dynamic depending on whether their structures change with time. From the field of application perspective, we have social networks, information networks, technological networks, epidemic networks, to mention a few. Each of these types of networks can be narrowed to specific networks. Graph classifications based on degree distribution exist. For instance, scale-free graphs, Poisson graphs. Graphs such as unipartite, bipartite or multipartite are based on the node types. For a general knowledge of graphs and their theory, refer to [Hofstad (2016); Frieze and M. Karonski (2015); Grimmett (2012); Newman (2002); Guichard (2017); van Lint and Wilson (2001); Keller and Trotter (2015); Brualdi (2010); Wilson (1996); Harju (2007) and Bondy and Murty (1979)].

Real world network are large, and in most cases it is virtually impossible to describe them in detail or to give an accurate model for how they came to be. To circumvent this problem, random graphs have been considered as network models. The field of random graphs was established in late 1950s and early 1960s. For detail, see Hofstad (2016).

In this article, our interest is in social networks and how they affect the epidemiology of diseases, especially, sexually transmitted infections. A social network is a social structure made up of individuals (or organizations) called nodes which are connected by some specific types of interdependency, such as friendship, enmity, common interest, financial exchange, dislike, sexual relationship or relationship of beliefs, knowledge or prestige. For detail of social network analysis, refer to Wasserman and Faust (1994). A sexual contact network is a set of individuals who are connected by sexual relationships (partnerships).

Graph Models for Sexually Transmitted Infection

We make a scanty review of graph models of interest, from where we pick our research question. For a review of graph or network-based models, refer to Quax (2008) and Tolentino (2014). Bai *et al* (2007) propose a network spreading model for HIV, wherein each individual is represented by a node of the transmission network and the edges are the connections between individuals along which infection may spread. The sexual activity of each individual, measured by its degree, is not homogeneous but obeys power law distribution. Slood and Ivanov (2007) did stochastic simulation of HIV population through complex networks. The node-degrees obey power law distribution while the time evolution of the network is determined by a Markov process. Kretzchmar *et al* (1996) did modeling prevention strategies for gonorrhea and chlamydia using stochastic network simulations. Their simulation model is discrete time Markov model describing pair formation and separation and disease transmission as stochastic processes. Morris and Kretzchmar (1995) used stochastic simulations to investigate the effect of concurrent partnerships on transmission dynamics in networks. Quax (2008) did modeling and simulation of propagation of infectious diseases in a homosexual population. The author constructed Kronecker graphs, with the node degrees obeying the power law distribution. In most of these studies, it is found out that, in time steps, either an edge is formed or dissolved between nodes with equal probability or that a new random graph is regenerated at every time step. In practice, all the nodes have varying partnership durations. While some partnerships are stable relationships with long durations, others are casual relationships with short term durations. The assumption of equal probability for the dissolution of every relationship or equal probability for relationship formation may not be realistic. Althaus and Roellin (2011) argue that sexual partnership durations are best described by a Weibull distribution, indicating increased robustness with ongoing duration. So, our graph model is based on the argument that the node-degrees obey the power law distribution and the partnership durations obey Weibull distribution.

Model and Algorithm

We construct a graph or network model as a dynamical bipartite graph, where a population is compartmentalized into two types of subpopulations, wherein each individual is represented by a node and the edges are the links between the individuals. Power-law distributions are used to generate degree sequences for the subpopulations and the graph constructed using the mechanism of configuration model. The power law distribution can be mathematically represented by

$$p(k) = k^{-\gamma} \quad k \leq k_{\max}$$

where k is the number of sexual partners *per year* and γ is a parameter of the distribution. Small γ denotes more limited sexual contact behaviour and corresponds to a smaller value of k_{\max} indicating the promiscuity and vice

versa. Latora et al (2006) reports that the sexual contact network in Burkina Faso is a scale-free network. They estimated the exponent γ in the distribution for the numbers of partners for the male population to be 2.9(0.1). The survey in Sweden has shown that the values of the exponent γ in the distributions of the numbers of female and male populations were 3.1(0.2) and 2.6(0.3) respectively.

We simulate epidemics on our graph based on the following procedure.

1. Specify the total population $T = N_1 + N_2$, where N_1 and N_2 are the female and male population sizes respectively.
2. Specify the degree distribution as a power law distribution with the parameter value γ .
3. Generate the graph by the mechanism of configuration model.
4. At each time step, apply the infection operator ξ_1 . A susceptible node may be infected by neighbouring infected nodes with probability p_i , which is determined by the number of infected nodes $i, i = 1, \dots, k$ and the infection stages of the infected nodes $L_j, j = 1, \dots, n$.
5. At each time step, apply local progression operator ξ_2 . A pathogen can spread within an infected node itself without external influences from one infection status to another with probability p_{L_j} , L_j is the stage number. A new p_{L_j} , is determined after every change of infection status.
6. At each time step, apply replacement operator ξ_3 . Our model assumes a constant population size and we enforce this by immediately replacing a node that is removed by natural death or disease-related death.
7. At each time step, apply edge operator ξ_4 . Existing edges are disconnected according to probabilities related to Weibull distribution of partnership durations. These disconnected edges are swapped between disconnected nodes.

Repeat these steps until statistical significance is obtained.

Remark1. Our model can also be applied in a homosexual population by replacing the females with the recipients and the males with the donors

III. Simulation

To validate our model, we use a basic model of HIV with only two compartments of susceptible and infected individuals. The specific realism of HIV epidemic is not our target here. For comprehensive knowledge of transmission and other processes, see Pinsky and Douglas (2009). The essence of simulation here is to determine how epidemics play out on this graph. So, the complexity involved in real HIV modeling is not treated. We assume an individual is either susceptible or infected. Therefore, the simulation is done on SI assumption. Thus, our simulation set up is as follows.

- (1) We set all the nodes to be susceptible except a few randomly selected infected individuals
- (2) At each time step for each susceptible node i , denote m_1 for the number of its neighbouring infected nodes. If the node i is a male, then the probability that i will become infected in the next time step is

$$p_1 = 1 - (1 - \beta)^{m_1}$$

β is the transmission probability per sexual partners. Similarly, for each susceptible female node i

$$p_2 = 1 - (1 - 2\beta)^{m_2},$$

because the male-female transmission is about two times as successful as female-to-male transmission.

We set $\beta = 0.2$. Note that the realism of HIV transmission dynamics is not the essence of this study.

- (3) At each time step, each infected node may die with probability ε_1 . We set $\varepsilon_1=0.10$ (corresponding to about 10 years to live).
- (4) At each time step, each susceptible node die with probability ε_2 . We set $\varepsilon_2 = 0.015$ (which corresponds to a life expectancy of about 65 years).
- (5) At each time step, the dead nodes are replaced each with probability ξ ($\xi = 0.27$).
- (6) At each time step, infected nodes proceed to AIDS status with probability $\lambda_1 = 0.108$ and AIDS patients on average, die within 1 year with probability $\lambda_2 = 1$.
- (7) At each time step, each sexual partnership is dissolved with a probability related to the probability distribution of partnership durations. To be specific, we use Weibull distribution. Also, all the nodes that have lost partnerships randomly re-connect to other disconnected nodes. This is common among casual partners like prostitutes and promiscuous men.

The MATLAB code developed Jaquet and Pechal (2009) was found useful in developing our own code.

IV. Results

The simulation results are presented as shown in Figures 1, 2 and 3 in the sequel.

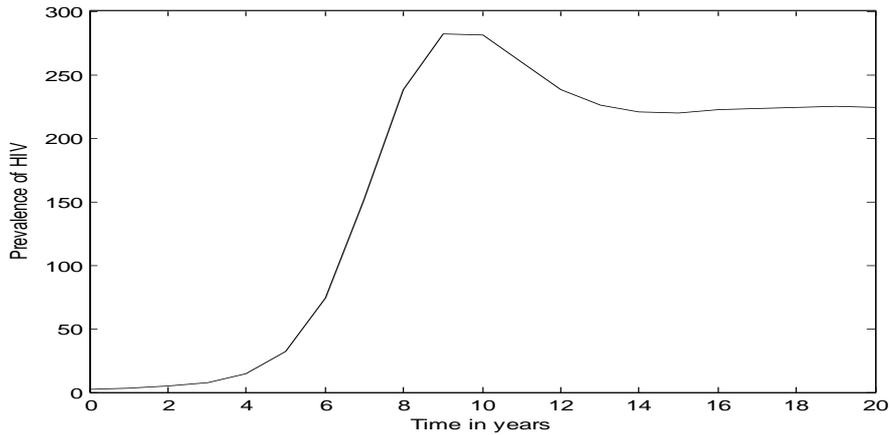


Figure 1: HIV prevalence under power – law and Weibull distributions

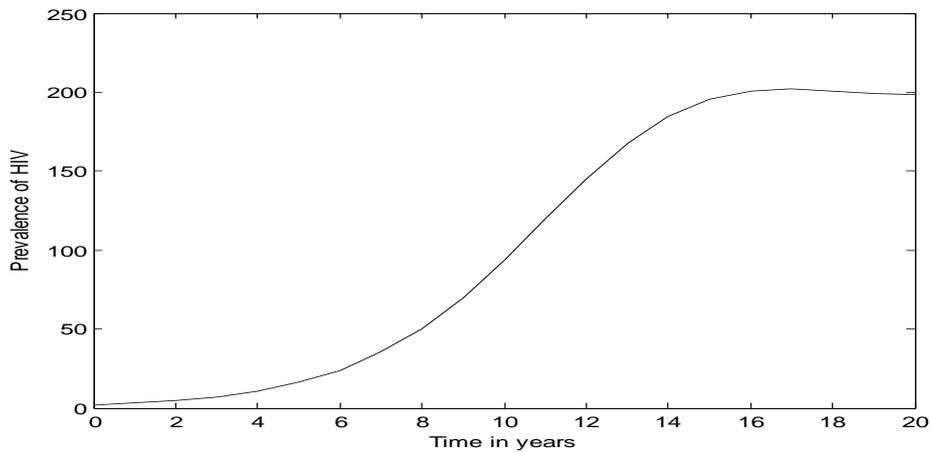


Figure 2: HIV prevalence under regeneration of a partnership network at every time step

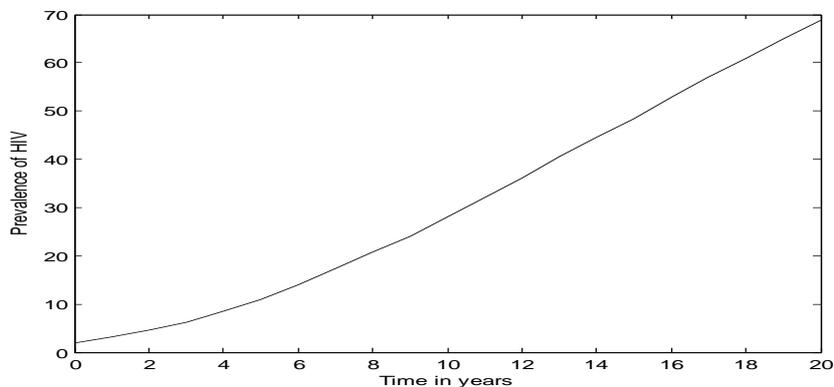


Figure 3: HIV prevalence under a static partnership network at every time step

V. Discussion

In this article a graph-based model was developed for simulating the epidemics of sexually transmitted diseases. The main result is in Figure 1. The essence of this research is to ascertain how epidemics of sexually transmitted diseases play out based on this model. Sexual networks in which the partnerships and demography change faster than epidemic time scale are far from being static or random. The assumption of static partnership structure in time steps is erroneous in real sexual networks for an infection like HIV because there might be partnerships that need to break within some time steps. Also, random connection assumption for all the

partnerships in each time step can be misleading because in a real sexual network, there are stable partners that spillover some time steps. Both scenarios lead to low epidemic outcome compared to our model. This can be seen in Figures 2 and 3.

VI. Conclusion

In this article we developed a graph-based model for simulating the epidemics of sexually transmitted diseases. This model is based on the assumption that the node-degrees follow the power law distribution and the partnership durations obey the Weibull distribution with the disconnected edges reconnected immediately to other disconnected nodes based on uniform matching assumption. The duration distribution gives some measures of stability to some partnerships while other relationships are casual, creating a fertile ground for higher epidemic outcome. Our model performs realistically and can be adopted for simulating the epidemics of sexually transmitted infections.

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