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# Stochastic Modeling of the Transmission Dynamics of HIV in a Heterosexual Population on Complex Graphs

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**Abstract** The objective of this study is to predict the prevalence of HIV prevalence in a heterosexual population through complex graphs. A heterosexual population together with the partnership connections is described by a complex graph. We considered two scenarios; first a situation where individuals have the numbers of partners distributed according to a power-law distribution and secondly a situation where individuals are restricted each to one partner. In each case, the partnership durations are described by Weibull distribution and the effects of condom use are investigated. The results show that monogamous forms of relationship and effective condom use are the best strategy for the control of HIV prevalence. Therefore, behavioural change from multiple partnership and unprotected sex is crucial for the control of HIV/AIDS.

**Keywords** sexual networks, HIV, sexually transmitted diseases, sexual partnerships

## 1. Introduction

The human immune-deficiency virus (HIV) together with the associated acquired immune deficiency syndrome (AIDS) is a pandemic [1-3]. AIDS is an illness that damages a person's ability to fight off disease, leaving the body open to attack from ordinarily innocuous infections and some forms of cancers. HIV disrupts the functioning of the immune system. A weakened immune system allows the development of a number of different infections and cancers, and it is these diseases which cause illness and death in people with AIDS. HIV also infects and causes direct damage to other types of cells [4].

Two-third of all HIV infected people live in Sub-Saharan Africa; Nigeria ranking third in the highest burden apart from South Africa and India. This calls for more concerted control effort to arrest this ugly trend.

Heterosexual contacts are most responsible for HIV infections compared to homosexual, drug injection and mother- to-child routes of transmission [5].

Several intervention methods are available. These range from sex abstinence, use of condoms, education and use of antiretroviral drugs and counseling. Condoms used correctly can reduce the likelihood of HIV transmission to an extremely low level. Combinations of antiretroviral medications that have been available since 1996 are slowing, stopping, and even reversing the progression of HIV disease. Antiretroviral drugs are allowing many HIV infected people (who otherwise would become ill) to live active, healthy lives with few or no symptoms. These drugs are not a cure for HIV; the medications now available must be continued indefinitely to prevent progression of the disease [4].

Two types of HIV are currently recognized: HIV-1 and HIV-2. The classification is based on differences in genetic structure. HIV-2 is the less common type and is found primarily in Western Africa. Both types of virus are transmitted in the same way and cause the same illnesses. However, it appears that HIV-2 is more difficult to transmit and that time from infection toillness is longer. In addition, a number of different sub-types or strains of HIV-1 have been classified. These subtypes (also known as "clades") are distinguished by smaller variations in their genetic composition. The sub-types are identified by letter. They are unevenly distributed geographically.

Sub-type B is found mostly in the Americas, Japan, Australia, the Caribbean, and Europe. Sub-types A and D are most common in sub-Saharan Africa [4].

As pointed out in Williams et al [3], the development of antiretroviral drugs to treat HIV has been a singular scientific achievement. Between 1995 and 2009 an estimated 14.4 million life-years has been gained globally among adults on ART but the rate of new infections is unacceptably high and still exceeds the number of people starting ART each year.

As presented in casels *et al* [5], ART reduces viral load and the probability of transmission. It also reduces HIV/AIDS-related mortality and, therefore, increases the life expectancy of infected individuals.

The plan of this paper is as follows. Introductory part is presented in section 1. Section 2 is devoted to graphs and modeling. The model description is presented in section 3. Simulations are carried out in section 4. Results, discussion and conclusive remarks are passed in sections 5, 6 and 7 respectively.

## 2. Graphs and Modeling

Stochastic models of HIV have been proposed and studied by researchers. For example, Peterson et al [6] applied Monte-Carlo simulation technique in a population of intravenous drug users.

Greenhalgh and Hay [7] studied a mathematical model of the spread of HIV/AIDS among injecting drug users. Dalal *et al* [8] examined a stochastic model of AIDS and condom use. Dalal, *et al* [9] also studied a stochastic model for internal HIV dynamics. Ding *et al* [10] carried out risk analysis for AIDS control based on a stochastic model with treatment rate. Tuckwell and Le Corfec [11] studied a stochastic model for early HIV-1 population dynamics. Waema and Olowofeso [12] studied a mathematical model for HIV transmission using generating function approach.

These 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 [13].

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 [14-24].

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 [14].

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 [25]. A sexual contact network is a set of individuals who are connected by sexual relationships (partnerships).

### 2.1. 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 [26] and Tolentino [27]. Bai *et al* [28] 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. Sloot *et al* [29] 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* [30] 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 [31] used stochastic simulations to investigate the effect of concurrent partnerships on transmission dynamics in networks. Quax [26] 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 [32] 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 may obey the power law or any other distribution and the partnership durations obey Weibull distribution.

## 3. Model Description

In this paper we consider a population that is divided into two types, namely, adult males and females, where each individual is in one of the states- susceptible, infected in the active, untreated infected, treated infected or AIDS stages. Initially susceptible individuals can become infected after contact with infected individuals. We adopt the recipe by Jaquet and Pechal [33] and represent each of the infected states by some arbitrary number L of states $I_n$ $(n = 1, \ldots, L)$, each corresponding to one "stage" of the disease. Each of these stages is characterized by a real parameter $\alpha_n$ which we call infectiousness and which determines the probability that an individual in that stage infects another susceptible individual.

### 3.1. Modeling of sexual contact networks

We construct a network model as a dynamical bipartite graph, where a population is compartmentalized into male and female susceptible subpopulations, wherein each individual is represented by a node and the edges are the links between the individuals. First, we use the power-law distribution 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

$p(k) = k^{-\gamma}, \ k \leq k_{max}$ where $k$ is the number of sexual partners *per year* and $\gamma$ is a parameter of the distribution. Small $\gamma$ denotes more limited sexual contact behaviour and corresponds to a smaller value of $k$max indicating the promiscuity and vice versa. Latora et al [1] reports that the sexual contact network in Burkina Faso is a scale-free network. They estimated the exponent $\gamma$ 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 $\gamma$ in the distributions of the numbers of female and male populations were 3.1(0.2) and 2.6(0.3) respectively. For a review of sexual contact network models and other standard epidemiological models, refer to Liljeros et al [13].

Secondly, we generate a degree sequence where every node has one link (partner) and generate the bipartite graph by the same mechanism of configuration model

### 3.2. Modeling the spread of HIV/AIDS on Graphs

The emphasis is on HIV/AIDS heterosexual contact network, wherein compartments of males and females are each subdivided into five states, comprising the susceptible, active infected phase, untreated, treated and AIDS individuals. We adopt the recipe by Bai *et al* (2007) with modification to reflect the realism of HIV transmission dynamics. As in their article, our model is implemented by computer simulation with a time step equal to one year. The simulation processes are in the sequel:

(1) We set the number of susceptible individuals and select a number of infected nodes randomly.

(2) At each time step for each susceptible node $i$, denote $m_1, m_2, m_3$ *and* $m_4$ for the numbers of its neighbouring infected nodes in the initial active phase, not in the process of antiretroviral (ARV), in the process of ARV and having AIDS respectively. If the node $i$ is a male, then the probability that $i$ will become infected in the next time step is

$p_1 = 1 - (1 - \beta_1)^{m_1}(1 - \beta_2)^{m_2}(1 - \beta_3)^{m_3}(1 - \beta_4)^{m_4}$

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

$$p_2 = 1 - (1 - 2\beta_1)^{m_1}(1 - 2\beta_2)^{m_2}(1 - 2\beta_3)^{m_3}(1 - 2\beta_4)^{m_4},$$

because the male-female transmission is about two times as successful as female-to-male transmission. As adopted by Bai *et al* [28], $\beta_2$ *and* $\beta_3$ are below 0.5 and since the ARV reduces transmission probability to as much as 60%, we set $\beta_3 = 0.4\beta_2$

(3) At each time step, each infected node may die with probability $\varepsilon_1$ (for the infected in the active phase), $\varepsilon_2$ (for the infected not on ARV), $\varepsilon_3$ (for the infected on ARV) and $\varepsilon_4$ (for AIDS patient). We set $\varepsilon_1$=0.108 (corresponding to about 9 years to live), $\varepsilon_2 = 0.15$ (about 7 years), $\varepsilon_3 = 0.08$ (about 12.5 years) and $\varepsilon_4 = 1$ (about one year).

(4) At each time step, each susceptible node die with probability $\varepsilon_5$ . We set $\varepsilon_5 = 0.015$ (which corresponds to a life expectancy of about 65 years.

(5) At each time step, the dead nodes are replaced each with probability $\xi$ ($\xi = 0.27$). This choice is made based on the assumption of constant population, with $\xi$ equal to the average of $\varepsilon_i, i = 1,..,5$.

(6) At each time step, infected nodes in the active phase proceed for ARV with probability $\lambda_1 = 0.6$ or remain untreated with probability $\lambda_2 = 0.4$. Infected nodes not on ARV progress to AIDS with probability $\lambda_3 = 0.16$ (about 6 years to live) while the infected nodes on ARV progress to AIDS with probability $\lambda_4 = 0.09$ (about 11.5 years to live. AIDS patients , on average, die within 1 year with probability $\lambda_5 = 1$.

(7) At each time step, each sexual partnership is dissolved based on 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.

**4. Simulation**

We perform the following simulation experiments. In all the experiments, it is assumed that the partnership durations follow the Weibull distribution. We fix the initial population size at 3000 with the number of males equal to the number of females and also the female and male degree sequences come from the same distribution. First, we consider a situation where there is no usage of condoms and only two individuals are randomly infected initially, with the degree sequence following the power law distribution. The result is displayed in Figure 1. Secondly, we consider a situation where 80% of the population imbibes the use of condoms and only two individuals are randomly infected initially, with the degree sequence following the power law distribution. The result is shown in Figure 2.

In the third experiment, we consider a situation where 99% of the population adopts the use of condoms and only two individuals are randomly infected initially, with the degree sequence following the power law distribution. The result is shown in Figure 3. In the fourth experiment we consider a situation where 80% of the population imbibes the use of condoms and only 300 individuals are randomly infected initially, with the degree sequence following the power law distribution. The result is shown in Figure 4. In the fourth experiment we consider a situation where 99% of the population imbibes the use of condoms and only 300 individuals are randomly infected initially, with the degree sequence following the power law distribution. The result is shown in Figure 5. In the sixth episode, we consider a situation where there is no usage of condoms and only two individuals are randomly infected initially, with the relationships being monogamous. The result is displayed in Figure 6. In the seventh experiment, we consider a situation where 99% of the population adopts usage of condoms and only 300 individuals are randomly infected initially, with the relationships being monogamous. The result is displayed in Figure 7. Lastly, in the eighth episode, we consider a situation where 99% of the

population adopts usage of condoms and only two individuals are randomly infected initially, with the relationships being monogamous. The result is displayed in Figure 8.

**5. Results**

The results of the simulation experiments are shown in the sequel.

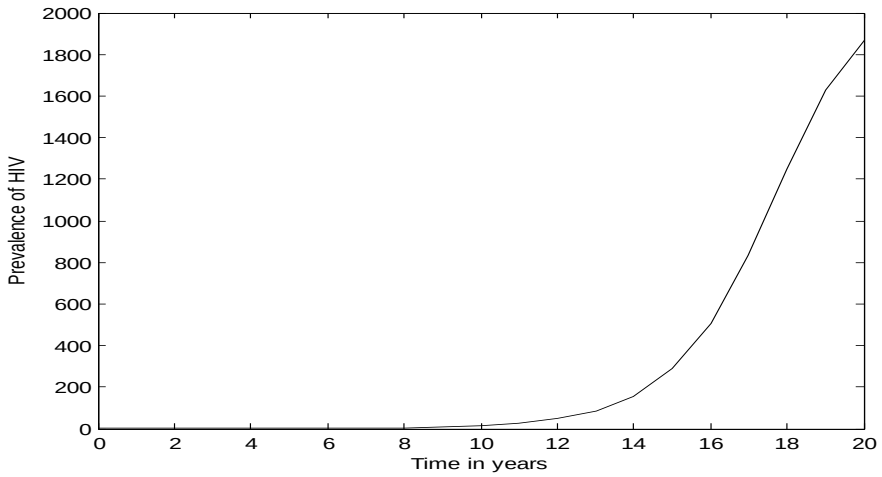


*Figure 1: HIV prevalence under power-law and Weibull distributions without condom; $S_0$=3000, I=2*

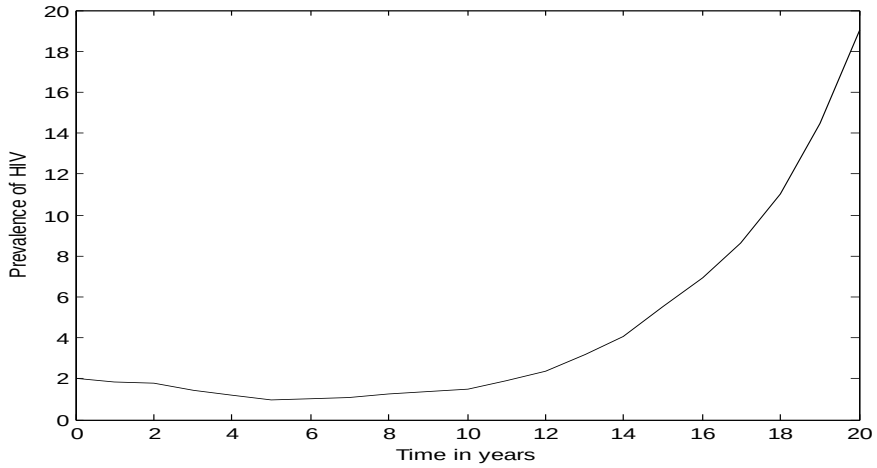


*Figure 2: HIV prevalence under power-law and Weibull distributions with condom (80%); $S_0$=3000, I=2*

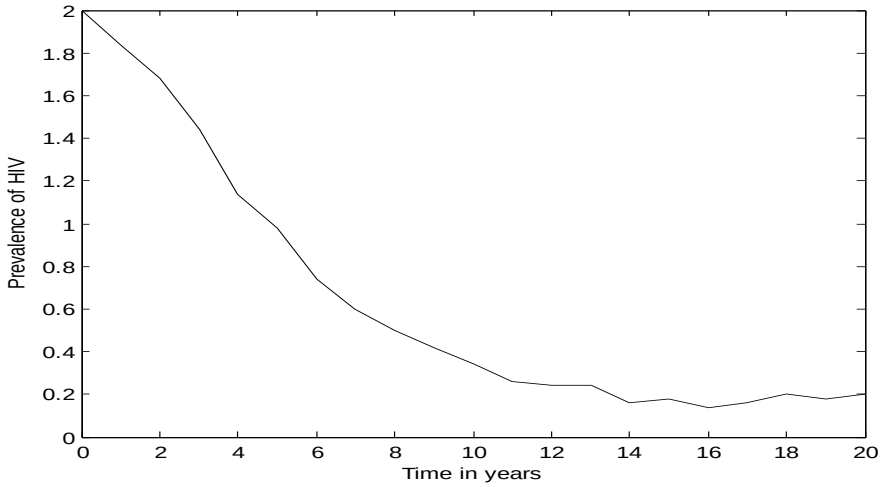


*Figure 3: HIV prevalence under power-law and Weibull distributions with condom (99%); $S_0$=3000,I=2*

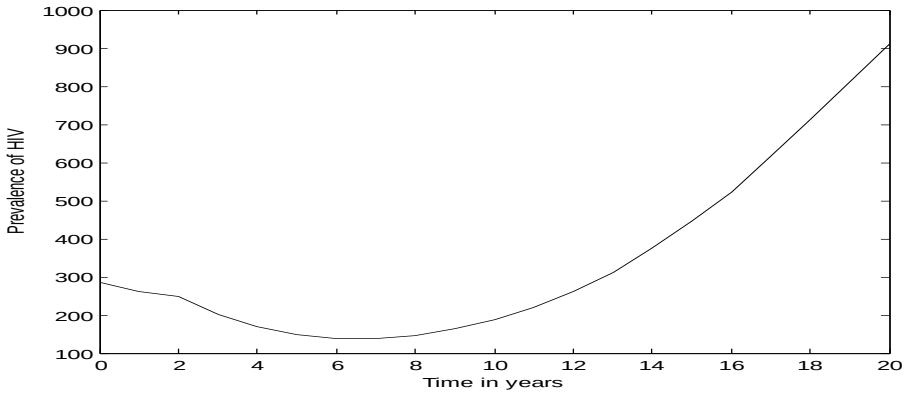


*Figure 4: HIV prevalence under power-law and Weibull distributions with condom (80%); $S_0$=3000, I=300*

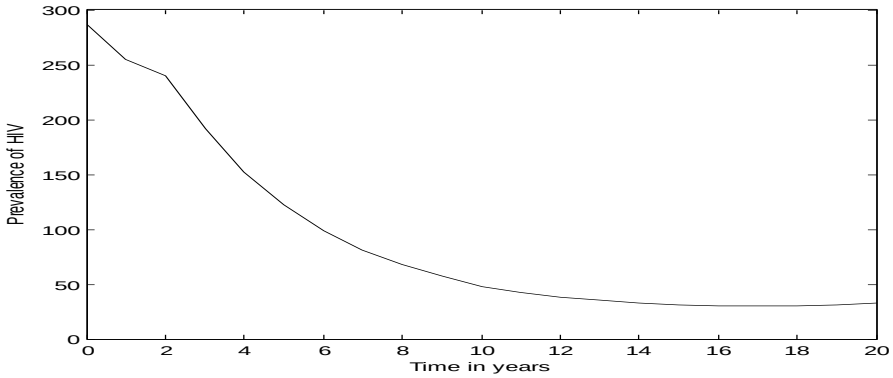


*Figure 5: HIV prevalence under power-law and Weibull distributions with condom (99%); S_0=3000, I=300*

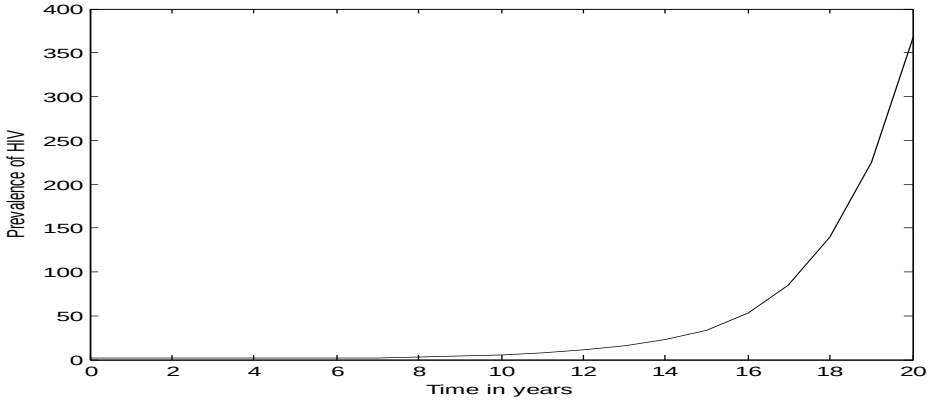


*Figure 6:HIV prevalence under monogamy and Weibull distribution without condom; $S_0$=3000,I=2*

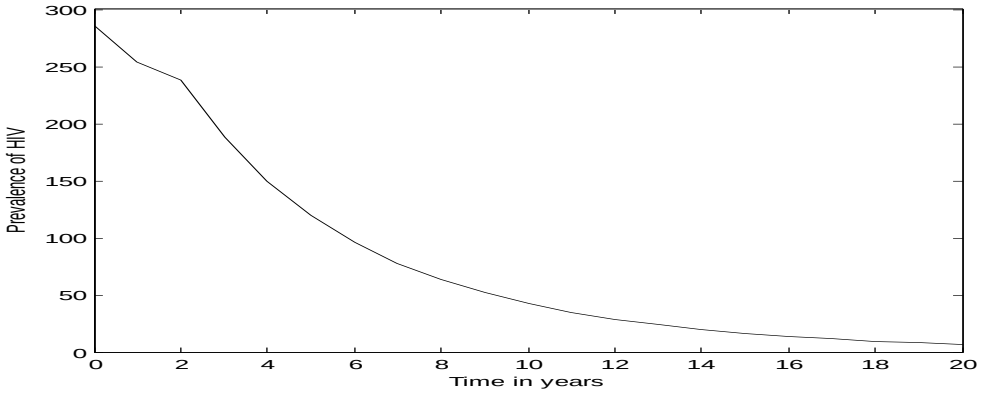


*Figure 7: HIV prevalence monogamy and Weibull distribution with condom (99%); $S_0$=3000, I=300*

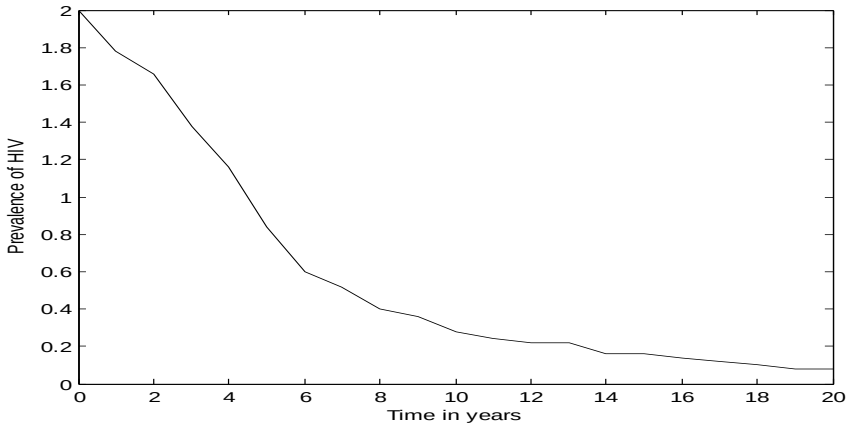


*Figure 8: HIV prevalence monogamy and Weibull distribution with condom (99%); $S_0$=3000, I=2*

## 6. Discussion

In this article, we have developed a graph-based model and simulated the transmission dynamics of HIV under different scenarios on it. The main results are shown in Figures 1 through 8. The result in Figure 1 shows that two index cases that randomly invade a population can cause an exponential increase in the spread of HIV under power law distribution of the degree sequence in the long run. The result in Figure 2 shows that, with 80% condom usage, two index cases that randomly invade a population precipitate a low prevalence of HIV in the long run. Figure 3 shows that, with 99% condom usage, there cannot be a take –off of epidemic. Figure 4 shows the prevalence of HIV when there is a level of endemicity in the population before 80% condom coverage is applied. The result show that HIV prevalence increases slowly under this scenario. In the extreme, Figure 5 shows that, with 99% condom coverage reduces the HIV prevalence rapidly. The result in Figure 6 shows that under monogamy and a few index cases, the HIV prevalence increases slowly, even without condom usage. This emphasizes the importance of behavioural change from multiple partnerships. Figure 7 shows that in a population where HIV is endemic, behavioral change from multiple partnerships to monogamy and effective condom usage can eliminate the prevalence. Figure 8 shows that with effective condom usage in monogamous relationships, there cannot be any epidemic take off. The findings in this study suggest that behavioural change from multiple partnership and effective condom usage is important for the control of HIV/AIDS.

## 7. Conclusion

In this article, we have developed and simulated the transmission dynamics of HIV on a complex graph. The partnership structures under power-law distribution of the degree sequence; and under monogamy were used. We assumed that the partnership durations obey the Webull distribution. The results emphasize the importance of monogamy and condom usage. We therefore, recommend that to ensure speedy recovery from HIV burden, the members of highly endemic population are urged to desist from multiple partnership; and should apply condoms during intercourse.

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