A Continuous-risk Model with Heterogeneous Mixing for Understanding Impact of Condom Use on Spread of Sexually Transmitted Infections Among Adolescents

Asma Azizi[1], Karen Ríos Soto[2], and Anuj Mubayi[3]

[1] Department of Mathematics, Tulane University, New Orleans , Louisiana

[2] Department of Mathematical Sciences, University of Puerto Rico at Mayaguez

[3] School of Human Evolution and Social Change; Simon A. Levin Mathematical Computational Modeling Science Center, Arizona State University, Tempe, Arizona

Abstract

Sexually Transmitted Infections (STI's) remain a significant public health challenge globally with a high burden of some diseases even in some parts of developed countries. Translation of the evidence regarding the protective role of condom use on STI, with sexual transmission rates into sexual behaviour patterns of infected subjects, remains largely unexplored. This study aims to describe and analyze the impact of inconsistent condom use and risky sexual behaviors on the prevalence and dynamic of STIs. A novel Susceptible-Infected-Susceptible (SIS) model with continuous-risk, defined as number of concurrent partner, for the spread of high infectious STI's such

as chlamydia, gonorrhea an syphilis in a homosexual and heterosexual community, is developed and analyzed. The model incorporates heterogeneous sexual behavior via a function describing the biased (preferential) mixing between individuals with different risks. Sensitivity analysis is carried out to assess the relative impact of condom use frequency by high-risk people on the fraction of infection at the steady state as well as the rule of distribution of infection on changing risk. Our results show that under the case partners of people have the risk close (but not equal) to their risk, condom use by high risk people has more impact on controlling the infection than the case people choose some fraction of their partners with exactly the same risk and the rest randomly. Also, high-risks attitude to condom use changes the shape of endemic equilibrium point as a function of risk: when people with maximum number of partners don't use condom frequently, they have the biggest chance to get infection among all risks, but when they start to use condom more, peak of infection at steady state disappears and the shape of infection at steady state becomes a flat function of risk.

1 Introduction

Sexually Transmitted Infections (STI) are one of the major health issues that can be a consequence of risky behavior or unprotected sexual activity. More than half of sexually active people in the United States of America will have an STD/STI at some point in their lifetime [12]. Recent estimates from the CDC show that there are 19.7 million new STIs every year in the U.S.A [16].

Currently, use of the male latex condom is the primary strategy for HIV and STI prevention in sexually active individuals worldwide. Condoms, if used correctly, can greatly reduce (though not eliminate) the risk of STI. However, differences in disease-specific infectivity and the number of exposures to an infected partner may reduce condom effectiveness [14]. Several studies show the attitude of adolescents, as sexually active population, to condom use [1, 2, 13, 15]. Six in ten high school students in U.S.A, who are sexually active, reported they used condoms at their most recent sexual intercourse. Condom use among this group increased from 46% in 1991, to 63% in 2003, and was 59% in 2013 [1]. Reece et.al. [15] also studied rates of condom use among sexually active individuals in the U.S. population. Based on their result, adolescents reported condom use during 79.1% of the past 10 vaginal intercourse events.

Beadnell et.al. [2] conducted a study on students in a large urban northwest school district were recruited and then surveyed annually for seven years. The sample is taken from 5 different grades (8−12th grades). In this study adolescents are in 3 different profiles: condom-user who are people with few partners and use condom consistently, few-partners:

who are the ones with few partners and use condom inconsistently, and the risk-takers: people who have lot's of partners and use condom inconsistently. Among the few-partners and risk-takers, risk takers use condom (68% of the sexual acts) more than few partners do (49% of the sexual acts). The fraction of individuals with few-partners is more than condom-users ones in grades 11 and 12. Therefore, we conclude that adolescents with at least age 15 who have few partners are less likely to use condom consistently.

Another study by Lescano et.al [13] examined the attitude of adolescent toward condom use by casual and main partners. Their study showed the number of partners in casual partners is more than those with main partners. That is, partners of people with lots of partners are mostly casual, and partners of people with few partners are the main ones. Individuals with casual partners reported to use condom more than those with main partners (47% vs. 37%, respectively). Therefore, based on these results, we assume, people in age $15-25$ with high number of partners are more positive toward using condom than people with the same age but few number of partners.

Mathematical models can provide frameworks to understand the underling epidemiology of diseases and how they are correlated to the social structure of the infected population [4, 5, 6, 7]. Transmission-based models can help the medical community to understand and to anticipate the spread of diseases in different populations, and help them to evaluate the potential effectiveness of different approaches for bringing the epidemic under control. The primary goal of our modeling effort is to create a model that can be used to understand the spread of STI's, and predicting the impact of having several concurrent

partners by individuals as well as the use of condom on STI epidemic.

The main goal of this project is to study impact of combination of risk and condom use to determine whether a particular behavior is safe or risky with regard to STIs prevention. In this study, we look at condom use as a function of risk, both risk and frequency of condom use are continuous variables per unit time. We analyze the model to identify the importance of these two factors in the spread or prevention of STIs.

Most of the parameters in the model are estimated within a reasonable level of accuracy in order for results to give qualitative and quantitative understanding of how the disease is spreading. We use local sensitivity analysis to identify the relative importance of condom use and numerical examples to illustrate how we can prioritize behavioral strategies by individuals based on their predicted effectiveness.

The reminder of this article is organized as follow: in section two, we explain the model and its parameters. Section three provides some numerical result of the model, and section four will summarize our results.

2 Mathematical Model

We developed and analyzed a continuous risk-based transmission model that can be used to understand the spread of the disease and quantify the relative effectiveness of accounting for different behaviors by individuals. In our model, the sexually active population is divided into the susceptible population (S), and the infectious population (I). Once a person has recovered from infection, they are again susceptible to infection. Therefore,

the model has a $S \to I \to S$(SIS) structure.

The number of partners a person has (his/her risk), and the number of partners that their partners have (his/her partners risk) both affect the spread of STIs. That is, different assumptions about the distribution of risk behavior for the population will result in different disease forecasts. We use the selective mixing model developed by Busenberg et.al. [3] to capture the heterogenous mixing among people with different numbers of partners. Our model is closely related to the STI models for the spread of the HIV/AIDS virus in a heterosexual network [10, 11]. These models account for the distribution of risk in a population based on realistic sexual contact networks [8, 9, 10, 11]. We assume the risk of contracting STI is primarily a function of a person's risk, the probability that a partner is infected, and the use of prophylactics (e.g. condoms).

We built an integro-differential equation model, where the risk is defined based on the number of partners a person has per unit time. The relative importance of the number of partners and the number of acts per partner on the spread of an STI depends on the disease infectiousness. A high infectious STI is the infection in that the probability of transmission per act, from an infected person to uninfected one is high; it means one act with an infected person may be enough to catch the infection. Therefore, the number of people a person infects (in a highly infectious STI), and a persons risk, depends mostly upon the number of partners he/she has rather than the number of sexual acts per partner. Chlamydia, gonorrhea, syphilis, and chancroid are example of high infectious diseases. So we predict our model is more appropriate for high infectious STIs.

Total population $N^g(r)$ of people with gender $g \in [m, w]$ and total number of partners or risk $r \in [r_0, r_\infty]$ is divided into susceptible , $S^g(t, r)$, and infectious , $I^g(t, r)$, at any time t. We assume people leave and enter the population with migration rate μ and susceptible people may become infectious at the infection rate λ and infectious individuals come back to susceptible status with rate γ. Based on these assumptions we have a heterogeneous SIS model

$$\frac{dS^g(t,r)}{dt} = \mu(N_0^g(r) - N^g(r)) - \lambda^g(t,r)S^g(t,r) + \gamma I^g(t,r), \tag{1}$$

$$\frac{dI^g(t,r)}{dt} = \lambda^g(t,r)^g S^g(t,r) - \gamma I^g(t,r) - \mu I^g(t,r), \tag{2}$$

$$S^g(0,r) = S_0^g(r), \quad I^g(0,r) = I_0^g(r). \tag{3}$$

Here $N_0^g(r)$ is total initial population of people with gender g and risk r in the absence of infection. Initial conditions of the model are perturbation of disease free equilibrium, i.e $I_0^g(r) > 0$ at least for one $r \in [r_0, r_\infty]$.

2.1 Migration and Disease Recovery Rates

We model a 15-25 year-old sexually active population and assume that the primary mechanism for migration is by aging into, and out of, the population. We consider migration rate $\mu = 0.1 = [(25 - 15)years]^{-1}$, with the assumption that death is negligible compared to the rate that people enter and leave the modeled population. We also assume that, in the absence of infection, equilibrium population for each risk group r of men and women

is given, and that everyone aging into the model population enters being a susceptible.

The rate at which infectious people are recovered, γ , depends upon the gender of the person and their risk level. We assume an infectious individual leaves the infectious compartment when they recover naturally. Natural recovery rate, γ is determined by assuming an exponential distribution for the average time to recovery $\frac{1}{\gamma}$.

2.2 Disease Transmission rate λ

We derive the transmission rate for the case where a susceptible person with gender g and risk r (shown by (g, r)) can be infected by someone of the opposite sex g' in any risk group r'. This force of infection, $\lambda^g(r)$, is the rate that people in (g, r) are infected through sexual acts. Here an act is any sexual activity that can transmit the disease between individuals. We define $\lambda^g(r)$ as the integral of the rate of disease transmission from each infected person in (g', r'), $I^{g'}(r')$, to the susceptible $S^g(r)$ by

$$\lambda^g(r) = \int_{r_0}^{r_\infty} \tilde{\lambda}^g(r, r')dr'. \tag{4}$$

The rate of disease transmission from the infected persons $I^{g'}(r')$ in group (g', r') to the susceptible individuals $S^g(r)$ in group (g, r), $\tilde{\lambda}$, is defined as the product of three factors:

$$\tilde{\lambda}^g(r, r') = \begin{pmatrix} \text{Number of } r'-\text{risk} \\ \text{partners of susceptible} \\ \text{with risk r, per unit time} \end{pmatrix} \begin{pmatrix} \text{Probability of} \\ \text{disease transmission} \\ \text{per partner} \end{pmatrix} \begin{pmatrix} \text{Probability that} \\ \text{partner with risk } r' \\ \text{is infected} \end{pmatrix}$$

$$= \quad p(r, r') \quad \beta(r, r') \quad \left(\frac{I^{g'}(r')}{N^{g'}(r')} \right) .$$

These terms are defined as:

- $p(r, r')$: the number of sexual partners per unit time that each individual in group (g, r) has with someone in group (g', r'), and
- $\beta(r, r')$: the probability of disease transmission per partner for a susceptible person in group (g, r) with their partner in (g', r') and
- $\frac{I^{g'}(r')}{N^{g'}(r')}$: the probability of that the person in (g', r') is infected.

2.2.1 Partnership Formation

A person with risk r has r partner per unit time. An individual selects his partners based on mixing function, such partners can be selected randomly, biased or with a linear combination of them.

Random Mixing Function: We use random mixing function, when individuals with risk r, do not show any preference for any risk, during choosing partners. The random

mixing function ρ_r, which r stands for random mixing are described as follow:

$$\rho_r = \frac{r' N^{g'}(r')}{\int_{r_0}^{r_\infty} u N^{g'}(u) du}. \tag{5}$$

Biased Mixing Function: In biased mixing, people with risk r prefer to have partners with same risk, which also called assortative mixing. However, because in this model risk is a continuous variable finding partners of exactly the same risk does not seem reasonable. Therefore it would be better to consider selecting partners on some neighborhood of r. In order to choose the radius of this neighborhood, we make some assumptions. First of all when risk of a person increases, the probability that he can find partners of the same risk decreases. That is when risk r increases the number of people with risk r decreases, so the variance of risk of his partners increases. Suppose $\sigma(r)$ is the standard deviation of risk of partners of a person with risk r, then we define $\rho_b(r, r')$ as a hat function

$$\rho_b(r, r') = \begin{cases} \frac{r' - r + \sigma(r)}{\sigma^2(r)} & r - \sigma(r) \leq r' \leq r \\ -\frac{(r' - r - \sigma(r))}{\sigma^2(r)} & r < r' < r + \sigma(r) \\ 0 & elsewhere, \end{cases} \tag{6}$$

where index b stands for biased mixing. Figure (1) shows these ρ_b functions for risks $r = 1, 3, 10$. Both functions ρ_r and ρ_b satisfy the condition

$$\int_{-\infty}^{\infty} \rho(r, r') dr' = 1.$$

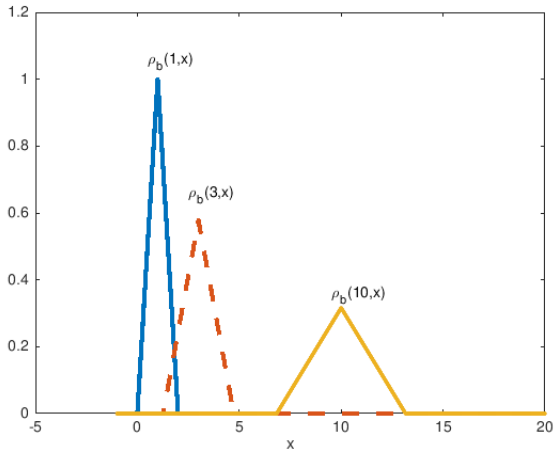


Figure 1: Plot of Hat Function $\rho_b(r, x)$ for $r = 1, 3, 10$. By increasing r the function becomes fatter and shorter.

In our model, we assume people choose some fraction of their partners based on their preference, and for the rest they do not have any preference (totally random mixing), that is we use a convex combination of ρ_r and ρ_b to define the mixing function $\rho(r, r')$. Suppose $\epsilon(r)$ fraction of partners of a person with risk r are selected preferentially and the rest randomly, therefore, we have [3]:

$$\rho(r, r') = \epsilon(r)\rho_b(r, r') + (1 - \epsilon(r))\rho_r(r, r'), \tag{7}$$

where, in that case function ρ_r changes, because people with risk r' choose $\epsilon(r')$ fraction of their partner preferentially as well. Therefore we have random mixing function given by:

$$\rho_r(r, r') = \frac{(1 - \epsilon(r')r'N(r'))}{\int_{r_0}^{r_\infty}(1 - \epsilon(u))uN^{g'}(u)du}.$$

Function $\epsilon(r)$ states what percentage of partners should be in the $\sigma(r)$ neighborhood of person with risk r. This value can be a constant number say 0.5, or a function of r. In case we take $\sigma(r)$ as a non-constant function of r, $\epsilon(r)$ is constant, but if $\sigma(r)$ is constant, we take $\epsilon(r)$ as a decreasing function of r. For instance, we can define $\sigma(r) = 1$, therefore, we have

$$\rho_b(r, r') = \begin{cases} r' - r + 1 & r - 1 \leq r' \leq r \\ r' - r - 1 & r < r' < r + 1 \\ 0 & elsewhere, \end{cases} \tag{8}$$

and then apply variance on $\epsilon(r)$. We point out that ϵ is a decreasing function of risk r, because when risk increases the diversity of risk of partners increases, for example we can think of $\epsilon(r) \propto \frac{1}{\sigma(r)}$. In our simulation we assume ρ_b is defined as Equation (8) and define several functions for $\epsilon(r)$:

1. $\epsilon_1(r) = 0$, that is random mixing function, this means nobody prefers nobody.
2. $\epsilon_2(r) = 0.50$, that means all people want to have half of their partners with the same risk as themselves.
3. $\epsilon_3(r) = 1$, that means people only want to have partners with same risk as themselves.
4. $\epsilon_4(r) = \frac{0.6}{\sqrt{r}}$,(for $\epsilon(r) = \frac{0.6}{r}$ the results were the same), and finally
5. $\epsilon_5(r) = e^{-2r} + 0.5$.

The last two functions are plotted in figure (2), By this definition, a person with risk r

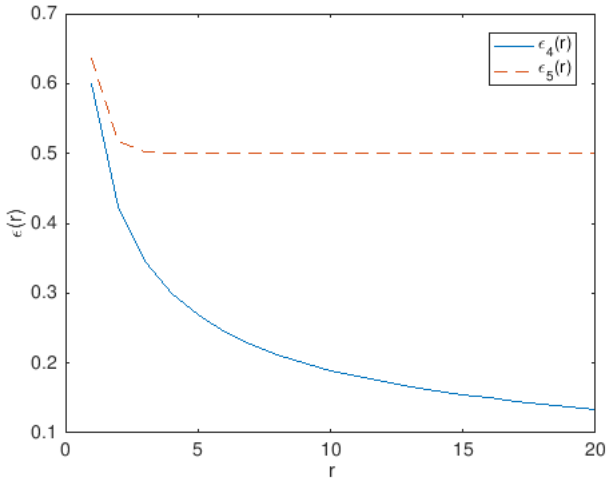


Figure 2: functions $\epsilon_4(r)$ and $\epsilon_5(r)$. The range of ϵ_4 is bigger than that of ϵ_5, for example in ϵ_4 1-partner people want to have 60% of their partners to be one-partner, and 20-partner people want to have 12% of their partners like themselves. For ϵ_5 the preference of lower risk ones changes from 65% to 50%, however higher risk ones all take 50%.

choose $\epsilon(r)\%$ of their partner from almost the same risk, the rest are chosen equally from all risk groups. Population of people in (g, r) is $N^g(r)$, so all individuals in (g, r) want to have $rN^g(r)\rho(r, r')$ partners in (g', r'). On the other hand all people in (g', r') want to have $r'N^{g'}(r')\rho(r', r)$ partners in in (g, r). Therefore, we define **actual** number of partnership between groups (g, r) and (g', r') as harmonic average of these two values:

$$H(r, r') = \frac{2rN(r)\rho(r, r') \times r'N(r')\rho(r', r)}{rN(r)\rho(r, r') + r'N(r')\rho(r', r)}. \tag{9}$$

Therefore, we define

$$p(r, r') = \frac{H(r, r')}{N(r)}, \tag{10}$$

as the number of partners for a person with risk r who have risk r'.

2.2.2 Probability of Transmission per Partner

The probability that a susceptible person catches infection from their infected partner depends upon the number of sexual acts between the individuals. We allow the number of acts per partner for a person with risk r, $a(r)$, to depend upon the number of his (her) partners,(r), if the total number of acts is given by A, then the number of acts per partner for a person with risk r is

$$a(r) = \frac{A}{r}. \tag{11}$$

However, the number of acts between a person with risk r and their partner with risk r', should be the same as the number of acts between a person with risk r' and their partner with risk r. To make it compatible, we define harmonic average $A(r, r')$ as

$$A(r, r') = \frac{2a(r)a(r')}{a(r) + a(r')}, \tag{12}$$

that is the number of acts between a person with risk r and their partner with risk r'. In some portion of acts, people use condom, we assume a person with risk r, uses condom in $c(r)$ fraction of their acts, where $c(r)$ is an increasing function of r, that means people with

more partners are more likely to use condom in their acts. At the end of this subsection we will introduce the function $c(r)$.

Now suppose a person with risk r has a sexual act with their partner of risk r'. We know person r use condom in $c(r)$ fraction of their acts and person r' use condom in $c(r')$. Therefore, we should make decision if they use condom in their particular act or not. T here are two different scenarios for that:

1. **Preference to low condom use**: The decision tend to no condom act, it means the person who is less likely to use condom wins, therefore

$$C_1(r, r') = \frac{2c(r)c(r')}{c(r) + c(r')}. \tag{13}$$

2. **Preference to high condom use**: The decision tend to condom act, it means the person who is more likely to use condom wins, therefore

$$1 - C_2(r, r') = \frac{2(1 - c(r))(1 - c(r'))}{2 - c(r) - c(r')},$$

or

$$C_2(r, r') = 1 - \frac{2(1 - c(r))(1 - c(r'))}{2 - c(r) - c(r')}. \tag{14}$$

Now, suppose probability of transmission per no-condom act is $\bar{\beta}$ and probability of transmission under condom use is $\bar{\beta}_c = 0.01\bar{\beta}$, it means condom is 99% effective. Therefore,

the probability that a person with risk r does not catch infection after one condom act is $1 - \bar{\beta}_c$.

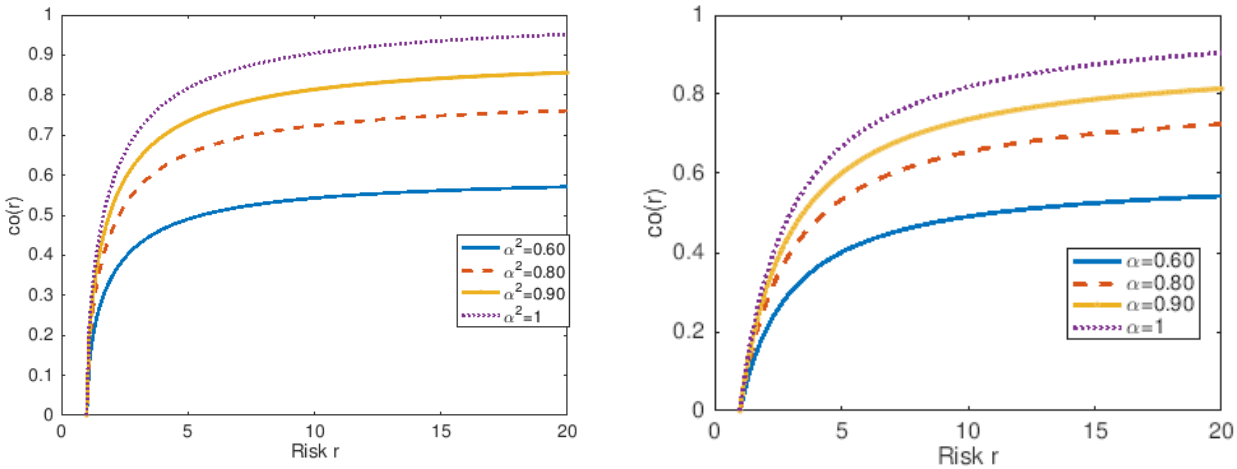
Assume a person with risk r has $A(r, r')$ act with their partner with risk r', and in $C(r, r')\%$ of the acts, they use condoms, therefore, they have a total of $C(r, r')A(r, r')$ acts with condom, and so the probability that the person with risk r doesn't catch infection from his infected partner with risk r' after finishing all condom acts is $(1 - \bar{\beta}_c)^{C(r,r')A(r,r')}$. Similarly, the probability that the person with risk r does not catch on infection from his infected partner with risk r' after finishing all no-condom acts is $(1 - \bar{\beta})^{(1-C(r,r'))A(r,r')}$. Finally the probability of catching infection after at least one act with partner r' is

$$\beta(r, r') = 1 - (1 - \bar{\beta}_c)^{C(r,r')A(r,r')}(1 - \bar{\beta})^{(1-C(r,r'))A(r,r')}. \tag{15}$$

The form of condom use function c(r): Now we are making several assumptions for condom use function $c(r)$ and define two different type of functions $c(r)$. The first assumption is that people with more partners use condom more [2, 13], therefore, $c(r)$ is an increasing function of r. Now the question is how fast this function grows. For this we made our own assumption: using condom for small value of r grows fast, however after some point it grows slowly. For that, the function should be concave down. The function should also be dimensionless, because it represents the fraction of times condom used by a person with r partners. Based on these assumptions we introduce two functions:

$$c_1(r) = \alpha\sqrt{\frac{r-r_0}{r+r_0}}, \quad \textit{and} \quad c_2(r) = \frac{\alpha(r-r_0)}{r+r_0}, \tag{16}$$

which are plotted for different α values in figure (3).



(a) $co_1(r) = \alpha\sqrt{\frac{r-r_0}{r+r_0}}$, (b) $co_2(r) = \alpha\frac{r-r_0}{r+r_0}$

Figure 3: Plot of two different condom use functions $c(r)$.

The value of α states, people with an infinite number of partners use condom in α fraction of their acts. That is

$$\lim_{r\to\infty} c(r) = \alpha.$$

Based on [15] people use condom at most at 50% of their sexual act, so we may assume $\alpha = 0.50$ at baseline.

To summarize we have the SIS model

$$\frac{dS^g(t,r)}{dt} = \mu(N_0^g(r) - N^g(r)) - \lambda^g(t,r)S^g(t,r) + \gamma I^g(t,r),$$

$$\frac{dI^g(t,r)}{dt} = \lambda^g(t,r)^g S^g(t,r) - \gamma I^g(t,r) - \mu I^g(t,r),$$

where all functions are defined in Table (1)

functions used in the model	
Function	Definition
$\lambda^g(t,r)$	$\int_{r_0}^{r\infty} \tilde{\lambda}^g(r,r')dr'$
$\tilde{\lambda}^g(r,r')$	$p(r,r')\beta(r,r')\frac{I^{g'}(t,r')}{N^g(t,r')}$
$p(r,r')$	$\frac{H(r,r')}{N(r)}$
$H(r,r')$	Harmonic average of $rN(r)\rho(r,r')$ and $r'N(r')\rho(r',r)$
$\rho(r,r')$	$\epsilon(r)\rho_b(r,r') + (1-\epsilon(r))\rho_r(r,r')$
$\epsilon(r)$	$\frac{0.6}{\sqrt{r}}$
$\beta(r,r')$	$1-(1-\bar{\beta})^{A(r,r')(1-C(r,r'))}(1-\bar{\beta}_c)^{A(r,r')C(r,r')}$
$A(r,r')$	Harmonic average of $a(r)$ and $a(r')$
$a(r)$	$\frac{A}{r}$
$C(r,r')$	Harmonic average of $c(r)$ and $c(r')$ (or 1− (Harmonic average of $1-c(r)$ and $1-c(r')$))
$c(r)$	$\alpha\sqrt{\frac{r-r_0}{r+r_0}}$

Table 1: The definition of functions used in the model.

3 Numerical Simulation

In our simulation, we assume for a period of one year, people have at least one and at most 20 concurrent partners. To find the number of people with risk r (N(r)), we use power law

distribution with parameter 3, it means

$$N(r) \propto r^{-3}.$$

For the initial condition we use current infection distribution over risk based on an individual data for Chlamydia. The Figure (4) shows the percentage of infection per risk. All other parameters and functions are fixed with the baseline values given in Tables (2) and (3), unless specifically defined otherwise.

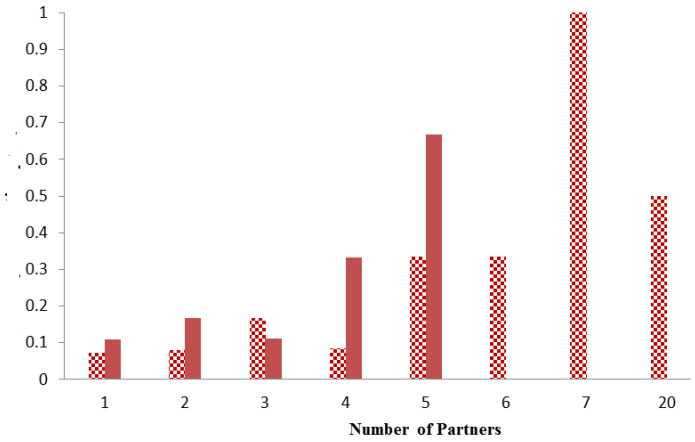


Figure 4: Initial Infection fraction for men and women, solid red columns refers to women and dashed red refers to men.

We aim to study the impact of condom use function $c(r)$ on the fraction of infected individuals at steady state that is a function of risk ($I^*(r)$) as well as the total fraction of infection for all risks ($\int_{r_0}^{r\infty} I^*(r)dr$). Figure (5) shows the function $I^*(r)$ for different

Model Quantities	Definition	Unit	Baseline Values
t	Time variable	Years	—
$S^g(t,r)$	Number of susceptible people with gender g and risk r at time t	People	—
$I^g(t,r)$	Number of infectious people with gender g and risk r at time t	People	—
N^g	Total population size of People with gender g.	People	1000
A	Total number of sexual acts per unit time.	Act	260
$\bar{\beta}$	Probability of transmission per unprotected act.	Act^{-1}	0.22
$\bar{\beta}_c$	Probability of transmission per protected act.	Act^{-1}	0.22×0.01
γ	Per capita recovery rate for humans from the infectious state to the susceptible state. $1/\gamma$ is the average duration of the infectious period.	$Year^{-1}$	2
μ	Migration rate.	$Year^{-1}$	0.10
$r_0(r_\infty)$	Minimum (maximum) number of partners	People	1(20)

Table 2: The definition of the model variables and parameters.

functions of risk r

Function	Description	Definition
$\rho_b(r,r')$	biased mixing function	$\begin{cases} \frac{r'-r+\sigma(r)}{\sigma^2(r)} & r-\sigma(r) \le r' \le r \\ -\frac{(r'-r-\sigma(r))}{\sigma^2(r)} & r < r' < r+\sigma(r) \\ 0 & elsewhere, \end{cases}$
$\rho_r(r,r')$	random mixing function	$\frac{(1-\epsilon(r')r'N(r'))}{\int_{r_0}^{r_\infty}(1-\epsilon(u))uN^{g'}(u)du}.$
$\epsilon(r)$	prefrence amount of risk r person to choose the same behavior partner.	$\frac{0.6}{\sqrt{r}}$
$a(r)$	total # of contacts for person of risk r pre day.	$\frac{A}{r}$
$c(r)$	fraction of times condom used by a person with risk r	$\alpha\sqrt{\frac{r-r_0}{r+r_0}}$

Table 3: The definition of functions of risk.

scenarios of condom use: when function $c(r)$ tends to α as r tends to ∞ ($\alpha\%$ condom), i.e

$$\lim_{r\to\infty} c(r) = \alpha$$

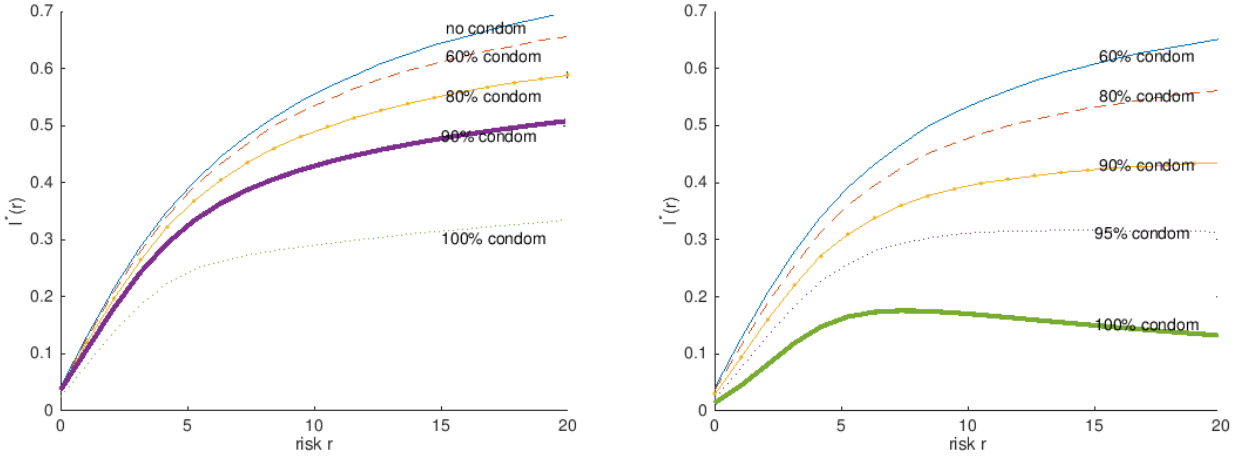
for $\alpha = 0, 60\%, 80\%, 90\%, 95\%, 100\%$. This means people with infinite number of partners use condom at $\alpha\%$ of their acts, and therefore, people with high but finite number of partners, use condom in some fraction close to but less than $\alpha\%$.

Figure (5.a) is the result when we apply preference to low condom use for $C(r, r')$, Equation (13). In this case, for all scenarios $I^*(r)$ is an increasing function of r, it means infection happen mostly among higher risk people, even if they use condom more. Increasing α only shifts the function $I^*(r)$ downward, without changing its shape. It means in any case, taking more partners increase your chance of getting infection. This is due to the fact that we take the Equation (13) for $C(r, r')$. The aformentioned strategy trusts more on lower-risk response regarding condom use. For example, if a person has risk 20 and reports to use condom 80% of the time and his partner has risk 10 and use condom in 50% of the time, Equation (13) finds a percentage to condom use that is closer to 50% other than 80%. Therefore, even if a person reports to use condom 100% of the time, the model doesn't apply 100% except for the case that his partner uses condom 100% of the times.

The strategy represented by Equation (14) is reverse, it trusts more on the response of higher-risk people regarding condom use. Figure (5.b) shows the result for when strategy

of Equation (14) is taken. In this case, by increasing condom use the graph of $I^*(r)$ drops down and becomes flatter. In this graph, we observe for each $\alpha > 80\%$ there is a sharp threshold, a risk r^* for which people with risk more than r^* have the same chance of catching infection. To see that we test condom function for more α values between 80% and 100% and found that r^* values, then we fitted a curve trough these points to predict r^* for all α values, the Figure (6) shows the result.

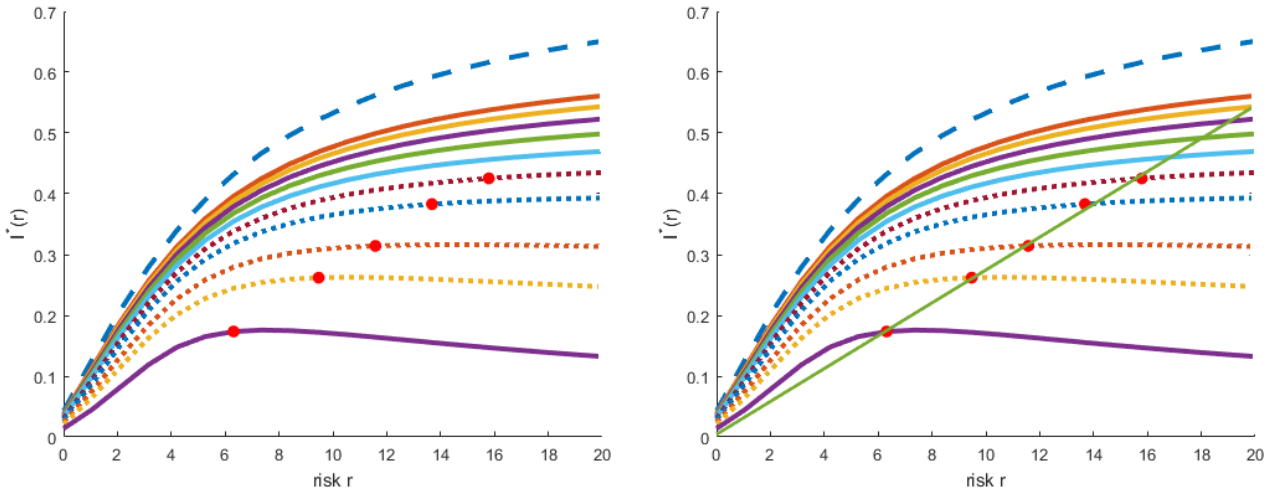
In all these simulations we used $\epsilon(r) = \epsilon_4(r) = \frac{0.6}{\sqrt{r}}$ (ϵ shown in Table (3)) for the mixing function. For other ϵ_i values we have the same results, however if we use $\epsilon_3 = 1$, for all strategies for $C(r, r')$ we have similar result to figure (5.b). Because taking $\epsilon_3 = 1$ means that people have only partners with the same risk as themselves, therefore higher risk ones have contact with only higher risk ones and vise versa, therefore, we have $C(r, r') = c(r) = c(r')$ and when high risk people use condom 100% of the time the infection disappears among them and therefore peak of infection happens among lower risk people.



(a) $C(r, r')$ follows equation (13)

(b) $C(r, r')$ follows equation (14)

Figure 5: Different Scenarios of condom use (different α) for ϵ_4 and function $co(r) = co_1$. For co_2 and $co_3(r)$ the result were similar, so we skip them. Increasing condom use by high-risk people does not save them from a possible infection.



(a) $C(r, r')$ follows equation (13)

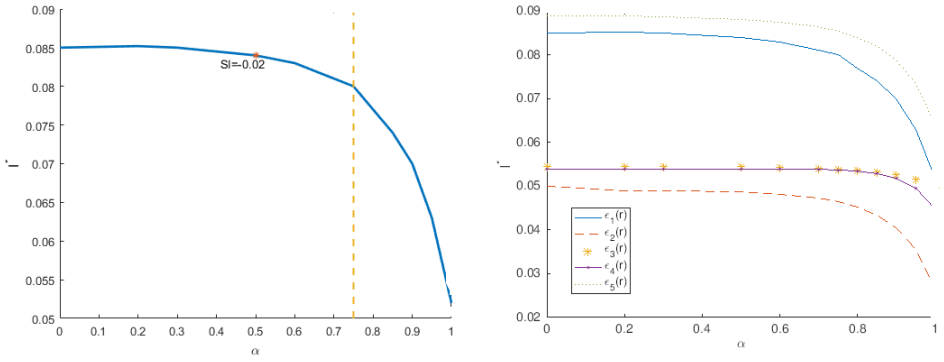
(b) $C(r, r')$ follows equation (13)

Figure 6: (a)$I^*(r)$ for $\epsilon = \frac{0.6}{\sqrt{r}}$, sharp threshold is observed in STI prevalence with increase in any risk r, however threshold decreases and shift to the left when condom use increases.(b) Fit a curve through r^* to find r^* for any $\alpha \in [0, 1]$.

These result also shows for $\alpha \in [80\%, 100\%]$, $I^*(r)$ decreases faster than other values. Therefore we plot the graph $I^* = \int_{r_0}^{r_\infty} I^*(r)dr$ v.s α to see how prevalence changes. Figure (7.a) shows how total fraction of infection at steady state ($I^* = \int_{r_0}^{r_\infty} I^*(r)dr$) changes by increasing condom use by high risk people. The baseline value for α is 0.5 (that is when people at ∞-risk use condom at 50% of their acts). At this point sensitivity index of I^* is -0.02, that is, at this point if α increases by 1% then I^* decreases by 0.02%. However, from the same figure, we observe that to drop down the prevalence, α needs to be at least 75%.

Again, in this simulation we used $\epsilon_4(r)$ in mixing function. Now we are going to test other mixing functions by taking different $\epsilon(r)$ functions. Figure (7.b) shows $I^* =$

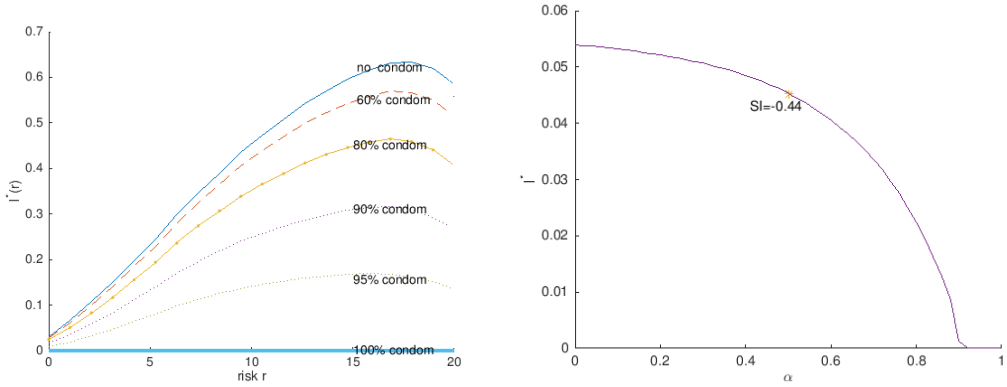
$\int_{r_0}^{r\infty} I^*(r)dr$ v.s α for different mixing functions. As we observe, for different mixing functions, I^* is not sensitive to percentage of time people with ∞ number of partners use condom.



(a) I^* v.s α for ϵ_4 (b) I^* v.s α for all ϵs

Figure 7: This figures report the simulation with condom function $c_1(r)$, for $c_2(r)$ results are similar.(a) The sensitivity of $I^* = \int_{r_0}^{r\infty} I^*(r)dr$ with respect to α. The sensitivity index is then the slope of the response curve at the baseline values, indicated by $*$. The response is linear near the baseline case and, therefore, the local sensitivity analysis is valid over a broad range of parameters. (b) For all mixing functions used here, α needs to be at least 80% to drop the infection down.

Therefore, it seems when we fix preference neighborhood and assign a value for this neighborhood ($\epsilon(r)$) prevalence of infection would not be sensitive to α near its baseline. Now we use Equation (6) for defining $\epsilon(r)\rho_b(r, r')$ and define $\epsilon(r) = 0.25$ and $\sigma(r) = \sqrt{r}$, it means a person with risk r wants to have 25% of his partners in domain of $(r-\sqrt{r}, r+\sqrt{r})$. That way by increasing the radius of preferred neighborhood for a person with risk r is expanded. The Figure (8) shows the result of this simulation: (8.a) is graph of I^* v.s risk, which shows for all scenarios high risk people are among the one with most chance of infection. Figure (8.b) is graph of I^* v.s α for when we use Equation (6) in the mixing



(a) I^* v.s α for ϵ_4 (b) I^* v.s α for ϵ_4

Figure 8: (a) Different Scenarios of condom use (different α) for $\epsilon = 0.25$ and function $c(r) = c_1$. Increasing condom use by high-risk people doesn't save them from infection. (b) The sensitivity of $I^* = \int_{r_0}^{r_\infty} I^*(r)dr$ with respect to α. The sensitivity index is then the slope of the response curve at the baseline values, indicated by $*$.

function. As we observe, by increasing the radius of preferred neighborhood, I^* becomes more sensitive to α. Sensitivity index at baseline is -0.44, and after 90% condom use infection will die out.

4 Discusion

We created a continuous risk sexual heterosexual SIS transmission model for the spread of highly infectious STIs with heterogeneous mixing partnership selection to investigate the impact of condom use by high risk people in controlling spread of STI's.

We implemented different condom use functions and studied their impact on fraction of infected people versus their risk. Our result show the spread of infection over the risk (shape of $I^*(r)$) depends on model structure, and how we define condom use function.

We implemented different mixing functions and different condom use scenarios and then we did sensitivity analysis of prevalence with respect to fraction of the times that high risk people use condom. Our result shows that when people have more partners with the risks close to (but not equal) their risk, the sensitivity index of prevalence with respect to condom use is more than the case people choose some percentage of their partner with exactly the same risk and rest randomly.

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