Behaviour Change and Treatment of Core Groups: Its Effect on the Spread of HIV/AIDS

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Abstract. A general model is considered for treatment and behaviour change of the Human Immunodeficiency Virus (HIV) infecteds in a highly sexually active core group of female commercial sex workers (CSW's) and a "bridge population" of young unpartnered males. In this model, the spread of HIV/AIDS in the community is carried out mainly through the sexual interaction between the core group and the bridge population which acts as a bridge for the spread of disease to the general population. We will consider the effect of treatment of the infecteds and/or the subsequent behaviour change when targeted toward the core group and the bridge population. Analytical results will be given for a strategy which targets treatment and behaviour change at either the core group or the bridge population. Numerical examples are also provided to illustrate the biological significance of the treatment/behaviour change and its effect on the threshold parameter values. The results show that if the contact rates and transmission probabilities of the treated individuals are sufficiently reduced, the treatment/behaviour change can eradicate the disease provided that the level of treatment in the infected population is sufficiently high. However, an ill-planned treatment program which fails to meet the required reductions in contact rate or transmission probability could have a detrimental effect on the spread of the epidemic.

1 Introduction

The spread of Human Immunodeficiency Virus/Acquired Immunodeficiency Syndrome (HIV/AIDS) in Asia, emerging only in the late 1980's, is relatively recent when compared with the spread of the epidemic in Africa, Western Europe, and North America. However, the scale of the rapidly spreading AIDS epidemic in Thailand, Myanmar, India, and other Asian countries reported in recent years (see e.g., [1]) has been alarming and has prompted many rather grim predictions. For example, Chin [2] used the EPIMODEL ([3]) with various "HIV scenarios" to project future spread of HIV in the world. The result points to projections that, by the year 2000, the number of new HIV infections in Asia may reach its peak, exceeding those of rest of the world combined, before tailing off. Among these Asian countries, the spread of HIV in Thailand has been most explosive and most well-documented. (See e.g. [4].) The key ingredients to the epidemic in Thailand are a "core group" of highly sexually active individuals (the female commercial sex workers, or CSW's, see e.g. [5]) which spreads the disease, and a "bridge population" (unpartnered young men, low-income male brothel visitors, and truck drivers) which provide a bridge for transmissions of HIV/AIDS between the core group and the general population of noncore females and their offsprings [6]. For theoretical studies of India, one may also add the professional blood donors to this group. While the important role of a core group such as CSW's in the transmission of sexually transmitted disease (STD) has been well-known (see e.g. [7]), the bridge population is somewhat a unique feature of developing countries like Thailand which needs further study. In recent years, the Thai government has been one of the most aggressive governments in the world in the fight against AIDS. AIDS prevention measures used in Thailand include establishing a Sentinel surveillance system to keep track of the new trends in the spread of HIV/AIDS, implementing comprehensive programs to increase AIDS awareness in the general public, and encouraging use of safe sex in commercial sex establishments via the "100% Condom Program" (see [8]) implemented in 1991 for distribution and promotion of condom use in sexual contacts, even with sanctions against those establishments with record of noncompliance. These measures seems to have taken effect. One evidence is the sharp drop in the STD

level reported at government STD clinics where in 1993 the STD level is only 29.26% of the 1990 STD level [9]. Moreover, Thongthai and Guest [10] reported from a 1993 survey that 10.1% of the males surveyed (age 15-49) had bought sex in the last 12 months, as compared to 21.8% in a similar survey conducted in 1990 by Sittitrai et al. [11]. Finally, the success of the 100% Condom Program is also clearly evident by comparing the two surveys. In the 1990 Survey only 33.3% of the male respondents who had commercial sex in the last 12 months used a condom every time they bought sex, while 34.1% never use condom when engaged in commercial sex. By 1993, the survey showed the corresponding numbers are 71.4% always use condom and 10.9% never use condom in commercial sex. However recent results of sustaining prevalence rates among the male army conscripts, pregnant women, and IVDU's from the Thai HIV Serosurveillance Survey, Round 16, June 1998 [12] do not give any clear indication that the prevention measures have had a positive impact. Whether the change in behaviour resulting from the prevention programs, along with the on-going development of vaccine, will be enough to slow down and eventually stop the spread of the epidemic is a question we must explore [13].

A model was proposed by Busenberg,Cooke, and Hsieh [14] aimed at studying the importance of the CSW's, although in that work the bridge population was expanded to include all unpartnered young men for the purpose of simplifying the model. The results showed that, among others, the recruitment rate of the CSW's and the relative difference in turnover rate (by death and retirement) of the CSW's once they become infected are important factors in determining whether the disease will persist.

In this work, we propose a model to further study the possible effect of treatment and behaviour change of the core group of CSW's and the bridge population in the society with the above-mentioned situation. A prevention program targeting CSW's for educational campaign and promoting use of condoms has been implemented in Thailand since 1994, although with only limited success (see [15]). Theoretical studies of the effect of treatment and/or behaviour change on spread of HIV/AIDS and other STD's can be found in, among others, [16, 17, 18, 19, 20, 21, 22, 23, 24]. Other studies on heterosexual transmissions with

a group of prostitutes include [25] and [26].

In our present model, it is assumed that treatment leads to a change in transmission probability of the treated individuals, and the behaviour change which occurs as a result of treatment and education program leads to reduced sexual contacts or less risky behaviour (such as use of condom). Both occurrences would affect the spread of the disease on the population level. To study its effect, we will use a model of linear treatment/behaviour change rate which assumes that the number taken into treatment or undergoing behaviour change is proportional to the number of untreated infecteds. (See [22] for a discussion on the choice of linear treatment rate.)

The model in [14] contains a "supply and demand" assumption on the recruitment of the prostitute core group which simply states that the recruitment rate of the CSW's is proportional to the number of potential male customers. In order to take into account of the behaviour change in the male customers, we have generalized this assumption to having the recruitment rate of CSW's proportional to the *total number of contacts* between males and females in the population. In the instances when no behaviour change occurs, this reduces to the model of [14].

In Section 2, we formulate the generalized model with treatment and behaviour change and give some general mathematical results which enables us to study a reduced system of equations. In Section 3 analytical results are given in the framework of screening and removal of the detected infecteds from sexually active population (see [27] for a similar model for gay population), i.e., the treated infecteds are confined to having sexual contacts only with other treated infecteds through education programs which lead to the change in behaviour. Some numerical examples are also given to illustrate the biological significance of the results. In Section 4 we describe some general mathematical results which enables us to reduce our model equations down to a four-dimensional system. In Section 5 we obtain relevant threshold parameters for the special case of treatment and behaviour change for only the bridge population. Local analysis is given followed by a discussion on the biological significance of these parameters with numerical examples. Finally Section 6 contains some

general remarks.

2 The Model

We consider four population groups of sexually active individuals: the core group of CSW's; the young unpartnered males; the young noncore females; and married couples. Within the core and young unpartnered males groups, there is a further division into susceptibles (non-infected), untreated infecteds, and treated infecteds. Thus we introduce the following symbols, all of which are assumed to vary with time.

F_0 = number of susceptible core females

U_0 = number of untreated infective core females

T_0 = number of treated infective core females

M_1 = number of susceptible unpartnered young males

U_1 = number of untreated infective unpartnered young males

T_1 = number of treated infective unpartnered young males

F_1 = number of susceptible noncore young females

f_1 = number of infective noncore young females

S_2 = number of couples in which both partners are susceptible

I_2 = number of couples in which one or both partners are infective.

We make note of the following assumptions, which we make to focus on the role of prostitution as the primary mode of spread.

Assumptions: Homosexual and drug activity are not included. Sexual contact of single males other than with prostitutes is neglected. Individuals in pairs do not have

extra-marital contacts. No break-up of pairs. All pairs are either susceptible or infective. No vertically transmitted HIV-infectives survive to join the sexually active population.

Moreover, we assume the "bridge population" to be the group of all unpartnered young men to keep our model simple. In a related work in preparation [28], different sexual activity levels will be assigned to the unpartnered young men with the group of highly sexually active unpartnered young men acting as the bridge population for the spread of epidemic.

We also introduce the following parameters for the model, all of which are assumed to be nonnegative (note that all parameters with the prime(') are the corresponding parameters for the treated classes):

$\alpha^*(c_m M_1 + c_m U_1 + c'_m T_1)$, the rate at which the core females (CSW's) are recruited, which is assumed to be proportional to the total number of required contacts per year by young men. This is a "supply and demand" assumption. α^*, a positive constant less than one, is the constant of proportionality at which the core prostitutes are recruited.

μ_i, $\bar{\mu}_i$, and $\bar{\mu}'_i$ (i = 0,1,2), removal rates due to death or removal from the geographic area or withdrawal from sexual activity in various populations.

c_f and c'_f, the contact rates or number of sexual contacts per unit time for untreated (including susceptible) and treated core females, respectively.

c_m and c'_m, the contact rates or number of sexual contacts per unit time for untreated (including susceptible) and treated young males.

β and β', the male-to-female transmission probabilities per sexual contact from untreated and treated young males, respectively.

$\bar{\beta}$ and $\bar{\beta}'$, the female-to-male transmission probabilities per sexual contact from untreated and treated core females, respectively. Note that we assume the male-to-female transmission probability is greater than that of female-to-male (i.e. $\beta > \bar{\beta}$).

$\rho_0, \bar{\rho}_0$, and $\bar{\rho}'_0$, the respective rates at which susceptible, infected untreated, and treated core females "retire" and move to the noncore female population.

$\sigma_1, \bar{\sigma}_1$, and $\bar{\sigma}'_1$, the respective pairing rates of susceptible, untreated and treated infective young males who form couples with noncore females. Note that we assume that these rates depend on the health status of the males, but not on the health status of the noncore females with whom they form pair. Thus the male is assumed no to know whether the female partner is infected at the time of pair-forming.

2b, the per capita rate at which new mature individuals enter the young male and young female groups (births per susceptible couple times the survival fraction). A one-to-one sex ratio is assumed.

ω, a factor multiplying b for births to infective couples, represents the reduced probability at which children of infective couples will survive to enter the sexually active population compared to children of non-infective couples.

We assume the following hypotheses on these parameters:

$$H1. \quad c_m(U_1 + M_1) + c'_m T_1 = c_f(U_0 + F_0) + c'_f T_0$$

This "conservation of total contacts" hypothesis states that the total number of contacts made by males with females, per unit time, is equal to the total number of contacts made by females with males, per unit time. Typically, $c_f > c_m$, $c'_f > c'_m$, and the young male population $U_1 + M_1 + T_1$ is larger than the core female population $U_0 + F_0 + T_0$. We note then that we have

$$\alpha^*[c_m(U_1 + M_1) + c'_m T_1] = \alpha[(U_0 + F_0) + c'_f/c_f T_0], \tag{1}$$

where $\alpha = c_f \alpha^*$. Since our model does not postulate constant population sizes, the parameters $c_m, c_f, c'_m, c'_f, \alpha$, and α^* will in general vary with time or according to the state of the system and the preference of the individuals. However, in this paper the contact rates are also assumed to remain constant in time (see [29] or [14] for a discussion). As a consequence, the population sizes of the core females and unpartnered men must vary to keep the number of total contacts balanced as the total population size varies. However, this is consistent with our "supply and demand" hypothesis where the CSW's are recruited in constant proportion to the number of contacts of unpartnered males.

$H2'$. $\quad \bar{\mu}_0 + \bar{\rho}_0 > \mu_0 + \rho_0, \quad \bar{\mu}_0 + \bar{\rho}_0 > \bar{\mu}'_0 + \bar{\rho}'_0,$

$H3$. $\quad c_m \geq c'_m, \quad c_f \geq c'_f, \quad \beta \geq \beta', \quad \bar{\beta} \geq \bar{\beta}', \quad \beta \geq \bar{\beta}, \quad \beta' \geq \bar{\beta}'.$

H2' is based on the plausible assumption that the rate of "removal" plus "retirement" from the group of untreated infected CSW's is greater than the same rates for the susceptible CSW's and the treated infected CSW's. H3 assumes that treatment results in lesser or equal contact rates and transmission probabilities for the treated individuals; and the male-to-female transmission probability is greater than or equal to the female-to-male transmission probability (see, e.g. [30]).

The next hypothesis concerns the nature of the mixing of subgroup members (see e.g. [31], [32]) where we assume proportional mixing. The incidence rate of new infections within the core group may then be written as

$$H4. \quad c_f F_0[\frac{c_m \beta U_1}{c_m(U_1 + M_1) + c'_m T_1} + \frac{c'_m \beta' T_1}{c_m(U_1 + M_1) + c'_m T_1}] =$$

$$c_f F_0[\frac{c_m \beta U_1}{c_f(U_0 + F_0) + c'_f T_0} + \frac{c'_m \beta' T_1}{c_f(U_0 + F_0) + c'_f T_0}].$$

The first quantity before the equal sign may be justified as the product of c_f , the number of contacts of a susceptible CSW times the number of susceptible CSW's, times the sum of the respective probabilities that a susceptible CSW will be infected by an untreated infected young man and a treated young man per contact. The equality is due to Hypothesis $H1$.

$H5'$. $\quad \bar{\mu}_1 + \bar{\sigma}_1 > \bar{\mu}'_1 + \bar{\sigma}'_1$

This intuitive hypothesis assumes that the removal plus pair-forming of the untreated infected young men is greater than that of the treated infected young men.

Finally, let $N_0 = F_0 + U_0 + T_0$ and $N_1 = M_1 + U_1 + T_1$ be the numbers of sexually active core female and unpartnered male populations, respectively. The respective numbers of infected CSW's and unpartnered men detected and treated at each time unit, $\bar{\sigma}_f(U_0, N_0)$ and $\bar{\sigma}_m(U_1, N_1)$ are assumed to depend on the population size of the yet untreated infecteds as well as the prevalence of untreated HIV-infected persons for each sex. Clearly we must have $\bar{\sigma}_j \geq 0, j = f, m$ and $\bar{\sigma}_f(0, N_0) = \bar{\sigma}_m(0, N_1) = 0$. Furthermore, in this paper we assume

the treatment terms to be linear functions of the untreated infecteds, i.e.

$$H6. \quad \bar{\sigma}_f(U_0, N_0) = \sigma_f U_0, \bar{\sigma}_m(U_1, N_1) = \sigma_m U_1,$$

where σ_f and σ_m are nonnegative constants less than one and measure the effectiveness of the treatment program in bringing untreated infecteds into the program. HIV models using linear rate of treatment include [16, 17, 22]. Also note that σ_f and σ_m are different from σ_1, the pairing rate of the susceptible males.

$$H7'. \quad \alpha + \bar{\mu}_1 + \bar{\sigma}_1 \geq \bar{\mu}_0 + \bar{\rho}_0 + \sigma_f$$

The last assumption $H7'$ says that the recruitment rate of the CSW's plus the total dispersal rate (removal and pairing) of an untreated infected single man must be greater or equal to the total dispersal rate (removal plus retirement and detection) of the untreated infected CSW's. This roughly implies that the dispersal of untreated single men and the recruitment of untreated CSW's must exceed the dispersal of the untreated infected CSW's, thereby maintaining the core group in balance. While less intuitive, H7' ensures the well-posedness of our model equations.

We have the following model equations, where $\frac{d}{dt}$ denotes derivative with respect to time.

$$\begin{aligned}
\frac{dF_0}{dt} &= \alpha^*[c_m(U_1 + M_1) + c'_m T_1] - (\mu_0 + \rho_0)F_0 - c_f F_0[\frac{c_m \beta U_1}{c_f(U_0 + F_0) + c'_f T_0} + \\
&\quad \frac{c'_m \beta' T_1}{c_f(U_0 + F_0) + c'_f T_0}] \qquad (2)\\
\frac{dU_0}{dt} &= c_f F_0[\frac{c_m \beta U_1}{c_f(U_0 + F_0) + c'_f T_0} + \frac{c'_m \beta' T_1}{c_f(U_0 + F_0) + c'_f T_0}] - (\bar{\mu}_0 + \bar{\rho}_0)U_0 - \sigma_f U_0\\
\frac{dT_0}{dt} &= \sigma_f U_0 - (\bar{\mu}'_0 + \bar{\rho}'_0)T_0\\
\frac{dM_1}{dt} &= b(S_2 + \omega I_2) - c_m M_1[\frac{c_f \bar{\beta} U_0}{c_f(U_0 + F_0) + c'_f T_0} + \frac{c'_f \bar{\beta}' T_0}{c_f(U_0 + F_0) + c'_f T_0}] - (\mu_1 + \sigma_1)M_1\\
\frac{dU_1}{dt} &= c_m M_1[\frac{c_f \bar{\beta} U_0}{c_f(U_0 + F_0) + c'_f T_0} + \frac{c'_f \bar{\beta}' T_0}{c_f(U_0 + F_0) + c'_f T_0}] - (\bar{\mu}_1 + \bar{\sigma}_1)U_1 - \sigma_m U_1\\
\frac{dT_1}{dt} &= \sigma_m U_1 - (\bar{\mu}'_1 + \bar{\sigma}'_1)T_1\\
\frac{dS_2}{dt} &= \sigma_1 \frac{M_1 F_1}{f_1 + F_1} - \mu_2 S_2
\end{aligned}$$

$$
\begin{aligned}
\frac{dI_2}{dt} &= \sigma_1 \frac{M_1 f_1}{f_1 + F_1} - \bar{\mu}_2 I_2 + \bar{\sigma}_1 U_1 + \bar{\sigma}_1' T_1 \\
\frac{dF_1}{dt} &= b(S_2 + \omega I_2) + \rho_0 F_0 - \mu_1 F_1 - \frac{F_1}{f_1 + F_1}(\sigma_1 M_1 + \bar{\sigma}_1 U_1 + \bar{\sigma}_1' T_1) \\
\frac{df_1}{dt} &= \bar{\rho}_0 U_0 + \bar{\rho}_0' T_0 - \bar{\mu}_1 f_1 - \frac{f_1}{f_1 + F_1}(\sigma_1 M_1 + \bar{\sigma}_1 U_1 + \bar{\sigma}_1' T_1)
\end{aligned}
$$

Detailed explanations of some of the equations were given in [14]. Here we will focus on what distinguishes the present generalized model from the model in [14]. The last two terms in the first equation represent the incidence of new infections with the extra term for the infections due to the treated young males. The first term in the first equation represents the recruitment of new core females, which is assumed to be proportional to the total number of contacts by young males (or total trade volume of the sex business). We are therefore implicitly assuming an unlimited resource for recruitment.

First two terms in the second equation represent the incidence of newly infecteds. The last term represents the detection and treatment of infected core females which in general depends on the size of the untreated infective core population U_0 as well as the total core female population N_0. The first term in the third equation is the newly treated individuals and the other term is the corresponding term for removal and transfer of treated infecteds.

In the equation for $\frac{dM_1}{dt}$, bS_2 gives the rate of birth and survival to maturity of young males from susceptible pairs, and $b\omega I_2$ the same rate for young males from infected pairs. There is no similar term in the equation for $\frac{dU_1}{dt}$ because vertical transmission is not considered in this model. The second term in the $\frac{dM_1}{dt}$ equation and the first term in the $\frac{dU_1}{dt}$ equation represent incidence of infection of males due to contact with infected core females (both untreated and treated). The terms $\mu_1 M_1$, $\bar{\mu}_1 U_1$, and $\bar{\mu}_1 T_1$ are for 'removals' and the terms $\sigma_1 M_1$, $\bar{\sigma}_1 U_1$, and $\bar{\sigma}_1 T_1$ give the rate at which males form new pairs. The last term in the equation for $\frac{dU_1}{dt}$ represents detection and treatment of previously untreated infecteds. Similarly for the terms in the equation for $\frac{dT_1}{dt}$.

Finally, detailed explanation of the terms representing formation of pairs can be found in [14]. More general discussion of such pairing functions may also be found, for example, in [33] or [25].

Using hypothesis $H1$, we replace $\alpha^*[c_m(U_1+M_1)+c'_mT_1]$ by $\alpha[(U_0+F_0)+c'_fT_0/c_f]$. We further use $H6$ to decouple the equations for F_0, U_0, T_0, U_1 and T_1 from the others. Moreover, by redefining μ_0 to be the former $\mu_0+\rho_0$, $\bar{\mu}_0$ to be the former $\bar{\mu}_0+\bar{\rho}_0$, $\bar{\mu}'_0$ to be the former $\bar{\mu}'_0+\bar{\rho}'_0$, $\bar{\mu}_1$ to be the former $\bar{\mu}_1+\bar{\sigma}_1$, and $\bar{\mu}'_1$ to be the former $\bar{\mu}'_1+\bar{\sigma}'_1$, we can write these equations in the following simpler form

$$\begin{aligned}
\frac{dF_0}{dt} &= \alpha[(U_0+F_0)+\frac{c'_f}{c_f}T_0]-\mu_0F_0-c_fF_0[\frac{c_m\beta U_1}{c_f(U_0+F_0)+c'_fT_0}+ \\
&\quad \frac{c'_m\beta'T_1}{c_f(U_0+F_0)+c'_fT_0}], \qquad (3)\\
\frac{dU_0}{dt} &= c_fF_0[\frac{c_m\beta U_1}{c_f(U_0+F_0)+c'_fT_0}+\frac{c'_m\beta'T_1}{c_f(U_0+F_0)+c'_fT_0}]-\bar{\mu}_0U_0-\sigma_fU_0, \qquad (4)\\
\frac{dT_0}{dt} &= \sigma_fU_0-\bar{\mu}'_0T_0, \qquad (5)\\
\frac{dU_1}{dt} &= c_f\bar{\beta}U_0+c'_f\bar{\beta}'T_0-(c_mU_1+c'_mT_1)\frac{c_f\bar{\beta}U_0+c'_f\bar{\beta}'T_0}{c_f(U_0+F_0)+c'_fT_0}-\bar{\mu}_1U_1-\sigma_mU_1 \qquad (6)\\
\frac{dT_1}{dt} &= \sigma_mU_1-\bar{\mu}'_1T_1. \qquad (7)
\end{aligned}$$

Hypothesis $H2', H5'$, and $H7'$ now take the following forms.

$H2.$ $\bar{\mu}_0>\mu_0, \bar{\mu}_0>\bar{\mu}'_0$

$H5.$ $\bar{\mu}_1>\bar{\mu}'_1$

$H7.$ $\alpha+\bar{\mu}_1\geq\bar{\mu}_0+\sigma_f$

3 Screening and Removal by Treatment from Contact with Active Population

Our first result concerns the special case for this system where the treated infecteds are refrained completely from sexual contacts in the susceptible sexually active population so that $c'_m=c'_f=0$ and, consequently, $N_0=F_0+U_0$ as T_0 is no longer part of the sexually active core female population. This assumption is appropriate in the instances where, through a treatment program which includes educational sessions that result in behaviour change, the

treated infected individuals confined all their sexual contacts to other treated infecteds. The model does not specifically include possible contacts of treated infected core females with treated infected unpartnered men, since we may assume that such contacts would have a negligible effect on the progress of the epidemic. For a similar model with homosexual populations, see [27]. Also see [24] for an STD epidemics model with isolation strategies.

Consequently, we can eliminate Equations (5) and (7) for T_0 and T_1 from our system of equations in (3)-(7). Moreover, we now introduce the notation

$$y_1 = \frac{F_0}{N_0}, \quad y_2 = \frac{U_0}{N_0}, \quad y_4 = \frac{U_1}{N_0}.$$

Using the fact that $y_2 = 1 - y_1$, our system becomes

$$\frac{dy_1}{dt} = -y_1 c_m \beta y_4 + (1 - y_1)[\alpha + (\bar{\mu}_0 + \sigma_f - \mu_0) y_1], \tag{8}$$

$$\frac{dy_4}{dt} = (c_f \bar{\beta} - c_m y_4 \bar{\beta})(1 - y_1) - y_4[\alpha + \bar{\mu}_1 - \mu_0 + \sigma_m - (\bar{\mu}_0 + \sigma_f - \mu_0)(1 - y_1)], \tag{9}$$

which is the same as (14)-(15) in [14] except y_3 becomes y_4, $\bar{\mu}_0$ becomes $\sigma_f + \bar{\mu}_0$, and $\bar{\mu}_1$ becomes $\bar{\mu}_1 + \sigma_m$. Hence the analysis follows similarly.

We define the following parameters:

$$S = \{(y_1, y_4) : 0 < y_1 < 1, 0 < y_4 < c_f/c_m\}$$

$$A = (\bar{\mu}_0 + \sigma_f - \mu_0)(c_m \bar{\beta} - \bar{\mu}_0 - \sigma_f + \mu_0)$$

$$B = c_m \bar{\beta}(c_f \beta + \alpha) - (\bar{\mu}_0 + \sigma_f - \mu_0)(c_m \bar{\beta} - \bar{\mu}_0 + \bar{\mu}_1 + 2\alpha - \sigma_f + \sigma_m)$$

$$C = -\alpha(c_m \bar{\beta} - \bar{\mu}_0 + \bar{\mu}_1 + \alpha + \sigma_m - \sigma_f)$$

$$R_f^2 = \frac{c_m c_f \beta \bar{\beta}}{(\alpha + \sigma_f + \bar{\mu}_0 - \mu_0)(\alpha + \sigma_m + \bar{\mu}_1 - \mu_0)}, \qquad R_f > 0.$$

$$R_0^2 = c_m c_f \beta \bar{\beta} / (\bar{\mu}_0 + \sigma_f)(\bar{\mu}_1 + \sigma_m).$$

$$R_1 = \begin{cases} \dfrac{\alpha}{\mu_0} & \text{if } R_f \leq 1 \\ \dfrac{\alpha}{\mu_0 + (\bar{\mu}_0 + \sigma_f - \mu_0) y_2^*} & \text{if } R_f > 1 \end{cases}$$

where y_2^* denotes an endemic equilibrium value of y_2.

$$R_1^* = \begin{cases} \dfrac{\alpha}{\mu_0} & \text{if } (y_1, y_2, y_4) \to (1, 0, 0) \\ \dfrac{\alpha}{\mu_0 + (\bar{\mu}_0 + \sigma_f - \mu_0)\bar{y}_2} & \text{if } (y_1, y_2, y_4) \to (\bar{y}_1, \bar{y}_2, \bar{y}_4) \end{cases}$$

where $(\bar{y}_1, \bar{y}_2, \bar{y}_4)$ could be any endemic equilibrium.

A, B, C, are the coefficients of the quadratic equation $Ay^2+By+C = 0$. The roots of the equation in $(0, 1)$, if they exist, yield the y_1 values of positive equilibria for System (8)-(9). R_f is the threshold parameter which determines the persistence of the endemic fractions in the population. R_0 is the basic reproductive number for the infected populations, while R_1 is a threshold parameter determining whether the total population goes to ∞ or 0. Note that all these parameters are the same as in [14] except $\bar{\mu}_0$ is replaced by $\bar{\mu}_0 + \sigma_f$ and $\bar{\mu}_1$ replaced by $\bar{\mu}_1 + \sigma_m$. Hence the following result for existence, uniqueness, and stability of positive equilibrium of System (8)-(9) is reproduced from Theorem 2 in [14] where "AS" denotes locally asymptotically stable:

TABLE 1

Analytical Result for Positive Equilibrium of Model

		R_f	Number of positive Equilibria	Stability
Case I	$A > 0$	> 1	1	AS
		≤ 1	0	-
Case II	$A = 0$	> 1	1	AS
		≤ 1	0	-
Case III	$A < 0$	> 1	1	AS
		$= 1$	$0(A \geq C)$	-
			$1(A < C)$	AS
		< 1	$0(B^2 < 4AC)$	-
			$1(B^2 = 4AC)$	Stable
			$2(B^2 > 4AC)$	One AS, one unstable

Furthermore, we also have the following results for the present model which were also proven in [14]:

Theorem 1. *(1) If $A \geq 0$, the disease-free equilibrium (abbreviated DFE) at $(1,0)$ is globally asymptotically stable (abbreviated G.A.S.) within the set S if $R_f \leq 1$. If $R_f > 1$, the unique endemic equilibrium is G.A.S. within S.*

(2) If $A < 0$, the above result still applies unless (i) $R_f = 1$ and $A < C$, or (ii) $R_f < 1$ but $B^2 \geq 4AC$. For case (i), DFE is linearly stable but not attracting in S. So the unique endemic equilibrium is G.A.S. in S. For case (ii), when $B^2 > 4AC$ there are two endemic equilibria in S where the one with smaller y_1 value is asymptotically stable and the other unstable. The stable manifold of the unstable endemic equilibrium divides S into two regions which are the domains of attraction for the asymptotically stable endemic equilibrium and the asymptotically stable DFE. Hence we have a saddle-node connection. When $B^2 = 4AC$, we have a saddle-point bifurcation of the previous case so that there is a unique endemic equilibrium. The stable manifold of the endemic equilibrium once again divides S into two regions which are the domains of attraction for itself and DFE.

Theorem 2. *Assume Cases I or II in Theorem 1. The limiting values of variables F_0, U_0, M_1, U_1 are given in Table 2.*

TABLE 2

Limiting values of variables for Cases I and II.

R_f	R_1	R_0	$N_0(t)$	(y_1, y_2, y_4)	(F_0, U_0, U_1, M_1)
≤ 1	< 1	$< 1^a$	0	(1,0,0)	(0,0,0,0)
> 1	< 1		0	(y_1^*, y_2^*, y_4^*)	(0,0,0,0)
> 1	> 1	$> 1^a$	∞	(y_1^*, y_2^*, y_4^*)	$(\infty, \infty, \infty, \infty)$
≤ 1	> 1	< 1	∞	(1,0,0)	$(\infty, 0, 0, \infty)$
≤ 1	> 1	> 1	∞	(1,0,0)	$(\infty, \infty, \infty, \infty)$

[a] means automatically satisfied.

For Case III, Table 2 is valid if: (i) $R_f > 1$ or (ii) $R_f \leq 1$ and

$$A \geq C$$

or (iii) $R_f < 1$ and $B^2 < 4AC$. When (a) $R_f = 1$ and $A < C$ or (b) $R_f < 1$ and $B^2 \geq 4AC$, asymptotic behaviour of the population depends on whether the initial value of the population is in the domain of attraction of the DFE or not. When $R_f < 1$ and $B^2 \geq 4AC$ there is the stable manifold of an positive equilibrium which separates the domains of attraction of the DFE and an asymptotically stable positive equilibrium (see Theorem 4 in [14] for a detailed discussion). Consequently, the asymptotic behaviour of the population once again depends on whether the initial value of the population is in the domain of attraction of the DFE or not. The results are summarized in Table 3 where $(\bar{y}_1, \bar{y}_2, \bar{y}_4)$ is a positive equilibrium.

TABLE 3

Limit values of variables for Case III when $R_f = 1$ and $A < C$ or $R_f < 1$ and $B^2 \geq 4AC$.

(y_1, y_2, y_4)	R_1^*	R_0	N_0	(F_0, U_0, U_1, M_1)
$(1,0,0)/(\bar{y}_1, \bar{y}_2, \bar{y}_4)$	< 1	$< 1^a$	0	(0,0,0,0)/(0,0,0,0)
$(\bar{y}_1, \bar{y}_2, \bar{y}_4)$	> 1	$> 1^a$	∞	$(\infty, \infty, \infty, \infty)$
$(1,0,0)$	> 1	< 1	∞	$(\infty, 0, 0, \infty)$
$(1,0,0)$	> 1	> 1	∞	$(\infty, \infty, \infty, \infty)$

[a] means automatically satisfied.

Table 3 follows directly from Table 2, except that the limiting value of (y_1, y_2, y_4) is placed in the first column since the value of R_1^* depends on the value of $\bar{y}_2$,

3.1 Numerical Examples and Discussion

We now consider the biological implications of our results, still under the assumption that $c'_m = c'_f = 0$. $\sigma_f, \sigma_m \in [0, 1]$ are the respective fractions of infective core females and infective

young men removed from sexual contacts with the active population at each time interval. It is clear that if $c_m c_f \beta\bar{\beta} > (1+\bar{\mu}_0+\alpha-\mu_0)(1+\bar{\mu}_1+\alpha-\mu_0)$, R_f will always be greater than one for all values of σ_f and σ_m and, by Table 1 and Theorem 1, a population with some infecteds will always approach the endemic equilibrium. Hence we only consider the case when $c_m c_f \beta\bar{\beta} \leq (1+\bar{\mu}_0+\alpha-\mu_0)(1+\bar{\mu}_1+\alpha-\mu_0)$.

We will use the following notations:

$$
\begin{aligned}
A_0 &= (\bar{\mu}_0-\mu_0)(c_m\bar{\beta}-\bar{\mu}_0+\mu_0)\\
B_0 &= c_m\bar{\beta}(c_f\beta+\alpha)-(\bar{\mu}_0-\mu_0)(c_m\bar{\beta}-\bar{\mu}_0+\bar{\mu}_1+2\alpha)\\
C_0 &= -\alpha(c_m\bar{\beta}-\bar{\mu}_0+\bar{\mu}_1+\alpha)\\
\bar{R}_f^2 &= \tfrac{c_m c_f \beta\bar{\beta}}{(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)}, \quad R_f > 0.
\end{aligned}
$$

That is, A_0, B_0, C_0, and $\bar{R}_f^2$ are the respective parameters obtained from A, B, C, R_f^2 by letting $\sigma_f = \sigma_m = 0$.

There are the following two cases in which the above-mentioned treatment program is needed to help drive the endemic fraction down to zero.

Case (i) If $A_0 > 0$, $\bar{R}_f^2 > 1$, and $\sigma_f \in (0, c_m\bar{\beta}-\bar{\mu}_0+\mu_0]$. The first two conditions indicate that without any such program ($\sigma_f = \sigma_m = 0$) the endemic fractions will persist in the population (see Table 1). In this situation $\sigma_f \in (0, c_m\bar{\beta}-\bar{\mu}_0+\mu_0]$ implies that the program will enable the population fractions to approach DFE if and only if $\sigma_m\sigma_f+(\bar{\mu}_0+\alpha-\mu_0)\sigma_m+(\bar{\mu}_1+\alpha-\mu_0)\sigma_f \geq [\bar{R}_f^2-1](\bar{\mu}_0+\alpha-\mu_0)(\bar{\mu}_1+\alpha-\mu_0)$. We then have $R_f^2 \leq 1$.

Case (ii) If (1) $A_0 > 0, \bar{R}_f^2 > 1, \sigma_f \in (c_m\bar{\beta}-\bar{\mu}_0+\mu_0, 1]$; or (2) $A_0 = 0$ and $\bar{R}_f^2 > 1$; or (3) $A_0 < 0$. In cases (1) and (2), the endemic fraction will persist unless certain additional conditions on treatment are met. In the scenario for (3), the endemic fraction will persist if $\bar{R}_f^2 > 1$. If $\bar{R}_f^2 = 1$, the endemic fraction will persist if and only if $A_0 < C_0$. If $\bar{R}_f^2 < 1$, the endemic fraction will go to zero if ${B_0}^2 < 4A_0C_0$, otherwise the persistence of endemic fraction depends on the initial fractions. In all situations where the endemic fraction persists, the program will help to drive the endemic fraction to zero if

(a) $\sigma_m\sigma_f+(\bar{\mu}_0+\alpha-\mu_0)\sigma_m+(\bar{\mu}_1+\alpha-\mu_0)\sigma_f = [\bar{R}_f^2-1](\bar{\mu}_0+\alpha-\mu_0)(\bar{\mu}_1+\alpha-\mu_0), A \geq C$; or

(b) $\sigma_m\sigma_f+(\bar{\mu}_0+\alpha-\mu_0)\sigma_m+(\bar{\mu}_1+\alpha-\mu_0)\sigma_f > [\bar{R}_f^2-1](\bar{\mu}_0+\alpha-\mu_0)(\bar{\mu}_1+\alpha-\mu_0), B^2 < 4AC.$

If the first condition in case (b) is met but we have $B^2 \geq 4AC$ instead of $B^2 < 4AC$, whether the program is helpful depends on whether the initial data is in the region of attraction of the DFE or the locally asymptotically stable endemic equilibrium.

Now let us consider a simplified case where $\sigma_m = 0$, i.e. only female core infecteds are treated. Here for the program to be helpful it is necessary that $c_m c_f \beta\bar{\beta} \leq (\bar{\mu}_1+\alpha-\mu_0)(\sigma_f + \bar{\mu}_0 + \alpha - \mu_0)$. Moreover, we have the following simpler expressions for A, B, C and R_f.

$$A = A_0 + \sigma_f(c_m\bar{\beta} - 2\bar{\mu}_0 + 2\mu_0 - \sigma_f)$$
$$B = B_0 + \sigma_f(2\bar{\mu}_0 - \mu_0 - \bar{\mu}_1 - c_m\bar{\beta} - 2\alpha + \sigma_f)$$
$$C = C_0 + \alpha\sigma_f$$
$$R_f^2 = \frac{c_m c_f \beta\bar{\beta}}{(\bar{\mu}_1 + \alpha - \mu_0)(\sigma_f + \bar{\mu}_0 + \alpha - \mu_0)}.$$

Furthermore, Hypotheses H2 and H7 yield $\bar{\mu}_1 + \alpha \geq \bar{\mu}_0 \geq \mu_0$.

We consider the three subcases in **Case (ii)** above separately.

(1) $A_0 > 0, \bar{R}_f^2 > 1, \sigma_f \in (c_m\bar{\beta} - \bar{\mu}_0 + \mu_0, 1]$.

The program is significant if

(a) $\sigma_f = (\bar{R}_f^2 - 1)(\bar{\mu}_0 - \mu_0 + \alpha)$ and $\sigma_f^2 - (c_m\bar{\beta} - 2\bar{\mu}_0 + 2\mu_0 - \alpha)\sigma_f \leq A_0 - C_0$.

or

(b) $\sigma_f > (\bar{R}_f^2 - 1)(\bar{\mu}_0 - \mu_0 + \alpha)$ and $4AC > B^2$.

To illustrate our result, we give the numerical example in Figs. 1-2. Note that the x-axis is the susceptible fraction y_1 of the core female population and the y-axis is the number of untreated infected young men divided by the total core female population y_4. In Fig.1, we let $\alpha = 0.3$, $\beta = 0.01$, $\bar{\beta} = 0.01$, $c_m = 15$, $c_f = 200$, $\mu_0 = 0.1$, $\bar{\mu}_0 = 0.2$, $\bar{\mu}_1 = 0.4$. Moreover, we assume no treatment, i.e., $\sigma_f = \sigma_m = 0$. As a result, $A_0 > 0$ and $\bar{R}_f^2 > 1$. There is an endemic equilibrium $(0.7682, 0.7580)$ which is G.A.S. in $S - (1, 0)$, while the DFE $(1, 0)$ is an unstable equilibrium. When we have a detection/removal program targeted toward the core females with $\sigma_f = 0.1$ and the latter inequality in (**1**a) satisfied, the DFE will become G.A.S. in the region S. Indeed, if we let $\sigma_f = 0.1$, i.e., the infected core females are detected and removed from the active population at 10% rate, DFE becomes G.A.S. for S (see Fig.2).

In fact, DFE is G.A.S. as long as $\sigma_f \in [0.1, 1]$ since it can be easily shown that, for $\sigma_f > 0.1$, the latter inequality in (**1**b) is also satisfied.

(2) $A_0 = 0$ and $\bar{R}_f^2 > 1$.

The program is helpful in this instance if

(a) $\sigma_f = (\bar{R}_f^2 - 1)(\bar{\mu}_0 - \mu_0 + \alpha)$ and $\sigma_f^2 - (c_m\bar{\beta} - 2\bar{\mu}_0 + 2\mu_0 - \alpha)\sigma_f \leq -C_0$.

or

(b) $\sigma_f > (\bar{R}_f^2 - 1)(\bar{\mu}_0 - \mu_0 + \alpha)$ and $4AC > B^2$.

(3) $A_0 < 0$.

The program is helpful if

(a) $\sigma_f = (\bar{R}_f^2 - 1)(\bar{\mu}_0 - \mu_0 + \alpha)$ and $\sigma_f^2 - (c_m\bar{\beta} - 2\bar{\mu}_0 + 2\mu_0 - \alpha)\sigma_f \leq A_0 - C_0$.

or

(b) $\sigma_f > (\bar{R}_f^2 - 1)(\bar{\mu}_0 - \mu_0 + \alpha)$ and $4AC > B^2$.

Here we give the following numerical example. Let $\alpha = 1, \beta = 0.1, \bar{\beta} = 0.1, c_m = 10, c_f = 100, \mu_0 = 1, \bar{\mu}_0 = 3.165, \bar{\mu}_1 = 3.165$. Fig.3 is Example 2 in [14] where there is an asymptotically stable endemic equilibrium at $(0.8252, 0.5903)$ and a hyperbolic endemic equilibrium (a saddle point) at $(0.9608, 0.1256)$. (Note that the range for the x-axis is from 0.5 to 1.0.) Depending on the initial population, the population may tend toward DFE at $(1, 0)$ or the endemic equilibrium at $(0.8252, 0.5903)$. Since $A_0 < 0$ and $R_f = 10/(3.165)^2 < 1$, the condition on σ_f in (3b) is always satisfied. If we let $\sigma_f = 0.003$, i.e., 0.3% of the infected core females detected and removed from the active core female population, Fig.4 shows that the basic dynamics of the system remains the same, except the asymptotically stable endemic equilibrium is now at $(0.8471, 0.5120)$ and the hyperbolic endemic equilibrium at $(0.9311, 0.2234)$. The reason is that the latter condition in (3b), $4AC > B^2$, is not satisfied. However when we let $\sigma_f = 0.1$, the only equilibrium is the DFE and it is G.A.S. in S (see Fig.5). Hence while a program that detected 0.3% of the infected core females would not make much difference, a program of 10% detected would be immeasurably beneficial in changing the course of the epidemic. Moreover, since the problem is well-posed for all $\sigma_f \in [0, 1]$, this program would be decisively beneficial for all values of $\sigma_f \in (0, 1]$.

In (1)-(3) above, the conditions (a) and (b) are only sufficient. Note that in Fig.4 although the dynamic behaviour of the system is unchanged, the hyperbolic equilibrium has shifted slightly from $(0.9608, 0.1259)$ to $(0.9311, 0.2234)$. Hence for an initial population in the region of attraction of the locally asymptotically stable endemic equilibrium and near $(0.9608, 0.1259)$, a program with $\sigma_f = 0.003$ may shift the same initial population into the domain of attraction of the DFE. Consequently, for some values of initial population, the program will still be helpful.

The case when the unpartnered men are treated, i.e. $\sigma_f = 0$ can be discussed in similar fashion and hence is omitted to save space. However we will make the following remark on the relative effectiveness of the two targeting programs (i.e. unpartnered men or CSW's). For a treatment program targeted at CSW's only ($\sigma_m = 0$), the necessary (but not sufficient) condition for eradication $R_f^2 \leq 1$ is equivalent to $\sigma_f \geq \sigma_f^*$ where σ_f^* is the threshold treatment rate given by

$$\sigma_f^* = \frac{c_m c_f \beta\bar{\beta} - (\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)}{\alpha + \bar{\mu}_1 - \mu_0}.$$

On the other hand, for a treatment program aimed at unpartnered men, the corresponding threshold treatment rate is

$$\sigma_m^* = \frac{c_m c_f \beta\bar{\beta} - (\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)}{\alpha + \bar{\mu}_0 - \mu_0}.$$

Note that the only difference in the two thresholds is one term in the denominators, namely, $\bar{\mu}_1$ in σ_f^* and $\bar{\mu}_0$ in σ_m^*. These terms are the respective AIDS-related removal rates for infected females and males which often are assumed to be the same in literature, due to the lack of evidence to the contrary. In most of the numerical examples in this paper, we also assume that $\bar{\mu}_1$ and $\bar{\mu}_0$ (and subsequently the threshold treatment rates σ_f^* and σ_m^*) are the same. Hence treating the two groups are essentially equally effective. However, we note that the CSW's group is much smaller in number when compared to unpartnered men. Consequently, treating at the same rate but aiming at the smaller CSW group would result in a much smaller number of individuals requiring treatment and thus be a more efficient and effective program in terms of budget cost for the program.

4 Treatment and behaviour Change

In this section we consider the general model where there is a community-wide program to detect and treat HIV-infecteds, or to alter the sex behaviour of the detected infecteds so that their probabilities to transmit the HIV virus to others are decreased. We now introduce the notation

$$\bar{N}_0 = F_0 + U_0 + \frac{c'_f}{c_f}T_0, \quad y_1 = \frac{F_0}{\bar{N}_0}, \quad y_2 = \frac{U_0}{\bar{N}_0}, \quad y_3 = \frac{c'_f}{c_f}\frac{T_0}{\bar{N}_0}, \quad y_4 = \frac{U_1}{\bar{N}_0}, \quad y_5 = \frac{T_1}{\bar{N}_0}.$$

Simple calculation then gives the following equations.

$$\begin{aligned}
\frac{d\bar{N}_0}{dt} &= \bar{N}_0[\alpha - \mu_0 - (\bar{\mu}_0 - \mu_0)y_2 - (\bar{\mu}'_0 - \mu_0)y_3] - \sigma_f y_2 \bar{U}_0(1 - \frac{c'_f}{c_f}), && (10)\\
\frac{dy_1}{dt} &= \alpha - y_1(c_m\beta y_4 + c'_m\beta' y_5)\\
&\quad -y_1[\alpha + \mu_0(1 - y_1) - \bar{\mu}_0 y_2 - \bar{\mu}'_0 y_3 - \sigma_f y_2(1 - \frac{c'_f}{c_f})], && (11)\\
\frac{dy_2}{dt} &= y_1(c_m\beta y_4 + c'_m\beta' y_5)\\
&\quad -y_2[\alpha + \sigma_f - \mu_0 y_1 + (\bar{\mu}_0 - \mu_0)(1 - y_2) - (\bar{\mu}'_0 - \mu_0)y_3 - \sigma_f y_2(1 - \frac{c'_f}{c_f})], && (12)\\
\frac{dy_3}{dt} &= \frac{c'_f}{c_f}\sigma_f y_2 - y_3[\alpha - \mu_0 y_1 - \bar{\mu}_0 y_2 + \bar{\mu}'_0(1 - y_3) - \sigma_f y_2(1 - \frac{c'_f}{c_f})], && (13)\\
\frac{dy_4}{dt} &= (\bar{\beta}y_2 + \bar{\beta}' y_3)[c_f - (c_m y_4 + c'_m y_5)]\\
&\quad -y_4[\alpha + \bar{\mu}_1 - \mu_0 + \sigma_m - (\bar{\mu}_0 - \mu_0)y_2 - (\bar{\mu}'_0 - \mu_0)y_3 - \sigma_f y_2(1 - \frac{c'_f}{c_f})], && (14)\\
\frac{dy_5}{dt} &= \sigma_m y_4 - y_5[\alpha + \bar{\mu}'_1 - \mu_0 - (\bar{\mu}_0 - \mu_0)y_2 - (\bar{\mu}'_0 - \mu_0)y_3 - \sigma_f y_2(1 - \frac{c'_f}{c_f})], && (15)
\end{aligned}$$

with $y_1 + y_2 + y_3 = 1$, $0 \le c_m y_4 + c'_m y_5 \le c_f$. Because of Hypotheses H2, H3, H5, and H7, these equations are well-posed and the set $\{y_i \ge 0, i = 1, 2, 3, 4, 5\}$ in the 5-dimensional space is invariant. Now we need only to consider the following four-dimensional system in the set $\mathcal{S} = \{y_i, i = 1, 2, 3, 4 \mid y_i \ge 0, y_1 + y_2 \le 1, c_m y_4 + c'_m y_5 \le c_f\}$:

$$\begin{aligned}
\frac{dy_1}{dt} &= \alpha - y_1(c_m\beta y_4 + c'_m\beta' y_5)\\
&\quad -y_1[\alpha - (\bar{\mu}_0 - \bar{\mu}'_0)y_2 - (\bar{\mu}'_0 - \mu_0)(1 - y_1) - \sigma_f y_2(1 - \frac{c'_f}{c_f})], && (16)
\end{aligned}$$

$$\begin{aligned}
\frac{dy_2}{dt} &= y_1(c_m\beta y_4 + c'_m\beta' y_5) \\
&\quad -y_2[\alpha+\sigma_f+(\bar{\mu}_0-\bar{\mu}'_0)(1-y_2)+(\bar{\mu}'_0-\mu_0)y_1-\sigma_f y_2(1-\frac{c'_f}{c_f})], \qquad (17)\\
\frac{dy_4}{dt} &= (\bar{\beta}y_2+\bar{\beta}'(1-y_1-y_2))[c_f-(c_m y_4+c'_m y_5)] \\
&\quad -y_4[\alpha+\bar{\mu}_1-\bar{\mu}'_0+\sigma_m-(\bar{\mu}_0-\bar{\mu}'_0)y_2+(\bar{\mu}'_0-\mu_0)y_1-\sigma_f y_2(1-\frac{c'_f}{c_f})], \qquad (18)\\
\frac{dy_5}{dt} &= \sigma_m y_4 - y_5[\alpha+\bar{\mu}'_1-\bar{\mu}'_0-(\bar{\mu}_0-\bar{\mu}'_0)y_2+(\bar{\mu}'_0-\mu_0)y_1-\sigma_f y_2(1-\frac{c'_f}{c_f})]. \qquad (19)
\end{aligned}$$

Due to the difficulty in complete analysis for the 4-dimensional system, we will only give partial results pertaining to the following threshold parameters.

$$\begin{aligned}
R_f^2 = &\frac{c_m c_f \beta\bar{\beta}}{(\alpha+\sigma_f+\bar{\mu}_0-\mu_0)(\alpha+\sigma_m+\bar{\mu}_1-\mu_0)}+ \\
&\frac{\sigma_f}{(\alpha+\bar{\mu}_0-\mu_0+\sigma_f)}\frac{c_m c'_f\beta\bar{\beta}'}{(\alpha+\bar{\mu}'_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0+\sigma_m)}+ \\
&\frac{\sigma_m}{(\alpha+\bar{\mu}_1-\mu_0+\sigma_m)}\frac{c_f c'_m\beta'\bar{\beta}}{(\alpha+\bar{\mu}'_1-\mu_0)(\alpha+\bar{\mu}_0-\mu_0+\sigma_f)}+ \\
&\frac{\sigma_f}{(\alpha+\bar{\mu}_0-\mu_0+\sigma_f)}\frac{\sigma_m}{(\alpha+\bar{\mu}_1-\mu_0+\sigma_m)}\frac{c'_f c'_m\beta'\bar{\beta}'}{(\alpha+\bar{\mu}'_1-\mu_0)(\alpha+\bar{\mu}'_0-\mu_0)}, \qquad R_f>0.
\end{aligned}$$

$$\begin{aligned}
R_0^2 = &\frac{c_m c_f\beta\bar{\beta}}{(\bar{\mu}_0+\sigma_f)(\bar{\mu}_1+\sigma_m)}+\frac{\sigma_f}{(\bar{\mu}_0+\sigma_f)}\frac{c_m c'_f\beta\bar{\beta}'}{\bar{\mu}'_0(\bar{\mu}_1+\sigma_m)}+ \\
&\frac{\sigma_m}{(\bar{\mu}_1+\sigma_m)}\frac{c_f c'_m\bar{\beta}\beta'}{\bar{\mu}'_1(\bar{\mu}_0+\sigma_f)}+\frac{\sigma_f}{(\bar{\mu}_0+\sigma_f)}\frac{\sigma_m}{(\bar{\mu}_1+\sigma_m)}\frac{c'_f c'_m\beta'\bar{\beta}'}{\bar{\mu}'_0\bar{\mu}'_1}, \qquad R_0>0.
\end{aligned}$$

$$R_1 = \begin{cases} \dfrac{\alpha}{\mu_0} & \text{if } R_f \le 1 \\ \dfrac{\alpha}{\mu_0+(\bar{\mu}_0+\sigma_f-\mu_0)y_2^*+(\bar{\mu}'_0+\sigma_f-\mu_0)y_3^*} & \text{if } R_f>1 \end{cases}$$

where y_2^*, y_3^* denotes endemic equilibrium values of y_2, y_3.

These parameters have similar epidemiological significance as those in Section 3. However, since we are unable to do the complete analysis, we will discuss what conclusions we have been able to draw from equations of the model.

4.1 Discussion

(i) First we note that the endemic fractions will always persist if $R_f > 1$. If $R_f \le 1$, the

endemic fractions may or may not persist depending on other parameter values. In that sense lowering R_f might be helpful. On the other hand, increasing R_f to exceed unity will always result in persistence of the epidemic. To show this we know that $R_f^2 > 1$ is equivalent to

$$[\frac{c_m c_f \beta\bar{\beta}}{(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)}-1]+\frac{\sigma_f}{\alpha+\bar{\mu}_0-\mu_0}[\frac{c_m c_f'\beta\bar{\beta}'}{(\alpha+\bar{\mu}_0'-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)}-1]+$$
$$\frac{\sigma_m}{\alpha+\bar{\mu}_1-\mu_0}[\frac{c_f c_m'\beta'\bar{\beta}}{(\alpha+\bar{\mu}_1'-\mu_0)(\alpha+\bar{\mu}_0-\mu_0)}-1]+$$
$$\frac{\sigma_f\sigma_m}{(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)}[\frac{c_f' c_m'\beta'\bar{\beta}'}{(\alpha+\bar{\mu}_1'-\mu_0)(\alpha+\bar{\mu}_0'-\mu_0)}-1]>0. \qquad (20)$$

If $c_m c_f \beta\bar{\beta} > (\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)$, the epidemic will persist without any treatment/behaviour change program, i.e. $\sigma_f = \sigma_m = 0$. However, the program can eradicate the disease if and only if the expression on the left of the inequality in (20) is negative. That can be achieved if

(a) at least one of the three inequalities: $c_m c_f'\beta\bar{\beta}' < (\alpha+\bar{\mu}_0'-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)$, $c_m' c_f\beta'\bar{\beta} < (\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1'-\mu_0)$, and $c_m' c_f'\beta'\bar{\beta}' < (\alpha+\bar{\mu}_0'-\mu_0)(\alpha+\bar{\mu}_1'-\mu_0)$ is met;

(b) σ_f and σ_m are sufficiently large.

In other words, the program can have a positive effect on eradicating the epidemic if and only if the net transmission rate is lowered via treatment or behaviour change so that Condition (a) above can be satisfied, and the program is sufficiently comprehensive so that the expression on the left of the inequality in (20) is negative. Note also that since σ_f and σ_m are bounded above by unity, it is conceivable that for some values of the parameters $c_f, c_m, \beta, \bar{\beta}, \alpha, \mu_0, \bar{\mu}_0$, and $\bar{\mu}_1$, no treatment program can help on the population level. To be more precise, treatment/behaviour change program will not lower R_f to below unity if

$$c_m c_f \beta\bar{\beta} > 1+(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)+(\alpha+\bar{\mu}_0-\mu_0)+(\alpha+\bar{\mu}_1-\mu_0).$$

If, on the other hand, $c_m c_f \beta\bar{\beta} \leq (\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)$, the disease might not persist. But treatment program will affect the spread of disease adversely by raising R_f to above unity if (a) either $c_m c_f \beta\bar{\beta} \geq c_m c'_f \beta\bar{\beta}' > (\alpha+\bar{\mu}'_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)$, or $c_m c_f \beta\bar{\beta} \geq c_f c'_m \beta'\bar{\beta} > (\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}'_1-\mu_0)$; and (b) σ_f or σ_m sufficiently large so that the expression in (20) becomes positive! This type of possible adverse effect of treatment/behaviour change program on the population level was also present in a model of homosexual population by Hsieh and Velasco- Hernandez[20]. We will give a numerical example of this phenomenon in the next section when we consider treatment targeted at bridge population only.

(ii) We now consider R_0 which is the basic reproductive number for the infected populations. If $c_m c_f \beta\bar{\beta} > \bar{\mu}_0\bar{\mu}_1$, the infected populations will persist without any treatment program, i.e. $R_0 > 1$. Since $R_0 > 1$ is equivalent to

$$[\frac{c_m c_f \beta\bar{\beta}}{\bar{\mu}_0\bar{\mu}_1} - 1] + \frac{\sigma_f}{\bar{\mu}_0}[\frac{c_m c'_f \beta\bar{\beta}'}{\bar{\mu}'_0\bar{\mu}_1} - 1] + \frac{\sigma_m}{\bar{\mu}_1}[\frac{c_f c'_m \beta'\bar{\beta}}{\bar{\mu}'_1\bar{\mu}_0} - 1] + \frac{\sigma_f\sigma_m}{\bar{\mu}_0\bar{\mu}_1}[\frac{c'_f c'_m \beta'\bar{\beta}'}{\bar{\mu}'_1\bar{\mu}'_0} - 1] > 0,$$

the program might be helpful if and only if (a) either $c_m c'_f \beta\bar{\beta}' \leq \bar{\mu}'_0\bar{\mu}_1$ or $c_f c'_m \beta'\bar{\beta} \leq \bar{\mu}'_1\bar{\mu}_0$, and (b) σ_f and σ_m sufficiently large so that the above expression becomes negative. Again, due to the upper bound of one for σ_f and σ_m, a program of this type cannot help to wipe out the infected populations if

$$c_m c_f \beta\bar{\beta} > 1 + \bar{\mu}_0\bar{\mu}_1 + \bar{\mu}_0 + \bar{\mu}_1.$$

If $c_m c_f \beta\bar{\beta} \leq \bar{\mu}_0\bar{\mu}_1$, the infected populations might not persist without any treatment program. But if a program is initiated where (a) either $c_m c'_f \beta\bar{\beta}' > \bar{\mu}'_0\bar{\mu}_1$ or $c_f c'_m \beta'\bar{\beta} > \bar{\mu}'_1\bar{\mu}_0$, and (b) σ_f and σ_m large enough, the expression above becomes positive and infected populations will definitely persist in the community.

(iii) Finally, we consider R_1, the threshold parameter which determines whether the total population increases to infinity or goes to 0 depending on whether R_1 is greater than unity or not. When R_f without treatment is less than or equal to one, the treatment program has no effect on the persistence of total population. When R_f without treatment is great than one, the treatment program (σ_f and σ_m in the denominator of R_1) will always make

R_1 smaller, thus affecting the persistence of population adversely. The magnitude of effect would depend on the relative size of the parameters involved.

5 Treatment and behaviour Change for Bridge Population Only

To further understand our model, we can analyze our model with the treatment and behaviour change targeted toward either the bridge population of young men or the core group of CSW's. In this section we consider System (3)-(7) but with treatment program for bridge population only. We do this in order to gain better understanding of what such program would do for the spread of the epidemic in the population. Moreover, we can then compare a treatment/behaviour change program with the detection/removal as discussed in Section 3. Subsequently we have $\sigma_f = 0$ and $y_3 = 0$. System (16)-(19) is simplified into the following 3-dimensional system:

$$\begin{aligned}
\frac{dy_1}{dt} &= \alpha - y_1(c_m\beta y_4 + c_m'\beta' y_5) \\
&\quad -y_1[\alpha - (\bar{\mu}_0 - \mu_0)(1 - y_1)], \qquad (21)\\
\frac{dy_4}{dt} &= \bar{\beta}(1 - y_1)(c_f - c_m y_4 - c_m' y_5) \\
&\quad -y_4[\alpha + \bar{\mu}_1 + \sigma_m - \bar{\mu}_0 + (\bar{\mu}_0 - \mu_0)y_1], \qquad (22)\\
\frac{y_5}{dt} &= \sigma_m y_4 - y_5[\alpha + \bar{\mu}_1' - \bar{\mu}_0 + (\bar{\mu}_0 - \mu_0)y_1] \qquad (23)
\end{aligned}$$

We will consider the system in the 3-dimensional region in the first octant $S_3 = \{(y_1, y_4, y_5)|0 \leq y_1 \leq 1, y_4, y_5 \geq 0, 0 \leq c_m y_4 + c_m' y_5 \leq c_f\}$. We also assume H1-H7 to hold for all analytical results that follow.

First we note that S_3 is invariant for System (21-23). Using local analysis about the DFE $(1, 0, 0)$, we have the following theorem:

Theorem 3. *Suppose* $c_f c_m \beta\bar{\beta} > (\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)$. *Let*

$$\bar{\sigma}_m^* = \frac{[c_m c_f \beta\bar{\beta} - (\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)](\alpha + \bar{\mu}_1' - \mu_0)}{(\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1' - \mu_0) - c_m' c_f \beta'\bar{\beta}}.$$

If $(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1'-\mu_0) \leq c_m' c_f \beta' \bar{\beta}$*, the DFE is unstable for System (21)-(23) for all values of* σ_m*. On the other hand, when* $(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1'-\mu_0) > c_m' c_f \beta' \bar{\beta}$*, the DFE is locally asymptotically stable if* $\sigma_m \geq \bar{\sigma}_m^*$ *and unstable if otherwise.*

Proof. The 3x3 Jacobian matrix for the system in question is

$$J = \begin{bmatrix} -c_m\beta y_4 - c_m'\beta' y_5 - \alpha + (1-2y_1)(\bar{\mu}_0-\mu_0) & -c_m\beta y_1 & -c_m'\beta' y_1 \\ -\bar{\beta}(c_f - c_m y_4 - c_m' y_5) - (\bar{\mu}_0-\mu_0)y_4 & -c_m\bar{\beta}(1-y_1) - \alpha - \bar{\mu}_1 & -c_m'\bar{\beta}(1-y_1) \\ & -\sigma_m + \bar{\mu}_0 - (\bar{\mu}_0-\mu_0)y_1 & \\ -(\bar{\mu}_0-\mu_0)y_5 & \sigma_m & -\alpha - \bar{\mu}_1' + \bar{\mu}_0 \\ & & -(\bar{\mu}_0-\mu_0)y_1 \end{bmatrix}.$$

At the DFE $(1,0,0)$, the Jacobian becomes

$$J(1,0,0) = \begin{bmatrix} -\alpha - (\bar{\mu}_0-\mu_0) & -c_m\beta & -c_m'\beta' \\ -c_f\bar{\beta} & -\alpha - \bar{\mu}_1 - \sigma_m + \mu_0 & 0 \\ 0 & \sigma_m & -\alpha - \bar{\mu}_1' + \mu_0 \end{bmatrix}.$$

H2, H5, and H7 imply $\mathrm{tr}J < 0$. By considering the cases where $\det J > 0$, the theorem follows directly. Q.E.D.

For analytical result regarding existence, uniqueness, and stability of positive equilibrium of System (21)-(23), we first recall the corresponding parameters for the model without treatment proposed in [14]:

$$\begin{aligned} R_f^2 &= \frac{c_m c_f \beta \bar{\beta}}{(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}_1-\mu_0)}, \qquad R_f > 0, \\ A &= (\bar{\mu}_0-\mu_0)(c_m\bar{\beta} - \bar{\mu}_0 + \mu_0), \\ B &= c_m\bar{\beta}(c_f\beta+\alpha) - (\bar{\mu}_0-\mu_0)(c_m\bar{\beta} - \bar{\mu}_0 + \bar{\mu}_1 + 2\alpha), \\ C &= -\alpha(c_m\bar{\beta} - \bar{\mu}_0 + \bar{\mu}_1 + \alpha). \end{aligned}$$

Note that the above expressions for R_f^2, A, B, and C are different from the ones given in Section 3 for the model with removal of infecteds.

For System (21)-(23), the positive equilibrium must satisfy the following cubic equation:

$$h(y) = C_1 y^3 + C_2 y^2 + C_3 y + C_4$$

with

$$C_1 = A(\bar{\mu}_0 - \mu_0),$$
$$C_2 = B(\bar{\mu}_0 - \mu_0) + A(\alpha + \bar{\mu}_1' - \bar{\mu}_0) + \sigma_m A',$$
$$C_3 = C(\bar{\mu}_0 - \mu_0) + B(\alpha + \bar{\mu}_1' - \bar{\mu}_0) + \sigma_m B',$$
$$C_4 = C(\alpha + \bar{\mu}_1' - \bar{\mu}_0) + \sigma_m C',$$

and

$$A' = (\bar{\mu}_0 - \mu_0)(c_m'\bar{\beta} - \bar{\mu}_0 + \mu_0),$$
$$B' = c_m'\bar{\beta}(c_f\beta' + \alpha) - (\bar{\mu}_0 - \mu_0)(c_m'\bar{\beta} - \bar{\mu}_0 + \bar{\mu}_1' + 2\alpha),$$
$$C' = -\alpha(c_m'\bar{\beta} - \bar{\mu}_0 + \bar{\mu}_1' + \alpha).$$

Note that A', B', and C' are, respectively, A, B, and C with c_m, β, and $\bar{\mu}_1$ replaced by their respective primed terms for the treated classes c_m', β', and $\bar{\mu}_1'$. We also know that C_4 is negative due to Hypothesis H7 and C_1 has the same sign as A due to H2.

To discuss stability of the system in question, we need the following result on nonexistence of nonconstant periodic solutions.

Theorem 4. *Suppose (i)* $c_m'\beta' \geq c_m\bar{\beta} + \bar{\mu}_0 - \mu_0$, *(ii)* $c_f\bar{\beta} + c_m'\bar{\beta} < \bar{\mu}_1' + 2\alpha - \mu_0$, *(iii)* $\sigma_m > (c_m'\beta' - \bar{\mu}_1' + \mu_0 - \alpha) + (c_m\bar{\beta} - \bar{\mu}_1 + \mu_0 - \alpha)$. *Then System (21)-(23) has no nonconstant periodic solutions in* S_3.

Proof. The proof utilizes Muldowney's result [34] on compound matrices. More precisely, we use Theorem 4.1 in Muldowney [34] which gives sufficient conditions for the nonexistence of nonconstant periodic solutions. The details of the proof are omitted to save space. We will only point out that, in the proof we employed the Lozinskii norm given by

$$\sup_j (Re\ a_j^j + \sum_{i \neq j} |\ a_i^j\ |).$$

Note also that the hypotheses H2-H3 and H7 are used in the proof. Q.E.D.

Now we are ready to give the theorem on local existence, uniqueness, and stability of positive equilibrium of System (21)-(23).

Theorem 5. *The local existence, uniqueness, and stability of positive equilibrium of System (21-23) is described in the following table*:

TABLE 4

Analytical Result for Positive Equilibrium of Model with Treatment

		$\bar{R}_f$	Number of positive Equilibria	Stability
Case I	$C_1 > 0$	> 1	$1, 2$, or $3 (C_3 > 0 > C_2)$	-
			1(otherwise)	AS
		≤ 1	$0, 1$ or $2 (C_3 > 0 > C_2)$	-
			0(otherwise)	-
Case II	$C_1 = 0$	> 1	1	AS
		$= 1$	$0 (C_2 \geq C_4)$	-
			$1 (C_2 < C_4)$	AS
		< 1	$0 ({C_3}^2 < 4C_2C_4)$	-
			$1 (C_3 2 = 4C_2C_4)$	-
			$2 ({C_3}^2 > 4C_2C_4)$	-
Case III	$C_1 < 0$	> 1	1	AS
		$= 1$	$0 (3C_1 + 2C_2 + C_3 \geq 0)$	-
			$1 (3C_1 + 2C_2 + C_3 < 0)$	-
		< 1	$0, 1$, or 2	-

where

$$\bar{R}_f^2 = \frac{c_m c_f \beta \bar{\beta}}{(\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \sigma_m + \bar{\mu}_1 - \mu_0)} + . \\ \frac{\sigma_m}{(\alpha + \sigma_m + \bar{\mu}_1 - \mu_0)} \frac{c_m' c_f \beta' \bar{\beta}}{(\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1' - \mu_0)} \qquad \bar{R}_f > 0.$$

Note that $\bar{R}_f^2 > 1$ is equivalent to $\sigma_m < \bar{\sigma}_m^*$.

The proof of the local existence and uniqueness of positive equilibrium makes use of Theorem 3 and elementary properties of cubic functions and calculus hence is omitted here. The global stability result for the cases with multiple positive equilibria is not obtained since the system (21)-(23) is not competitive in the sense of [35].

We now give the following epidemiologically important threshold parameters for System (21)-(23):

$$\bar{R}_0^2 = \frac{c_m c_f \beta \bar{\beta}}{\bar{\mu}_0(\bar{\mu}_1 + \sigma_m)} + \frac{\sigma_m}{\bar{\mu}_0} \frac{c_m' c_f \beta' \bar{\beta}}{\bar{\mu}_1'(\bar{\mu}_1 + \sigma_m)} \qquad \bar{R}_0 > 0.$$

$$\bar{R}_1 = \begin{cases} \dfrac{\alpha}{\mu_0} & \text{if } \bar{R}_f \leq 1 \\ \dfrac{\alpha}{\mu_0 + (\bar{\mu}_1 + \sigma_m - \mu_0)y_4^* + (\bar{\mu}_1' + \sigma_m - \mu_0)y_5^*} & \text{if } \bar{R}_f > 1 \end{cases}$$

where y_4^*, y_5^* denotes the unique endemic equilibrium values of y_4, y_5. Asymptotic results of $\bar{R}_0$ and $\bar{R}_1$ similar to Tables 2-3 in Section 3 can be easily obtained and hence are omitted here. Note also that here $\bar{R}_f$, $\bar{R}_0$, and $\bar{R}_1$ are different from their corresponding threshold parameters R_f, R_0, and R_1 in Section 4.

5.1 Discussions

First we note that all results discussed in Section 5 on targeting the bridge population for treatment and behaviour change can be obtained similarly for targeting the core group of CSW's. We want to compare the two targeting strategies, and hence no longer necessarily assume $\sigma_f = 0$ as in (21)-(23). To begin we observe from Table 4 that, given a treatment program targeted at the bridge population of unpartnered men, in order for the disease to be eventually eradicated for all initial endemic fractions ($(y_1, y_4, y_5) \neq (1, 0, 0)$), it is necessary that $\bar{R}_f^2 \leq 1$ or, equivalently, $\sigma_m \geq \bar{\sigma}_m^*$. In other words, for the program to be successful, it is necessary for the level of comprehensive detection and treatment of the infected unpartnered men to be no less than the threshold treatment rate $\bar{\sigma}_m^*$. Whether it does indeed eradicate the disease in the community depends on the initial endemic fraction at the onset of the epidemic.

We would like to compare the relative effectiveness of treating core females as opposed to treating unpartnered males. It can be easily shown that for a targeting program aimed at the core population of CSW's, the corresponding threshold treatment rate $\bar{\sigma}_f^*$ is

$$\bar{\sigma}_f^* = \frac{[c_m c_f \beta \bar{\beta} - (\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)](\alpha + \bar{\mu}_0' - \mu_0)}{(\alpha + \bar{\mu}_0' - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0) - c_m c_f' \beta \bar{\beta}'}.$$

Unlike the case of removal by treatment in Section 3 where the threshold treatment rates, σ_f^* and σ_m^*, are virtually the same, $\bar{\sigma}_f^*$ and $\bar{\sigma}_m^*$ are quite different. We rewrite the two

threshold treatment rates as follow:

$$\bar{\sigma}_f^* = \frac{c_m c_f \beta\bar{\beta} - (\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)}{\alpha + \bar{\mu}_1 - \mu_0 - \frac{c_m c'_f \beta\bar{\beta}'}{\alpha + \bar{\mu}'_0 - \mu_0}}.$$

$$\bar{\sigma}_m^* = \frac{c_m c_f \beta\bar{\beta} - (\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)}{\alpha + \bar{\mu}_0 - \mu_0 - \frac{c'_m c_f \beta'\bar{\beta}}{\alpha + \bar{\mu}'_1 - \mu_0}}.$$

Note the only difference is in the fraction in the denominators involving the contact rates, transmission probabilities, and removal rates of the treated infected individuals. Moreover, $\bar{\sigma}_f^*$ and $\bar{\sigma}_m^*$ without the fraction in the denominators (i.e. the treated individuals having no sexual contact outside the treated class) would be the same as the threshold treatment rates σ_f^* and σ_m^* in Section 3. If $(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}'_1-\mu_0) \leq c'_m c_f \beta'\bar{\beta}$, either treatment program will be unable to eradicate the epidemic. If $(\alpha+\bar{\mu}_0-\mu_0)(\alpha+\bar{\mu}'_1-\mu_0) > c'_m c_f \beta'\bar{\beta}$, the smaller value for the fraction in the denominator would result in a smaller threshold value. Consequently, assuming no significant difference in removal rates for the treated unpartnered males and core females, lower contact rate and transmission rate would lead to smaller threshold rate value. Given the much smaller number of the core female group (CSW's), this would indicate that, with the same budget, treating the core female group will be more effective in efficiently reducing the threshold as well as the actual number required to be treated to exceed the threshold treatment rate.

As mentioned earlier in the discussion in Subsection 4.1, a treatment program which does not meet all criteria on lowering the transmission probability $\bar{\beta}$ and the contact rate c_f could have an adverse effect on the spread of epidemic. To illustrate this possibility, we now give the following numerical examples. Note that the equivalent condition for $\bar{R}_f > 1$ is

$$[\frac{c_m c_f \beta\bar{\beta}}{(\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}_1 - \mu_0)} - 1] + \frac{\sigma_m}{\alpha + \bar{\mu}_1 - \mu_0}[\frac{c'_m c_f \beta'\bar{\beta}}{(\alpha + \bar{\mu}_0 - \mu_0)(\alpha + \bar{\mu}'_1 - \mu_0)} - 1] > 0$$

In all following 3-dimensional figures, the x-, y-, and z-axes denote respectively the susceptible fraction of core females, the untreated infected fraction of core females, and the untreated infected fraction of unpartnered males. First we let $\alpha = 0.2, \beta = \bar{\beta} = 0.01, \mu_0 = 0.5, \bar{\mu}_0 = \bar{\mu}_1 = 1.3, c_f = 90, c_m = 120$. Here $c_m c_f \beta\bar{\beta} > (\bar{\mu}_0 - \mu_0 + \alpha)(\bar{\mu}_1 - \mu_0 + \alpha)$ and

DFE at $(1, 0, 0)$ is unstable. Fig.6 shows that all populations tend to the endemic steady state at $(0.7792, 0.2208, 0.2592)$. Suppose a treatment program is implemented in the bridge population of young men with a lower contact rate at $c'_m = 100$, a lower removal rate $\bar{\mu}'_1 = 1.1$, a lower transmission probability $\beta' = 0.005$, and 20% of the infected bridge population treated ($\sigma_m = 0.2$). The expression above will become negative and the DFE will be globally asymptotically stable for S_3 (see Fig.7). Hence a treatment program in this scenario would be decidedly beneficial to the population.

We now demonstrate the possible adverse effect of an ill-planned treatment program. Let α, β, $\bar{\beta}$, μ_0, $\bar{\mu}_0$, $\bar{\mu}_1$ and c_m be the same as before, but $c_f = 80$. Now the DFE is G.A.S. in S_3 (Fig.8). In other words, the disease will by itself be eradicated without any community treatment program. However, if we target a treatment program in the bridge population with $c'_m = 100$, $\bar{\mu}'_1 = 0.7$, $\beta' = 0.01$, and $\sigma_m = 0.2$, it would result in the above equivalent expression for $\bar{R}_f > 1$ changing from negative to positive, creating an endemic equilibrium which is G.A.S. in $S_3 - (1, 0, 0)$ and causing a perverse turn of the epidemic for the worse. The example shows that if the treatment program slows down the progression to AIDS of the treated infected males without sufficiently lowering the contact rate with susceptible core females or the transmission probability, then it could increase the spread of the infection.

6 Concluding Remarks

Mathematical modeling of HIV transmission and treatment have suggested that lowering the contact rate c or the transmission probability β of the infecteds is necessary for the treatment program to be beneficial on the population level (see [16] or [18]) but is not sufficient (see [20]). All of the above- mentioned work considered models with male gay population which is reasonable since common sense would dictate a targeting strategy aiming toward high-risk groups. By the same reasoning, we consider in this model a public health policy which targets its resources at the sexually active young men or the core group of CSW's. The results show that if the contact rates and transmission probabilities of the treated individuals are

sufficiently reduced, the treatment can eradicate the disease if the level of treatment (σ_m or σ_f) is also sufficiently high. Moreover we discussed the extreme case when the program will adversely affect the spread of the disease. The work was presented to point out the complicated possibilities in the design of control programs for HIV/AIDS in countries with a large core group of sexually active individuals.

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References

[1] T.Brown and P.Xenos, AIDS in Asia: The gathering storm, *Asia-Pacific*, Issue No.16, Honolulu: East-West Center, (1994).

[2] J. Chin, Scenarios for the AIDS epidemics in Asia, *Asia-Pacific Population Research Reports*, No.2, East-West Center, Honolulu (1995).

[3] J. Chin and S. K. Lwanga, Estimation and projection of adult AIDS cases: A simple epidemiological model. *Bull. WHO* **69**:399-406.

[4] B. Weniger, K. Limpakarnjanarat, K. Ungchusak, S. Thanprasertsuk, K. Choopanya, S. Vanichseni, T. Uneklabh, P. Thongcharoen, and C. Wasi, The epidemiology of HIV infection and AIDS in Thailand, *AIDS* **5**(suppl 2) S71-S85 (1991).

[5] Bhassorn L., Noppavan C., Penporn T., and Wattana A., *The Demographic and behavioural Study of Female Commercial Sex Workers in Thailand,* Institute of Population Studies, Chulalongkorn University, Bangkok, (1993).

[6] M. Morris, C. Podhisita, M.J. Wawer, and M.S. Handcock, Bridge populations in the spread of HIV/AIDS in Thailand, *AIDS* **10** 1265-1271 (1996).

[7] H. Hethcote and J.A. Yorke, *Gonorrhea Transmission Dynamics and Control*, Springer-Verlag, Berlin (1984).

[8] W. Rojanapithayakorn and R. Hanenberg, The 100% condom program in Thailand, *AIDS* **10**:1-7 (1996).

[9] T. Brown, C. Gullaprawit, W. Sittitrai, S. Thanprasersuk, and A. Chamratrithirong, *Projection for HIV/AIDS in Thailand: 1987-2020*, Thai Red Cross Society Program on AIDS, Bangkok (1994).

[10] V. Thongthai and P. Guest, Thai sexual attitudes and behaviours: results from a recent national survey, Report for Gender and Sexuality in Modern Thailand Conference, July 11-12, 1995.

[11] Sittitrai, W, P. Phanuphak, J. Barry, and T. Brown, *Thai Sexual behaviour and Risk of HIV Infection: A Report of the 1990 Survey of Partner Relations and Risk of HIV infection in Thailand*, Program on AIDS, Thai Red Cross Society, and Institute of Population Studies, Chulalongkorn University, Bangkok, (1992).

[12] HIV surosurveillance in Thailand: result of the 16th round, June 1998, *Monthly Epidemiological Surveillance Report*, **30**:1, Division of Epidemiology, Royal Thai Ministry of Public Health, Bangkok, (1999).

[13] T.D. Mastro and K. Limpakarnjanarat, Condom use in Thailand: how much is it slowing the HIV/AIDS epidemic? *AIDS* **9**:523-525 (1995).

[14] S. Busenberg, K. Cooke, and Y.-H. Hsieh, A model for HIV in Asia, *Math. Biosciences*, **128**, 185-210, (1995).

[15] G.J. van Griensven, B. Limanonda, S. Ngaokeow, S.I. Ayuthaya, and V. Poshyachinda, Evaluation of atargeted HIV prevention programme among female commercial sex workers in the south of Thailand, *Sex. Transm. Infec.*, **74**(1),54-8 (1998).

[16] R. M. Anderson, S. Gupta, and R. M. May, Potential of community wide chemotherapy or immunotherapy to control the spread of HIV-1, *Nature* **350**,356-359 (1991).

[17] G. Scalia-Tomba, The effect of structural behaviour change on the spread of HIV in a one-sex population, *Math. Biosciences*, **107**, 547-555, (1991).

[18] J. X. Velasco-Hernandez and Y. H. Hsieh, Modelling the effect of treatment and behavioural change in HIV transmission dynamics, *J. Math. Biology*, **32**,233-249 (1994).

[19] S.M. Blower and A.R. McLean, Prophylactic vaccines, risk behaviour change, and the probability of eradicating HIV in San Francisco, *Science*, **265**, 1451-1454, (1994).

[20] Y.-H. Hsieh and J.X. Velasco-Hernandez, Community treatment of HIV-1: Initial stage and asymptotic dynamics,*Biosystems*, **35**, 75-81, (1994).

[21] J.X. Velasco-Hernandez, F. Brauer, and C. Castillo-Chavez, Effects of treatment and prevalence-dependent recruitment on the dynamics of a fatal disease. *IMA J. Math. Appl. Med. Biology* **13**, 175-192 (1996)

[22] Y.-H. Hsieh, A two-sex model for treatment of HIV/AIDS and behaviour change in a population of varying size, *IMA J. Math. Appl. Med. Biology*, **13**, 151-173, (1996).

[23] J.M. Hyman and J. Li, behaviour changes in SIS STD models with selective mixing, *SIAM J. Applied Math.* **57**(4), 1082-1094(1997).

[24] J.M. Hyman and J. Li, Modeling the effectiveness of isolation strategies in preventing STD epidemics, *SIAM J. Applied Math.* **58**(3), 912-925(1998).

[25] R. Waldstätter, Pair formation in sexually-transmitted diseases, in *Mathematical and Statistical Approaches to AIDS Epidemiology* (Lect. Notes in Biomath., **83**) C. Castillo-Chavez ed., pp.260-274, Springer-Verlag, Berlin, (1989).

[26] W.Y. Tan and X. Zhu, A stochastic model of the HIV epidemic for heterosexual transmission involving married couples and prostitutes: I. The probabilities of HIV transmission and pair formation, preprint.

[27] Y.-H. Hsieh, Modelling the effect of screening in HIV transmission dynamics, *Differential Equations Models in Biology, Epidemiology and Ecology*, Lect. Notes in Biomath., **92**, (S. Busenberg and M. Martelli, eds.), pp.99-120, Springer-Verlag, Berlin, (1991).

[28] Y.-H. Hsieh, A HIV model for behaviour change in CSW's and sexually active men, in preparation.

[29] F. LePont and S. M. Blower, The supply and demand dynamics of sexual behaviour: implications for heterosexual HIV epidemics, *J. Acquir. Immun. Defic. Syndr.* **4**,987-999 (1991).

[30] N.S. Padian, S.C. Shiboski, S.O. Glass, and E. Vittinghoff, Heterosexual transmission of human immunodeficiency virus (HIV) in northern California: results from a ten-year study, *Am. J. Epidemiol.* **146**(4),350-357 (1997).

[31] S. Busenberg and C. Castillo-Chavez, A general solution of the problem of mixing of subpopulations and its application to risk- and age-structured epidemic models for the spread of AIDS, *IMA J. Math. Appl. Med. Biol.* **81**,1-29 (1991).

[32] C. Castillo-Chavez and S. Busenberg, On the solution of the two-sex problem, in *Differential Equations Models in Biology, Epidemiology, and Ecology* (Lect. Notes Biomath. 92), S. Busenberg and M. Martelli, Eds., pp. 80-98, Springer-Verlag, Berlin, (1991).

[33] K. P. Hadeler, R. Waldstätter, and A. Worz-Busekros, Models for pair formation in bisexual populations, *J. Math. Biology* **26**,633-649 (1988).

[34] J.S. Muldowney, Compound matrices and ordinary differential equations. *Rocky Mountain J. of Math.* **20**(4),857-872 (1990).

[35] M.Y. Li and J.S. Muldowney, Global stability for the SEIR model in epidemiology. *Math. Biosci.* **125**(2), 155–164 (1995).

Figure Legend

Figure 1. Simulation of a population with no treatment and with $\alpha = 0.3, \beta = \bar{\beta} = 0.01, c_m = 15, c_f = 200, \mu_0 = 0.1, \bar{\mu}_0 = 0.2, \bar{\mu}_1 = 0.4$. y_1-axis is the susceptible fraction in core females, y_4-axis is the untreated infected fraction in young males. DFE at $(1, 0)$ is unstable. There is an asymptotically stable endemic steady state at $(0.7682, 0.7500)$.

Figure 2. Simulation of the same population in Fig. 1 but with screening and removal of the infecteds in the female core group with $\sigma_f = 0.1$. DFE at $(1, 0)$ is the unique equilibrium and is asymptotically stable in S.

Figure 3. Simulation of a population with no treatment and with $\alpha = 1, \beta = \bar{\beta} = 0.1, c_m = 10, c_f = 100, \mu_0 = 1.0, \bar{\mu}_0 = \bar{\mu}_1 = 3.165$. y_1-axis is the susceptible fraction in core females, y_4-axis is the untreated infected fraction in young males. There is an locally asymptotically stable endemic steady state at $(0.8252, 0.5903)$ and a hyperbolic endemic equilibrium at $(0.9608, 0.1255)$. DFE is locally asymptotically stable.

Figure 4. Simulation of the same population in Fig. 3 but with screening and removal of the infecteds in the female core group with $\sigma_f = 0.003$. Again, there is an locally asymptotically stable endemic steady state at $(0.8471, 0.5120)$ and a hyperbolic endemic equilibrium at $(0.9311, 0.2234)$. DFE is also locally asymptotically stable.

Figure 5. Simulation of the same population in Fig. 3 but with screening and removal of the infecteds in the female core group with $\sigma_f = 0.1$. DFE at $(1, 0)$ is the unique equilibrium and is asymptotically stable in S.

Figure 6. Simulation of a population with no treatment and with $\alpha = 0.2, \beta = \bar{\beta} = 0.01, c_f = 90, c_m = 120, \mu_0 = 0.5, \bar{\mu}_0 = \bar{\mu}_1 = 1.3$. x-axis is the susceptible fraction of core females, y-axis is the untreated infected fraction of core females, and z-axis is the untreated infected fraction in unpartnered males. DFE at $(1, 0, 0)$ is unstable. There is a asymptotically stable endemic steady state at $(0.7792, 0.2208, 0.2592)$.

Figure 7. Simulation of the same population in Fig. 6 but with treatment and behaviour change. $\sigma_m = 0.2, \beta' = 0.005, c'_m = 90$, and $\bar{\mu}'_1 = 1.1$. DFE is the unique equilibrium and is asymptotically stable in S_3.

Figure 8. Simulation of a population with no treatment and with $\alpha = 0.2, \beta = \bar{\beta} = 0.01, c_f = 80, c_m = 120, \mu_0 = 0.5, \bar{\mu}_0 = \bar{\mu}_1 = 1.3$. x-axis is the susceptible fraction of core females, y-axis is the untreated infected fraction of core females, and z-axis is the untreated infected fraction in unpartnered males. DFE is the unique equilibrium and is asymptotically stable in S_3.

Figure 9. Simulation of the same population in Fig. 8 but with treatment and behaviour change. $\sigma_m = 0.2, \beta' = 0.01, c'_m = 100$, and $\bar{\mu}'_1 = 0.7$. DFE is unstable and there is an asymptotically stable endemic steady state at $(0.5997, 0.2112, 0.4342)$.