

A MATHEMATICAL MODEL TO DEMONSTRATE THE SPREAD OF AN EPIDEMIC

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ABSTRACT

Many models for the spread of infectious diseases in populations have been analyzed mathematically and applied to specific diseases. Non-linear dynamical method of projecting the transmission of an epidemic is accurate if the input parameters are reliable. In this paper, a mathematical model is constructed for predicting an epidemic of HIV/AIDS with respect to the presence of infected individuals in the population. For the model, a formula for the basic reproduction number, R_0 (the expected number of secondary infectious caused by a single new infective introduced into a susceptible population) is determined. The six dimensional model is analyzed qualitatively to determine the stability of equilibria. Analysis of this model includes identifying the threshold R_0 that determines whether the disease dies out or an epidemic occurs.

Key words: Non-linear dynamical method, infectious diseases, epidemic stability, HIV/AIDS.

1. Introduction

Models developed for infectious diseases, such as measles or influenza, with short infectious periods have usually contained only one infectious stage [1, 7, 8]. However, these models are generally not suitable for the disease AIDS (Acquired Immunodeficiency Syndrome) caused by HIV (Human Immunodeficiency Virus) because the average infectious period from HIV infection to AIDS is approximately 10 years. For the past several decades mathematical principles have had an important role in disease control strategies [11, 1] and will continue to do so in future. Application of the models becomes easier if there are sufficiently accurate data for the variables used and the concerned parameter values. Mathematical models of transmission dynamics of HIV plays an important role in better understanding of epidemiological patterns and methods for disease control as they provide short and long term prediction of HIV and AIDS incidence and its dependence on various factors. The modeling study is also helpful in determining the demographic and economic impact of the epidemic, which in turn helps us to develop reasonable, scientifically and socially sound intervention plans in order to reduce the spread of the infection. Mathematical modeling studies have shown that the

AIDS epidemic is very sensitive to the human behaviors that spread HIV, including: the amount of risky behavior, the manner in which that risky behavior is distributed in the population and the social network structures within which people practice those risky behaviors. In fact, these models have shown that if we do not understand all three of these factors, then we can not hope to predict and control the spread of HIV and other sexually transmitted diseases [9, 10]. Mathematical and statistical models can serve as tools for understanding the epidemiology of HIV and AIDS if they are constructed carefully. Here an attempt is made to model the spread of HIV in a comprehensive manner with limited data. We have proposed a mathematical model for predicting an epidemic of HIV/AIDS into the population. We discuss the model using a simple mathematical approach and calculate the basic reproduction number (R_0) for the model to make a decision for the stability of equilibria. In addition we show that R_0 is the threshold parameter for the local stability of the disease free equilibria (DFE). Analysis of the centre manifold is done to determine the existence and stability of the endemic equilibria (EE) near the threshold, $R_0 = 1$. Numerical simulations have been carried out to delineate the various analytical results as well.

2. Model formulation

In order to derive the model equations, first we divide the population into two classes: Male and Female. Denote the populations of those not infected by HIV as M_0, F_0 , those infected as M_1, F_1 and those who subsequently develop AIDS as M_2, F_2 for males and females respectively. Here, it is assumed that HIV-infected individuals will clinically progress to AIDS (the advanced stage of HIV infection) with an average incubation period $1/\eta_1$ (for males), $1/\eta_2$ (for females). Infection is assumed to transmit from male to female and vice versa. No other mode of transmission is considered in the model. Females transmit the virus to their male counterparts with a probability of β_1 (at contact rate c_1), while males transmit to females with a probability of β_2 (at contact rate c_2). Males, females enter the susceptible class (susceptible here means those who can get the infection but are not infected yet) at constant rates λ_1 and λ_2 respectively.

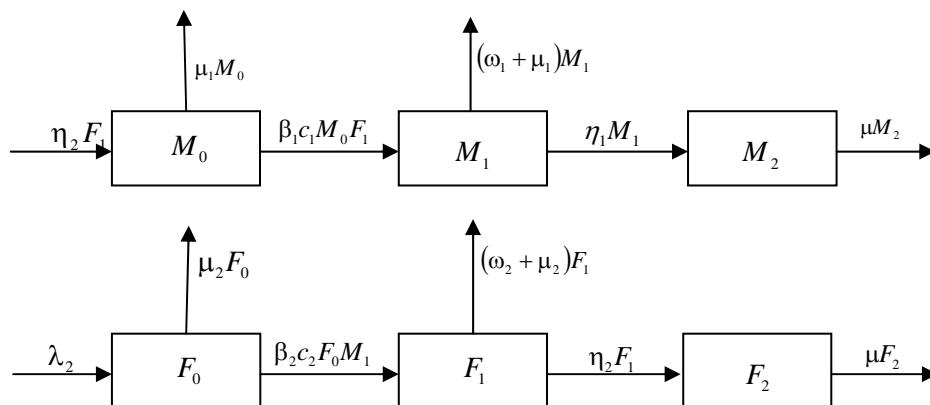


Figure 1: Model structure. The model describes transmission among two classes of people, Male (M) and Female (F).

Infected individuals are allowed to withdraw from risk behavior (at rates ω_1 and ω_2 , say) and die naturally (at rates μ_1 and μ_2 , say). These death rates are applicable for non-infected individuals. Deaths which are due to AIDS are assumed to be the same (at rate μ , say) for male and female. Here, all the parameters are assumed to be positive. The structure of HIV transmission is summarized in Fig. 1.

The differential equations of the model are given by:

$$\frac{dM_0}{dt} = \lambda_1 - \beta_1 c_1 M_0 F_1 - \mu_1 M_0 \quad (2.1)$$

$$\frac{dM_1}{dt} = \beta_1 c_1 M_0 F_1 - (\omega_1 + \eta_1 + \mu_1) M_1 \quad (2.2)$$

$$\frac{dM_2}{dt} = \eta_1 M_1 - \mu M_2 \quad (2.3)$$

$$\frac{dF_0}{dt} = \lambda_2 - \beta_2 c_2 F_0 M_1 - \mu_2 F_0 \quad (2.4)$$

$$\frac{dF_1}{dt} = \beta_2 c_2 F_0 M_1 - (\omega_2 + \eta_2 + \mu_2) F_1 \quad (2.5)$$

$$\frac{dF_2}{dt} = \eta_2 F_1 - \mu F_2 \quad (2.6)$$

3. Stability analysis of disease free equilibria

3.1 Disease free equilibrium of the model

The disease free equilibrium (DFE) for the system (2) is given as

$$\begin{aligned} x_0 &= (M_0, M_1, M_2, F_0, F_1, F_2)_{DFE} \\ &= \left(\frac{\lambda_1}{\mu_1}, 0, 0, \frac{\lambda_2}{\mu_2}, 0, 0 \right) \end{aligned}$$

where 0 indicates that there is no infected people (i.e. no disease in the population).

3.2 Jacobian matrix at DFE and local stability

In order to find the Jacobian at disease free equilibrium we consider the system (2) as

$$f_1 = \beta_1 c_1 x_3 x_2 - k_1 x_1 \quad (3.2a)$$

$$f_2 = \beta_2 c_2 x_4 x_1 - k_2 x_2 \quad (3.2b)$$

$$f_3 = \lambda_1 - \beta_1 c_1 x_3 x_2 - \mu_1 x_3 \quad (3.2c)$$

$$f_4 = \lambda_2 - \beta_2 c_2 x_4 x_1 - \mu_2 x_4 \quad (3.2d)$$

where $M_0 = x_3, M_1 = x_1, F_0 = x_4, F_1 = x_2, k_1 = (\omega_1 + \eta_1 + \mu_1)$ and $k_2 = (\omega_2 + \eta_2 + \mu_2)$. Let us consider $f = [f_1, f_2, f_3, f_4]^T$ and $x = [x_1, x_2, x_3, x_4]^T$ then the Jacobian matrix at DFE is

$$J_0 = D_x f(x_0) = \begin{pmatrix} -k_1 & \frac{\beta_1 c_1 \lambda_1}{\mu_1} & 0 & 0 \\ \frac{\beta_2 c_2 \lambda_2}{\mu_2} & -k_2 & 0 & 0 \\ 0 & -\frac{\beta_1 c_1 \lambda_1}{\mu_1} & -\mu_1 & 0 \\ -\frac{\beta_2 c_2 \lambda_2}{\mu_2} & 0 & 0 & -\mu_2 \end{pmatrix} \quad (3.2e)$$

where the notation $D_x f(x_0)$ indicates the partial derivative of f with respect to x evaluated at $x = x_0$.

Since all the eigenvalues of the matrix J_0 have negative real parts, the DFE is locally asymptotically stable.

4. Existence and stability analysis of endemic equilibria

4.1 Endemic equilibrium of the model

The model has also an endemic equilibrium (EE). By setting the left hand side of system (2) equal to 0, the EE of the model is found and given as

$$\begin{aligned} x^* &= (M_0, M_1, M_2, F_0, F_1, F_2)_{EE} \\ &= \left(\frac{1}{\mu_1} \left(\lambda_1 - \frac{\mu_1 A}{BF \beta_2 c_2} - \frac{\omega_1 A}{BF \beta_2 c_2} - \frac{\eta_1 A}{BF \beta_2 c_2} \right), \frac{A}{BF \beta_2 c_2}, \frac{\eta_1 A}{BF \mu \beta_2 c_2}, \right. \\ &\quad \left. \frac{1}{\mu_2} \left(\lambda_2 - \frac{\mu_2 A}{DE \beta_1 c_1} - \frac{\omega_2 A}{DE \beta_1 c_2} - \frac{\eta_2 A}{DE \beta_1 c_1} \right), \frac{A}{DE \beta_1 c_1}, \frac{\eta_2 A}{DE \mu \beta_1 c_1} \right) \end{aligned} \quad (4.1a)$$

where,

$$A = \lambda_1 \beta_1 c_1 \lambda_2 \beta_2 c_2 - \mu_1^2 \mu_2^2 - \mu_1 \omega_1 \mu_2^2 - \mu_1 \eta_1 \mu_2^2 - \mu_1^2 \mu_2 \omega_2 - \mu_1 \omega_1 \mu_2 \omega_2 - \mu_1 \eta_1 \mu_2 \omega_2 - \mu_1^2 \mu_2 \eta_2 - \mu_1 \omega_1 \mu_2 \eta_2 - \mu_1 \eta_1 \mu_2 \eta_2 \quad (4.1b)$$

$$B = \mu_1 + \omega_1 + \eta_1 \quad (4.1c)$$

$$D = \lambda_1 \beta_2 c_2 + \mu_1 \mu_2 + \omega_1 \mu_2 + \eta_1 \mu_2 \quad (4.1d)$$

$$E = \mu_2 + \omega_2 + \eta_2 \quad (4.1e)$$

$$F = \beta_1 c_1 \lambda_2 + \mu_1 \mu_2 + \mu_1 \omega_2 + \mu_1 \eta_2 \quad (4.1f)$$

4.2 Jacobian matrix at EE and global stability

Using the system of equations (3.2) the Jacobian matrix at endemic equilibrium states is given by

$$J_1 = D_x f(x^*) = \begin{pmatrix} -k_1 & \beta_1 c_1 M_0^* & \beta_1 c_1 F_1^* & 0 \\ \beta_2 c_2 F_0^* & -k_2 & 0 & \beta_2 c_2 M_1^* \\ 0 & -\beta_1 c_1 M_0^* & -(\beta_1 c_1 F_1^* + \mu_1) & 0 \\ -\beta_2 c_2 F_0^* & 0 & 0 & -(\beta_2 c_2 M_1^* + \mu_2) \end{pmatrix} \quad (4.2a)$$

where,

$$M_0^* = \frac{1}{\mu_1} \left(\lambda_1 - \frac{\mu_1 A}{BF\beta_2 c_2} - \frac{\omega_1 A}{BF\beta_2 c_2} - \frac{\eta_1 A}{BF\beta_2 c_2} \right) \quad (4.2b)$$

$$F_0^* = \frac{1}{\mu_2} \left(\lambda_2 - \frac{\mu_2 A}{DE\beta_1 c_1} - \frac{\omega_2 A}{DE\beta_1 c_1} - \frac{\eta_2 A}{DE\beta_1 c_1} \right) \quad (4.2c)$$

$$M_1^* = \frac{A}{BF\beta_2 c_2} \quad (4.2d)$$

$$F_1^* = \frac{A}{DE\beta_1 c_1} \quad (4.2e)$$

and the values of A, B, D, E and F are given above in equation (4.1b–4.1f).

Since it is not easy to find out the eigenvalues of matrix J_1 at EE analytically, we use the data from Table 1 and after calculating we have seen that all eigenvalues are negative. So, easily we can say that the endemic solution is also stable.

5. The basic reproduction number

The basic reproduction number, denoted R_0 is “the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual”[4]. If $R_0 < 1$, then on average an infected individual produces less than one new infected individual over the course of its infectious period, and the infection cannot grow. Conversely, if $R_0 > 1$, then each infected individual produces, on average, more than one new infection, and the disease can invade the population (see the survey paper by Hethcote[6]).

Here, we have found the basic reproduction number using the method discussed in [14]. To find R_0 the following notation is used:

$$\begin{bmatrix} \frac{dx_1}{dt} \\ \frac{dx_2}{dt} \end{bmatrix} = \begin{bmatrix} F_1 \\ F_2 \end{bmatrix} - \begin{bmatrix} V_1 \\ V_2 \end{bmatrix} \quad (5.1)$$

where,

$$\begin{bmatrix} F_1 \\ F_2 \end{bmatrix} = \begin{bmatrix} \beta_1 c_1 x_3 x_2 \\ \beta_2 c_2 x_4 x_1 \end{bmatrix} \quad (5.2)$$

and

$$\begin{bmatrix} V_1 \\ V_2 \end{bmatrix} = \begin{bmatrix} k_1 x_1 \\ k_2 x_2 \end{bmatrix} \quad (5.3)$$

Then, letting $y = [x_1, x_2]^T$, we let F and V be the Jacobian. Now we have

$$F = \frac{\partial F}{\partial y} = \begin{pmatrix} \frac{\partial F_1}{\partial x_1}(x_0) & \frac{\partial F_1}{\partial x_2}(x_0) \\ \frac{\partial F_2}{\partial x_1}(x_0) & \frac{\partial F_2}{\partial x_2}(x_0) \end{pmatrix} \quad (5.4)$$

$$= \begin{pmatrix} 0 & \beta_1 c_1 x_3 \\ \beta_2 c_2 x_4 & 0 \end{pmatrix} \quad (5.5)$$

and

$$V = \frac{\partial V}{\partial y} = \begin{pmatrix} \frac{\partial V_1}{\partial x_1}(x_0) & \frac{\partial V_1}{\partial x_2}(x_0) \\ \frac{\partial V_2}{\partial x_1}(x_0) & \frac{\partial V_2}{\partial x_2}(x_0) \end{pmatrix} \quad (5.6)$$

$$= \begin{pmatrix} k_1 & 0 \\ 0 & k_2 \end{pmatrix} \quad (5.6)$$

Thus, following reference [14], FV^{-1} is the next generation matrix for the model and

$$R_0 = \rho(FV^{-1})$$

$$\begin{aligned}
&= \left(\frac{\beta_1 c_1 \beta_2 c_2 x_3 x_4}{k_1 k_2} \right)^{\frac{1}{2}} \\
&= \left(\frac{\beta_1 c_1 \beta_2 c_2 \lambda_1 \lambda_2}{\mu_1 \mu_2 (\omega_1 + \eta_1 + \mu_1) (\omega_2 + \eta_2 + \mu_2)} \right)^{\frac{1}{2}} \tag{5.8}
\end{aligned}$$

where $\rho(FV^{-1})$ denotes the spectral radius of the matrix FV^{-1} .

Suppose $R_0 > 1$. Then

$$\begin{aligned}
R_0 &> 1 \\
&\Leftrightarrow (\beta_1 c_1 \beta_2 c_2 \lambda_1 \lambda_2)^{\frac{1}{2}} > (\mu_1 \mu_2 (\omega_1 + \eta_1 + \mu_1) (\omega_2 + \eta_2 + \mu_2))^{\frac{1}{2}} \\
&\Leftrightarrow \beta_1 c_1 \beta_2 c_2 \lambda_1 \lambda_2 > \mu_1 \mu_2 (\omega_1 + \eta_1 + \mu_1) (\omega_2 + \eta_2 + \mu_2) \tag{5.9}
\end{aligned}$$

If $R_0 < 1$. Then

$$\begin{aligned}
R_0 &< 1 \\
&\Leftrightarrow (\beta_1 c_1 \beta_2 c_2 \lambda_1 \lambda_2)^{\frac{1}{2}} < (\mu_1 \mu_2 (\omega_1 + \eta_1 + \mu_1) (\omega_2 + \eta_2 + \mu_2))^{\frac{1}{2}} \tag{5.10} \\
&\Leftrightarrow \beta_1 c_1 \beta_2 c_2 \lambda_1 \lambda_2 < \mu_1 \mu_2 (\omega_1 + \eta_1 + \mu_1) (\omega_2 + \eta_2 + \mu_2)
\end{aligned}$$

6. Analysis of the centre manifold near $x=x_0$, $R_0=1$

In this section we consider the nature of the equilibrium solutions of the disease transmission model near the bifurcation point $x=x_0$, $R_0=1$ [14]. Since R_0 is often inconvenient to use directly as bifurcation parameter, we introduce a bifurcation parameter θ . Let θ be a bifurcation parameter such that $R_0 < 1$ for $\theta < 0$ and $R_0 > 1$ for $\theta > 0$ and such that x_0 is a DFE for all values of θ . Let us consider the system

$$\dot{x} = f(x, \theta) \tag{6.1}$$

where f is as described in equation (3.2). The choice of θ is given below, when the quality b is calculated. The position of the DFE depends particularly on the choice of θ and the local stability changes at the point $(x_0, 0)$. The results of centre manifold theory [15] are used here to show that there are nontrivial (endemic) equilibria near the bifurcation point $(x_0, 0)$.

We use the notation $J_0 = D_x f(x_0, 0)$ for the partial derivative of f with respect to x evaluated at $x=x_0$ and $\theta=0$. Let v and u be the corresponding left and right eigenvectors chosen such that $vJ_0=0$ and $J_0u=0$ with $vu=1$ where $v=[v_1, v_2, v_3, v_4]$ and

$u = [u_1, u_2, u_3, u_4]^T$. Following reference [14], we define

$$a = \frac{v}{2} D_{xx} f(x_0, 0) u^2 = \frac{1}{2} \sum_{i,j,k=1}^n v_i u_j u_k \frac{\partial^2 f_i}{\partial x_j \partial x_k}(x_0, 0) \quad (6.2)$$

$$b = v D_{x\theta} f(x_0, 0) u = \sum_{i,j=1}^n v_i u_j \frac{\partial^2 f_i}{\partial x_j \partial \theta}(x_0, 0) \quad (6.3)$$

For our model, we have $n=4$ and now we find the values of a and b . The sign of a as well as the value of b will help in determining the nature of the endemic equilibria near the bifurcation point.

For $i=1$

$$\begin{aligned} a_1 &= \frac{1}{2} \sum_{j,k=1}^4 v_1 u_j u_k \frac{\partial^2 f_1}{\partial x_j \partial x_k}(x_0, 0) \\ &= \frac{1}{2} v_1 u_2 u_3 \beta_1 c_1 + \frac{1}{2} v_1 u_2 u_3 \beta_1 c_1 \\ &= v_1 u_2 u_3 \beta_1 c_1 \end{aligned}$$

Similarly, for $i=2,3,4$ we get $a_2 = v_2 u_1 u_4 \beta_2 c_2$, $a_3 = -v_3 u_2 u_3 \beta_1 c_1$ and $a_4 = -v_4 u_1 u_4 \beta_2 c_2$ respectively. Thus we have

$$\begin{aligned} a &= a_1 + a_2 + a_3 + a_4 \\ &= v_1 u_2 u_3 \beta_1 c_1 + v_2 u_1 u_4 \beta_2 c_2 - v_3 u_2 u_3 \beta_1 c_1 - v_4 u_1 u_4 \beta_2 c_2 \\ &= u_2 u_3 \beta_1 c_1 (v_1 - v_3) + u_1 u_4 \beta_2 c_2 (v_2 - v_4) \end{aligned} \quad (6.4)$$

In order to find the value of b , let me consider R_0 as a function of c_1 i.e. $R_0 = R_0(c_1)$ and fix all other parameters $c_2, \beta_i, \mu_i, \lambda_i, \omega_i, \eta_i$. Let c_1^* be the value of c_1 such that $R_0(c_1^*) = 1$. Let $\theta = c_1 - c_1^*$, then $R_0 = R_0(\theta)$ with $R_0(0) = 1$.

For $i=1$

$$\begin{aligned} b_1 &= \sum_{j=1}^4 v_1 u_j \frac{\partial^2 f_1}{\partial x_j \partial \theta}(x_0, 0) \\ &= v_1 u_2 \beta_1 x_3 \\ &= \frac{v_1 u_2 \beta_1 \lambda_1}{\mu_1} \end{aligned}$$

Similarly, for $i=2,3,4$ we get $b_2 = 0$, $b_3 = -v_3 u_2 \beta_1 x_3 = -\frac{v_3 u_2 \beta_1 \lambda_1}{\mu_1}$ and $b_4 = 0$ respectively. Thus we have

$$\begin{aligned}
b &= b_1 + b_2 + b_3 + b_4 \\
&= \frac{v_1 u_2 \beta_1 \lambda_1}{\mu_1} + 0 - \frac{v_3 u_2 \beta_1 \lambda_1}{\mu_1} + 0 \\
&= \frac{u_2 \beta_1 \lambda_1}{\mu_1} (v_1 - v_3)
\end{aligned} \tag{6.5}$$

Now using the condition $vJ_0=0$ and $J_0u=0$, we can find v and u as

$$v = \left(v_1^*, \frac{\beta_1 c_1 \lambda_1 v_1^*}{k_2 \mu_1}, 0, 0 \right) \tag{6.6}$$

$$\text{and } u = \left(u_1^*, \frac{\beta_2 c_2 \lambda_2 u_1^*}{\mu_2 k_2}, -\frac{\beta_1 \beta_2 c_1 c_2 \lambda_1 \lambda_2 u_1^*}{\mu_1^2 \mu_2 k_2}, -\frac{\beta_2 c_2 \lambda_2 u_1^*}{\mu_2^2} \right) \tag{6.7}$$

Since $R_0=1$ i.e. $k_1 k_2 \mu_1 \mu_2 - \beta_1 \beta_2 c_1 c_2 \lambda_1 \lambda_2 = 0$ then $v_1 = v_1^* \neq 0$ and $u_1 = u_1^* \neq 0$.

Let $u_1^* = 1$. Then the condition $uv=1$ gives

$$v_1^* = \frac{1}{Q} \tag{6.8}$$

where

$$Q = 1 + \frac{\beta_1 \beta_2 c_1 c_2 \lambda_1 \lambda_2}{k_2^2 \mu_1 \mu_2} \tag{6.9}$$

Substituting the values of v and u in equations (6.4) and (6.5), we get

$$\begin{aligned}
a &= v_1 u_2 u_3 \beta_1 c_1 + v_2 u_1 u_4 \beta_2 c_2 \\
&= -\frac{\beta_1^2 \beta_2^2 c_1^2 c_2^2 \lambda_1 \lambda_2}{Q k_2^2 \mu_1^2 \mu_2^2} - \frac{\beta_1 \beta_2^2 c_1 c_2^2 \lambda_1 \lambda_2}{Q k_2 \mu_1 \mu_2^2}
\end{aligned} \tag{6.10}$$

and

$$\begin{aligned}
b &= \frac{u_2 \beta_1 \lambda_1}{\mu_1} v_1 \\
&= \frac{\beta_1 \beta_2 c_2 \lambda_1 \lambda_2}{Q \mu_1 \mu_2 k_2}
\end{aligned} \tag{6.11}$$

Thus, it is obvious that $a < 0$ and $b \neq 0$ and hence by theorem 2 [14] there are locally asymptotically stable endemic equilibria near x_0 for $0 < \theta < \delta$ where $\delta > 0$. Therefore, the bifurcation as R_0 passes through 1 is a forward bifurcation.

Hence, the DFE is locally asymptotically stable if R_0 is less than one (i.e. $\theta < 0$), if R_0 is greater than one then the DFE is unstable and there is a locally asymptotically stable EE near the DFE.

7. Numerical computation and discussion

To illustrate the various theoretical results discussed in this paper, the model is simulated using the parameter values/ranges shown in Table 1. Choice of numerical values for the model's parameter values is based upon published data on the transmission dynamics of HIV in one of the major cities, Delhi of India [2, 3, 5, 12, 13]. Since AIDS is a sexually transmitted disease, we restrict our analysis to the population that is age 15 or older. Here, we have used MATLAB 6.1 package for plotting the solutions of our model. It is easily observed from Fig. 2 that the final total population size is a lot smaller than the initial population size. So, HIV/AIDS has the potential impact to cause a population crush (i.e. an epidemic occurs) if all the parameter values remain constant.

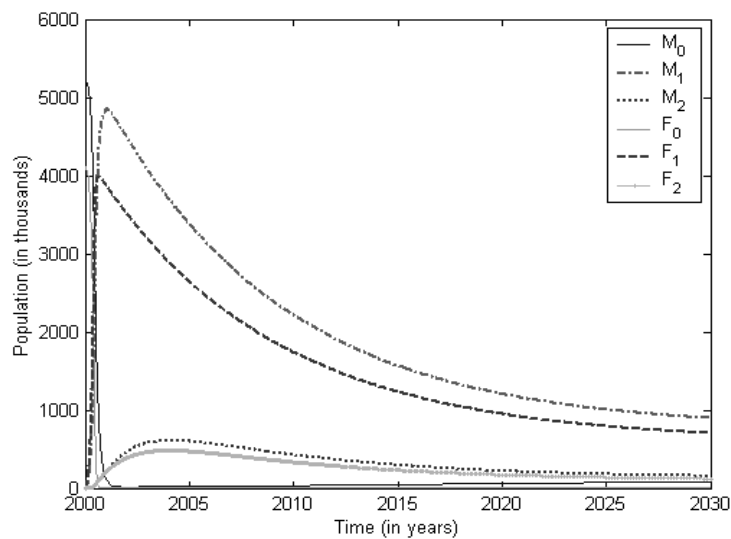


Figure 2: Trends of HIV, AIDS and susceptible population.

The basic reproduction number, R_0 (given by 5.8) is a threshold parameter for the model. Here, $R_0 = 117.308 > 1$ and the disease persists limiting to the endemic equilibrium point (EEP). Moreover, the analysis of the centre manifold yields a second parameter, a (given by 6.2) whose sign indicates the existence and stability near $x = x_0$ and $R_0 = 1$. Note that $a = -2.08783$ (i.e. negative). Thus for $R_0 < 1$, the DFE is stable where as for $R_0 > 1$, the DFE is unstable and the EEP is stable.

Conclusion

Application of non-linear differential equations model in predicting the course of epidemics is well established. The model presented here captures the dynamics of virus transmission and full-blown disease in males and females. The model is analyzed to investigate the existence and stability of the associated equilibria. Numerical simulations were carried out using reasonable sets of parameter values to assess the spread and the persistency of HIV/AIDS epidemic in the country. The model shows that there is a possibility of an epidemic if all the parameter values remain constant (i.e. no initiatives

are taken for changing the behavioural parameters). This model can contribute to the planning of preventive procedures in case of HIV transmission into the population. Behavioural parameters can help public health planning as well.

Table 1: Description and estimation of parameters.

| Parameter | Description | Estimation value/range |
|-------------------|---|------------------------|
| λ_1 | Recruitment rate of susceptible males into the community (in thousands) | 92.58 (year) |
| λ_2 | Recruitment rate of susceptible females into the community (in thousands) | 69.95 (year) |
| $\frac{1}{\mu_1}$ | Average life expectancy for males | 55.6 years |
| $\frac{1}{\mu_2}$ | Average life expectancy for females | 58.8 years |
| β_1 | Probability of females transmit the virus to their male counterparts | 0.00155 |
| β_2 | Probability of males transmit the virus to their female counterparts | 0.00105 |
| c_1 | Contact rate of females | 1.001 |
| c_2 | Contact rate of males | 5.440 |
| ω_1 | Withdrawal rate from risk behavior for males | 0 |
| ω_2 | Withdrawal rate from risk behavior for females | 0 |
| η_1 | Incubation period for males | 0.1 year |
| η_2 | Incubation period for females | 0.1 year |
| μ | Natural death rate | 0.6 |

REFERENCES

1. Anderson R M, May R M 1991 Infectious diseases of humans: Dynamics and control (London: Oxford University Press).
2. Census of India 2001, "Report of the technical group on population projections constituted by the national commission on population", (2006).
3. Delhi State AIDS Control Society, Government of Delhi, Population Foundation of India and Population Reference Bureau, "HIV/AIDS in DELHI, Meeting the Challenge", New Delhi, (2005).
4. Diekmann, O., Heesterbeek, J. A. P. and Metz, J. S. J., "On the definition and the computation of the basic reproduction number ratio R_0 in models for infectious diseases in heterogeneous populations", J. Math. Bio. **28**, 365-382, (1990).
5. Gisselquist, David and Correa, Mariette, "How much does heterosexual commercial sex contribute to India's HIV epidemic?" International Journal of STD and AIDS **17**: 736-742, 2006.
6. Hethcote, H. W., "The mathematics of infectious disease", SIAM Rev. **42**, 599-653, (2000).
7. H. W. Hethcote, Qualitative analysis of communicable disease models, Math. Biosci. **28**: 335-356 (1976).
8. H. W. Hethcote and J. W. Van Ark, Epidemiological models for heterogeneous populations: proportionate mixing, parameter estimation and immunization programs, Math. Biosci. **84**: 85-118 (1987).

9. Hyman, JM, and Stanley, EA. Using Mathematical Models to Understand the AIDS epidemic. *Math. Biosci.*, **90**: 415-473, (1988.).
10. Hyman, JM, and Stanley, EA. 1994. A Risk-Based Heterosexual Model for the AIDS Epidemic with Biased Sexual Partner Selection. *Modeling the AIDS Epidemic: Planning, Policy and Prediction*, Raven Press, Ltd.
11. Murray J D (1989) *Mathematical biology* (Berlin: Springer-Verlag).
12. Rao, Arni S. R. Srinivasa and Kakehashi, Masayuki, "A combination of differential equations and convolution in understanding the spread of an epidemic", *Sadhana*, **29**, 305-313, (2004).
13. Rao, Arni S. R. Srinivasa, "Mathematical modeling of AIDS epidemic in India", *Current Science*, **84**, (2003).
14. Van den Driessche, P. and Watmough, James, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission", *Elsevier (Math. Biosci.)*, (2002).
15. Wiggins, S., "Introduction to Applied Nonlinear Dynamical Systems and Chaos", Springer-Verlag, Berlin, (1990).