A Mathematical Model of HIV Transmission Dynamics in Closed Population

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Abstract: In this study we proposed a mathematical model of HIV transmission dynamics, the population is partitioned into four compartments of Susceptible S (t), Infected I (t), Removed R (t) and the Controlled U (t). Extreme conditions are imposed on the model equations to check for stability of free equilibrium states and it is confirmed that the disease free equilibrium states is locally asymptotically stable.

Key words: Compartmental model, free equilibrium states, HIV, dynamics, susceptible, extreme

INTRODUCTION

The application of mathematics to HIV epidemic and epidemiology in general cannot be over emphasis. Two decades ago, people know little about mathematics of HIV/AIDS particularly, mathematical or epidemiological models of HIV epidemic. Today, mathematical models play an important role in better understanding of infectious diseases, the impact, characteristics features and the behavior of the host population.

It is a known fact that there is no single medical cure for HIV/AIDS presently, the so-called Antiretroviral Drugs (ARD) do not cure HIV, they only burst the immune system of the infected individuals against secondary infection thereby prolonging their life span (Kimbir and Aboiyar, 2003; Hsieh, 1996; May and Anderson, 1987, 1991).

In this study we want to see the effect of preventive measures at various stages of the epidemic. First, we consider a situation when the susceptible individuals used a preventive measure also we consider when the infected individuals used a preventive measure and then, we consider a situation when both susceptible and the infected population used a preventive measure.

Model parameters:

S (t) = Number of susceptible at time t
I (t) = Number of infected at time t
R (t) = Number of infected receiving ART at time t
U (t) = Number of susceptible using a preventive measure at time t
b = Population birth rate
μ = Population death rate
α_0 = Population death rate of infected not receiving ART
α = Population death rate of infected receiving ART
T = Maximum lifespan after infection
k = Efficacy of ART per unit time
C_0 = Average number of sexual partners of members of class I
C = Average number of sexual partners of members of class R
β_0 = Probability of transmission by members of class I
β = Probability of transmission by members of class R
σ = Proportion of infected receiving ART per unit time
λ = Proportion of susceptible using a preventive measure
ρ = Proportion of susceptible using a preventive measure but become infected
π = Efficacy of the preventive measure

Formulation of the model: The diagram can be found useful in formulating the model equations (Fig. 1). The model equations are:
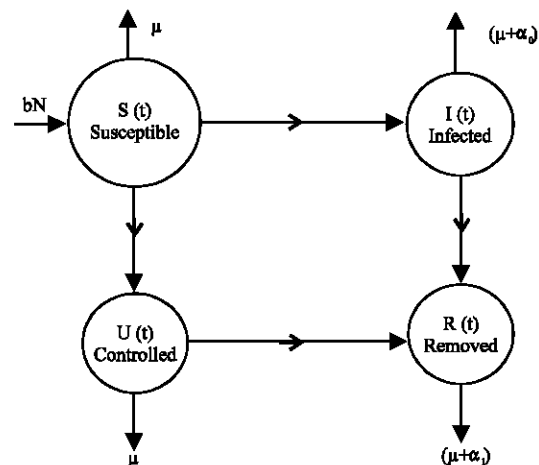

Fig. 1: Pictorial representation of the model flow

$$\frac{dS}{dt} = bN - (B + \mu + \lambda)S(t) \qquad (1)$$

$$\frac{dI}{dt} = BS(t) - (\mu + \sigma + \alpha_0)I(t) \qquad (2)$$

$$\frac{dR}{dt} = \sigma I(t) + \rho U(t) - (\mu + \alpha_1)R(t) \qquad (3)$$

$$\frac{dU}{dt} = \lambda S(t) - (\mu + \rho)U(t) \qquad (4)$$

where, $\lambda = \pi/\rho$ and $B = c_0\beta_0 I + c\beta R/N$ (Kimbir and Aboiyar, 2003).

Now rewrite these equations into equivalence in difference equations using the classical Euler's method:

$$S_{n+1} = S_n bN - (B + \mu + \lambda)S_n(t)$$
$$I_{n+1} = I_n BS_n(t) - (\mu + \sigma + \alpha_0)I_n(t)$$
$$R_{n+1} = R_n + \sigma I_n(t) - \rho U_n(t) - (\mu + \alpha_1)R_n(t)$$
$$U_{n+1} = U_n + \lambda S_n(t) - (\mu + \rho)U_n(t)$$

Stability analysis of the free equilibrium states: Here it check the disease free equilibrium states using the next generation operator by Diekmann (Umar, 2007).

We would categorize the population into two cohorts (classes) as $X = (S, U)$ and $Z = (I, R)$. Then we would have thus:

$$X = f(X, Z) = bN - (c_0\beta Z + c\beta Z)\frac{X}{N} - (2\mu + \rho)$$

$$Z = h(X, Z) = (c_0\beta Z + c\beta Z)\frac{X}{N} + \rho X - (2\mu + \alpha_0 + \alpha_1)Z$$

$$\text{Now let } H = \frac{\partial h}{\partial Z} \Rightarrow H = c_0\beta - (2\mu + \alpha_0 + \alpha_1)$$

Letting $H = M-D$ with $M>0$, $D>0$ is a diagonal matrix, then,

$$M + c_0\beta \text{ and } D = (2\mu + \alpha_0 + \alpha_1)$$

The basic reproduction number of the infective is defined as the spectral radius (dominant eigenvalues) of the matrix MD^{-1}:

$$R_0 = \phi(MD^{-1}) = \frac{c_0\beta}{2\mu + \alpha_0 + \alpha_1} < 1$$

$$\Rightarrow R_0 < 1$$

Since all the parameters are positive, hence the expression for the reproduction number is strictly less one. This means we this model the HIV epidemic can totally be eradicated.

CONCLUSION

Since, $R_0 < 1$, this implies for every one primary infection would generate less than one secondary infection, hence this deadly scourge can die out within a fine time. Therefore, it conclude the disease free equilibrium states of the model is locally asymptotically stable.

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