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A Delay Model for the Spread of HIV/Aids in A Heterosexual Population

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Abstract: *Mathematical models for the spread of HIV infection have made a considerable contribution on the understanding of HIV/AIDS dynamics. In this paper, an HIV/AIDS epidemic model in a heterosexual population is analyzed through modification of Susceptible-Infective-Removed (SIR) model by incorporating time lags (delay) for one to become infective and the other to become fully blown in a given population.By application of the next generation matrix, the reproduction number R_0 is determined. By construction of Lyapunov function and using La Salleâ™s invariance principle, it is proven that if the reproduction number is less than or equal to unity, the HIV/AIDS free equilibrium is globally asymptotically stable and the disease dies out; and if the reproduction number is greater than unity, the endemic equilibrium is globally asymptotically stable, and hence the disease becomes endemic.*

Keywords: *Time delay, stability*

I. Introduction

Human Immuno deficiency Virus(HIV) is the virus which causes Acquired Immune Deficiency Syndrome (AIDS). Epidemiological research on HIV/AIDS has been marked with much activity for the last decade. It is considered as the worldâ™s serious epidemic of this century. Although much is un-known about HIV, much about its transmission dynamics in populations have been discovered by researchers ([], [])).

Kenya is considered one of the countries in Africa which has the worldâ™s worst HIV and AIDS epidemics (as observed in []). From [], approximately 1.5 million people in Kenya are considered to b e living with HIV. This ever increasing numbers of HIV/AIDS related cases has led to the development of mathematical models to explain its spread and transmission dynamics. Over the years, mathematical modeling has been of great concern to many researchers (like for example in [] and []). It has been useful in the analysis of various disease dynamics such as malaria, tuberculosis, and HIV/AIDS. It plays a bigger role in the understanding of epidemiological patterns for disease control. From epidemiology, HIV is primarily transmitted through the intimate ex-change of body fluids, such as semen, blood, vaginal secretion, and motherâ™s milk. HIV can also b e passed to a child from infected mother during birth (vertical transmission). Its long infection time (delay) which ranges from a few months to years is the main characteristic of HIV before the onset of AIDS.

Hence, the formulation of the model in this research is similar to that proposed by Luboobi et al. [], but with the inclusion of a second time delay. That is, when a susceptible individual draws a uniformly random person from the population and the individual chosen is infectious, the susceptible individual is assumed to get the virus. After a time lag, $\tau_1>0$, the individual when tested will become infectious. Without drug intervention, an infected individual will then progress to fully blown after time $\tau_2>0$. Each full blown individual remains full blown till death.

II. The Model

We sub-divide a population in a clinical set up into; Susceptible (S(t)) individuals, Infective (I(t)) individuals, and Fully Blown (A(t)) (AIDS) individuals. The susceptible population is assumed to be recruited into the compartment of Susceptibles by birth at the rate denoted by B, while the population can decrease due to natural deaths at a rate μ or due to infection as a result of interaction with infected individuals I(t). Infected individuals may die due to natural death at a rate μ or progress to become fully blown individuals at a rate ν. After progression to the compartment of fully blown, individuals are removed from this compartment due to natural death at a rate μ or die due disease induced death at a rate d. Each individual that is susceptible draws a uniformly random person from the population. If the individual chosen is infectious, the susceptible individual is assumed to get the virus with a probability β. In a clinical set up, an individual after being in contact with an infective, takes some time lag, say $\tau_1>0$, to be clinically infected. Without drug intervention, an infected individual will then progress to fully blown after some time $\tau_2>0$. Each full blown individual remains full blown till death. These dynamics of the disease leads to the modification of Equation (**Error! Reference source not found.**) as follows;

$$\begin{aligned}\dot{S}(t) &= B-\mu S(t)-\frac{\beta C I(t)S(t)}{N(t)},\\ \dot{I}(t) &= \frac{\beta C I(t-\tau_1)S(t-\tau_1)}{N(t-\tau_1)}-(\nu+\mu)I(t),\\ \dot{A}(t) &= \nu I(t-\tau_2)-(d+\mu)A(t). \qquad (1)\end{aligned}$$

Let $\tau=\max\{\tau_1,\tau_2\}$,and $C:=\mathcal{C}([-\tau,0],R^3_+)$, $\varphi(\theta):=(S(\theta),I(\theta),A(\theta))$ $\theta\in[-\tau,0]$;

$\varphi\in C$, with the norm of φ defined as $\|\varphi\|=\sup_{-\tau\le\theta\le 0}|\varphi(\theta)|$ where $|\cdot|$ is a norm in R^3.

The initial condition for Equation (1) is;

$$\varphi(\theta)=(S_0(\theta),I_0(\theta),A_0(\theta)). \qquad (2)$$

where all elements are nonnegative for all $\theta\in[-\tau,0]$ with $S(\theta)\ge 0$, $I(\theta)\ge 0$, and $A(\theta)\ge 0$. Equation (1) subject to (2), has a unique solution, see for instance [].

III. Local stability

The stable steady states are the non infected steady state $E_0=(S_0,0,0)$ and the infected steady state $E_1=(S^*,I^*,A^*)$. To study the stable steady state,we linearize the system about the equilibrium point E_1. Let's define

$$\begin{aligned}x(t) &= S(t)-S^*,\\ y(t) &= I(t)-I^*,\\ z(t) &= A(t)-A^*. \qquad (3)\end{aligned}$$

and by Taylor series expansion of Equation (1) about (S^*,I^*,A^*) and ignoring higher order terms, we obtain

$$\begin{aligned}\dot{x}(t) &= -(\mu+\frac{\beta C I^*}{N^*})x(t)-\frac{\beta C S^*}{N^*}y(t),\\ \dot{y}(t) &= \frac{\beta C I^*}{N^*(t-\tau_1)}x(t-\tau_1)-(\mu+\nu)y(t)+\frac{\beta C S^*}{N^*(t-\tau_1)}y(t-\tau_1),\\ \dot{z}(t) &= \nu y(t-\tau_2)-(d+\mu)z(t). \qquad (4)\end{aligned}$$

For simplification we let $\tau=\max\{\tau_1,\tau_2\}$ and thus Equation (4) can be expressed in a matrix form as;

$$\dot{Y}(t)=AY(t)+BY(t-\tau) \qquad (5)$$

where

A:=–(μ+ $\frac{\beta C I^*}{N}$) EQ – \F(βCS\s\up5(*),N) EQ 00 EQ –(μ+υ)

EQ 00 EQ 0 EQ –(d+μ)\, B:=0 EQ 0 EQ 0

\F(βCI\s\up5(*),N) EQ \F(βCS\s\up5(*),N) EQ 00 EQ ν EQ 0\,

$Y(t):=x(t)y(t)z(t)$,and $Y(t-\tau):=x(t-\tau)y(t-\tau)z(t-\tau)$.

Equation (5) is a linear system and to solve it, we assume a solution of the form

$Y(t)=Y_0e^{\lambda t}$, Y_0 is a constant 3×1 vector

which upon substitution in Equation (5) yields;

$$Y_0\lambda e^{\lambda t}=AY_0e^{\lambda t}+BY_0e^{\lambda t} \qquad (6)$$

For a nontrivial solution and $Y_0\neq 0$, we need to have;

$$\xi(\lambda):=|\text{ matrix not implemented }|=0 \qquad (7)$$

At E_0, with $I^*,A^*=0$ and $S^*=S_0=\frac{B}{\mu}$, $E_0=(S_0,0,0)$ and Equation (7) becomes;

$$H(\lambda):= \text{| matrix not implemented |}=0 \quad (8)$$

On computing, it yields

$\lambda=-\mu, -(d+\mu)$ and $(\frac{\beta CS^*}{N})e^{-\tau\lambda}-(\mu+\nu)$.

The first two eigenvalues are negative and for asymptotic stability of the disease free equilibrium, the Equation

$$(\frac{\beta CS^*}{N})e^{-\tau\lambda}-(\mu+\nu)-\lambda=0, \quad (9)$$

should satisfy;

$$\text{Re } \lambda<0 \quad (10)$$

To have Equation (10) hold, we state the following theorem;

Theorem 1 The disease free equilibrium exists if the reproduction rate $R_0<1$ and $\tau(\mu+\nu)>1$.

To prove Theorem
, we use the following Lemma by Bellman and Cooke []

Lemma 1 All roots of the equation $(z+a)e^z+b=0$, where a and b are real, have negative real parts if and only if;
(i) $a>1$,
(ii) $a+b>0$,
(iii) $b<\zeta\sin\zeta-a\cos\zeta$

where ζ is the root of $\zeta=-a\tan\zeta$, $0<\zeta<\pi$, if $a\neq0$ and $\zeta=\frac{\pi}{2}$ if $a=0$.

[Sorry. Ignored `\begin{proof} ... \end{proof}`]

This shows that for asymptotic stability at disease free equilibrium, we have that; $\tau>\frac{1}{\mu+\nu}$, $R_0<1$, and $\frac{\pi}{2}<\zeta<\pi$.

At endemic equilibrium, $E_1=(S^*,I^*,A^*)$, Equation (7) becomes;

$$\xi(\lambda):= \text{| matrix not implemented |}=0 \quad (11)$$

Clearly, one of the eigenvalues is $-(d+\mu)$. For the other eigenvalues, λ, we have;

$$\text{| matrix not implemented |}=0 \quad (12)$$

On evaluating the eigenvalue problem of (12), we obtain the following characteristic equation

$$\lambda^2+(2\mu+\nu+\frac{\beta CI^*}{N^*})\lambda+\mu^2+\mu\nu+(\mu+\nu)\frac{\beta CI^*}{N^*}-(\frac{\beta CS^*}{N^*}\lambda+\frac{\beta CS^*\mu}{N^*})e^{-\lambda\tau}=0 \quad (13)$$

Let $H(\lambda):=\lambda^2+(2\mu+\nu+\frac{\beta CI^*}{N^*})\lambda+\mu^2+\mu\nu+(\mu+\nu)\frac{\beta CI^*}{N^*}$

and $D(\lambda):=-\frac{\beta CS^*}{N^*}\lambda-\frac{\beta CS^*\mu}{N^*}$.

Hence, Equation (13) can be rewritten thus;

$$H(\lambda)+D(\lambda)e^{-\lambda\tau}=0. \quad (14)$$

If the roots of Equation (14) are negative, then the endemic equilibrium is asymptotically stable. This leads as to the following Theorem;

Theorem 2 For all values of $\tau>0$ and $R_0>1$, the disease equilibrium E_1,is positively bounded and asymptotically stable.

To check whether the roots of Equation(14) are negative, we use the following Lemma by Boese [].

Lemma 2 For the roots of (14) to lie to the left of the complex plane, it is necessary that;
(i) All zeros of $H(\lambda)$ satisfy $Re\lambda \leq 0$,
(ii) $|H_0| \geq |D_0|$, where $H_0 := H(0)$, and $D_0 := D(0)$.

[Sorry. Ignored `\begin{proof} ... \end{proof}`]

IV. Global stability

We shall use Lyapunov function for global stability of the disease-free equilibrium.

Theorem 3 The disease free equilibrium is globally stable if $R_0 \leq 1$.

[Sorry. Ignored `\begin{proof} ... \end{proof}`]

Theorem 4 The endemic equilibrium E_1, is globally stable if $R_0 > 1$.

[Sorry. Ignored `\begin{proof} ... \end{proof}`]

V. Numerical simulations

We use Matlab software to illustrate the numerical simulations describing the theoretical results for model (1). We describe the variables and parameters values to enable us make numerical simulations. Parameter values are hypothetical.

Table: Data for the HIV/AIDS model

Initial or values	**default Source**
4000	Estimate
800	Estimate
97	Estimate
29 per year	Estimate
0.011-0.95	[],[]
3 per year	[]
0.01562	[]
0.333 per year	[]
0.125 per year	[]

VI. Simulation for the HIV/AIDS free equilibrium

For numerical simulation of the stable steady state, E_0, of (1), we use the following initial conditions

$S_0=4000, I_0=800, A_0=97$

Figure 1 shows the solution dynamics of model (1) when reproduction number R_0, is less than one. In this case, the only stable steady state is the HIV/AIDS free equilibrium E_0.

Figure 1: Numerical solution of model (1) when $R_0 < 1$.

From figure 1, we observe that the population of infectives and fully blown individuals will eventually decrease to 0, but the susceptible population converges to $S^* \leq \frac{B}{\mu}$. In other words, the solutions converge to HIV/AIDS free steady state E_0, where the disease is wiped out.

VII. Simulation for the disease equilibrium

If $R_0 > 1$, the HIV/AIDS free equilibrium becomes unstable while the endemic equilibrium E_1 becomes stable. Additionally, if $R_0 > 1$ by proposition 2, the endemic equilibrium is asymptotically stable. In figure 2, solutions converge to E_1.

Figure 2: Numerical solution of model (1) when $R_0 > 1$.

From figure 2, the infection persists in the population, that is, the number of infectives in the population will increase until it attains an equilibrium E_1. Figure 2 shows the convergence of the endemic equilibrium which is in line with preposition 3 for $R_0 > 1$.

When the delay parameter $\tau>0$ is large, the infectious individuals in the population will take a longer time to be eliminated (removed) in the population, hence increasing the force of infection leading to more infectives in the population. This leads to an increase of infective population as numerically shown in figure 3 below.

Figure 3: Numerical solution of model (1) when $\tau>0$ is large.

If the delay parameter τ is not large, the infected individuals will die out faster i.e, infected individuals are eliminated from the population faster as the rate at which they progress to fully blown is small. The computer simulation for this case is as shown in figure 4.

Figure 4: Numerical solution of model (1) when $\tau>0$ is small.

Globally, if the spread of the infection is not addressed, the susceptibles population will decrease in comparison to the infected population. This can be illustrated by the following numerical simulation

Figure 5: Numerical solution of model (1) if the force of infection is not reduced.

Conclusion

We have formulated a HIV/AIDS delay model and investigate its dynamical behaviors. By means of next generation matrix, we obtained a basic reproduction number, R_0, which plays an important role in controlling the spread of AIDS. From the stability analysis, decreasing R_0 below unity reduces the spread of the disease. The numerical simulations show that the disease dies out (or is controlled) when $R_0>1$ or persists in the population (endemically) when $R_0>1$. The use of intervention programs such as social and medical intervention encourages the reduction of R_0. For example, the use of educational programs encourages the reduction of the parameter C (the average number of sexual partners)and the parameter through abstinence, faithfulness, and use of condoms. On the hand, medical intervention (which involves the use of Anti-Retro viral drugs), suppresses the intensity of HIV progression by prolonging the delay. This in turn results in the prolonging the rate of conversion,ν, of infected individuals to fully blown.

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