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Modelling the Effect of Treatment in The Dynamics of HIV/AIDS in An Age-Structured Population

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Abstract

In this paper, we use a continuous age-structured model to derive a two-age groups HIV/AIDS epidemic model. We assume that HIV infection confers treatment, and the infective agent can be transmitted not only by horizontally but also vertically from adult individuals to their newborn. The model is first derived as a system of partial differential equations, and then age groups are defined so that by adding up all the individuals within each age group, the model reduces to a system of ordinary differential equations. In the analysis of the model, keen interest is put on the role of treatment; in the dynamics of the spread of the epidemic. The model is analyzed when the force of infection is a constant. In the this case, the only possible equilibrium is the endemic equilibrium. The model is analyzed by using stability at both the disease-free and endemic equilibrium exists. The model is analyzed by using stability theory of differential equation and numerical simulation. The model analysis shows that the increase in treatment will decrease the epidemic and the epidemic slows down more rapidly if the treated infectives do not take part in the sexual contact. Finally, in order to verify our theoretical results, some numerical simulations are also included.

Keywords: Vertical Transmission, Treatment, Age-Structure, HIV-Prevalence, Local Stability, Global Stability.

Introduction

In this paper, we consider a mathematical model for the vertical transmission for an epidemic spreading in an age-structured population where the transmission coefficient depends on age. The term vertical transmission means the transmission of a disease from infected mothers to their unborn or newly born babies. It is commonly referred to as mother to child transmission. Examples of the disease that can be transmitted vertically such as gonorrhea, syphilis, herpes, tuberculosis and most recently HIV/AIDS. HIV in children is generally more serious than adults due to faster disease complications and progression [3-8, 13-23]. Vertical transmission of HIV/AIDS has been the principal cause of 80-90% of HIV-infected children [21]. The age-structured epidemic model with vertical transmission have been analyzed by several authors, especially we can refer to Mugisha and Luboobi, Busenberg and Cooke [20, 22].

Review of Literature

Age–structured models are most commonly used to see the most serious impact of HIV/AIDS on a particular age group of interest. such models give clear clue as to which age group of society should be concentrated on in terms of treatment, education and the kind of strategies for containing the spread[9-12]. In particular, Blynthe & Anderson et al. [2] developed an age–structured model to study the effect of sexual activity levels. In Anderson et al. [1], Anderson et al. presented an age–structured model to study the role of sexual contact and proportionate mixing in a population with HIV/AIDS. Loboobi [16] and Mugisha & Luboobi [18] worked with models for the study of the dynamics of HIV/AIDS in a three-age group population. in the models a population divided into three age groups was studied. Mugisha & Luboobi [19] models, the dynamics of HIV/AIDS with a possible vaccination strategy was studied in a two age groups population.

All above described models involve partial differential equation. Our model is derived as a system of partial differential equation then the model is reduced to a system of ordinary differential equation [20, 24]. Our model is the advancement of the model of J.Y.T. Mugisha and L. S.

Luboobi [20] following respect: herein we consider four dimensional system while they used three dimensional system. We also taken vertical transmission through treated infectives.

In view of the above, in this paper, we have proposed and analyzed a continuous age distribution model of HIV/AIDS with vertical transmission. The numerical analysis of the proposed model is also carried out to investigate the influence of some important parameters on the spread of the disease.

The Basic System

Let us divide the host population into four subpopulations; the susceptible class, the normal infective class, the treated infective class and the AIDS patients. The age-density functions of each class are denoted by *S*(*a, t*), *I*(*a, t*), *U*(*a, t*) and *A*(*a, t*). Let $\alpha(a,t)$ is the age-specific force of infection due to normal infcetves, $\gamma(a,t)$ is the age-specific force of infection due to treated infcetves, $\sigma(a)$ the rate at which normal infectives at age *a* become treated, $\nu(a)$ the rate at which normal infectives at age *a* become AIDS patients, $\theta(a)$ the rate at which treated infectives at age *a* become AIDS patients, $\mu(a)$ the HIV/AIDS epidemic-free mortality at age *a* and $d(a)$ the rate at which AIDS patients at age *a* are dying due to AIDS. Then the basic system(age-structured model) with vertical transmission can be formulated as follows:

$$\frac{\partial S}{\partial a}+\frac{\partial S}{\partial t}=-[\alpha(a,t)+\gamma(a,t)+\mu(a)]S(a,t) \quad (2.1)$$

$$\frac{\partial I}{\partial a}+\frac{\partial I}{\partial t}=[\alpha(a,t)+\gamma(a,t)]S(a,t)-[\sigma(a)+\nu(a)+\mu(a)]I(a,t) \quad (2.2)$$

$$\frac{\partial U}{\partial a}+\frac{\partial U}{\partial t}=\sigma(a)I(a,t)-[\theta(a)+\mu(a)]U(a,t) \quad (2.3)$$

$$\frac{\partial A}{\partial a}+\frac{\partial A}{\partial t}=\theta(a)U(a,t)+\nu(a)I(a,t)-[d(a)+\mu(a)]U(a,t) \quad (2.4)$$

With boundary conditions given by

$$S(0,t)=\int_0^M [S(a,t)+(1-\varepsilon)I(a,t)+bU(a,t)]\lambda(a)da \quad (2.5)$$

$$I(0,t)=\int_0^M [(1-p)\varepsilon I(a,t)]\lambda(a)da \quad (2.6)$$

$$U(0,t)=\int_0^M [\varepsilon pI(a,t)+(1-b)U(a,t)]\lambda(a)da \quad (2.7)$$

Where $\lambda(a)$ is the per capita birth rate age *a*, $S(0,t)$ is the total number of babies born uninfected, $I(0,t)$ is the total number of babies born infected which are not subjected to treatment and $U(0,t)$ is the total number of babies born infected which are subjected to treatment and $M<\infty$ is the upper bound of age. ε is the ratio of that newborns produced from normal infected individuals are vertically infected and remaining part (1-ε) of newborns are susceptibles. *b* is the fraction of babies born HIV free by treated infective mothers.

The force of infection is given by

$$\alpha(a,t)=\frac{\int_0^M \rho(a,\bar a)I(\bar a,t)d\bar a}{\int_0^M n(a,t)da},$$

$$\gamma(a,t)=\frac{\int_0^M \eta(a,\bar a)U(\bar a,t)d\bar a}{\int_0^M n(a,t)da}, \quad (2.8)$$

Where $\rho(a,\bar a)$ be the transmission rate between the susceptible individual aged a and the normal infective individual aged $\bar a$. Similarly $\eta(a,\bar a)$ be the transmission rate between the susceptible individual aged *a* and the treated infective individual aged $\bar a$.

We shall also assume that the AIDS patients have full-blown symptoms and are easily noticeable and not sexually interacted with any other class then the sexually active and interacting number of adults,

$$N(a,t)=S(a,t)+I(a,t)+U(a,t)$$

The initial conditions are given by

$$S(a,t)=S_0(a),\ N(a,t)=N_0(a),$$
$$I(a,t)=I_0(a),\ U(a,t)=U_0(a), \quad (2.9)$$

Where $\rho(a,\bar a)$ is the infection coefficient, also commonly interpreted as the probability that a susceptible individual age *a* interacts with a normal infective individuals aged $\bar a$ and becomes infected.

$$S(t)=\int_0^M S(a,t)da,\ I(t)=\int_0^M I(a,t)da,$$
$$U(t)=\int_0^M U(a,t)da,$$

We use this model to formulate an HIV/AIDS model with two age groups mopdel where Group I is made up of sexually immature children and Group II is made up of sexually mature and active adults. We model the dynamics of the spread in heterosexual transmission made up of ordinary differential equations.

Derivation of the Two-Age Groups HIV/AIDS Model

Let the population be divided in 2-age groups by the age intervals $[a_j, a_{j-1})$ for j =1, 2, where $0 = a_0 < a_1 < a_2 = M$. The respective number of susceptibles and infective cases in the jth age group $[a_j, a_{j-1})$ is given by

$$S_j(t) = \int_{a_{j-1}}^{a_j} S(a,t)da$$

$$I_j(t) = \int_{a_{j-1}}^{a_j} I(a,t)da$$

$$U_j(t) = \int_{a_{j-1}}^{a_j} U(a,t)da$$

$$A_j(t) = \int_{a_{j-1}}^{a_j} A(a,t)da \qquad (3.1)$$

Assume that at the start of epidemic, the population is at steady age distribution with exponential growth in all the classes so that $N(a,t) = e^{qt}W(a)$ and the number of individuals in the age interval $[a_j, a_{j-1})$ is

$$N_j(t) = \int_{a_{j-1}}^{a_j} N(a,t)da = e^{qt}\int_{a_{j-1}}^{a_j} W(a)da = e^{qt}P_j \qquad (3.2)$$

Where $\int_{a_{j-1}}^{a_j} W(a)da = P_j$ is the size of he *j*th age group at steady state at time t = 0 and $W(a)$ is the total population at a and q is he intrinsic rate of growth of population at steady age distribution. For $a_{j-1} \le a \le a_j$ let $\mu(a) = \mu_j$, $\nu(a) = \nu_j$, $\sigma(a) = \sigma_j$. Let the age specific infection rate be class-dependent and written as $\alpha(a,t) = \alpha_j$ and $\gamma(a,t) = \gamma_j$ and assume a constant birth rate $\lambda(a) = \lambda_j$ such that our renewal equations become

$$S(0,t) = \int_0^M [S(a,t) + (1-\varepsilon)I(a,t) + bU(a,t)]\lambda(a)da$$

$$S(0,t) = \sum_{j=1}^{2}[S_j(t) + (1-\varepsilon)I_j(t) + bU_j(t)]\lambda_j \qquad (3.3)$$

$$I(0,t) = \int_0^M [(1-p)\varepsilon I(a,t)]\lambda(a)da$$

$$I(0,t) = \sum_{j=1}^{2}[(1-p)\varepsilon I_j(a)]\lambda_j \qquad (3.4)$$

$$U(0,t) = \int_0^M [\varepsilon pI(a,t) + (1-b)U(a,t)]\lambda(a)da$$

$$U(0,t) = \sum_{j=1}^{2}[\varepsilon pI_j(t) + (1-b)U_j(t)]\lambda_j \qquad (3.5)$$

With

$$N(0,t) = S(0,t) + I(0,t) + U(0,t) = e^{qt}W(0) = \sum_{j=1}^{2}\lambda_j P_j$$

For each j = 1,2, we allow transfer between the two age groups to be through constants c_i called transfer rate constants so that the way an individual, in each epidemiological class, crosses into another age group is described by

$$S(a_j,t) = c_j S_j(t),\ I(a_j,t) = c_j I_j(t),$$
$$U(a_j,t) = c_j U_j(t),\ A(a_j,t) = c_j A_j(t),$$
$$W(a_j) = c_j P_j$$

The transfer rate constants c_j are given by the reciprocal of the average length of the *j*th interval 11, 17],

$$c_j = \frac{1}{a_j - a_{j-1}}$$

Consider the fractions of the *j*th group in the epidemiological classes as

$$s_j(t) = \frac{S_j(t)}{N_j(t)} \quad s_j(t) = \frac{S_j(t)}{e^{qt}P_j} \qquad (3.6)$$

$$s'_j(t) = \frac{S'_j(t)}{e^{qt}P_j} - qs_j(t)$$

$$i_j(t) = \frac{I_j(t)}{N_j(t)} \quad i_j(t) = \frac{I_j(t)}{e^{qt}P_j} \qquad (3.7)$$

$$i'_j(t) = \frac{I'_j(t)}{e^{qt}P_j} - qi_j(t)$$

$$u_j(t) = \frac{U_j(t)}{N_j(t)} \quad u_j(t) = \frac{U_j(t)}{e^{qt}P_j} \qquad (3.8)$$

$$u'_j(t) = \frac{U'_j(t)}{e^{qt}P_j} - qu_j(t)$$

For the force of infection defined in equation (2.8), let the constant rate $\rho(a,\bar{a}) = \rho_{jk}$, for $a \in [a_j, a_{j-1})$ represent a constant interaction between susceptibles in the *j*th age group and infectives in the *k*th age group

$$\alpha_j(t)=\frac{\sum_{k=1}^{2}\rho_{jk}I_k(t)}{\sum_{j=1}^{2}N_k(t)}=\frac{\sum_{k=1}^{2}\rho_{jk}e^{qt}P_k i_k(t)}{\sum_{j=1}^{2}e^{qt}P_j}=\sum_{k=1}^{2}\rho_{jk}P_k i_k(t)$$

From this, we have for j=1, the force of infection in Group I given by

$$\alpha_1(t)=\sum_{k=1}^{2}\rho_{1k}P_k i_k(t)=\rho_{11}P_1 i_1(t)+\rho_{12}P_2 i_2(t)$$

and for j=2 , the force of infection in Group II given by $\alpha_2(t)=\sum_{k=1}^{2}\rho_{2k}P_k i_k(t)=\rho_{21}P_1 i_1(t)+\rho_{22}P_2 i_2(t)$

Similarly $\eta(a,\bar{a})=\eta_{jk}$

$$\eta_j(t)=\frac{\sum_{k=1}^{2}\eta_{jk}U_k(t)}{\sum_{j=1}^{2}N_k(t)}=\frac{\sum_{k=1}^{2}\eta_{jk}e^{qt}P_k u_k(t)}{\sum_{j=1}^{2}e^{qt}P_j}=\sum_{k=1}^{2}\eta_{jk}P_k u_k(t)$$

for j=1 $\gamma_1(t)=\sum_{k=1}^{2}\eta_{1k}P_k i_k(t)=\eta_{11}P_1 u_1(t)+\eta_{12}P_2 u_2(t)$

for j=2 $\gamma_2(t)=\sum_{k=1}^{2}\eta_{2k}P_k i_k(t)=\eta_{21}P_1 u_1(t)+\eta_{22}P_2 u_2(t)$

their no sexual interaction among individuals in group I and between individuals in group I and group II, we have all the terms in ρ_{11}, ρ_{12}, $\rho_{21},\eta_{11},\eta_{12}$ and η_{21} zero. Thus, we have $\alpha_1(t)=0$, $\gamma_1(t)=0$, $\alpha_2(t)=\rho_{22}P_2 i_2(t)$ and $\gamma_2(t)=\eta_{22}P_2 u_2(t)$. Integrating equation (2.1) w.r.t. a, over $[a_j,a_{j-1})$ gives

$$S(a_j,t)-S(a_{j-1},t)+\frac{dS_j}{dt}=-\alpha_j\int_{a_{j-1}}^{a_j}S(a,t)da-\gamma_j\int_{a_{j-1}}^{a_j}S(a,t)da-\mu_j\int_{a_{j-1}}^{a_j}S(a,t)da \quad (3.9)$$

and using the first expression of eq. 3.1

$$S(a_j,t)-S(a_{j-1},t)+\frac{dS_j}{dt}=-\alpha_j S_j(t)-\gamma_j S_j(t)-\mu_j S_j(t) \quad (3.10)$$

for j=1 eq. (3.10) gives

$$S(a_1,t)-S(0,t)+\frac{dS_1}{dt}=-\alpha_1 S_1(t)-\gamma_1 S_1(t)-\mu_1 S_1(t)$$

$$s'_1(t)=\frac{S'_1(t)}{e^{qt}P_1}-qs_1(t)$$

$$s'_1(t)=\frac{1}{e^{qt}P_1}[S(0,t)-S(a_1,t)-\alpha_1 S_1(t)-\gamma_1 S_1(t)-\mu_1 S_1(t)]-qs_1(t)$$

$$s'_1(t)=\frac{1}{e^{qt}P_1}[\lambda_2\{S_2(t)+(1-\varepsilon)I_2(t)+bU_2(t)\}-c_1 S_1(t)-\mu_1 S_1(t)]-qs_1(t)$$

$$s'_1(t)=\frac{\lambda_2 P_2}{P_1}[s_2+(1-\varepsilon)i_2(t)+bu_2(t)]-(q+c_1+\mu_1)s_1(t) \quad (3.11)$$

Similarly we get other equations

For j=2 $S(a_2,t)-S(a_1,t)+\frac{dS_2}{dt}=-\alpha_2 S_2(t)-\gamma_2 S_2(t)-\mu_2 S_2(t)$

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$$s'_2(t)=\frac{S'_2(t)}{e^{qt}P_2}-qs_2(t)$$

$$s'_2(t)=\frac{1}{e^{qt}P_2}\left[S(a_1,t)-S(a_2,t)-\alpha_2S_2(t)-\gamma_2S_2(t)-\mu_2S_2(t)\right]-qs_2(t)$$

$$s'_2(t)=\frac{\lambda_2P_1}{P_2}s_1(t)-(\alpha_2+\gamma_2+q+c_2+\mu_2)s_1(t) \qquad (3.12)$$

$$I(a_j,t)-I(a_{j-1},t)+\frac{dI_j}{dt}=\alpha_j\int_{a_{j-1}}^{a_j}S(a,t)da+\gamma_j\int_{a_{j-1}}^{a_j}S(a,t)da-(\sigma_j+\nu_j+\mu_j)\int_{a_{j-1}}^{a_j}I(a,t)da$$

for j=1 $I(a_1,t)-I(0,t)+\frac{dI_1}{dt}=\alpha_1S_1(t)+\gamma_1S_1(t)-(\sigma_1+\nu_1+\mu_1)I_1(t)$

$$i'_1(t)=\frac{I'_1(t)}{e^{qt}P_1}-qi_1(t)$$

$$i'_1(t)=\frac{1}{e^{qt}P_1}\left[I(0,t)-I(a_1,t)+\alpha_1S_1(t)+\gamma_1S_1(t)-(\sigma_1+\nu_1+\mu_1)I_1(t)\right]-qi_1(t)$$

$$i'_1(t)=\frac{\varepsilon(1-p)P_2\lambda_2}{P_1}i_2(t)-(q+c_1+\sigma_1+\nu_1+\mu_1)i_1(t) \qquad (3.13)$$

for j=2 $I(a_2,t)-I(a_1,t)+\frac{dI_2}{dt}=\alpha_2S_2(t)+\gamma_2S_2(t)-(\sigma_2+\nu_2+\mu_2)I_2(t)$

$$i'_2(t)=\frac{I'_2(t)}{e^{qt}P_2}-qi_2(t)$$

$$i'_2(t)=\frac{1}{e^{qt}P_2}\left\{I(a_1,t)-I(a_2,t)+\alpha_2S_2(t)+\gamma_2S_2(t)-(\sigma_2+\nu_2+\mu_2)I_2(t)\right\}-qi_2(t)$$

$$i'_2(t)=\frac{c_1P_1}{P_2}i_1(t)+\alpha_2s_2(t)+\gamma_2s_2(t)-(q+c_2+\sigma_2+\nu_2+\mu_2)I_2(t) \qquad (3.14)$$

$$U(a_j,t)-U(a_{j-1},t)+\frac{dU_j}{dt}=\sigma_j\int_{a_{j-1}}^{a_j}I(a,t)da-(\theta_j+\mu_j)\int_{a_{j-1}}^{a_j}U(a,t)da$$

$$U(a_j,t)-U(a_{j-1},t)+\frac{dU_j}{dt}=\sigma_jI_j(t)-(\theta_j+\mu_j)U_j(t)$$

for j=1

$$\mathrm{U}(\mathrm{a}_1,\mathrm{t})-\mathrm{U}(0,\mathrm{t})+\frac{\mathrm{dU}_1}{\mathrm{dt}}=\sigma_1\mathrm{I}_1(\mathrm{t})-(\theta_1+\mu_1)\mathrm{U}_1(\mathrm{t})$$

$$u'_1(t)=\frac{U'_1(t)}{e^{qt}P_1}-qu_1(t)$$

$$u'_1(t)=\frac{1}{e^{qt}P_1}\left[U(0,t)-U(a_1,t)+\sigma_1I_1(t)-(\theta_1+\mu_1)U_1(t)\right]-qu_1(t)$$

$$u'_1(t)=\frac{P_2\lambda_2}{P_1}\left[\varepsilon pi_2(t)+(1-b)u_2(t)\right]+\sigma_1i_1(t)-(q+c_1+\theta_1+\mu_1)u_1(t) \qquad (3.15)$$

for j=2 $U(a_2,t)-U(a_1,t)+\frac{dU_2}{dt}=\sigma_2I_2(t)-(\theta_2+\mu_2)U_2(t)$

$$u'_2(t)=\frac{U'_2(t)}{e^{qt}P_2}-qu_2(t)$$

$$u'_2(t)=\frac{1}{e^{qt}P_2}\left[U(a_1,t)-U(a_2,t)+\sigma_2 I_2(t)-(\theta_2+\mu_2)U_2(t)\right]-qu_2(t) \quad (3.16)$$

Then, equation (3.11)-(3.16) give the two-age groups HIV/AIDS epidemic model as

$$s'_1(t)=\frac{\lambda_2 P_2}{P_1}\left[s_2+(1-\varepsilon)i_2(t)+bu_2(t)\right]-(q+c_1+\mu_1)s_1(t)$$

$$s'_2(t)=\frac{\lambda_2 P_1}{P_2}s_1(t)-(\alpha_2+\gamma_2+q+c_2+\mu_2)s_1(t)$$

$$i'_1(t)=\frac{\varepsilon(1-p)P_2\lambda_2}{P_1}i_2(t)-(q+c_1+\sigma_1+\nu_1+\mu_1)i_1(t)$$

$$i'_2(t)=\frac{c_1P_1}{P_2}i_1(t)+\alpha_2 s_2(t)+\gamma_2 s_2(t)-(q+c_2+\sigma_2+\nu_2+\mu_2)I_2(t)$$

$$u'_1(t)=\frac{P_2\lambda_2}{P_1}\left[\varepsilon p i_2(t)+(1-b)u_2(t)\right]+\sigma_1 i_1(t)-(q+c_1+\theta_1+\mu_1)u_1(t)$$

$$u'_2(t)=\frac{P_1c_1}{P_{21}}u_1(t)+\sigma_2 i_2(t)-(q+c_2+\theta_2+\mu_2)u_2(t)$$

Analysis of the Model

Assuming a Constant HIV Prevalence

Consider the case where the HIV prevalence, in the sexually active adult group, is a constant. Then the infection rate $\alpha_2(t)$ and $\gamma_2(t)$ can be taken constant. Here, we will assume that there is no sexual interaction with the AIDS group and as such, in epidemiological class we will have $s_j+i_j+u_j=1$ for *j*=1, 2**.** Thus, the system can be reduced to a 4-dimensional system with $s_1=1-i_1-u_1$ and $s_2=1-i_2-u_2$, to give

$$i'_1(t)=\frac{\varepsilon(1-p)P_2\lambda_2}{P_1}i_2(t)-(q+c_1+\sigma_1+\nu_1+\mu_1)i_1(t) \quad (4.1)$$

$$i'_2(t)=\frac{c_1P_1}{P_2}i_1(t)+(\alpha_2+\gamma_2)(1-i_2(t)-u_2(t))-(q+c_2+\sigma_2+\nu_2+\mu_2)i_2(t) \quad (4.2)$$

$$u'_1(t)=\frac{P_2\lambda_2}{P_1}\left[\varepsilon p i_2(t)+(1-b)u_2(t)\right]+\sigma_1 i_1(t)-(q+c_1+\theta_1+\mu_1)u_1(t) \quad (4.3)$$

$$u'_2(t)=\frac{c_1P_1}{P_2}u_1(t)+\sigma_2 i_2(t)-(q+c_2+\theta_2+\mu_2)u_2(t) \quad (4.4)$$

Positivity of Solutions

In this section, we prove that all solutions of the system (4.1)-(4.4) with positive initial data will remain positive for all times *t* >0.

Lemma 1

Let the initial data be $i_1(0)=i_{10}>0$, $i_2(0)=i_{20}\geq 0$, $u_1(0)=u_{10}\geq 0$, $u_2(0)=u_{20}\geq 0$ for all *t*. Then, the solution ($i_1(t)$, $i_2(t)$, $u_1(t)$, $u_2(t)$) of the model remain positive for all time *t* >0.

Proof

From equation (4.1), we have

$$\frac{di_1(t)}{dt}=\frac{\varepsilon(1-p)P_2\lambda_2}{P_1}i_2(t)-(q+c_1+\sigma_1+\nu_1+\mu_1)i_1(t)$$

$$\frac{di_1(t)}{dt}\geq-(q+c_1+\sigma_1+\nu_1+\mu_1)i_1(t)$$

From which we get,

$$i_1(t)\geq c_1\, exp\{-(q+c_1+\sigma_1+\nu_1+\mu_1)t\}>0.$$

Where c_1 is a constant of integration. A similar reasoning on the remaining equations shows that they are always positive for *t* >0.

Stability Analysis

In this section, we present the results of stability analysis of model (4.1)-(4.4) equilibria.

Equilibra of the Model

For simplicity we can write the eq. of system (4.1)-(4.4)

$$i'_1(t) = m_1 i_2(t) - m_2 i_1(t) \quad (5.1)$$

$$i'_2(t) = m_3 i_1(t) + m_4 - m_4 u_2 - m_5 i_2(t) \quad (5.2)$$

$$u'_1(t) = m_6 i_2(t) + m_7 u_2(t) + \sigma_1 i_1(t) - m_8 u_1(t) \quad (5.3)$$

$$u'_2(t) = m_3 u_1(t) + \sigma_2 i_2(t) - m_9 u_2(t) \quad (5.4)$$

where, $m_1 = \dfrac{\varepsilon(1-p)P_2\lambda_2}{P_1}$,

$m_2 = (q + c_1 + \sigma_1 + \nu_1 + \mu_1)$, $m_3 = \dfrac{c_1 P_1}{P_2}$,

$m_4 = (\alpha_2 + \gamma_2)$,

$m_5 = (q + \alpha_2 + \gamma_2 + c_2 + \sigma_2 + \nu_2 + \mu_2)$,

$m_6 = \dfrac{\varepsilon p P_2 \lambda_2}{P_1}$, $m_7 = \dfrac{(1-b)P_2\lambda_2}{P_1}$,

$m_8 = (q + c_1 + \theta_1 + \mu_1)$

$m_9 = (q + c_2 + \theta_2 + \mu_2)$

The endemic equilibrium for the above system of equation is given by

$E_1(i_1^*, i_2^*, u_1^*, u_2^*)$

$$i_1^* = \frac{m_1}{m_2} i_2^*,$$

$$i_2^* = \frac{m_4}{m_4\left[\dfrac{\sigma_2}{m_9} + m_3\omega\right] + \dfrac{m_5 m_2 - m_1 m_3}{m_2}},$$

$$u_1^* = m_9 \omega i_2^*, \quad u_2^* = \left[\frac{\sigma_2}{m_9} + m_3\omega\right] i_2^*,$$

Where

$$\omega = \frac{1}{[m_8 m_9 - m_3 m_7]}\left[m_6 + \frac{m_7\sigma_2}{m_9} + \frac{m_1\sigma_1}{m_2}\right]$$

Endemic equilibrium will exist if $m_8 m_9 > m_3 m_7$ and $m_2 m_5 > m_1 m_3$. In terms of parameters condition can be written as

$$\lambda_2(1-b)c_1 > (c_1 + q + \theta_1 + \mu_1)(c_2 + q + \theta_2 + \mu_2)$$

$$(q + \alpha_2 + \gamma_2 + c_2 + \sigma_2 + \nu_2 + \mu_2)$$

$$(q + c_1 + \sigma_1 + \nu_1 + \mu_1) > \varepsilon(1-p)c_1\lambda_2$$

Local Stability of the Equilibrium

To determine the local stability of E_1, the following variational matrix of the system (5.1)-(5.4) is computed around E_1 as,

$$M_1 = \begin{bmatrix} -m_2 & m_1 & 0 & 0 \\ m_3 & -m_5 & 0 & -m_4 \\ \sigma_1 & m_6 & -m_8 & m_7 \\ 0 & \sigma_2 & m_3 & -m_9 \end{bmatrix}$$

The characteristic equation corresponding to the matrix is given by

$$f(x) = \lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0 \quad (5.5)$$

Where,

$$a_1 = (m_2 + m_5 + m_8 + m_9)$$

$$a_2 = \{m_5 m_8 + m_2 m_9 + m_2 m_8 + m_5 m_9 + (m_8 m_9 - m_3 m_7) + \sigma_2 m_4 + (m_2 m_5 - m_1 m_3)\}$$

$$a_3 = (m_8 + m_9)(m_2 m_5 - m_1 m_3) + m_2 m_5 m_9 + (m_2 + m_5)(m_8 m_9 - m_3 m_7) + \sigma_2 m_2 m_4 + \sigma_2 m_4 m_8 + m_3 m_4 m_6$$

$$a_4 = (m_2 m_5 - m_1 m_3)(m_8 m_9 - m_3 m_7) + \sigma_2 m_2 m_4 m_8 + m_2 m_3 m_4 m_6 + \sigma_1 m_1 m_3 m_4$$

Since endemic equilibrium will exist if $m_8 m_9 > m_3 m_7$ and $m_2 m_5 > m_1 m_3$. Therefore, a_i>0 for i=1,2,3,4. Thus by Routh-Hurwith criteria, E^* is locally asymptotically stable as if the remaining conditions $a_1 a_2 - a_3 > 0$, and $a_1 a_2 a_3 - a_3^2 - a_1^2 a_4 > 0$ are satisfied.

Global Stability of the Equilibrium

To show the globally stability behavior of E_1, we need the bounds of dependent variables involved. For this we find the region of attraction stated in the form of following lemma.

Lemma 2

The set

$$\Omega = \{(i_1, i_2, u_1, u_2) \ ; \ 0 \le i_1 + u_1 \le 1; \ 0 \le i_2 + u_2 \le 1\}$$

is a region of attraction for the system (5.1)-(5.4).

Theorem 1

If the endemic equilibrium E_1 exists, then it is globally asymptotically stable provided the following sufficient condition are satisfied in Ω,

$$3[m_1 + m_3]^2 < 2 m_2 m_5 \quad (5.6)$$

Proof. Consider the following positive definite function about E_1;

$$V = \frac{1}{2}(i_1 - i_1^*)^2 + \frac{1}{2}k_1(i_2 - i_2^*)^2 + \frac{1}{2}k_2(u_1 - u_1^*)^2 + \frac{1}{2}k_3(u_2 - u_2^*)^2 \quad (5.7)$$

where the constants k_1, k_2, k_3 and k_4 can be chosen suitably

The derivative of V along the solution of the system (5.1)-(5.4) can be written as

$$\frac{dV}{dt} = (i_1 - i_1^*)\frac{di_1}{dt} + k_1(i_2 - i_2^*)\frac{di_2}{dt} + k_2(u_1 - u_1^*)\frac{du_1}{dt} + k_3(u_2 - u_2^*)\frac{du_2}{dt}$$

$$\frac{dV}{dt} = -m_2(i_1 - i_1^*)^2 - m_5 k_1 (i_2 - i_2^*)^2 - m_8 k_2 (u_1 - u_1^*)^2 - m_9 k_3 (u_2 - u_2^*)^2$$

$$+ [m_1 + k_1 m_3](i_1 - i_1^*)(i_2 - i_2^*) + [k_3 \sigma_2 - k_1 m_4](i_2 - i_2^*)(u_2 - u_2^*)$$

$$+ k_2 m_6 (i_2 - i_2^*)(u_1 - u_1^*) + [k_2 m_7 + k_3 m_3](u_1 - u_1^*)(u_2 - u_2^*) + k_2 \sigma_1 (i_1 - i_1^*)(u_1 - u_1^*)$$

Thus, a sufficient condition for *dV/dt* to be negative definite that

$$[m_1 + k_1 m_3]^2 < \frac{2}{3} m_2 m_5 k_1 \qquad (5.8)$$

$$[k_3 \sigma_2 - k_1 m_4]^2 < \frac{2}{3} m_5 m_9 k_1 k_3 \qquad (5.9)$$

$$k_2^2 m_6^{\ 2} < \frac{4}{9} m_5 m_8 k_1 k_2 \qquad (5.10)$$

$$[k_2 m_7 + k_3 m_3]^2 < \frac{2}{3} m_8 m_9 k_2 k_3 \qquad (5.11)$$

$$k_2^2 \sigma_1^2 < \frac{2}{3} m_2 m_8 k_2 \qquad (5.12)$$

After maximizing the LHS and minimizing the RHS and choosing k_1=1, the stability condition can be obtained as follows,

$$3[m_1 + m_3]^2 < 2 m_2 m_5$$

where the constants k_i>0 (i =1, 2, 3) can be chosen such that

$$k_3 = \frac{m_4}{\sigma_2} \text{ and}$$

$$k_2 < min\left(\frac{2 m_2 m_8}{3\sigma_1^2}, \frac{4 m_5 m_8}{9 m_6^{\ 2}} \right),$$

$$3[k_2 m_7 \sigma_2 + m_4 m_3]^2 < 2 m_8 m_9 \sigma_2^2 k_2$$

Numerical Analysis and Discussion

We give here numerical simulation of the equilibrium and stability conditions of the model (4.1-4.4).

We integrate the system (4.1-4.4) by fourth order Runge-Kutta method using the following set of parameter values: P_2 = 3000, P_1 = 1000, ε =.002, p = .003, λ_2 = 1.43, α_2 = .02, σ_2 = .2, γ_2 = .124, c_2 = .1, q = .2, μ_2 = .03, v_2 =.03, θ_2 = .05, σ_1 = .1, c_1 = .3, μ_1 = .02, v_1 =.004, θ_1 = .003, with initial values $i_1(0)$= .0396, $i_2(0)$= .32, $u_1(0)$ = .068 and $u_2(0)$= .115, the co-infection equilibrium values are computed as,

i_1^*=.03983271411, i_2^*=.3257746976,

u_1^*=.06865540307, u_2^*=.1202275282,

The eigenvalues corresponding to the endemic equilibrium E_1 are given by,

-.4836058512, -.6432554463, -1.023694293, -.8314444099

Since all the eigen values are negative, the endemic equilibrium E_1 is locally asymptotically stable.

The nonlinear stability behavior of E_1 in $i_2 - u_2$ and $i_1 - u_1$ plane is shown in Fig.1 and Fig.2 respectively. We see from these figures that all the trajectories tend towards the equilibrium point E_1. Hence, we infer that the system (4.1)-(4.4) may be globally stable about the endemic equilibrium E_1 for the above set of parameters. The results of numerical simulation are displayed graphically in Figs.(3-10). Fig.(3-4) depicts the variation of sexually mature normal infective population and the population of pre-mature infective children with time for different treatment rates. It is found that with the increase in the treatment rate σ_2, the sexually mature normal infective population decreases and the population of pre-mature normal infective children also decreases which in turn increases the sexually mature treated infective population and pre-mature treated infective children (see Figs.5-6) . Figs.(7-10) show the effect of age-specific force of infection γ_2 on all the classes. It is clear that with increase in the value of γ_2, the population of all the classes increase which make the disease more endemic.

Fig.1. Global stability in $i_2 - u_2$ plane

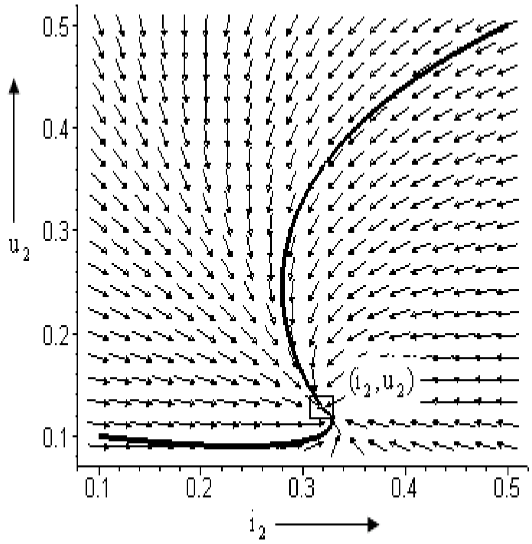


Fig.2. Global Stability in i_1-u_1 plane

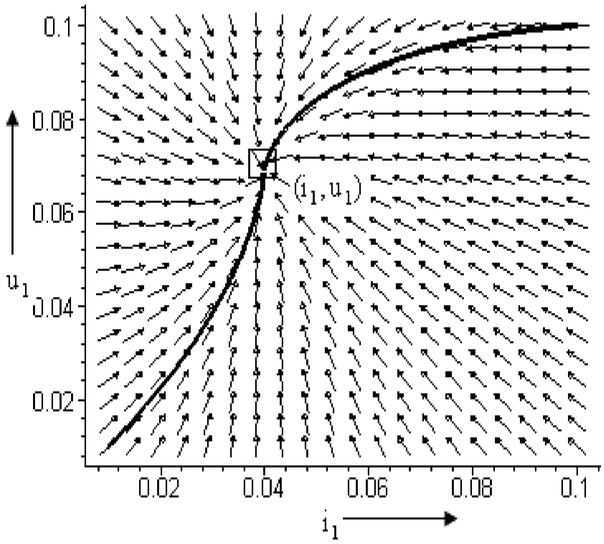


Fig3. Variation of sexually mature normal infectives with time for different rate of σ_2

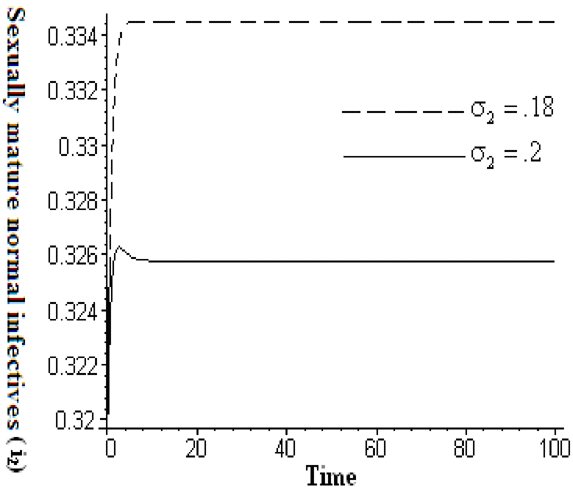


Fig4. Variation of sexually immature normal infective children with time for different rate of σ_2

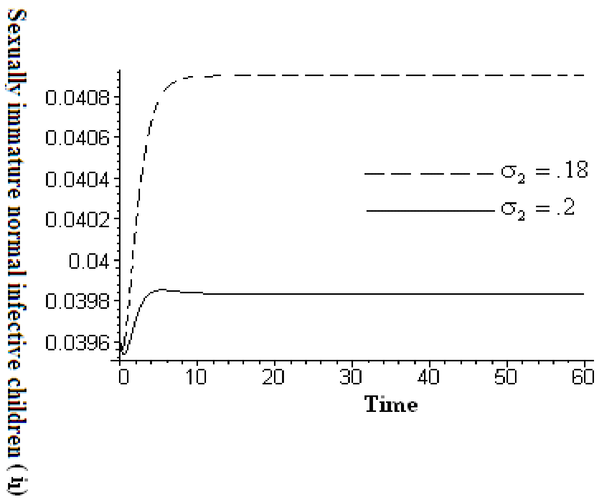


Fig5. Variation of sexually mature treated infectives with time for different rate of σ_2

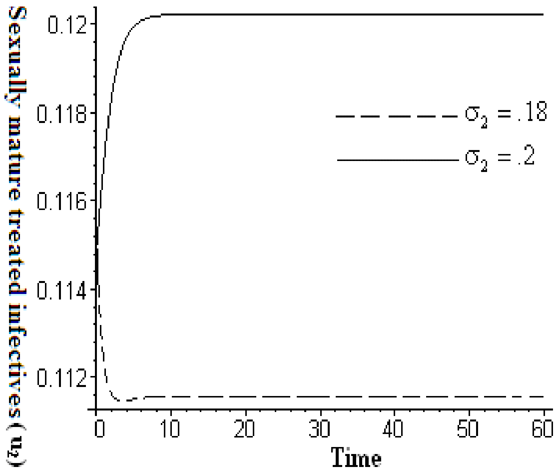


Fig6. Variation of sexually immature treated infective children with time for different rate of σ_2

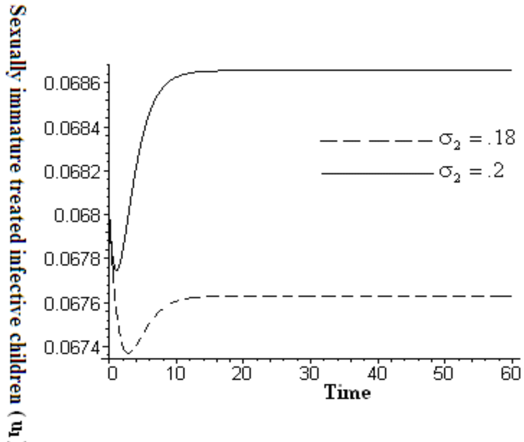


Fig7. Variation of sexually immature treated infective children with time for different rate of γ_2

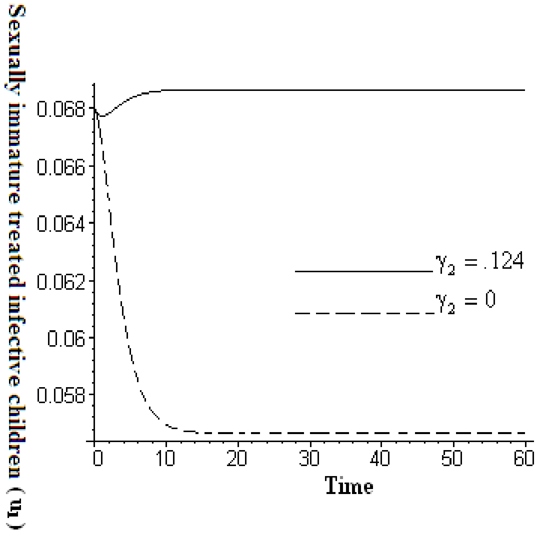


Fig8. Variation of sexually immature normal infective children with time for different rate of γ_2

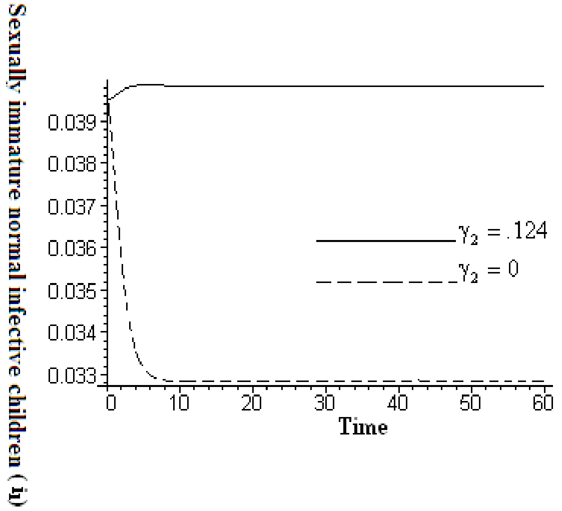


Fig9. Variation of sexually mature normal infectives with time for different rate of γ_2

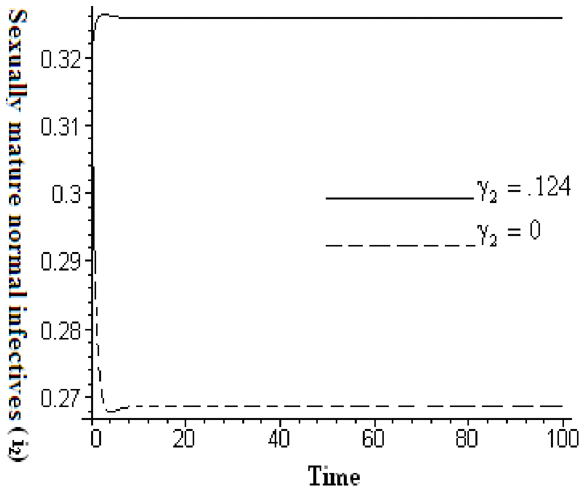
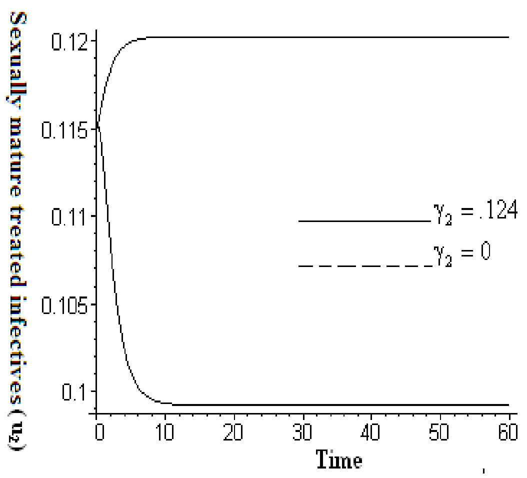


Fig10. Variation of sexually mature treated infectives with time for different rate of γ_2



Conclusion

In this paper, a continuous age-structured model has been taken to derive a two-age groups HIV/AIDS epidemic model. It is assumed that HIV infection confers treatment, and the infective agent can be transmitted not only by horizontally but also vertically from adult individuals to their newborn. The model is first derived as a system of partial differential equations, and then age groups are defined so that by adding up all the individuals within each age group, the model reduces to a system of ordinary differential equations. The model is analyzed by using stability theory of differential equation and numerical simulation. We show that both the disease-free and endemic equilibrium exists. The model analysis shows that the increase in treatment will decrease the epidemic and the epidemic slows down more rapidly if the treated infectives do not take part in the sexual contact. It is also noted that disease can be kept under control upto the desired level by reducing the contact rate between susceptible and normal infective

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