Mathematical Model Approach To HIV/AIDS Transmission From Mother To Child

Basavarajaiah.D. M. B. Narasimhamurthy, K. Maheshappa. B. Leelavathy

ABSTRACT:- AIDS is a devastating disease, more than 2.50 million of the infected populations died every year (NACO).For the control of diseases transmission need to be implementation of public health program, i.e., it helps to minimize the destruction caused by AIDS epidemic. Mathematical models and underlying transmission mechanism of the HIV can help the scientific, medical and researcher to understand and anticipate its spread in different population. Present study fitted mathematical models, which exhibit two equilibriums namely, the disease-free and the endemic equilibrium. It is found that if the basic reproduction number *R*0 <1, the disease-free equilibrium is always locally asymptotically stable and in such a case the endemic equilibrium does not exist. If R0 >1, a unique equilibrium exist which locally asymptotically stable and becomes globally asymptotically stable under certain conditions showing that the disease becomes endemic due to vertical transmission.

Key words: AIDS, HIV, PMTCT, DTSM, ARV's, Vertical transmission, NACO

I. INTRODUCTION:

Epidemiology is the study of the distribution and determinants of diseases both infectious and non-infectious. Originally the term was used to refer only to the study of epidemic infectious diseases but it is now applied more broadly to other diseases as well (Johnson, 2004). Mathematical models have been used extensively in research into the epidemiology of HIV/AIDS, to help improve our understanding of major contributing factors in a giving epidemic (Naresh *at. el.,* 2006).The goal of any modelling exercise is to extract as much information as possible from available data and provide an accurate representation of both the knowledge and uncertainty about the epidemic. A number of different models of HIV and AIDS have been developed, ranging from simple extrapolations of past curves to complex transmission models. A major tradition in modelling HIV/AIDS epidemics has been to use back calculation, or back projection, techniques. These techniques produce statistical solutions to convolution equations that relate the number of AIDS diagnoses over time to past trends in HIV infection, and to the distribution of the HIV incubation period (Salomon and Murray, 2001).In this study we have, therefore, developed a model for transmission of HIV into a population of varying size with vertical transmission and other demographics and epidemiological factors. Our purpose is to formulate a model for AIDS epidemic that may be transmuted either horizontally or vertically in populations.

II. Equation:

The PMTCT (Vertical transmission) data collected from ART centres of different government hospitals of Karnataka state, data were analysed by Mat lab -6.50 version, DTSM –diseases free and equilibrium model was fitted and diagnostically tested by simulation

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Disease transmission and Susceptible model (DTSM-MODEL):

Model Variables Description: ***N***- Total population, ***S***- Susceptible class, ***I***- Infective class, ***P***- Pre-AIDS class, ***T***- Treated class, ***A***- AIDS class.

Definitions of Symbols used frequently:

π — Rate of recruitment into susceptible population.

c- Average number of sexual partners per unit time

β- Sexual contact rate

δ — Rate of movement from infectious class

ε —Fraction of new-borns infected with HIV who dies immediately after birth

θ — Rate of newborns infected with HIV

μ — Natural mortality rate

α — Induced death rate due to AIDS

$\sigma 1$ — Fraction of δ joining the pre — AIDS class

γ —Rate of movements of pre-AIDS class individuals into AIDS Class

$\sigma 2$ — Fraction of δ joining treated class

v — Rate at which AIDS group get treatment

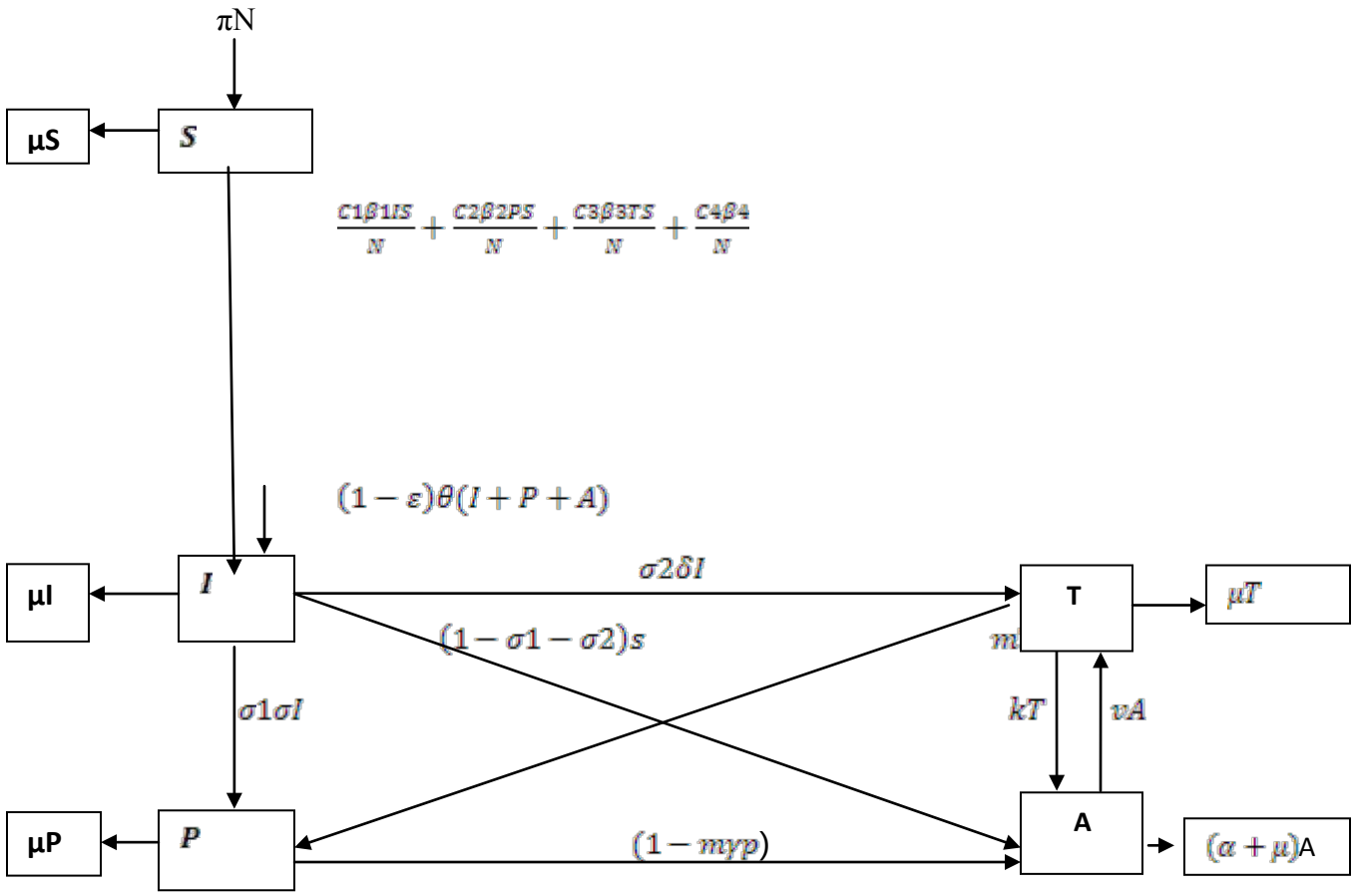
m — Fraction of γ who get treatment

k — Rate at which treated group becomes full blown AID

III. Formulation of the Model:

Consider a population of size $N(t)$at time *t* with constant inflow of susceptible with rate πN. The population size $N(t)$ is divided into five subclasses which are susceptible $S(t)$ invectives $I(t)$ (also assumed to be infectious), pre-AIDS Patients $P(t)$ treated class $T(t)$ and AIDS patients $A(t)$ with natural mortality rateμ in all classes. $\propto$ *i*s the disease induced death rate in the AIDS patients' class andψ the rate at which AIDS patients get treatment. In the model, it is assumed that the susceptible become HIV infected via sexual contacts with infective which may also lead to the birth of infected children. It is assumed that a fraction of new born children are infected during birth and hence are directly recruited into the infective class with a rate $(1-\varepsilon)\theta$and others die effectively at birth$(0 \le \varepsilon \le 1)$. We do not consider direct recruitment of the infected persons but by vertical transmission only. It is assumed that some of the infectives join pre-AIDS class, depending on the viral counts, with a rate $\sigma 1\delta$ and then proceed with a rate γ to develop full blown AIDS, it is also assumed that some of the infectives move to join treated class with a rate $\sigma 2\delta$ and then proceed with a rate *k* to develop full blown AIDS while others with serious infection directly join the AIDS class with a rate$(1-\sigma 1-\sigma 2)\delta$.The interaction between susceptible and infectives is assumed to be of standard mass action type.

Flow diagram of HIV Model (Flow chart).



The above figure that showed the disease transmission had governed by the differential equation.

$$\frac{ds}{dt}=\pi N-\frac{C1\beta 1IS}{N}-\frac{C2\beta 2PS}{N}-\frac{C3\beta 3TS}{N}-\frac{C4\beta 4AS}{N}-\mu\frac{dI}{dt}$$

$$\frac{dI}{dt}=\frac{C1\beta 1IS}{N}+\frac{C2\beta 2PS}{N}+\frac{C3\beta 3TS}{N}+\frac{C4\beta 4AS}{N}-(\delta+\mu)I+(I-\epsilon)\theta(I+P+A)$$

$$\frac{dP}{dT}=\sigma 2\delta I-(\gamma+\mu)p \qquad Eqn\ (3.11)$$

$$\frac{DT}{dt}=\sigma 2\delta I+mrp+vA-(k+\mu)T,$$

$$\frac{dA}{dt}=(1-\sigma 1-\sigma 2)\delta I+(1-m)\gamma p+kT-(v+\alpha+\mu)A$$

The intial condition of the HIV diseases the model becomes

$S(0)=S_0$, $I(0)=I_0$, $P(0)=P_0$,$T(0)=T_0$ and $A(0)=A_0$

To simplify the model, it is reasonable to assume that the AIDS women patients and those in Pre-AIDS classes are isolated and sexually inactive and hence they are not capable of producing children i.e. $(1-\varepsilon)\theta p=(1-\delta)\theta A=0$ and also they do not contribute to RNA viral transmission horizontally i.e. $\beta 2$and $\beta 2$ are taken negligible (Naresh *et.al*., 2006).

In view of the above assumptions, the system can now be written as follows:

$$\frac{ds}{dt}=\pi N-\frac{C1\beta 1IS}{N}-\frac{C3\beta 3TS}{N}-\mu k$$

$$\frac{dI}{dt}=\frac{C1\beta 1IS}{N}+\frac{C3\beta 3TS}{N}-(\delta+\mu)I+(1-\varepsilon)\theta I$$

$$\frac{dP}{dt}=\sigma 1\delta I-(\gamma+\mu)P \qquad (3.2)$$

$$\frac{dT}{dt}=\sigma 2\delta I+myp+vA-(k+\mu)T$$

$$\frac{dA}{dt}=(1-\sigma 1-\sigma 2)\delta I+(1-m)\gamma p+kT-(v+\alpha+\mu)A$$

From the equation (3.2), it is pointed out here that not all infected individuals take part in spreading the disease, as in the case of infected children, but they will all develop their own AIDS. However, the model can be modified to include a delay to make the infected children become adult to further spread the infection either vertically or horizontally.

The population N has calculated

N=S+I+P+T+A

$$\frac{dN}{dt}=\frac{dS}{dt}+\frac{dI}{dt}+\frac{dP}{dt}+\frac{dT}{dt}+\frac{dA}{dt},$$

$$\frac{dN}{dt}=\pi N-\frac{C1\beta 1IS}{N}-\frac{C3\beta 3TS}{N}-\mu S+\frac{C1\beta 1IS}{N}+\frac{C3\beta 3TS}{N}-(\delta+\mu)I+(1-\varepsilon)\theta I+\sigma 1\delta I-$$

$$(\gamma+\mu)P+\sigma 2\delta I+myP+vA-(k+\mu)P+\sigma 2\delta I(1-m)\gamma P+kT-(v+\alpha+\mu)A.$$

Therefore,

$$\frac{dN}{dt}=\pi N-\mu N-\alpha A+(1-\varepsilon)\theta I$$

Thus, we normalize the model. Without loss of generality let $S=\frac{S}{N}$, $i=\frac{I}{N}$

$$P=\frac{P}{N},h=\frac{T}{N},\ \alpha=\frac{A}{N}$$

Therefore, the normalized system can be calculated as follows

$$S=sN$$

$$\frac{dS}{dt}=S\frac{dN}{dt}+N\frac{dS}{dt}$$

$$\frac{dS}{dt}=\frac{1}{N}\left(\frac{dS}{dt}-S\frac{dN}{dt}\right)$$

Therefore,

$$\frac{ds}{dt}=\pi-C_1\beta_1 is-C3\beta 3hs-(\pi-\alpha a+(1-\varepsilon)\theta i)S$$

$$i=iN$$

$$\frac{dI}{dt}=i\frac{dN}{dt}+N\frac{di}{dt}$$

$$\frac{di}{dt}=\frac{1}{N}\left[\frac{dI}{dt}-i\frac{dN}{dt}\right]$$

$$\therefore\ \frac{di}{dt}=C_1\beta_1 is+c3\beta 3hs+(1-\varepsilon)\theta i-(\pi+\delta-\alpha a+(1-\varepsilon)\theta i)i$$

$$P=PN$$

$$\frac{dP}{dt}=P\frac{dN}{dt}+N\frac{dP}{dt}$$

$$\frac{dP}{dt}=\frac{1}{N}\left[\frac{dP}{dt}-P\frac{dN}{dt}\right]$$

$$\therefore\ \frac{dP}{dt}=\sigma_1\delta i-[\pi+\gamma-\alpha a+(1-\varepsilon)\theta i]P$$

H=Hn

$$\frac{dT}{dt}=h\frac{dN}{dt}+N\frac{dH}{dt}$$

$$\frac{dh}{dt}=\frac{1}{dN}\left[\frac{dT}{dt}-h\frac{dN}{dt}\right]$$

$$\frac{dh}{dt}=\sigma 2\delta i+myp+va-(\pi+k-\alpha a+(1-\varepsilon)\theta i)h$$

$$A=\alpha N$$

$$\frac{dA}{dt} = a\frac{dN}{dt} + N\frac{da}{dt}$$

$$\frac{da}{dt} = \frac{1}{N}\left[\frac{dA}{dt} - a\frac{dN}{dt}\right]$$

$$\frac{da}{dt} = (1-\sigma 1-\sigma 2)\delta I + (1-m)\gamma p + kh - [\pi + v + \alpha - \alpha a + (1-\varepsilon)\theta i]a$$

Now the system of equation was follows

$$\frac{di}{dt} = C_1\beta_1 is + C_3\beta_3 hs + (1-\varepsilon)\theta i - [\pi + \delta - \alpha a + (1-\varepsilon)\theta i]i$$

$$\frac{dp}{dt} = \sigma 1\delta i - [\pi + \gamma - \alpha a + (1-\varepsilon)\theta i]p$$

(3.3)

$$\frac{dh}{dt} = \sigma 2\delta i + m\gamma p + va - (\pi + k - \alpha a + (1-\varepsilon)\theta i)h$$

$$\frac{da}{dt} = (1-\sigma 1-\sigma 2)\delta i + (1-m)\gamma p + kh - [\pi + \gamma + \alpha - \alpha a + (1-\varepsilon)\theta i]a,$$

Such that,

$$s + i + p + h + a += 1$$

TABLES AND FIGURES

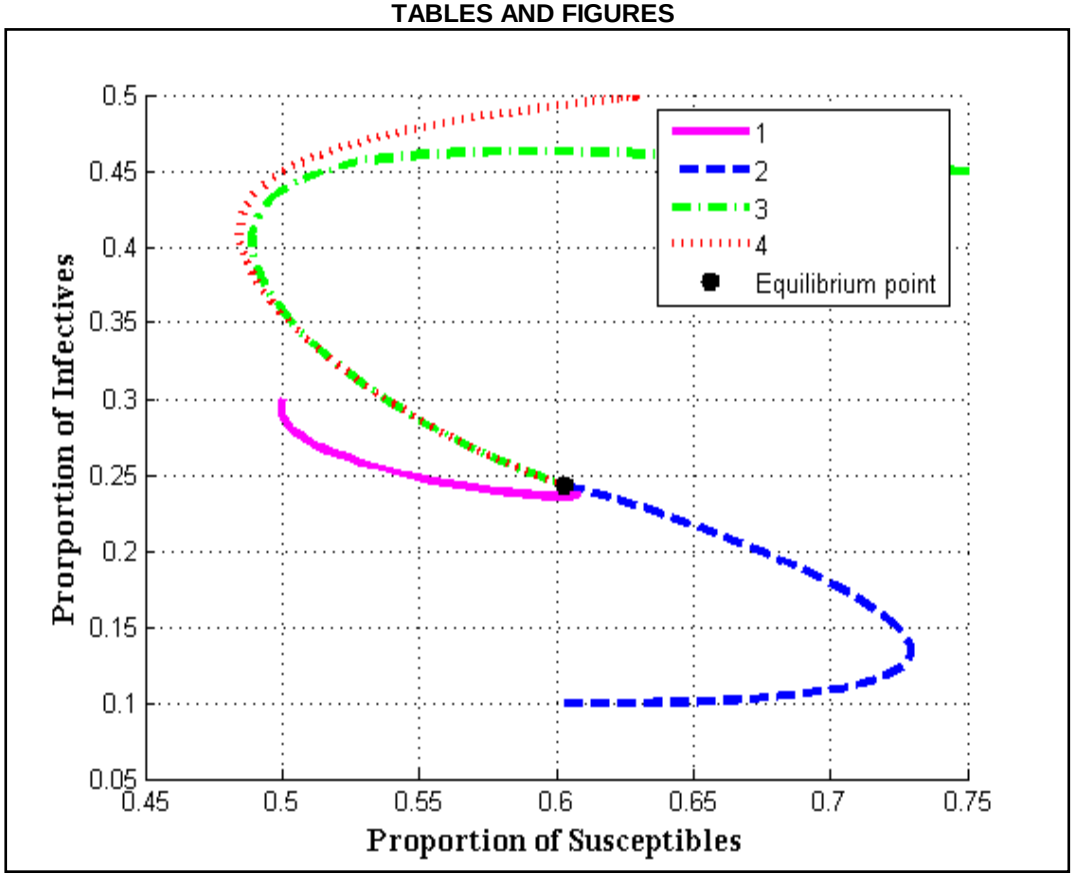


Figure (1): Endemic equilibrium of proportion of infectives with Susceptibles.

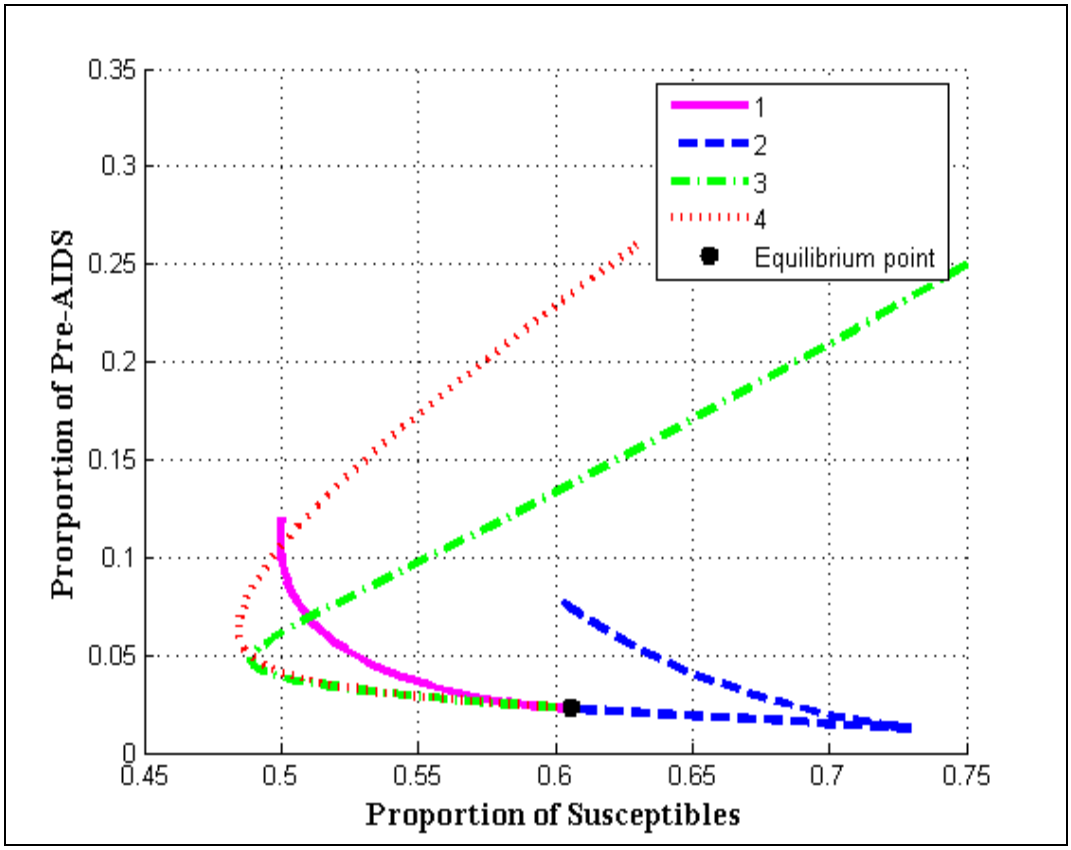


Figure 1(a). Endemic equilibrium of proportion of Pre-AIDS population.

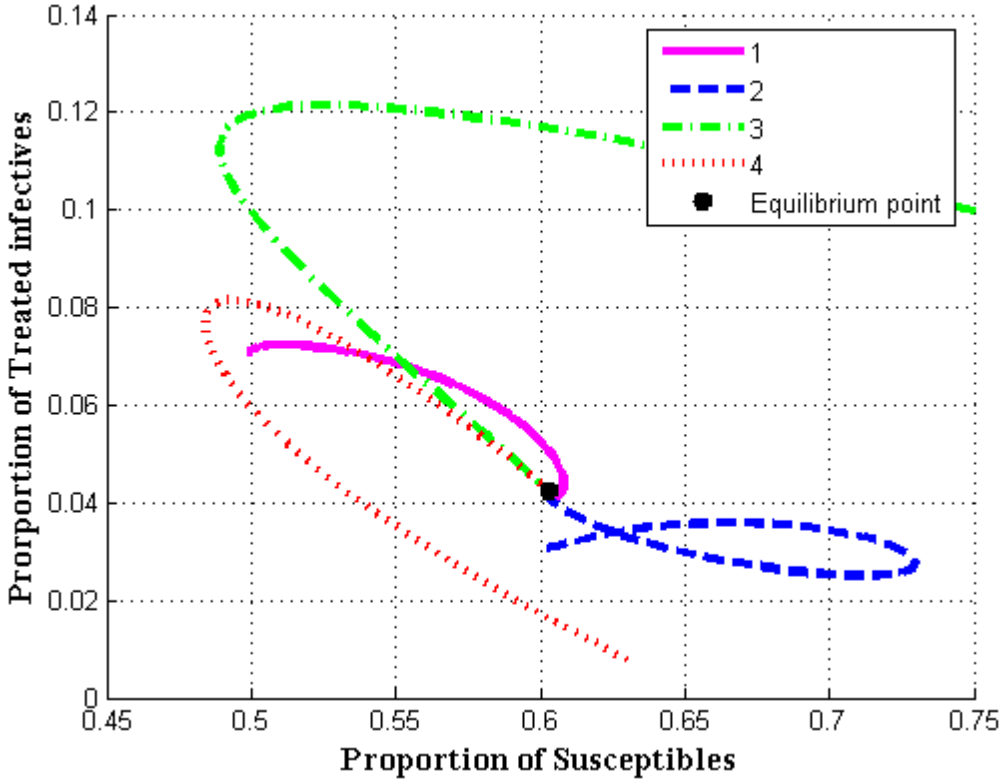


Figure (2): Endemic equilibrium of proportion of treated class

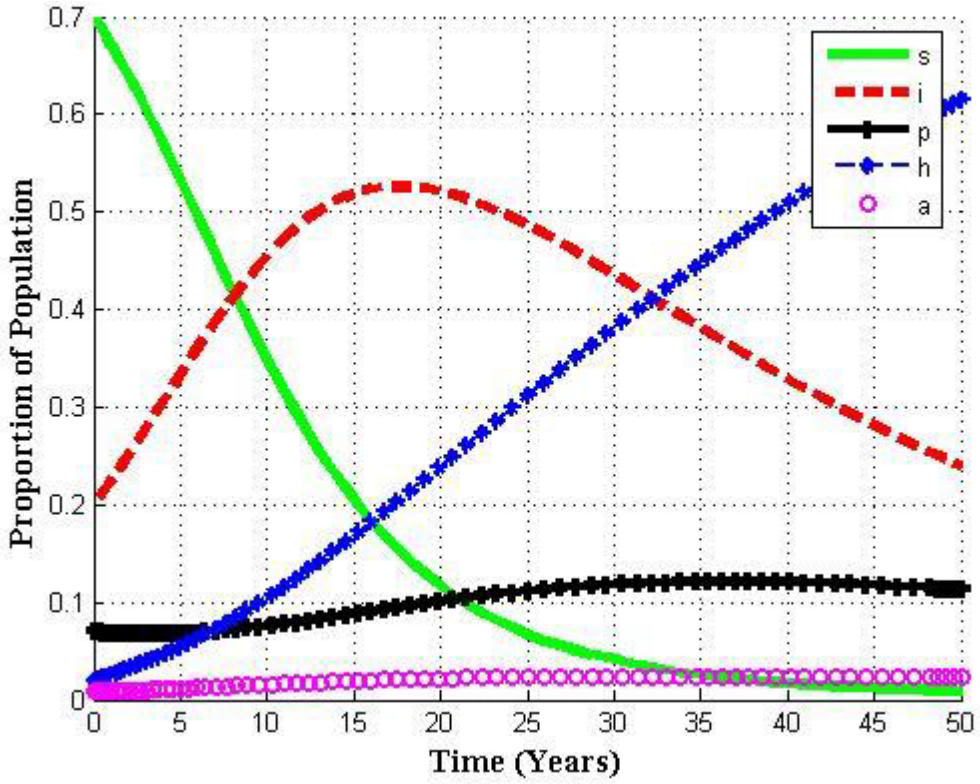


Figure: 2(a) Variation of population in different classes for $\pi = 0$ and $\theta = 0$

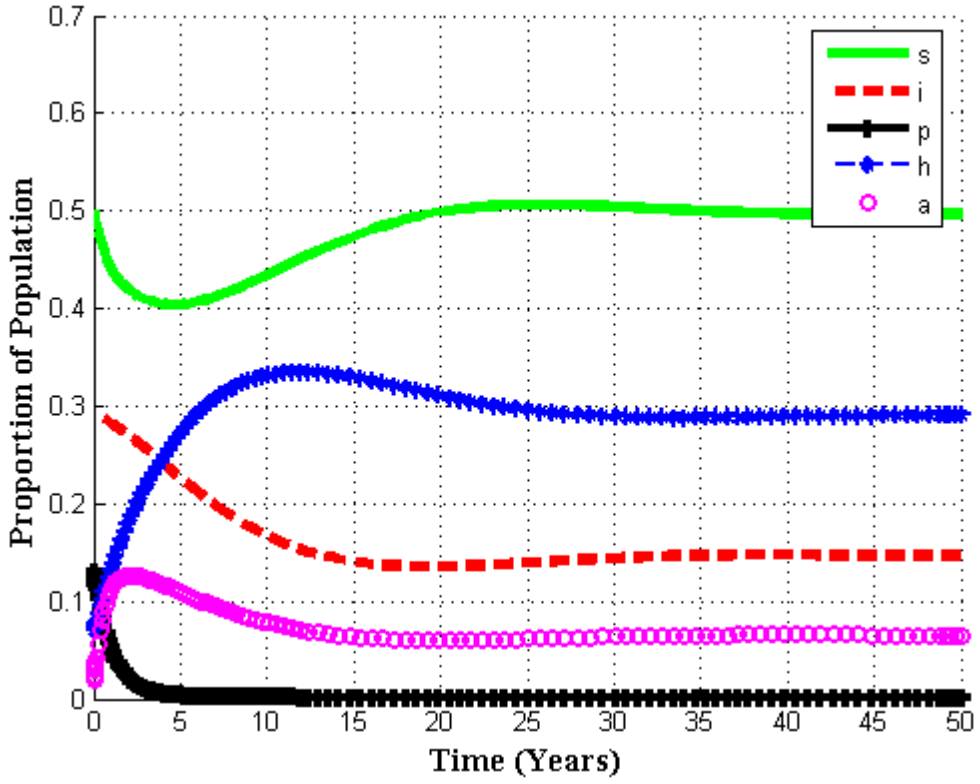


Figure: 2(b) Variation of population in different classes for $\pi = 0.1$ and $\theta = 0.20$

THEORAM AND PROOF

Positivity of Solutions: For the model (3.3) to be epidemiological meaningful and well posed, we need to prove that all state variables are non-negative $\forall \geq 0.$

Theorem (1.0): Let
$\Omega = \{(s,i,p,h,a)\} \in \mathbb{R}+: s+i+p+h+a = 1\}$,
then the solution $\{s(t), i(t), p(t), h(t), a(t)\}$ of the system 3.1.3 are the $\forall \geq 0.$

To P.V.T the theoram ,we have to use the differential equation of the system (3.3) using the 1st equation ,we have

$$\frac{ds}{dt} \leq \pi - \pi S$$

$$\frac{ds}{dt} + \pi s \leq \pi$$

We was find out the integrating factor
$IF = e^{\pi} \int dt = e^{\pi t}$.

$$\frac{d}{dt} = (s\, e^{\pi t}) \leq \pi e^{\pi t}$$

Intigrating both the side,

$$S(t) \leq 1 + Ce^{-\pi t}$$

Applaying initial condition ;when
$t = 0, s(t)s(0), s(0) \leq 1 + C.$

$$s(t) \leq 1 + (s(o) - 1)e^{-\pi t}$$

When $t \to \infty, s(t) \leq 1$

There fore

$$0 \leq s(t) \leq 1$$

Similarly, using the second of the system equation 3.30, we get

$$\frac{di}{dt} \geq -(\delta + \pi)$$

$$IF = e \int (\delta + \pi)dt = e^{(-\delta+\pi)t}$$

$$\frac{d}{dt}\left(ie^{\delta+\pi t}\right) \geq 0$$

Integarating both sides $t = 0, i(t) = i(o), i(0) \geq 0$

$$i(t) \geq i(0)e^{(\delta+\pi)t}$$

$$t \to \infty, i(t) \geq 0$$

Therefore,

$$i(t) \geq 0$$

Also in the third equation of the system (3.3)

$$\frac{dp}{dt} \geq -(\pi + \gamma p) \qquad (3.6)$$

$$\frac{dp}{p} \geq -(\pi + \gamma p)dt$$

Integrating both sides, we get

$$p(t) \geq p(0)e^{-(\pi+\gamma)t}$$

Applying initail conditions at $t = 0, p(t) \geq p(0).$

When $t \to \infty, p(t) \geq 0$

Similarly, using euation of the system (3.3) we have

$$\frac{dh}{dt} \geq -(\pi + k)h$$

$$\frac{dh}{h} \geq -(\pi + k)dt$$

Integarting both sides, we get

$$h(t) \geq h(o)e^{-(\pi+k)t}$$

Applying initail conditions at $t = 0, h(t) \geq h(0)$

When, $t \to \infty, h(t) \geq 0$

Finally, using equation of the system(3.3) we have

$$\frac{da}{dt} \geq (\pi + v + \alpha)a$$

$$\frac{da}{a} \geq -(\pi + v + \alpha)dt$$

Integrating both sides, we get

$$a(t) \geq a(0)e^{-(\pi+\gamma+\alpha)t}$$

Applaying initail condition at $t = 0, a(t) \geq a(0)$

When $t \to \infty, a(t) \geq 0$

3.3) Stability Analysis of the model. In this section, we present the result of stability analysis of the equalibrium points

3.4) Equalibrium points of the model. The model (3.3) has two non negative equlibrium points which are; the diseases free equalibrium pointE_0, and endemic equalibrium E^*

At equalibrium points

$$\frac{ds}{dt} = \frac{di}{dt} = \frac{dp}{dt} = \frac{dh}{dt} = \frac{da}{dt} = 0.$$

Hence the following system of equations is solved for equalibrium points

$$0 = \pi - C_1\beta_1 is - C_3\beta_3 hs - (\pi - \alpha a + (1-\varepsilon)\theta i)s$$

$$0 = C_1\beta_1 is + C_3\beta_3 hs + (1-\varepsilon)\theta i - [\pi + \delta - \alpha a + (1-\varepsilon)\theta i]i$$

$$0 = \sigma 1\delta i - [\pi + \gamma - \alpha a + (1-\varepsilon)\theta i]p$$

$$0 = \sigma_2\delta i + m\gamma p + va - (\pi + k - \alpha a + (1-\varepsilon)\theta i)h$$

$$o = (1-\sigma_1-\sigma_2)\delta i + (1-m)\gamma p + kh - [\pi + v + \alpha - \alpha a + (1-\varepsilon)\theta i]a$$

For the disease-free equalibrium $i = p = h = a = 0$ when substituted above, the system of equations reduced to

$$\pi - s\pi = 0, hence\ s = 1$$

Therefore, the disease-free equalibrium $E_0$is $(1,0,0,0,0)$.

The linear stability of E_0 can be established by its basic reproduction number. It is determined by using next generation method on the equation (3.3) in the form of matrices *F* and *V.*

Let F_i be the rate of appearance of new infection in compartment and V*i* be the transfer of individuals out of compartment by another means X_0 be the disease free equilibrium

R_0 is the largest eigenvalue of $\left[\frac{\partial Fi(x0)}{\partial(xi)}\right]\left[\frac{\partial Vi(x0)}{\partial(xj)}\right] - 1$

(3.9)

3.5 Computation of the Basic Reproduction Number, R_0

The basic reproduction number *R*0 is defined as the effective number of secondary infection caused by typical infected individual during his periods of infectiousness (Diekman *et al.,* 1990). It is obtained by taking the largest (dominant) Eigen value (spectral radius) of

$$F = \begin{bmatrix} \pi+\sigma-(1-\varepsilon)\theta & 0 & 0 & 0 \\ -\sigma\delta & \pi+\gamma & 0 & 0 \\ 0- & -m\gamma & \pi+k & -v \\ -(1-\sigma 1-\sigma 2\delta & (1-m)\gamma & -k & \pi+v+\alpha \end{bmatrix}$$

$$R_0 = FXV^{-1}$$

$$R_0 = \frac{c1\beta 1}{\pi+\delta-\theta+\theta\varepsilon} + \frac{c_3\beta_3(\sigma_2\pi^2+\sigma_2\pi\alpha+\sigma_2\gamma\pi+\sigma_2\gamma\alpha+\sigma_1 m\gamma\pi+\sigma_1 m\gamma\alpha+v\pi+v\gamma+\sigma_1 v\pi)\gamma}{(\pi+\delta-\theta+\theta\varepsilon)(\pi+\gamma)(\alpha\pi+\pi k+\pi^2+\alpha k+\gamma\pi)}$$

(3.10)

Thus, if $R_0 > 1$ the infection triggers an epidemic otherwise its prevalence is zero i.e. for $R_0 < 1$. From the solution, it is noted that with an increase in R_0, which can be viewed as a function of *c,* the number of sexual partners. The number of infectives increases which in turns increases the AIDS patient population. Thus in order to keep the spread of the disease at minimum, the number of sexual partners should be restricted.

The Endemic Equilibrium and Local Stability:

The endemic equilibrium point of the model (3.3) is given by $E^* = (s, i^*, p^*, h^*, a)$, to obtain an endemic equilibrium $E^*$of this model, we set to zero each equation in the model. Then by solving the system of equations in (3.3) we express each equilibrium point in terms of i^* and a^* at steady state, we get

$$\pi - C_1\beta_1 is - C_3\beta_3 hs - [\pi - \alpha a + \sigma_1 - \varepsilon)\theta i]s \qquad (a.1)$$

$$C_1\beta_1 is + C_3\beta_3 hs + (1-\varepsilon)\theta i - [\pi + \delta - \alpha a + (1-\varepsilon)\theta i]i \qquad (a.2)$$

$$\sigma_1\delta i - [\pi + \gamma - \alpha a + (1-\varepsilon)\theta i]p \qquad (a.3)$$

$$\sigma 2\delta i + m\gamma p + va - [\pi + k - \alpha a + (1-\varepsilon)\theta i]h \qquad (a.4)$$

$$(1-\sigma_1-\sigma_2)\delta i + (1-m)\gamma p + kh - [\pi + v + \alpha - \alpha a + (1-\varepsilon)\theta i]a \qquad (a.5)$$

Add equation (a.1) and (a.2) we get the value of s^*

$$S^* = \frac{\pi + (1-\varepsilon)\theta^* - (\pi + \delta - \alpha a^* + (1-\varepsilon)\theta^*)i^*}{\pi - \alpha a^* + (1-\varepsilon)\theta i^*}$$

Using the equation (a.3) and (a.4) to get the value p^*

$$p^* = \frac{\boldsymbol{\sigma_1}\delta i^*}{\pi + \gamma - \alpha a^* + (1-\varepsilon)\theta i^*}$$

Solve Eqns (a.4) and (a.5) to get the value of $h^* and\ a^*$ we get

$$h^* = \frac{k}{\emptyset\omega}$$

$$a^* = \frac{(1-\boldsymbol{\sigma_1}-\sigma_2)\delta i^*\emptyset\psi + (1-m)\boldsymbol{\sigma_1}\gamma\delta i\psi + k(\sigma 2\delta i\emptyset + m\gamma\boldsymbol{\sigma_1}\delta i^*}{\emptyset(\omega\psi - kv)}$$

Where,

$$\phi = (\pi + \gamma - \alpha a^* + (1-\varepsilon)\theta i^*)$$

$$\psi = (\pi + k - \alpha a^* + (1-\varepsilon)\theta i^*)$$

$\omega = (\pi + v + \alpha - \alpha a^* + (1-\varepsilon)\theta i^*$, and

$$k = \sigma 2\delta i^*\emptyset + m\gamma\sigma 1\delta i^* + \frac{v(1-\sigma 1-\sigma 2)\delta i^*\emptyset\psi + (1-m)\sigma 1\gamma\delta i^*\psi + k(\sigma 2\delta i^*\emptyset + m\gamma\sigma 1\delta i^*}{\omega\psi - kv}$$

The value $i^* are\ in\ the\ form\ of\ ploynomial$

$$i^*(A_5 i^* + A_4 i^* + A_2 i^* + A_1 i^* + A_0) = 0 \qquad (3.1.3)$$

After some algebraic calculation, the expression can be reduced as

$$\boldsymbol{A i^{*2} + B i^* = 0} \qquad (3.1.4)$$

Where,

$$\boldsymbol{A = -(\pi + k - \alpha a^*)(\pi + \delta - \alpha a^*)\Gamma}$$

$$\Gamma = C_1\beta_1\pi^3 - C_1\beta_1(\alpha a^*)2 - 2C_1\beta_1\pi v\alpha a^* - 2C_1\beta_1\pi\alpha^2 a^* + C_1\beta_1\pi k\alpha - C_1\beta_1 k\alpha a^* - C_1\beta_1\gamma v\alpha a^* + C_1\beta_1\gamma k\alpha - C_1\beta_1\gamma\alpha^2 a^* + C_1\beta_1\pi\gamma k - 2C_1\beta_1\pi\gamma\alpha a^* + C_3\beta_3\delta\pi\sigma_2\gamma + C_3\beta_3\delta\pi m\gamma\sigma 1 - C_3\beta_3\delta\gamma\alpha a^* + C_3\beta_3\delta\gamma\sigma_1\sigma_2\sigma + C_3\beta_3\delta m\gamma\sigma_1\alpha + C_3\beta_3\delta\gamma v - C_3\beta_3\delta\gamma\sigma_2\alpha a^* + C_3\beta_3\delta\sigma_2\pi^2 - C_1\beta_1 k\alpha^2 a^* - 2C_1\beta_1\pi k\alpha a^* + C_3\beta_3\delta\sigma_2\pi\alpha + C_3\beta_3\delta v\pi - C_3\beta_3\delta\sigma_1 v\pi - 2C_3\beta_3\delta\sigma_2\pi\alpha a^* + C_3\beta_3\delta v\alpha a^* - C_3\beta_3\delta v\alpha a^* + C_3\beta_3\delta\sigma_2\pi(\alpha a^*)2 + C_1\beta_1\pi\gamma v + C_1\beta_1\pi\gamma\alpha - 3C_1\beta_1\pi^2\alpha a^* + C_1\beta_1\pi^2 k + C_1\beta_1 k(\alpha a^*)2 + 3C_1\beta_1 k(\alpha a^*)2 + 3C_1\beta_1\pi(\alpha a^*)2 + C_1\beta_1\pi^2 v - C_3\beta_3\delta\sigma 2\alpha^2 a^*$$

$$\boldsymbol{B = (\pi + k - \alpha a^*)\Lambda}$$

$$\Lambda = -\pi^4 k + 4\pi^3\alpha a^* - \pi^3\alpha k - \pi^3\delta v + 4\pi^3\alpha^2 a^* - \pi^3\delta\alpha + 3\pi^2\delta\alpha^2 a^*$$

$$-\pi^2\gamma v - \pi^2\delta k\alpha + 3\pi^2 k\alpha^2 a^* - \sigma\pi^2 v(\alpha a^*)^2 - \sigma\pi^2\alpha(\alpha a^*)^2$$

$$+4\pi v(\alpha a^*)^4 + 4\pi v(\alpha a^*)^3 - \pi^4 v - \pi^4\alpha - \pi^4\gamma - \gamma(\alpha a^*)^4$$

$$+k\gamma(\alpha a^*)^4 - \alpha(\alpha a^*)^4 + 4\pi\alpha(\alpha a^*)^3 - \pi^4 v - \pi^4 v - \pi^4\alpha - \pi^4\gamma$$

$$-\boldsymbol{\gamma}(\alpha a^*)^3 - k\gamma(\alpha a^*)^3 - \pi^3 k\gamma + \delta k\gamma\alpha^2 a^* + 4\pi^3\gamma\alpha a^*$$

$$+2\pi\delta\gamma\alpha^2 a^* + \delta v(\alpha a^*)^3 + \gamma v(\alpha a^*)^3 + c_1\beta_1\pi^4 + 3\pi^2\gamma k\alpha a^* - \pi^5 + 2\pi\gamma ak\alpha a^* + 2\pi\delta v\alpha a^*$$

$$-\pi\gamma a\delta k + 4\pi\gamma(\alpha a^*)^3 - a\delta k(\alpha a^*)^2 - \gamma(\alpha a^*)^4 - 3k\gamma\pi(\alpha a^*)^2 - \pi^2\gamma\delta k + 3\pi^2\gamma\delta\alpha a^* - 3\pi\gamma\delta$$

$$(\alpha a^*)^2 + c_1\beta_1\pi^3\alpha + c_1\beta_1\pi^3 v + c_1\beta_1\pi^3\gamma - 3c_1\beta_1\pi^3\alpha a^* + 3c_1\beta_1\pi^2(\alpha a^*)^2 + c_1\beta_1\pi^3 k - c_1\beta_1\pi(\alpha a^*)^2 + \gamma a(\alpha a^*)^3 + 2\pi\delta k\alpha^2 a^* - 3\pi k\alpha(\alpha a^*)^2 - 3\pi\delta\alpha(\alpha a^*)^2 - 3\pi\delta v(\alpha a^*)^2 + 3\pi^2\gamma\alpha^2 a^* + 3\pi^2\gamma v\alpha a^* - \pi^2 k\gamma\alpha - \pi^2\gamma\delta\alpha - \pi^2\gamma\delta v - 3\pi\alpha^2 a^* - 3\pi\gamma v - 3\pi\gamma v(\alpha a^*)^2 - k\gamma\alpha(\alpha a^*)^2 - \delta\gamma v(\alpha a^*)^2 - \delta\gamma\alpha(\alpha a^*)^2 + C_3\beta_3\delta\sigma_2\pi^3 - \sigma\pi^2\gamma(\alpha a^*)^2 - \delta\gamma v(\alpha a^*)^2 - \delta\gamma\alpha(\alpha a^*)^2 + C_3\beta_3\delta m\gamma a\sigma_1\pi + C_3\beta_3\delta\gamma v\pi + C_1\beta_1\pi\gamma v\alpha a^* - C_3\beta_3\delta v\pi\alpha a^*$$

-

$$C_3\beta_3\delta\sigma_2\pi\alpha^2 a^* + C_3\beta_3\delta\sigma_1 v\alpha a^* + C_1\beta_1\pi v(\alpha a^*)^2 + C_1\beta_1\pi v(\alpha a^*)^2 + C_1\beta_1\pi\alpha(\alpha a^*)^2 - C_1\beta_1\pi\alpha^2 a^* + C_1\beta_1\pi^2 kv - C_3\beta_3\delta m$$

THE NUMERICAL SIMULATIONS OF THE MODEL

Model Simulation

To study the dynamical behaviour of the model (3.3) numerically, the system is integrated by using Runge-Kutta method using the following set of parameter values:

$$\theta = 0.30\ \ \varepsilon = 0.20\ v = 0.10\ \beta_1 = 0.40\ \ \beta_3 = 0.05\ \sigma_1 = 0.20\ \sigma_2 = 0.01\ k = 0.08\ \gamma = 0.90\ c_1 = 3$$

$$c_3 = 1\ m = 0.4\ \ \pi = 0.40\ \delta = 0.6\ \ \alpha = 9$$

With initial values

$$S(0) = 0.50\ I(0) = 0.30\ p(0) = 0.12\ \ h(0) = 0.07\ \ a(0) = 0.01$$

The endemic equilibrium values are computed as shown graphically Fig (1), Fig (2), and Fig (3) in Fig910- Fig (2) .It is shown the $i^*\ p^*\ and\ h^*$ and a^* is plotted against the proportion of susceptible population s^* The results of numerical simulation are shown graphically in Figures 2. In figure 2(a) the distribution of proportion of population with time is shown in different classes with neither new infected children into the population nor recruitments i.e. $\pi = 0$ and $\theta = 0$. It is seen that in the absence of vertical transmission into the community, the proportion of susceptible population decreases continuously as the population is closed which results in an increase in proportion of infective population first and then it decreases as all infectives subsequently develop full blown AIDS and the die out by natural or disease-induced death rate. The proportion of treated class is Increase continuously since the total population being constant in this case. Figure (2)

shows the variation of proportion of population in all classes with both recruitment of susceptible and fraction of new born children which are infected at birth. It is found that susceptible first decrease with time after using ARVs they prolong life time they increase and then reaches its equilibrium position. Since due to vertical transmission from infectives, susceptible population increase continuously therefore infection becomes more endemic, following that $R_0 > 1$

IV. CONCLUSION:

In this research, a non-linear mathematical model is proposed and analysed to study the transmission of HIV/AIDS in a population of varying size with treatments and vertical transmission under the assumption that due to sexual interaction of susceptibles with infectives, the infected babies are born to increase the growth of infective population directly. It is assumed that people in pre-AIDS and AIDS classes are exposed and incapable of producing children. By analysing the model, we have found a threshold parameter *R*0. It is noted that when $R_0 < 1$ then the disease dies out and when $R_0 > 1$, the disease becomes endemic. The model has two non-negative equilibrium namely the disease-free equilibrium, E_0 (1, 0, 0, 0, 0) and the endemic equilibrium $E^* = (s^* i^* p^* h^* a^*)$. It is found that the disease-free equilibrium 0 $E0^*$ is locally asymptotically stable if $R_0 < 1$ and for $R_0 > 1$ it is unstable and the infection is maintained in the population. The endemic equilibrium E*, which exist only when $R_0 > 1$ is always locally asymptotically stable. The equilibrium is also shown to be globally asymptotically stable under certain conditions. It is found that an increase in the rate of vertical transmission leads to increase the population of infectives which in turn increases the pre-AIDS and AIDS population.

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