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AIDS Epidemic Modeling With Different Demographic Structures

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Abstract

The most urgent public health problem today is to devise effective strategies to minimize the destruction caused by the AIDS epidemic. Mathematical models based on the underlying transmission mechanisms of the AIDS virus can help the medical/scientific community understand and anticipate its spread in different populations and evaluate the potential effectiveness of different approaches for bringing the epidemic under control. In this paper, we present the framework of conventional compartmental models for the spread of HIV infection to investigate the effect of various types of growths of host population. The model presented has been studied qualitatively using stability theory of differential equations. The equilibrium and stability analysis have been carried out by establishing local and global stability results and some inferences have been drawn to understand the spread of the disease. A numerical study in each case is also performed to see the influence of certain parameters on the disease spread and to support the analytical results. The model analysis has also been applied to compare the theoretical results with the known Indian HIV data.

Key words: HIV/AIDS epidemic, immigration, reproductive number, bifurcation, logistic growth.

1. Introduction

The AIDS epidemic has stimulated a large amount of research on the structure and variability of the Human Immuno-deficiency Virus (HIV) and on the natural history and epidemiology of AIDS. Recently, a growing effort in modeling the transmission of HIV and control strategies has emerged. Only models that are founded on the transmission mechanisms of HIV can show how the early infection of high-risk groups, behavioral changes, and future medical advances such as treatments and vaccine will affect the future courses of this epidemic. In developing the mathematical models, we are creating a logical structure that organizes existing information on AIDS into a coherent framework. Models can provide qualitative insights, even when data are lacking, and can help prioritize data collection.

Essentially all conventional mathematical models for epidemic or endemic infections of humans assume that the host population is constant in size, with births exactly balancing deaths. Several epidemiological models with varying population size are analyzed mathematically in Bailey [3], Busenberg and Hadeler [8], Busenberg and Van den Driessche [9], and Mena-Lorca and Hethcote [19]. Many models for AIDS have varying population size (Fan et al. [10], Hyman and Stanley [12], Jacquez et al. [13], Massad [15], May and Anderson [17], May et al. [18], Naresh et al. [21] and Tripathi et al. [25]). Naresh et al. [20] presented a model for vertical transmission of HIV/AIDS in a population with constant inflow of susceptibles. Naresh and Tripathi [22] developed a model for HIV-TB co-infection in a variable size population with constant immigration.

The assumption that the population is closed and fixed is often a reasonable approximation when modeling epidemics where the disease spreads quickly in the population and dies out within a short time. However, if the population growth or decrease is significant or the disease causes enough deaths to influence the population size, then it is not reasonable to assume that the population size is constant [19].

An approach used by Anderson and May [1] for laboratory population of mice is constant immigration at rate A and deaths proportional to the population size with a

rate constant d. Then,

$$\frac{dN}{dt} = A - dN \ , \qquad N(0) = N_0 \tag{1.1}$$

In this case the population size approaches A/d as t goes to infinity. This form is called constant immigration with exponential deaths.

Some models assume a more natural demographic process where the birth and death rates are proportional to the population size. Anderson et al. [2] and May and Anderson [16] proposed a variety of models for infectious diseases with varying total population sizes. A disadvantage of the models with birth and death rates proportional to the population size are that the population size decreases or grows exponentially except in the special case where births exactly balance deaths [11].

If $N(t)$ is the total population size as function of time t, b is the birth rate constant and d is the death rate constant, then

$$\frac{dN}{dt} = (b-d)N \quad , \quad N(0) = N_0 \tag{1.2}$$

If the net growth rate $r = b - d$, so that the population size $N(t)$ grows exponentially for $r > 0$, is constant if $r = 0$ and decays exponentially if $r < 0$.

Extinction of the population by exponential decay is demographically unlikely, also exponential growth to infinity is unrealistic in human and animal populations since finite resources always eventually limit the growth. Models with restricted growth due to density dependence have been considered by Anderson et al. [2], Brauer [5], Bremermann and Thieme [7], Gao and Hethcote [11] and Pugliese [24].

A demographic structure with density-dependent restricted population growth is given by the logistic equation.

$$\frac{dN}{dt} = r\left(1-\frac{N}{K}\right)N \tag{1.3}$$

where $N(t)$ is total population size as a function of time t, r is the positive growth rate constant and K is the carrying capacity of the environment.

In this paper, we propose a nonlinear deterministic mathematical model for AIDS epidemic and analyze for different population growth rates as described above. A numerical simulation of the model system is also performed to investigate the results. The model is applied to compare the theoretical results with Indian HIV data.

2. Mathematical model

We propose a simple nonlinear model for a population of total size $N(t)$ with growth rate function $Q(N)$, dependent on population size N. The total population is divided into three classes that is susceptibles $S(t)$, Infectives or HIV positives $I(t)$ and that of AIDS patients $A(t)$. It is assumed that the susceptibles become HIV

infective via sexual contacts with infectives with transmission coefficient β. The transfer diagram is given below,

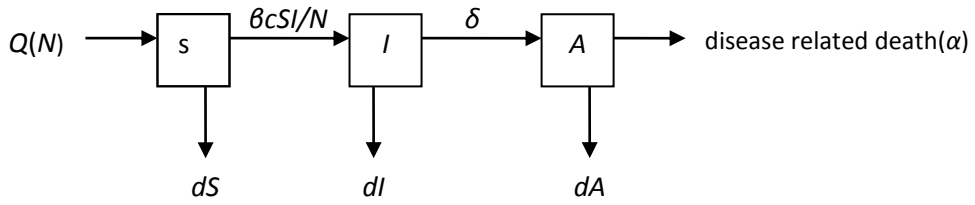

Fig.1 Transfer diagram of the model

In view of the above, the model equations are given by a set of nonlinear ordinary differential equations,

$$\frac{dS}{dt} = Q(N) - \frac{\beta cSI}{N} - dS \tag{2.1}$$

$$\frac{dI}{dt} = \frac{\beta cSI}{N} - (\delta + d)I \tag{2.2}$$

$$\frac{dA}{dt} = \delta I - (\alpha + d)A \tag{2.3}$$

$S(0) = S_0 > 0$, $I(0) = I_0 \geq 0$ and $A(0) = A_0 \geq 0$

where c is the number of sexual partners in a unit time, d is the natural mortality rate in all the classes, δ is the movement rate of infectives to the AIDS class and α is the disease related death rate constant.

Continuity of right hand side of system (2.1)-(2.3) and its derivative imply that the model is well posed for $\beta c > (\delta + d)$ and $N > 0$. As N tends to zero S, I and A also tend to zero. Hence, each of these terms tends to zero as N does. It is, therefore, natural to interpret these terms as zero at N=0. It is also assumed that all the dependent variables and parameters of the model are non-negative.

Since $N(t) \cong S(t) + I(t) + A(t)$, therefore the model (2.1)-(2.3) can be rewritten as (using $\beta c = \beta_1$),

$$\frac{dN}{dt} = Q(N) - dN - \alpha A \tag{2.4}$$

$$\frac{dI}{dt} = \frac{\beta_1 (N - I - A)I}{N} - (\delta + d)I \tag{2.5}$$

$$\frac{dA}{dt} = \delta I - (\alpha + d)A \tag{2.6}$$

In the following, we consider different forms of growth function $Q(N)$ to study the model dynamics. First we consider that all immigrants are susceptible with a constant inflow rate. In the next, we assume that some of the immigrants are infective followed by a model with density-dependent birth and death rate.

3. When all the immigrants are susceptible

In this case, we consider that there is a constant inflow at a rate Q_0 of new susceptible members into the population. The model (2.4)-(2.6), can be written as,

$$\frac{dN}{dt} = Q_0 - dN - \alpha A \tag{3.1}$$

$$\frac{dI}{dt} = \frac{\beta_1 (N - I - A)I}{N} - (\delta + d)I \tag{3.2}$$

$$\frac{dA}{dt} = \delta I - (\alpha + d)A \tag{3.3}$$

It is also assumed that the AIDS patients are sexually inactive as they are isolated and hence do not contribute to viral transmission.

From the model, it is noted that in the absence of infection, population size approaches the steady state value Q_0/d. During the early stage of epidemic, if it is assumed that $S \cong N \cong \frac{Q_0}{d}$ then the growth of infectious people $I(t)$ can be approximately governed by the following equation,

$$\frac{dI}{dt} = [\beta_1 - (\delta + d)]I \tag{3.4}$$

which gives $I(t)=I_0 \exp\left[\frac{R_0-1}{T}\right]t$,

where $R_0=\frac{\beta_1}{(\delta+d)}$, the basic reproduction number, and $T=\frac{1}{(\delta+d)}$ the time during which people remain infective. The doubling time t_d of the epidemic can be obtained as,

$$t_d=\frac{(\ln 2)T}{R_0-1} \tag{3.5}$$

Thus if $R_0 > 1$, the infection triggers an epidemic otherwise for $R_0 < 1$ its prevalence is zero. From the solution $I(t)$, it is noted that with an increase in R_0 the number of infectives increases which in turn increases the AIDS patients population.

3.1 Positivity of solutions

Lemma 1. Let the initial data be $N(0)= N_0>0$, $I(0)= I_0\geq 0$ and $A(0)= A_0>0$ for all $t \geq 0$. Then, the solution $(N(t), I(t), A(t))$ of the model remain positive for all time $t \geq 0$.

Proof. From equation (3.2), we have

$I'(t) \geq -(\delta+d)I(t)$ and by applying a theorem on differential inequalities [4] we obtain

$I(t) \geq c_1 e^{\{-(\delta+d)t\}} > 0$. Here c_1 is a constant of integration. A similar reasoning on the remaining equations shows that they are always positive in Ω_1 for $t > 0$.

3.2 Boundedness of solutions

The invariant region where solution exists is obtained as follows:

$$\frac{Q_0}{(\alpha+d)} \leq \text{lim inf } N(t) \leq \text{lim Sup } N(t) \leq \frac{Q_0}{d} \text{ (as } t\to\infty)$$

Since $N(t) > 0$ for all $t \geq 0$. Therefore, from (3.1), total population cannot blow up to infinity in finite time and consequently, the model system is dissipative (solutions are bounded). Thus, the solution exist globally for all $t > 0$ in the invariant and compact set.

$$\Omega_1 = \{(N, I, A);\ 0 < N \leq \overline{N};\ 0 \leq I \leq \bar{I};\ 0 \leq A \leq \overline{A}\}$$

which is a region of attraction for any arbitrary small $\varepsilon > 0$ starting in the region [$0 \leq I, A$ and $N \geq I + A$].

where $\bar{N} = \frac{Q_0}{d} + \varepsilon$, $\bar{I} = \frac{Q_0}{d}\left(1 - \frac{1}{R_0}\right)$ and $\bar{A} = \frac{\delta \bar{I}}{(\alpha + d)}$

3.3 The effect of R_0 and bifurcation behavior of the model

In epidemiological modeling the basic reproduction number, a fundamental parameter governing the spread of the disease, is the most crucial threshold quantity.

Bifurcation, in general, is a set of parameter values at which equilibrium values or fixed point of the system being considered changes stability and/or appears. In epidemiology, bifurcation phenomenon is associated with threshold parameter.

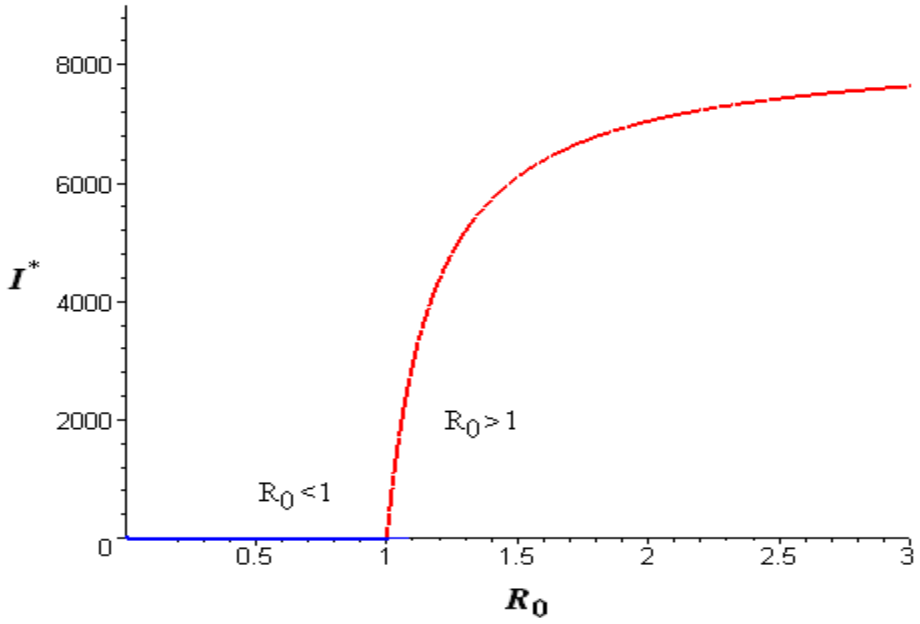

Fig.3.1. The bifurcation diagram showing forward bifurcation

From Fig. 3.1, we observe that the reproduction number $R_0 = 1$ is the bifurcation point which changes the stability behavior between disease free equilibrium and endemic equilibrium. It is noted that the disease- free equilibrium is always stable for $R_0<1$ and in this case there is no possibility for endemic equilibrium to exist and thus the disease is eradicated from the population. The system shows a forward bifurcation if reproduction number R_0 slightly exceeds one and disease-free equilibrium becomes unstable and an endemic equilibrium appears. Thus, it is observed that the HIV infection can be eradicated from the population if we reduce the reproduction number R_0 below one successfully and in that case the endemic equilibrium does not exist for $R_0<1$.

The behavior of reproduction number is also described comprehensively in the Figs. (3.2-3.4). From the Fig. 3.2, it is observed that when the reproduction number is less than one, the susceptible population increases tremendously. The level of susceptible population in this case is very high while it decreases when the reproduction number is greater than one. From Figs. (3.3-3.4), we see the effect of basic reproduction number R_0 on the different epidemiological classes. It is noted that the number of infectives increases for all values of $R_0 > 1$ which in turn reduces the susceptible population (see Fig. 3.3). It can also be seen that for $R_0<1$, the infective population tends to zero in the long run showing that the disease can not set off in the population. Similar phenomenon is observed for AIDS population (see Fig. 3.4)

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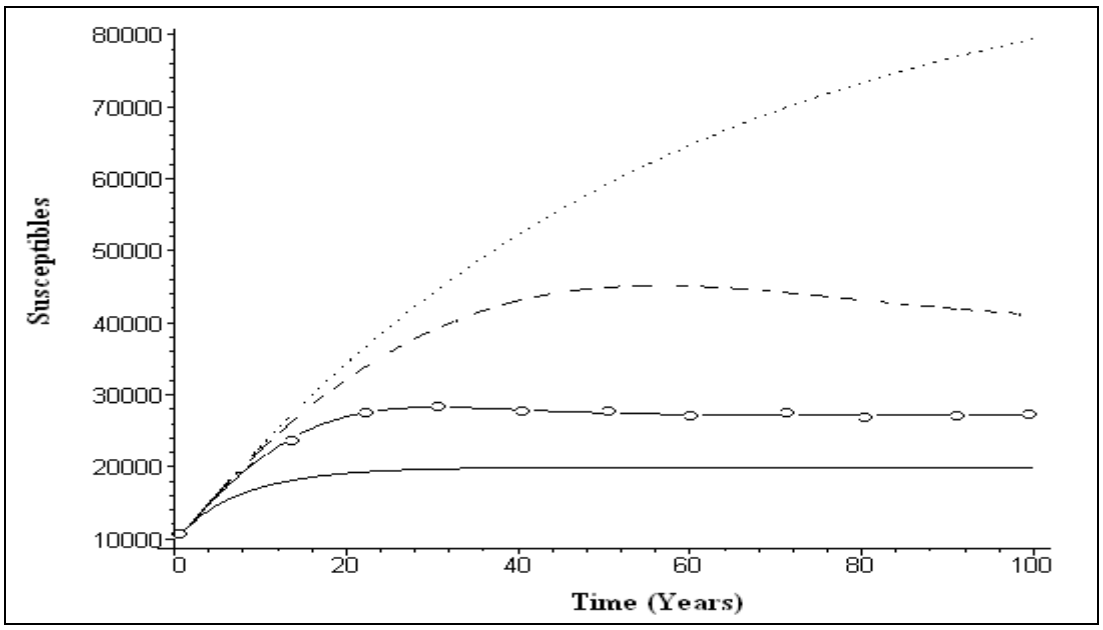

Fig.3.2. Variation of susceptibles for different values of reproduction number (R_0)

(Here ····· for $R_0 = 0.99$, - - - - for $R_0 = 1.5$, -∘–∘– for $R_0 = 2.5$, —— for $R_0 =$ (10)

Thus, the HIV infective population and the AIDS population become stable and reach their endemic level with time for reproduction number greater than one otherwise they will be unstable.

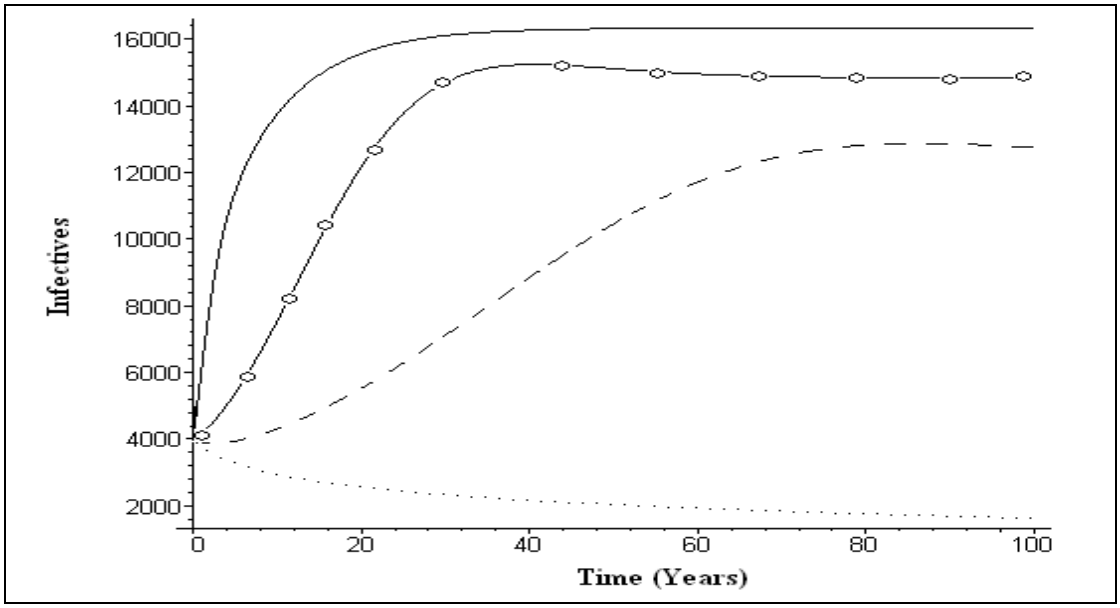

Fig.3.3 Variation of infectives for different values of reproduction number (R_0)

(Here ····· for $R_0 = 0.99$, - - - - for $R_0 = 1.5$, -∘–∘– for $R_0 = 2.5$, —— for $R_0 = 10$)

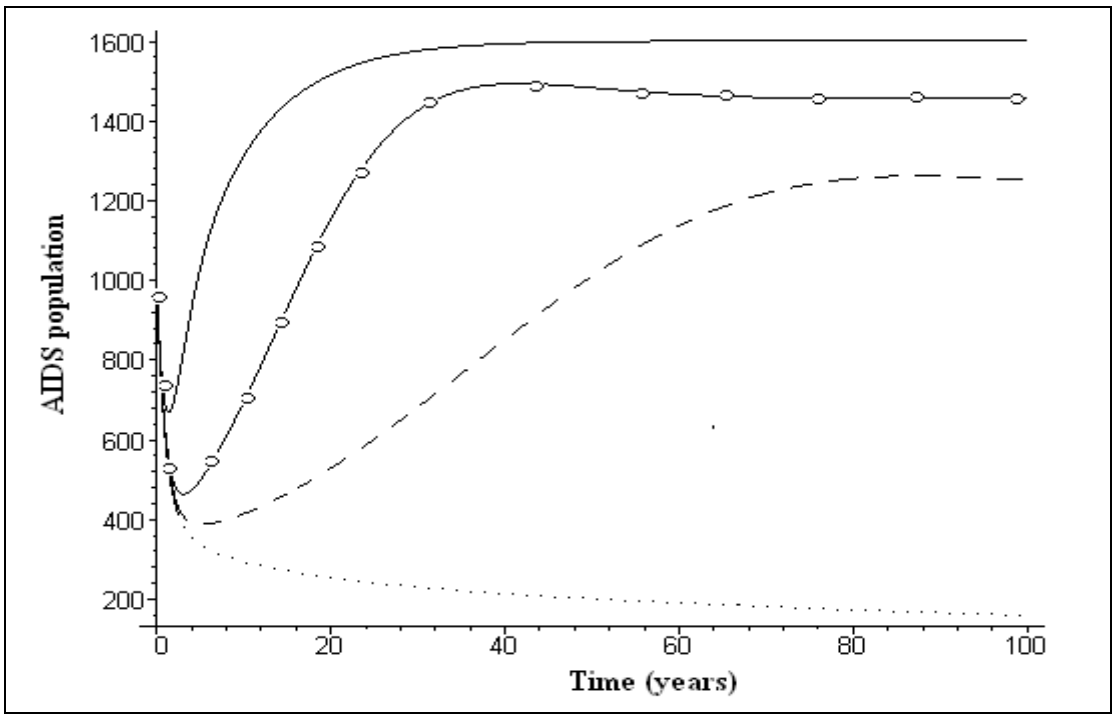

Fig.3.4. Variation of AIDS population for different values of reproduction number(R_0)

(Here ····· for $R_0 = 0.99$, - - - - for $R_0 = 1.5$, -∘–∘– for $R_0 = 2.5$, —— for $R_0 = 10$)

3.4. Stability analysis

The model (3.1)-(3.3) has two non-negative equilibria namely,

(i) E_0 (Q_0/d, 0, 0), the disease free equilibrium.

(ii) E^* (N^*, I^*, A^*), the endemic equilibrium.

where

$$N^* = \frac{Q_0 R_0(\alpha+\delta+d)}{R_0 d(\alpha+\delta+d)+\alpha\delta(R_0-1)}$$

$$I^* = \frac{Q_0 (R_0-1)(\alpha+d)}{R_0 d(\alpha+\delta+d)+\alpha\delta(R_0-1)}$$

$$A^* = \frac{Q_0 (R_0-1)\delta}{R_0 d(\alpha+\delta+d)+\alpha\delta(R_0-1)}$$

It is noted that the endemic equilibrium E^* exist only when, $R_0 > 1$. It is found that equilibrium level of infectives I^* increases as Q_0 increases leading to increase in A^*. The equilibrium level of AIDS patients A^* decreases as the disease induced death rate α increases. It is also noted that when the disease remain endemic, the disease-induced deaths reduce the equilibrium population size from Q_0/d to N^*.

Now to determine the local stability of E_0, the following variational matrix is computed corresponding to equilibrium point E_0,

$$M_0 = \begin{bmatrix} -d & 0 & -\alpha \\ 0 & [\beta_1 - (\delta+d)] & 0 \\ 0 & \delta & -(\alpha+d) \end{bmatrix}$$

From M_0, it is clear that E_0 is locally asymptotically stable provided $\beta_1 < (\delta+d)$ i.e. for $R_0 < 1$, the disease dies out and under this condition the equilibrium E^* does not exists as expected. If $R_0 > 1$ then E^* exists and the infection is maintained in the population.

The variational matrix about the equilibrium point E^* is given by,

$$M^* = \begin{bmatrix} -d & 0 & -\alpha \\ [\beta_1 - (\delta + d)]\dfrac{I^*}{N^*} & \dfrac{-\beta_1 I^*}{N^*} & \dfrac{-\beta_1 I^*}{N^*} \\ 0 & \delta & -(\alpha + d) \end{bmatrix}$$

The characteristic equation corresponding to M^* is obtained as,

$$f(\lambda) = \lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0 \tag{3.6}$$

where $a_1 = \alpha + 2d + \dfrac{\beta_1 I^*}{N^*}$

$$a_2 = d(\alpha + d) + (\alpha + d + \delta)\frac{\beta_1 I^*}{N^*}$$

$$a_3 = [\beta_1 d(\alpha + d + \delta) + \alpha\delta\{\beta_1 - (\delta + d)\}]\frac{I^*}{N^*}$$

It can seen easily that a_i>0 (i =1, 2, 3) and $a_1 a_2 - a_3$> 0. Thus, E^* is locally asymptotically stable.

Now to show that E^* is globally asymptotically stable, we propose the following theorem..

Theorem 1. The endemic equilibrium E^* is globally asymptotically stable provided the following condition is satisfied in Ω_1,

$$4\alpha^2\delta < d^2(\alpha + d) \tag{3.7}$$

Proof. Consider the following positive definite function about E^*,

$$V = \frac{1}{2}\left(N - N^*\right)^2 + k_1\left(I - I^* - I^* \ln\frac{I}{I^*}\right) + \frac{1}{2}k_2\left(A - A^*\right)^2 \tag{3.8}$$

The derivative of V along the solutions can be written as,

$$\frac{dV}{dt} = \left(N - N^*\right)\left(Q_0 - dN - \alpha A\right) + k_1\left(\frac{I - I^*}{I}\right)\left[\frac{\beta c(N - I - A)I}{N} - (d + \delta)I\right]$$

$$+ k_3\left(A - A^*\right)\left[\delta I_1 - (d + \alpha)A\right]$$

which can be further written as,

$$\frac{dV}{dt} = -d\left(N - N^*\right)^2 - \alpha\left(N - N^*\right)\left(A - A^*\right) - \frac{\beta c k_1}{N^*}(I - I^*)^2 - k_2(\alpha + d)(A - A^*)^2$$

$$+\frac{\beta c k_1}{NN^*}(I+A)(I-I^*)(A-A^*)+\left(k_2\delta-\frac{\beta c k_1}{N^*}\right)(I-I^*)(A-A^*)$$

Now for dV/dt to be negative definite, the following conditions must be satisfied:

$$\frac{\beta c}{N^*}\left(\frac{I+A}{N}\right)^2 k_1 < d \tag{3.9}$$

$$\alpha^2 < d(\alpha+d)k_2 \tag{3.10}$$

$$\left[k_2\delta-\frac{\beta c k_1}{N^*}\right]^2 < (\alpha+d)\frac{\beta c k_1}{N^*}k_1 k_2 \tag{3.11}$$

After maximizing the LHS and minimizing the RHS of above inequalities (3.9)-(3.11), the stability condition can be obtained as follows:

$$4\alpha^2\delta < d^2(\alpha+d)$$

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

$$\frac{\alpha^2\delta N^*}{\beta_1 d(\alpha+d)} < k_1 < \frac{dN^*}{4\beta_1} \text{ and } k_2 = \frac{\beta c k_1}{\delta N^*}$$

Hence, V is a Liapunov function with respect to E^* whose domain contains Ω_1, proving the theorem.

***Remark* 1.** *It is noted that the system* (3.1)–(3.3) *is bounded by the system* (3.1)–(3.3) *when* $\alpha = 0$*, which implies that the solution of* (3.1)–(3.3) *is bounded by the solution of the latter. If* $\alpha = 0$*, the system is globally stable without any condition. Hence, we speculate that the endemic equilibrium of system* (3.1)–(3.3) *may be globally asymptotically stable as given in the theorem.*

4. When some of the immigrants are infected

In this case, we consider that some of the immigrants are infected which directly increases the infective population. Thus, infected individuals are introduced into the population by the arrival of infectives from outside the population. For example, travelers may return home from a foreign trip with an infection acquired abroad, individuals who are HIV positive may migrate to other habitat, or infective truck drivers may enter into the city. Truck drivers are at an increased risk of infection due to the migratory nature of their job and their prolonged absence from home. As a result, such individuals are more likely to have sexual interactions with commercial sex workers, who often provide them with affordable food and lodging during their journeys. The spread of AIDS is further

exacerbated by the highly sexually active lifestyles of both the truck drivers and the prostitutes they visit [6, 14]. This is the more realistic situation than the previous case where all immigrants are taken to be susceptible. Thus, the model (2.1)-(2.3) can be written as follows,

$$\frac{dS}{dt} = Q_0 - \frac{\beta_1 SI}{N} - dS \tag{4.1}$$

$$\frac{dI}{dt} = Q_1 + \frac{\beta_1 SI}{N} - (\delta + d)I \tag{4.2}$$

$$\frac{dA}{dt} = \delta I - (\alpha + d)A \tag{4.3}$$

As before, we can rewrite the above system (4.1)-(4.3) as follows,

$$\frac{dN}{dt} = Q_0 + Q_1 - dN - \alpha A \tag{4.4}$$

$$\frac{dI}{dt} = Q_1 + \frac{\beta_1 (N - I - A)I}{N} - (\delta + d)I \tag{4.5}$$

$$\frac{dA}{dt} = \delta I - (\alpha + d)A \tag{4.6}$$

If $\beta_1 = 0$, so that the infectives are only those who enter the population from outside. This reduces the equation (4.5) to,

$$\frac{dI}{dt} = Q_1 - (\delta + d)I \tag{4.7}$$

For which every solution approaches,

$$\breve{N} = \frac{1}{d}\left[Q_0 + Q_1 - \frac{\alpha\delta\breve{I}}{\alpha + d}\right], \quad \breve{I} = \frac{Q_1}{\delta + d} \text{ and } \breve{A} = \frac{\delta\breve{I}}{\alpha + d}$$

It is observed from system (4.1)-(4.3) that if immigration of infective individuals tends to zero, the endemicity of the infection is reduced. This can simply be shown by comparing $N_{Q_1=0}$ and $N_{Q_1\neq 0}$ using a crude assumption,

(H_1) Let only $I(t)$ be zero at equilibrium in equation (4.1), then, $\frac{N_{Q_1=0}}{N_{Q_1\neq 0}} = \frac{Q_0}{Q_0 + Q_1} < 1$, this implies that the introduction of infective immigrants reduces S_0 and increases $I(t)$.

4.1. Stability analysis

The model has only one non-negative endemic equilibrium $\hat{E}(\hat{N}, \hat{I}, \hat{A})$ for $\beta_1>0$ due to direct inflow of infectives. Here $\hat{N}$, $\hat{I}$ and $\hat{A}$ are positive solutions of the equations obtained by putting right hand side of system (4.4)-(4.6) equal to zero and are given by,

$$\hat{N} = \frac{\frac{\beta_1(\alpha+d)}{\delta}\left(\frac{Q_0+Q_1-d\hat{N}}{\alpha}\right)^2\left(\frac{\alpha+\delta+d}{\delta}\right)}{Q_1+[\beta_1-(\delta+d)]\frac{(\alpha+d)}{\delta}\left(\frac{Q_0+Q_1-d\hat{N}}{\alpha}\right)} \tag{4.8}$$

$$\hat{I} = \frac{(\alpha+d)}{\delta}\left(\frac{(Q_0+Q_1)-d\hat{N}}{\alpha}\right) \tag{4.9}$$

$$\hat{A} = \frac{(Q_0+Q_1)-d\hat{N}}{\alpha} \tag{4.10}$$

To show the existence of $\hat{E}$ we write $F(\hat{N})$ from eq.(4.8) as,

$$F(\hat{N}) = Q_1\hat{N}+[\beta_1-(\delta+d)]\frac{(\alpha+d)}{\delta}\left(\frac{Q_0+Q_1-d\hat{N}}{\alpha}\right)\hat{N}$$

$$-\frac{\beta_1(\alpha+d)}{\delta}\left(\frac{Q_0+Q_1-d\hat{N}}{\alpha}\right)^2\left(\frac{\alpha+\delta+d}{\delta}\right) \tag{4.11}$$

It would be sufficient if we show that $F(\hat{N}) = 0$ has a unique positive root.

To prove this, we have,

$$F(0) = -\frac{\beta_1(\alpha+d)}{\delta}\left(\frac{Q_0+Q_1}{\alpha}\right)^2\left(\frac{\alpha+\delta+d}{\delta}\right) < 0 \tag{4.12}$$

$$F\left(\frac{Q_0+Q_1}{d}\right) = \frac{Q_1(Q_0+Q_1)}{d} > 0 \tag{4.13}$$

Also

$$F'(\hat{N}) = Q_1+[\beta_1-(\delta+d)]\frac{(\alpha+d)}{\delta}\left(\frac{Q_0+Q_1-d\hat{N}}{\alpha}\right)-[\beta_1-(\delta+d)]\frac{(\alpha+d)d\hat{N}}{\delta\alpha}$$

$$+\frac{2\beta_1(\alpha+d)d}{\delta\alpha}\left(\frac{Q_0+Q_1-d\hat{N}}{\alpha}\right) \tag{4.14}$$

It is noted that $F'(\hat{N}) > 0$ if

$$Q_1+\left[[\beta_1-(\delta+d)]+\frac{2\beta_1 d}{\alpha}\right]\frac{(\alpha+d)}{\delta}\left(\frac{Q_0+Q_1-d\hat{N}}{\alpha}\right)>[\beta_1-(\delta+d)]\frac{(\alpha+d)d\hat{N}}{\delta\alpha}$$

Thus, $F(\hat{N}) = 0$ has exactly one root (say $\hat{N}$) between 0 and $\frac{Q_0+Q_1}{d}$. Using $\hat{N}$, the values of $\hat{I}$ and $\hat{A}$ can be found easily.

Remark 2. It is observed from system (4.4)-(4.6) that if immigration of infectives tends to zero then endemic equilibrium $\hat{E}\to E^*$. Thus, the endemicity of the infection is reduced when immigration of infectives is restricted i.e. $Q_1 = 0$.

The characteristic equation corresponding to the variational matrix with respect to $\hat{E}$ is obtained as,

$$g(\lambda)=\lambda^3+b_1\lambda^2+b_2\lambda+b_3=0 \tag{4.15}$$

where $b_1=\alpha+d+\frac{\beta_1\hat{I}}{\hat{N}}+\frac{Q_1}{\hat{I}}$

$$b_2=d(\alpha+d)+(\alpha+2d)\left[\frac{Q_1}{\hat{N}}+\frac{\beta_1\hat{I}}{\hat{N}}\right]+\frac{\beta_1\delta\hat{I}}{\hat{N}}$$

$$b_3=d(\alpha+d+\delta)\frac{\beta_1\hat{I}}{\hat{N}}+d(\alpha+d)\frac{Q_1}{\hat{I}}+\alpha\delta\left[\frac{Q_1+[\beta_1-(\delta+d)]\hat{I}}{\hat{N}}\right]$$

Here again $b_i > 0$ (i =1, 2, 3) and $b_1b_2-b_3 > 0$ holds. Thus, $\hat{E}$ is locally asymptotically stable without any condition.

Lemma 2. The region of attraction in this case is given as,

$\Omega_2 = \{(N, I, A); 0 < N \le \overline{N}\ ; 0 \le I \le \overline{I}\ ; 0 \le A \le \overline{A}\ \}$ is a region of attraction.

where

$$\overline{N}=\frac{Q_0+Q_1}{d},$$

$$\bar{I} = \frac{(Q_0 + Q_1)[\beta_1 - (\delta + d)] + (Q_0 + Q_1)\sqrt{[\beta_1 - (\delta + d)]^2 + 4Q_1\beta_1 d}}{2\beta_1 d}$$

and $\bar{A} = \dfrac{\delta \bar{I}}{(\alpha + d)}$

Theorem 2. The endemic equilibrium $\hat{E}$ is globally asymptotically stable if the following inequality is satisfied in Ω_2,

$$4\beta_1\alpha^2\delta < d^2(\alpha + d)\hat{N}\left[\frac{Q_1}{\bar{I}\,\hat{I}} + \frac{\beta_1}{\hat{N}}\right] \tag{4.16}$$

It can be proved by using the following positive definite function about $\hat{E}$

$$V = \frac{1}{2}\left(N - \hat{N}\right)^2 + m_1\left(I - \hat{I} - \hat{I}\ln\frac{I}{\hat{I}}\right) + \frac{1}{2}m_2\left(A - \hat{A}\right)^2 \tag{4.17}$$

where the constant $\dfrac{\alpha^2\delta}{(\alpha + d)} < m_1 < \dfrac{d^2\hat{N}\xi}{4\beta_1}$ and $m_2 = \dfrac{\beta_1 k_1}{\delta\hat{N}}$

Here $\xi = \left[\dfrac{Q_1}{\bar{I}\,\hat{I}} + \dfrac{\beta_1}{\hat{N}}\right]$

Remark 3. *It is also noted that if $Q_1 = 0$ then condition* (4.16) *for global stability reduces to the condition (3.7).*

5. When population grows logistically

In order to investigate disease dynamics for the model with more demographic effects, it should be assumed that birth and death rates are density dependent. In this case, the epidemiological model formulated has population dynamics corresponding to the logistic equation where the restricted growth is due to density dependence in both the birth and death rates. The birth rate decreases and the death rate increases as the population size increases towards its carrying capacity.

$$\frac{dS}{dt} = \left[b - a\frac{rN}{K}\right]N - \frac{\beta_1 SI}{N} - \left[d + (1-a)\frac{rN}{K}\right]S \tag{5.1}$$

$$\frac{dI}{dt} = \frac{\beta_1 SI}{N} - \left[\delta + d + (1-a)\frac{rN}{K}\right]I \tag{5.2}$$

$$\frac{dA}{dt} = \delta I - \left[\alpha + d + (1-a)\frac{rN}{K}\right]A \qquad (5.3)$$

$S(0) > 0$, $I(0) \geq 0$, $A(0) \geq 0$

where b and d are natural birth and death rates, $r = b - d > 0$ is the growth rate constant, $K > 0$ is the carrying capacity of the human population density in the natural environment. For $0<a<1$, the birth rate decreases and the death rate increases as N increases to its carrying capacity K. When $a = 1$, the model could be called simply a logistic birth model as all of the restricted growth is due to a decreasing birth rate and the death rate is constant. Similarly, when $a = 0$, it could be called a logistic death model as all of the restricted growth is due to an increasing death rate and the birth rate is constant. The birth rate is density independent when $a = 0$ and the death rate is density independent when $a = 1$. These are consistent with the limited resources associated with density dependence.

Since $N(t) = S(t) + I(t) + A(t)$; therefore, we can write above system as following,

$$\frac{dN}{dt} = rN\left[1 - \frac{N}{K}\right] - \alpha A \qquad (5.4)$$

$$\frac{dI}{dt} = \frac{\beta_1 (N - I - A)I}{N} - \left[\delta + d + (1-a)\frac{rN}{K}\right]I \qquad (5.5)$$

$$\frac{dA}{dt} = \delta I - \left[\alpha + d + (1-a)\frac{rN}{K}\right]A \qquad (5.6)$$

$N(0) > 0$, $I(0) \geq 0$, $A(0) \geq 0$

Also $r = (b\text{-}d)$ is the growth rate constant. If we consider the case where $r > 0$ so the logistic equation really does describe restricted growth. If $r = 0$ and there is no disease, then the population size remains constant. If $r < 0$ and there is no disease, then the population size decreases to zero.

Lemma 3. The region of attraction in this case is given by,

$$\Omega_3 = \{(N, I, A);\ 0 < N \leq \mathrm{K};\ 0 \leq I \leq \bar{I}\ ;\ 0 \leq A \leq \bar{A}\ \}$$

where $\bar{I} = K\left[1 - \frac{1}{R_1}\right]$ and $\bar{A} = \left(\frac{\delta}{\alpha + d + (1-a)r}\right)\left[1 - \frac{1}{R_1}\right]K$.

As in Section 3, it is easy to note that the solution of model system (5.4)-(5.6) remains positive for all $t>0$.

5.1 Stability analysis

The model (5.4)-(5.6) has two non-negative equilibria namely,

(i) W_0 (K, 0, 0), the disease-free equilibrium.

(ii) $\vec{E}(\vec{N},\vec{I},\vec{A})$, the endemic equilibrium.

where $\vec{I} = \dfrac{r\vec{N}\left[\alpha+d+(1-a)\dfrac{r\vec{N}}{K}\right]\left[1-\dfrac{\vec{N}}{K}\right]}{\alpha\delta}$

$$\vec{A} = \frac{r\vec{N}}{\alpha}\left[1-\frac{\vec{N}}{K}\right]$$

and $\vec{N}$ is given by the quadratic equation,

$$G(\vec{N}) = A\vec{N}^2 + B\vec{N} + C = 0 \tag{5.7}$$

where $A=\dfrac{\beta_1 r^2(1-a)}{K^2\alpha\delta}$

$$B=\frac{\beta_1 r(1-a)}{\alpha\delta K}\left[\frac{\alpha+\delta+d}{(1-a)}-\frac{\alpha\delta}{\beta_1}-r\right]$$

$$C=\left[\{\beta_1-(\delta+d\}-\frac{\beta_1 r(\alpha+d+\delta)}{\alpha\delta}\right]$$

It would be sufficient if to show that $G(\vec{N}) = 0$ has a unique positive root.

To prove this we have,

$$G(0) = \left[\{\beta_1-(\delta+d\}-\frac{\beta_1 r(\alpha+d+\delta)}{\alpha\delta}\right] \tag{5.8}$$

It is noted that $G(0) < 0$ provided the following condition is satisfied

$$[\beta_1-(\delta+d] < \frac{\beta_1 r(\alpha+d+\delta)}{\alpha\delta} \tag{5.9}$$

And

$$G(K) = [\delta + d + (1-a)r][R_1 - 1]K \qquad (5.10)$$

Thus, if $R_1 > 1$ then $G(K) > 0$, where $R_1 = \frac{\beta_1}{\delta + d + r(1-a)}$ is defined in (5.13).

Also

$$G'(\vec{N}) = \frac{1}{\alpha \delta K^2}[2\beta_1 r^2(1-a) + K\{\beta_1(\alpha + \delta + d) - (1-a)(\alpha\delta + \beta_1 r)\}] \qquad (5.11)$$

which is positive if

$$\beta_1(\alpha + \delta + d) > (1-a)(\alpha\delta + \beta_1 r) \qquad (5.12)$$

Thus, $G(\vec{N}) = 0$ has exactly one root (say $\vec{N}$) between 0 and K under condition (5.12). Using $\vec{N}$, the values of $\vec{I}$ and $\vec{A}$ can be found easily.

We find that the equilibrium W_0 is locally asymptotically stable if $\beta_1 < [\delta + d + r(1-a)]$, the disease dies out and under this condition the equilibrium $\vec{E}$ does not exist. If $\beta_1 > [\delta + d + r(1-a)]$, then W_0 is unstable and there exists unique endemic equilibrium $\vec{E}$ and the infection is maintained in the population.

We define the basic reproduction number in this case as,

$$R_1 = \frac{\beta_1}{\delta + d + r(1-a)} \qquad (5.13)$$

and note that if $R_1 < 1$the infection dies out and for $R_1 > 1$it always persists in the population.

The characteristic equation corresponding to the variational matrix with respect to $\vec{E}$ is given by,

$$h(\lambda) = \lambda^3 + c_1\lambda^2 + c_2\lambda + c_3 = 0 \qquad (5.14)$$

where, $c_1 = \alpha + d - r + \frac{\beta_1 \vec{I}}{\vec{N}} + (3-a)\frac{r\vec{N}}{K}$

$$c_2 = \left[\alpha + d + (1-a)\frac{r\vec{N}}{K}\right]\left[\frac{\beta_1 \vec{I}}{\vec{N}} + \left(\frac{2r\vec{N}}{K} - r\right)\right] + \frac{\beta_1 \vec{I}}{\vec{N}}\left[\delta - r + \frac{2r\vec{N}}{K}\right] + \alpha(1-a)\frac{r\vec{A}}{K}$$

$$c_3 = \frac{\beta_1 \ddot{I}}{\ddot{N}}\left[\alpha + d + \delta + (1-a)\frac{r\ddot{N}}{K}\right]\left(\frac{2r\ddot{N}}{K} - r\right) + \alpha\delta\left[\frac{\beta_1(\ddot{I}+\ddot{A})}{\ddot{N}^2} - \frac{(1-a)r}{K}\right]\ddot{I}$$

$$-\alpha\beta_1\left[(1-a)\frac{r\ddot{A}}{K}\right]\frac{\ddot{I}}{K}$$

Thus by Routh-Hurwitz criteria, $\ddot{E}$ is locally asymptotically stable as it can be shown that $c_1 > 0$, $c_2 > 0$, $c_3 > 0$ and $c_1c_2 - c_3 > 0$.

Theorem 3. Let the following inequality hold, the endemic equilibrium $\ddot{E}$ is globally asymptotically stable in Ω_3.

$$\eta^2 \tau^2 \delta < \varepsilon^2 p \qquad (5.15)$$

where $\eta = \left[\frac{\alpha}{\ddot{N}} + \frac{k_2(1-a)r\bar{A}}{K}\right]$, $\varepsilon = \frac{\beta_1}{\ddot{N}}\left[\frac{r}{K} - \frac{\alpha}{\ddot{N}}\right]$, $\tau = \left[\frac{2\beta_1}{\ddot{N}} - \frac{(1-a)r}{K}\right]$ and $p = \left[(\alpha + d) + \frac{(1-a)r\ddot{N}}{K}\right]$.

Proof: Consider the following positive definite function about $\ddot{E}$

$$V = \left(N - \ddot{N} - \ddot{N}\ln\frac{N}{\ddot{N}}\right) + k_1\left(I - \ddot{I} - \ddot{I}\ln\frac{I}{\ddot{I}}\right) + \frac{1}{2}k_2\left(A - \ddot{A}\right)^2 \qquad (5.16)$$

where the constant $\frac{\eta^2\delta}{\varepsilon p} < k_1 < \frac{\varepsilon}{\tau^2}$ and $k_2 = \frac{\beta_1 k_1}{\delta\ddot{N}}$

It can be shown easily, as before, that $\ddot{E}$ is globally asymptotically stable.

Remark 4. If the movement rate of HIV infectives to AIDS class tends to zero i.e. $\delta = 0$, then the condition for global stability is automatically satisfied showing that this parameter has destabilizing effect on the system.

6. Numerical Simulations

We give here numerical simulation of the models for different epidemiological situations. First we see the nonlinear behavior of the system (3.1)-(3.3) and (4.4)-(4.6) numerically. It is noted that, on considering $Q_1 = 0$, we get the reduced model (3.1)-(3.3). We integrate the system (4.4)-(4.6) by fourth order Runge-Kutta method using the following set of parameter values:

$Q_0 = 2000$, $Q_1 = 400$, $d = 0.02$, $\beta_1 = 0.4$, $\alpha = 1$, $\delta = 0.1$, $p = 0.2$

with initial values $N(0) = 10000$, $I(0) = 4000$ and $A(0) = 1000$, the equilibrium values are computed as

$$\hat{N} = 22686,\ \hat{I} = 15772,\ \hat{A} = 1546$$

and equilibrium values for $Q_1 = 0$ and keeping the value of all other parameters same we get,

$$N^* = 24242,\ I^* = 15455,\ A^* = 1515.$$

The results are displayed graphically in Figs. 6.1 - 6.2. In these figures, the infective population is plotted against the AIDS population. We see from these figures that the solution curves tend to the endemic equilibrium E^* and $\hat{E}$. Hence, we infer that the systems (3.1)-(3.3) and (4.4)-(4.6) are globally stable about the endemic equilibrium E^* and $\hat{E}$ for the above set of parameter values.

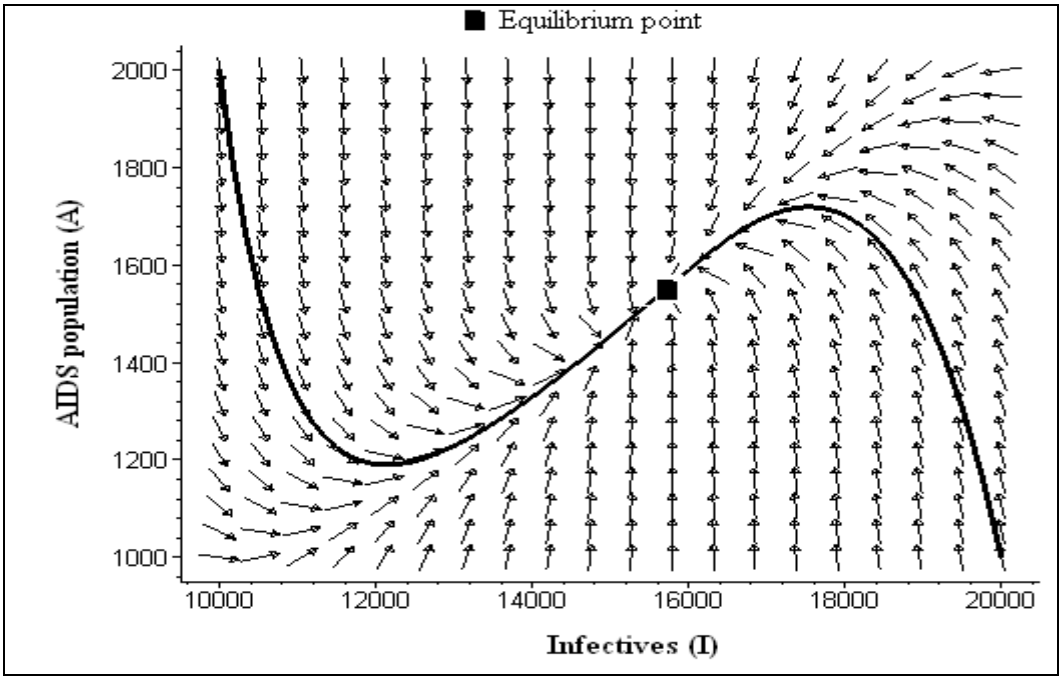

Fig. 6.1. Variation of infective population (I) and AIDS population (A) when all the immigrants are susceptible i.e.$Q_1 = 0$

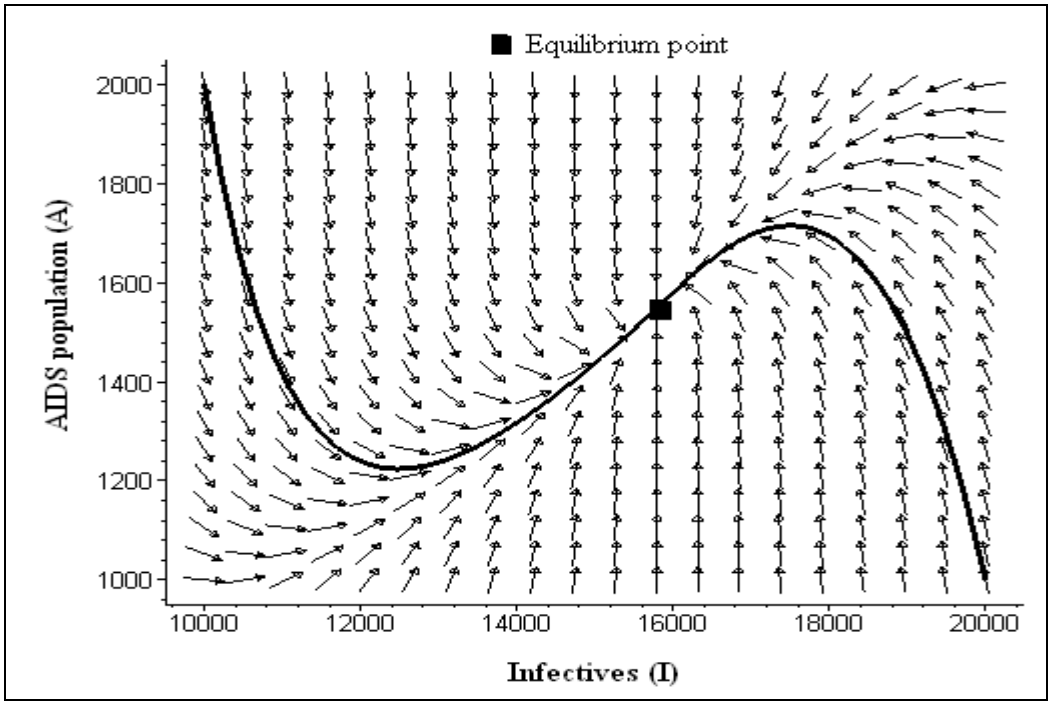

Fig. 6.2. Variation of infective population (I) and AIDS population (A) when some of the immigrants are infected i.e. $Q_1 \neq 0$

Now we integrate the system (5.4)-(5.6) by fourth order Runge-Kutta method using the following set of parameter values:

$$r = 0.2,\ d = 0.02,\ \beta_1 = 0.4,\ \alpha = 1,\ \delta = 0.1,\ K = 20000,\ a = 0.7$$

and initial values $N(0) = 10000$, $I(0) = 4000$ and $A(0) = 1000$. The equilibrium values are computed as

$$\vec{N} = 14953,\ \vec{I} = 8036 \text{ and } \vec{A} = 755.$$

In the Fig. 6.3, the infective population is plotted against the AIDS population for logistically growing population. We see from the figure that the solution curve converges to the endemic equilibrium $\vec{E}$. Hence, we infer that the system (5.4)-(5.6) is also globally stable about this endemic equilibrium for the above set of parameter values. In Figs. 6.4 and 6.5 we plot the total population and infective population respectively for different demographic states with time. It is seen that the level of total population and infective population is higher in the case when some of the immigrants are infectives. Thus, the endemicity of infection is higher if the direct inflow of infectives is allowed in the population whereas the endemicity of infection is low if the population undergoes logistic growth.

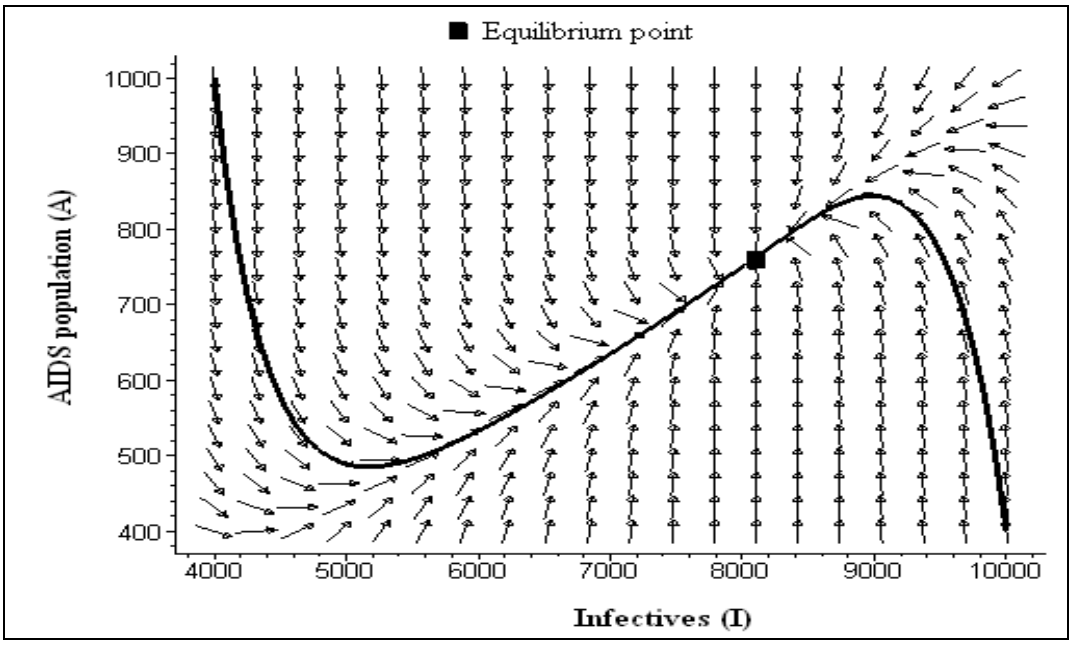

Fig. 6.3. Variation of infective population and AIDS population when population grows logistically

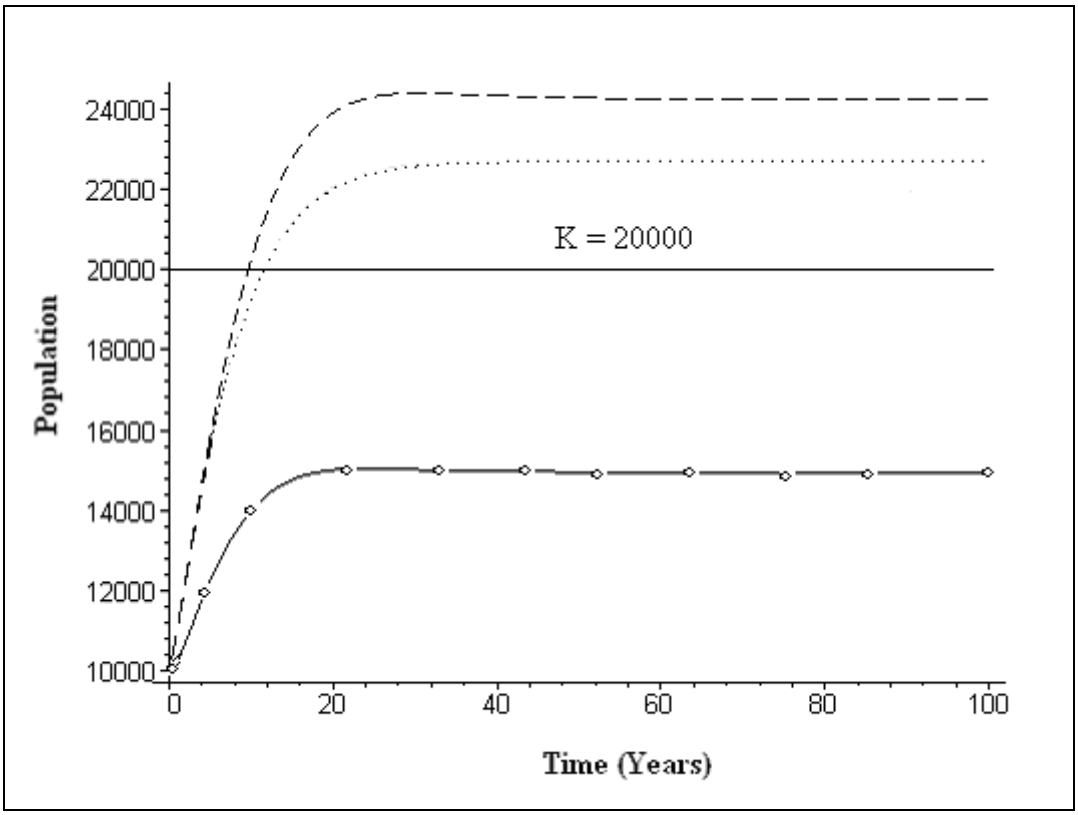

Fig.6.4. Variation of population with time for different demographic states

(Here ..... when all the immigrants are susceptibles, - - - - when some of the immigrants are infected and -∘-∘- for logistically growing population)

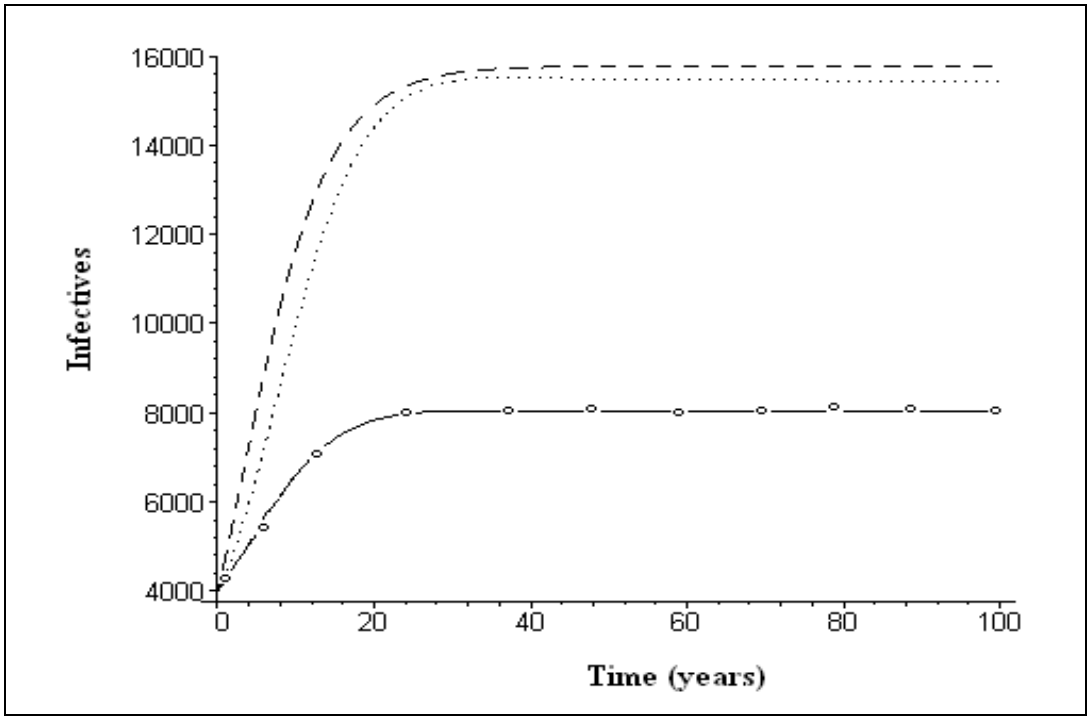

Fig.6.5. Variation of infective population with time for different demographic states

(Here ..... when all the immigrants are susceptibles, - - - - when some of the immigrants are infected and -∘-∘- for logistically growing population)

7. Model application to the Indian HIV data

To estimate and validate the models (3.1)-(3.3) and (5.4)-(5.6) by comparison with reported values for the HIV positive cases in India, we use the following parameter values.

Table 7.1. Parameter values for validation of model (3.1)-(3.3)

Parameter	Symbol	Values
Natural mortality rate of individuals per year	d	0.02
Movement rate of HIV infective individuals	δ	0.1
AIDS related death rate	α	1
Contact rate of susceptibles with HIV infectives	β_1	0.4

Most of the parameter values used in simulation are adopted from previously published articles while others are estimated intuitively. The unit of parameters is in per year. We also use initial values for simulation [12, 15, 17, 18, 23]

$N(0)$ =100000000, adult population that were found in 1990, as initial population size,

$I(0)$= 200000, number of reported HIV positives at the end of 1990,

$A(0)$= 57, number of AIDS cases reported HIV positives at the end of 1990,

Q_0 = 2000000, yearly immigrated adult persons (estimated from $N\,d = Q_0$ [15])

Table 7.2.Reported HIV positive cases (Approx.) in millions by year: 1990-2005 [23]

Year	1990	1994	1998	1999	2000	2001	2002	2003	2005
HIV+	0.2	1.75	3.5	3.7	3.86	3.97	4.58	5.1	5.7

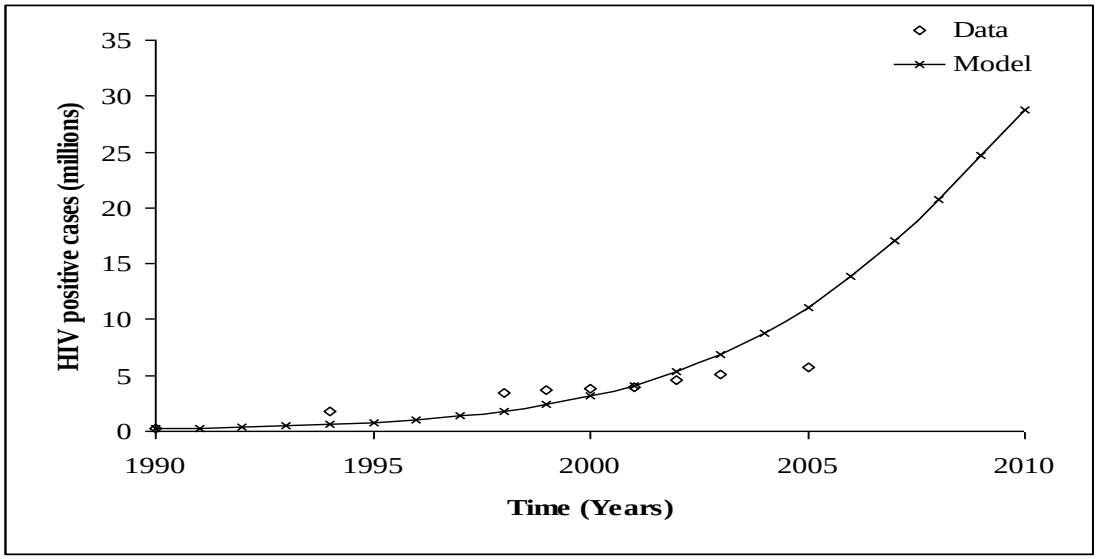

Fig. 7.1. HIV positive cases in India

In the Fig.7.1, the result of the simulation are displayed where we can see that the trend of data as reported in Table 7.2 and the curve representing estimated values given by the model for HIV infected persons using the above parameter values. From the Fig.7.1, it is seen that approximately 28 millions people would be living with HIV/AIDS by 2010.

Now to validate the model (5.4)-(5.6) we use same parameter values, given in the Table 7.1 and convex constant (a) = 0.7, growth rate constant (r) = 0.2 and carrying capacity (K) = 600000000.

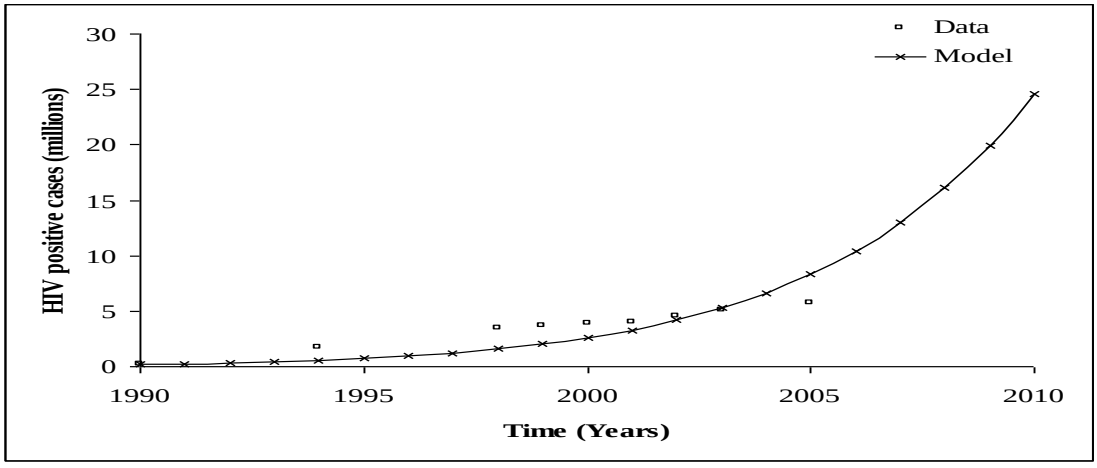

Fig. 7.2. HIV positive cases in India

From the Fig.7.2, it is seen that the number of HIV infected persons estimated by the model, for the same set of parameter values that are given in the Table 7.1, are closer to the reported Indian HIV data. From the Fig.7.2, it is observed that up to 25 millions people would live with HIV/AIDS by 2010. This result match with the National AIDS Control Organization (2002) [23] which also suggested that in India approximately 25 million people will live with HIV/AIDS by 2010.

8. Conclusion

In this paper we have proposed a nonlinear mathematical model which has been analyzed to encompass various well known growth forms describing different demographic states. These states denote the population growth when all the immigrants are susceptible, when some of the immigrants are infected and when the population has density dependent structure. We found a threshold quantity in terms of basic reproduction number for the models with different demographics. If the basic reproduction number is less than or equal to one, the disease-free equilibrium is locally asymptotically stable. If it is greater than one, a unique endemic equilibrium exists which is globally asymptotically stable in the interior of the feasible region, so that the disease persists in the population if it is initially present.

The model application for Indian HIV data is also given and it seems that for logistically growing population model, the future prediction of HIV in India gives nearly closer result to the NACO prediction [23].

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