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DETERMINISTIC MODELING FOR HIV AND AIDS EPIDEMICS WITH VIRAL LOAD DETECTABILITY

PETER EMEDA TENGAA[1,*], SAMUEL MWALILI[2], GEORGE OTIENO ORWA[3]

[1]Department of Mathematics and Statistics, Pan African University Institute of Basic Sciences Technology and Innovation, Nairobi, Kenya

[2]Department of Statistics and Actuarial Sciences, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

[3]Department of Mathematics and Statistics, Bomet University College, Bomet, Kenya

Abstract. We proposed and analyzed a nonlinear ordinary differential equation model for HIV and AIDS epidemics with viral load detectability and derived the interaction mechanisms between model compartments. The model is studied qualitatively and obtain a threshod parameter that represents the largest eigenvalue by using next-generation approach. Furthermore, local and global stability conditions for disease free and endemic equilibria are determined, similarly, we perfomed birfucation analysis and sensitivity analysis of the model. In addition, using the numerical results, we showed the condition on which the disease can die out ($R_0^d < 1$) and also when the disease invade the population ($R_0^d > 1$). Lastly, the results showed that people living with HIV to lower the viral loads to Undetectable level by taking the prescribed dozes as shown in Figure (7) resulting to viral suppression.

Keywords: HIV and AIDS model; viral load detectability; stability; birfucation; numerical simulation.

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*Corresponding author
E-mail address: emedason@gmail.com
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1. INTRODUCTION

Human Immunodeficiency Virus (HIV), is the virus that causes Acquired Immunodeficiency Syndrome (AIDS). HIV targets and infecting immune cells, the type of white blood cells called CD4+T cells which protects human from illness. HIV gradually destroys the immune system until it fails to fight against other infections. With deterioration of the immune system of the body, then the body develops opportunistic infections such as pneumonia, meningitis, cancers and others of the like that leads to Acquired Immune Deficiency Syndrome (AIDS) [17]. HIV and AIDS epidemics still remains at the forefront of public health burdens facing developing countries. Since the first cases of AIDS were identified in 1981, the number of HIV infected people and AIDS deaths per year has continued to rise rapidly. Globally it is estimated that 37.9 million people living with HIV at the end of 2018 and 24.5 million people were receiving Antiretroviral Therapy (ART) till the end of 2018. Worldwide, between 25% to 50% of patients do not take their medications as recommended, this is after drug resistant test which shows the number of viral load coppies in their blood [19]. The mathematical models have received much attention from researchers after pioneering work of Kermack and Mckendrick contributing to the mathematical theory of epidemics [10]. A lot of studies have been done to study HIV and AIDS epidemic transmission dynamics, some of them are [9, 18, 20] while on other hand several schoolars has extended HIV models to include control strategies to obtain the optimality of the strategies such studies are [15, 16], also other scholars has gone further to investigate the co-infection of HIV and other diseases and study the effects of each other in a population [1, 2, 3, 11]. People who take ART daily as prescribed and achieve and maintain an undetectable viral load have effectively no risk of sexually transmitting the virus to an HIV negative partner [7]. The use of ART improves the health of people living with HIV, therefore we need to lower the viral load rate in order to increase undetectable viral load population into the model. However, to the best of our knowledge, no one has investigated on HIV and AIDS models incorporating detectable viral load and undetectable viral load. Therefore, in this paper, HIV and AIDS model is well formulated by including the viral load detectability. The paper is arranged as follows:- In Section 2, we described and formulated the model using Ordinary Differential Equation (ODE)

system with assumptions. In Section 3, we investigate the quantitative analysis of the model such as invariant region, positivity of the solution, stability analysis , bifurcation analysis and sensitivity analysis. Section 4 shows the numerical solution of the model and lastly in Section 5 showed a concluding remarks.

2. PRELIMINARIES

2.1. Model formulation and descriptions. The model divides the total population N_t into five subclasses according to their disease status. Susceptibe individuals (S(t)) indicates HIV susceptibles, Infected individuals (I(t)) represent positive HIV individuals who are not showing AIDS symptoms, AIDS individuals on ARVTs (A(t)) indicates AIDS patients on ART, Detectable viral load individuals (D(t)) represents HIV and AIDS detectable viral load individuals and Undetectable viral load individuals (U(t)) represents HIV and AIDS undetectable viral load individuals. The S(t) class is increased from constant recruitment (Λ). However, frequency dependent transmission is assumed and individuals from S(t) move to I(t) with force of infection $\lambda = \beta \frac{I}{N(t)}$, where β is the rate of transmission between S(t) and I(t). The HIV positive individuals not yet showing AIDS symptoms I(t) can be increase by the proportion $(1-\rho)$ from infected mothers who give birth to infected children, also I(t) can progress to AIDS symptoms class and join the AIDS patients on antiretroviral therapy class A(t) with a rate of θ_1. Moreover, AIDS patients on antiretroviral therapy class A(t) after failure of therapy they can either join detectable viral load class D(t) with detectable viral load rate of ψ or can join undetectable viral load class U(t) with a viral load rate of $(1-\psi)$.

In turn with HIV and AIDS viral load test or drug resistance tests while also HIV replicates at an extremely rapid rate then individuals in detectable viral load class D(t) can be treated with a rate θ_2 and individuals in undetectable viral load class U(t) can be treated with a rate of θ_3 to move back to AIDS patients on antiretroviral therapy class A(t). In all compartments μ is the natural mortality rate while α is the death due to HIV and AIDS infected individuals. The above model description can be represented diagrammatically with schematic flow diagram as in Figure (1).

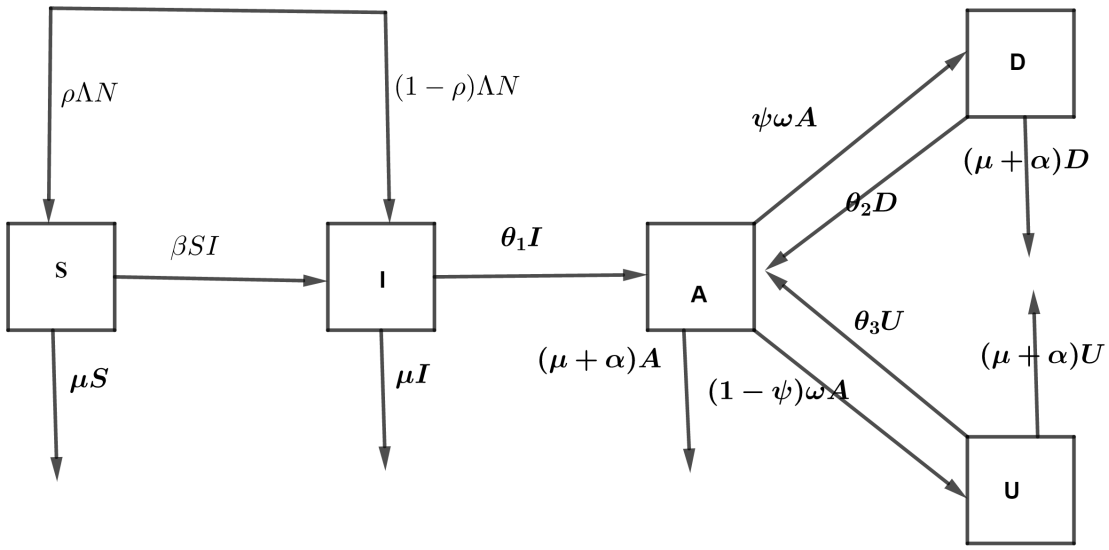

FIGURE 1. Flow diagram for basic HIV and AIDS with viral load detectability

Basing on assumptions made and relationship that exists between variables shown in Figure (1), the five ordinary differential equations that describes the dynamics of HIV and AIDS is given as follows:

$$
\begin{cases}
\dfrac{\mathrm{d}S}{\mathrm{d}t} &= \rho\Lambda N - \mu s(t) - \frac{\beta SI}{N} \\
\dfrac{\mathrm{d}I}{\mathrm{d}t} &= (1-\rho)\Lambda N + \frac{\beta SI}{N} - (\mu+\theta_1)I(t) \\
\dfrac{\mathrm{d}A}{\mathrm{d}t} &= \theta_1 I(t) + \theta_2 D(t) + \theta_3 U(t) - (\mu+\alpha+\omega)A(t) \\
\dfrac{\mathrm{d}D}{\mathrm{d}t} &= \psi\omega A(t) - (\mu+\alpha+\theta_2)D(t) \\
\dfrac{\mathrm{d}U}{\mathrm{d}t} &= (1-\psi)\omega A(t) - (\mu+\alpha+\theta_3)U(t)
\end{cases}
\tag{2.1}
$$

with initial condition $S(0) = S_0$, $I(0) = I_0$, $A(0) = A_0$, $D(0) = D_0$, $U(0) = U_0$ By adding the state equations in (2.1) we end up with rate of change of population as

$$
\begin{aligned}
\frac{\mathrm{d}N}{\mathrm{d}t} &= \frac{\mathrm{d}S}{\mathrm{d}t} + \frac{\mathrm{d}I}{\mathrm{d}t} + \frac{\mathrm{d}A}{\mathrm{d}t} + \frac{\mathrm{d}D}{\mathrm{d}t} + \frac{\mathrm{d}U}{\mathrm{d}t} \\
\frac{\mathrm{d}N}{\mathrm{d}t} &= (\Lambda-\mu)N - \alpha(A+D+U)
\end{aligned}
\tag{2.2}
$$

2.2. Normalization of the Model. The model (2.1) can easily be analyzed after being normalized such that the total population proportion is one. The normalization is done by scaling the population of each compartment by the total population. We transform the actual proportions by setting:

$$s = \frac{S}{N}, i = \frac{I}{N}, a = \frac{A}{N}, d = \frac{D}{N}, u = \frac{U}{N} \tag{2.3}$$

where by $s+i+a+d+u=1$, substituting (2.3) into (2.2) we end up with

$$\frac{\mathrm{d}N}{\mathrm{d}t} = [(\Lambda-\mu)-\alpha(a+d+u)]N \tag{2.4}$$

Thus, the nondimensionalized system of equations becomes:

$$\begin{cases} \frac{\mathrm{d}s}{\mathrm{d}t} = \rho\Lambda - [\beta i + \Lambda - \alpha(a+d+u)]s \\ \frac{\mathrm{d}i}{\mathrm{d}t} = (1-\rho)\Lambda + [\beta s - \theta_1 - \Lambda + \alpha(a+d+u)]i \\ \frac{\mathrm{d}a}{\mathrm{d}t} = \theta_1 i + \theta_2 d + \theta_3 u - [\alpha + \omega + \Lambda - \alpha(a+d+u)]a \\ \frac{\mathrm{d}d}{\mathrm{d}t} = \psi\omega a - [\alpha + \theta_2 + \Lambda - \alpha(a+d+u)]d \\ \frac{\mathrm{d}u}{\mathrm{d}t} = (1-\psi)\omega a - [\alpha + \theta_3 + \Lambda - \alpha(a+d+u)]u \end{cases} \tag{2.5}$$

subject to condition $s+i+a+d+u=1$. All the feasible solutions of system (2.5) enters the region of biological interest defined by

$$\Omega = \left\{(s,i,a,d,u) \in \Re_+^5 : s+i+a+d+u = 1\right\}$$

that is positive invariant solution. We consider the dynamics of the flow generated by system (2.5) in Ω. In this region, therefore the model (2.5) is considered to be both biologically and mathematically well posed.

3. Qualitative Analysis

3.1. Invariant Region. The solutions of the system (2.5) is uniformly bounded in the proper subset $\Omega \in \Re_+^5$, then the total population at any time t is given by $s+i+a+d+u=1$, then

from (2.4) we get:

$$\begin{aligned}
\frac{\mathrm{d}N}{\mathrm{d}t} &= [(\Lambda-\mu)-\alpha(a+d+u)]N,\\
\frac{\mathrm{d}N}{\mathrm{d}t} &\le (\Lambda-\mu)N \quad \text{if there is no death from HIV}\\
\frac{\mathrm{d}N}{N} &\le (\Lambda-\mu)dt \quad \text{separating variables}\\
\int\frac{\mathrm{d}N}{N} &\le \int(\Lambda-\mu)dt \quad \text{integrating both sides}\\
\ln|N| &\le (\Lambda-\mu)t\\
N &\le \exp(\Lambda-\mu)t\\
N &\le \exp(\Lambda-\mu)t \longrightarrow 1 \quad \text{as} \quad t\longrightarrow\infty
\end{aligned} \tag{3.1}$$

$\therefore$ The population size $N \longrightarrow 1$ and hence, $\Omega = \left\{(s,i,a,d,u)\in\Re_+^5 : 0\le N\le 1\right\}$, thus all the solution set of (2.5) is bounded in Ω.

3.2. Positivity of the solutions. We need to show that the model equtions in (2.5) has nonnegative solutions, this due to fact that human populations can not be negative.Therefore, we need to pose the conditions under which the model being studied has non-negative solutions.

Theorem 3.1. Let $\Omega = \left\{(s,i,a,d,u)\in\Re_+^5 : s_0>0, i_0>0, a_0>0, d_0>0, u_0>0\right\}$ then the solution of $\Omega = \{(s,i,a,d,u)\}$ are positive for $t\ge 0$.

Considering first equation of (2.5) we have:

Proof.

$$\begin{aligned}
\frac{\mathrm{d}s}{\mathrm{d}t} &= \rho\Lambda-[\beta i+\Lambda-\alpha(a+d+u)]s,\\
\frac{\mathrm{d}s}{\mathrm{d}t} &\ge -\Lambda s,\\
\frac{\mathrm{d}s}{s} &\ge -\Lambda dt \quad \text{separating variables}\\
\int\frac{\mathrm{d}s}{s} &\ge -\int\Lambda dt \quad \text{integrating both sides}\\
s(t) &\ge s_0\mathrm{e}^{-\Lambda t}\ge 0
\end{aligned} \tag{3.2}$$

Upon considering the second equation from (2.5) we have:

$$\begin{aligned}
\frac{\mathrm{d}i}{\mathrm{d}t} &= (1-\rho)\Lambda + [\beta s - \theta_1 - \Lambda + \alpha(a+d+u)]i, \\
\frac{\mathrm{d}i}{\mathrm{d}t} &\geq -(\theta_1+\Lambda)i, \\
\frac{\mathrm{d}i}{i} &\geq -(\theta_1+\Lambda)dt \quad \text{separating variables} \\
\int \frac{\mathrm{d}i}{i} &\geq -\int (\theta_1+\Lambda)dt \quad \text{integrating both sides} \\
i(t) &\geq i_0 \mathrm{e}^{-(\theta_1+\Lambda)t} \geq 0 \qquad (3.3)
\end{aligned}$$

The third, Fouth and fifth equation in similar manner becomes:

(3.4)

$$a(t) \geq a_0 \mathrm{e}^{-(\alpha+\omega+\Lambda)t} \geq 0, \quad d(t) \geq d_0 \mathrm{e}^{-(\alpha+\theta_2+\Lambda)t} \geq 0 \quad \text{and} \quad u(t) \geq u_0 \mathrm{e}^{-(\alpha+\theta_3+\Lambda)t} \geq 0$$

□

3.3. Existence of Disease Free Equilibrium. To obtain equilibrium points we equate model equations to zero, then the Disease Free Equilibrium (DFE) involves setting infected individuals to zero and solving for the non-infected variables. Let E_0 denotes the DFE then system (2.5) then the DFE is given follows:

$$\begin{aligned}
E_0 &= (s^0, i^0, a^0, d^0, u^0), \quad \text{for} \quad i = a = d = u = 0 \\
\frac{\mathrm{d}s}{\mathrm{d}t} &= \rho\Lambda - (\beta i + \Lambda - \alpha(a+d+u))s = 0 \\
\Rightarrow s = \rho \Longrightarrow \quad E^0 &= (\rho, 0, 0, 0, 0) \qquad (3.5)
\end{aligned}$$

3.4. Basic Reproduction Number. In this subsection we obtained the threshold parameter that governs the spread of the disease, most epidemic models have a threshold which determines the diseases ability to establish itself or clear from the population. Therefore R_0^d for the system of equation (2.5) will be obtained as follows:

The model equations are re-written by starting with newly infective group of individuals:

$$\frac{\mathrm{d}i}{\mathrm{d}t} = (1-\rho)\Lambda + [\beta s - \theta_1 - \Lambda + \alpha(a+d+u)]i$$
$$\frac{\mathrm{d}a}{\mathrm{d}t} = \theta_1 i + \theta_2 d + \theta_3 u - [\alpha + \omega + \Lambda - \alpha(a+d+u)]a$$
$$\frac{\mathrm{d}d}{\mathrm{d}t} = \psi\omega a - [\alpha + \theta_2 + \Lambda - \alpha(a+d+u)]d$$

f_i : appearance rate for new infection in i compartment, then

$$f_i = \begin{bmatrix} \beta si & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

The Jacobian matrix of f_i at DFE is given by $F_i = \dfrac{\partial f_i}{\partial(i,a,d)}|_{(E_0)}$

$$F_i = \begin{bmatrix} \beta\rho & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \tag{3.6}$$

If v_i : net transition between compartment i, v_i^- : transfers rate into the compartment i, v_i^+ : transfers rate out of the compartment i. The transfer of individuals into/out of the compartment i is given by $v_i = v_i^- - v_i^+$

$$v_i = \begin{bmatrix} (\theta_1+\Lambda)i + (1-\rho)\Lambda + \alpha(a+d+u)i \\ (\alpha+\omega+\Lambda)a - (\alpha(a+d+u)a + \theta_1 i + \theta_2 d + \theta_3 u) \\ (\alpha+\theta_2+\Lambda)i - (\alpha(a+d+u)d + \psi\omega a) \end{bmatrix}$$

The Jacobian matrix of v_i at DFE is given by $V_i = \dfrac{\partial v_i}{\partial(i,a,d)}|_{(E_0)}$

$$V_i = \begin{bmatrix} (\theta_1+\Lambda) & 0 & 0 \\ \theta_1 & \alpha+\omega+\Lambda & \theta_2 \\ 0 & \psi\omega & (\alpha+\theta_2+\Lambda) \end{bmatrix}$$

By using Next Generation Method (NGM) we obtain R_0^d which is given as:

$$G = F_i V_i^{-1} = \left(\frac{\partial f_i}{\partial (i,a,d)} |_{(E_0)} \right) \left(\frac{\partial v_i}{\partial (i,a,d)} |_{(E_0)} \right)^{-1}$$

$$G = \begin{pmatrix} \frac{\beta\rho}{\theta_1+\Lambda} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \Longrightarrow G = \frac{\beta\rho}{(\theta_1+\Lambda)} \tag{3.7}$$

Therefore, reproduction number $R_0^d = \dfrac{\beta\rho}{(\theta_1+\Lambda)}$. When a single infective in an entirely susceptible population is introduced with propotion of HIV free individuals ρ it becomes infective and makes β transmission rates per unit time. The rate of transmission(β) and propotion of HIV free individuals ρ multiplied by average infective period ($\dfrac{1}{(\theta_1+\Lambda)}$) for infective class. This is the threshold quantity which determines the diseases ability to establish itself or clear from the population. If $R_0^d < 1 \Rightarrow \dfrac{\beta\rho}{(\theta_1+\Lambda)} < 1$, therefore HIV and AIDS in model (2.1) clear from the population, hence the disease will fade away. While in turn if $R_0^d > 1 \Rightarrow \dfrac{\beta\rho}{(\theta_1+\Lambda)} > 1$ then, HIV and AIDS in model (2.5) establishes itself from the population, hence the disease will grow up.

3.5. Local stability of disease free equilibrium.

Theorem 3.2. The DFE point is locally asymptotically stable if $R_0^d < 1$ and unstable if $R_0^d > 1$.

Proof. To prove local stability of DFE, we obtained the Jacobian matrix (variational matrix) of the system of differential equations (2.5) at DFE(E_0) as:

$$J|_{(E_0)} = \begin{pmatrix} -\Lambda & \beta-\rho & \alpha\rho & \alpha\rho & \alpha\rho \\ 0 & \beta\rho-\theta_1-\Lambda & 0 & 0 & 0 \\ 0 & \theta_1 & -\alpha-\Lambda-\omega & \theta_2 & \theta_3 \\ 0 & 0 & \psi\omega & -\alpha-\theta_2-\Lambda & 0 \\ 0 & 0 & (1-\psi)\omega & 0 & -\alpha-\theta_3-\Lambda \end{pmatrix} \tag{3.8}$$

The system (3.8) has five eigenvalues since we have a 5×5 matrix. We note that one of the eigenvalue is $\lambda^\star = -\Lambda$, then the other eiegenvalues can be found as follows:

$$J|_{(E_0)} = \begin{pmatrix} \beta\rho - \theta_1 - \Lambda & 0 & 0 & 0 \\ \theta_1 & -\alpha - \Lambda - \omega & \theta_2 & \theta_3 \\ 0 & \psi\omega & -\alpha - \theta_2 - \Lambda & 0 \\ 0 & (1-\psi)\omega & 0 & -\alpha - \theta_3 - \Lambda \end{pmatrix} \tag{3.9}$$

The determinant of (3.8) will be as:

$$|J|_{(E_0)} - \lambda^\star I| = 0$$

$$\begin{vmatrix} \beta\rho - \theta_1 - \Lambda - \lambda^\star & 0 & 0 & 0 \\ \theta_1 & -\alpha - \Lambda - \omega\lambda^\star & \theta_2 & \theta_3 \\ 0 & \psi\omega & -\alpha - \theta_2 - \Lambda - \lambda^\star & 0 \\ 0 & (1-\psi)\omega & 0 & -\alpha - \theta_3 - \Lambda - \lambda^\star \end{vmatrix} = 0$$

The characteristic equation is given as:

$$p(\lambda^\star) = \lambda^{\star 4} + a_1\lambda^{\star 3} + a_2\lambda^{\star 2} + a_3\lambda^\star + a_4 = 0$$

where

$$a_1 = 3\alpha - \beta\rho + \theta_1 + \theta_2 + \theta_3 + 4\Lambda + \omega > 0$$

$$a_2 = \omega(2\alpha - \beta\rho + 3\Lambda) + 3(\alpha + \Lambda)(\alpha - \beta\rho + 2\Lambda)$$

$$\theta_3 + (2\alpha - \beta\rho + 3\Lambda + \psi\omega) + \theta_2(2\alpha - \beta\rho + \theta_3 + 3\Lambda - \psi\omega + \omega)$$

$$+ \theta_1(3(\alpha + \Lambda) + \theta_2 + \theta_3 + \omega)$$

$$a_3 = (\alpha + \Lambda)(\omega(\alpha - 2\beta\rho + 3\Lambda) + (\alpha + \Lambda)(\alpha - 3\beta\rho + 4\Lambda))$$

$$\theta_3 + (\psi\omega(\alpha - \beta\rho + 2\Lambda) + (\alpha + \Lambda)(\alpha - 2\beta\rho + 3\Lambda)) +$$

$$\theta_2\left(\alpha^2 + \theta_3(\alpha - \beta\rho + 2\Lambda + \psi\omega - \psi\omega) + \alpha(-2\beta\rho + 4\Lambda - \psi\omega + \omega) - 2\Lambda(\beta\rho + \psi\omega - \omega) + \beta\rho(\psi\omega - \omega) + 3\Lambda^2\right)$$

$$+ \theta_1(\theta_3(2(\alpha + \Lambda) + \psi\omega) + \theta_2(2\alpha + \theta_3 + 2\Lambda - \psi\omega + \omega) + (\alpha + \Lambda)(3(\alpha + \Lambda) + 2\omega))$$

$$a_4 = -\beta\rho + \theta_1 + \Lambda\mathbb{K}$$

$$\mathbb{K} = (\alpha+\Lambda)\left(\theta_3(\alpha+\Lambda+\psi\omega)+(\alpha+\Lambda)(\alpha+\Lambda+\omega)\right)$$

$$+\theta_2\left(\theta_3(\alpha+\Lambda+\psi\omega-\psi\omega)+(\alpha+\Lambda)(\alpha+\Lambda-\psi\omega+\omega)\right)$$

The necessary and sufficient condition for local stability of the system (3.9) is that all the eigenvalues of 4×4 have negative real part. By using Routh-Hurwitz Criteria the following underlying conditions should be satisfies :

$$\begin{cases} \text{Condition 1}: \quad a_1 > 0, a_3 > 0 \quad \text{and} \quad a_4 > 0 \\ \text{Condition 2}: \quad a_1a_2a_3 > a_3^2 + a_1^2a_4 > 0 \end{cases}$$

$$\begin{aligned} \text{Consider} \quad a_4 > 0 \Longrightarrow \quad & (-\beta\rho + \theta_1 + \Lambda)\mathbb{K} > 0 \\ & (\theta_1+\Lambda)\left(-\frac{\beta\rho}{(\theta_1+\Lambda)}+1\right)\mathbb{K} > 0 \\ & (\theta_1+\Lambda)(-R_0+1)\mathbb{K} > 0 \\ & -(\theta_1+\Lambda)(R_0-1)\mathbb{K} > 0 \\ & (\theta_1+\Lambda)(R_0-1)\mathbb{K} < 0 \\ \Longrightarrow a_4 > 0 \quad & \text{iff} \quad \mathbb{K} < 0 \end{aligned}$$

Similarly, $a_1 > 0$ and $a_3 > 0$ and $a_1a_2a_3 > a_3^2 + a_1^2a_4 > 0$. Thus, the DFEof (2.5) is Locally Asymptotically Stable (LAS) as the two conditions above are satisfied. □

3.6. Global stability of disease free equilibrium.

Theorem 3.3. The DFE is Globally Asymptotically Stable (GAS) in the feasible region if $R_0^d < 1$

Proof. To prove this theorem, we use theorem by [5] and we first required to write system of equation (2.1) as follows:

$$\begin{cases} \dfrac{\mathrm{d}X}{\mathrm{d}t} &= M(X,Z) \\ \dfrac{\mathrm{d}Z}{\mathrm{d}t} &= N(X,Z), \quad N(X,0)=0 \end{cases} \tag{3.10}$$

where $X \in \Re^1_+$ is the uninfected components including S(t) and $Z \in \Re^4_+$ denotes infected components including I(t), A(t), D(t) and U(t) with $E^0 = (X^*, 0)$ denotes the DFE of the system. The two conditions H1 and H2 must be met to guarantee GAS:

$$\begin{cases} \text{H1}: & \dfrac{\mathrm{d}X}{\mathrm{d}t} &= M(X,0), X^* \quad \text{is GAS.} \\ \text{H2}: & N(X,Z) &= G(X,Z)Z - \hat{N}(X,Z) \geq 0, \quad \text{for} \quad (X,Z) \in \Omega \end{cases} \tag{3.11}$$

where $G = \dfrac{\partial N}{\partial Z}|_{(X^*,0)}$ is an M-matrix (are the off diagonal elements of G which are non negative) and Ω is the region where the model makes biological sense. □

Theorem 3.4. The fixed point $E^0 = (X^*, 0)$ is a globally asymptotically stable equilibrium of system (2.1) provided that $R_0^d < 1$ and the assumptions H1 and H2 are satisfied.

Proof. From system of (2.5) we have $X = s$ (Uninfected) and $Z = i, a, d, u$ (Infected). Upon considering Uninfected compartment, we have

$$\begin{aligned} M(X,Z) &= \frac{\mathrm{d}X}{\mathrm{d}t} = \frac{\mathrm{d}s}{\mathrm{d}t} \\ M(X,Z) &= \frac{\mathrm{d}s}{\mathrm{d}t} = \rho\Lambda - [\beta i + \Lambda - \alpha(a+d+u)]s \\ \Rightarrow \frac{\mathrm{d}s}{\mathrm{d}t} &= \rho\Lambda - \Lambda s_t \end{aligned}$$

By using separation of variables, the solution becomes

$$\begin{aligned} \int_0^t \frac{ds}{\rho\Lambda - \Lambda s_t} &= \int_0^t dt \\ \Longrightarrow s(t) &= \rho + s_0 \mathrm{e}^{-\Lambda t} \\ \lim_{t \longrightarrow \infty} s(t) &= \rho + \lim_{t \longrightarrow \infty} s_0 \mathrm{e}^{-\Lambda t} \end{aligned} \tag{3.12}$$

Thus, as $t \longrightarrow \infty$ then $s(t) \longrightarrow \rho = X^*$ for, $s_0 = 0$. Hence, we conclude that the system (2.5) is GAS at the equilibrium $(\rho, 0)$, therefore H1 is satisfied.

Upon considering infected compartment, matrix $N(X;Z)$ is given by

$$N(X,Z) = \frac{\mathrm{d}Z}{\mathrm{d}t} = \frac{\mathrm{d}(i,a,d,u)}{\mathrm{d}t} = \begin{pmatrix} (1-\rho)\Lambda + [\beta s - \theta_1 - \Lambda + \alpha(a+d+u)]i \\ \theta_1 i + \theta_2 d + \theta_3 u - [\alpha + \omega + \Lambda - \alpha(a+d+u)]a \\ \psi\omega a - [\alpha + \theta_2 + \Lambda - \alpha(a+d+u)]d \\ (1-\psi)\omega a - [\alpha + \theta_3 + \Lambda - \alpha(a+d+u)]u \end{pmatrix} \tag{3.13}$$

Taking partial derivative with respect to $Z(i,a,d,u)$ to get G at equalibrium poin $X^*, 0$, we have

$$G = \frac{\partial N}{\partial Z}|_{(X^*,0)} = \begin{pmatrix} -\theta_1 - \Lambda + \beta\rho & 0 & 0 & 0 \\ \theta_1 & -\alpha - \Lambda - \omega & \theta_2 & \theta_3 \\ 0 & \psi\omega & -\alpha - \theta_2 - \Lambda & 0 \\ 0 & (1-\psi)\omega & 0 & -\alpha - \theta_3 - \Lambda \end{pmatrix}$$

From (3.11), to show H2:

$$N(X,Z) = G(X,Z)Z - \hat{N}(X,Z) \geq 0, \quad \text{for} \quad (X,Z) \in \Omega$$

$$\hat{N}(X,Z) = \begin{pmatrix} -\theta_1 - \Lambda + \beta\rho & 0 & 0 & 0 \\ \theta_1 & -\alpha - \Lambda - \omega & \theta_2 & \theta_3 \\ 0 & \psi\omega & -\alpha - \theta_2 - \Lambda & 0 \\ 0 & (1-\psi)\omega & 0 & -\alpha - \theta_3 - \Lambda \end{pmatrix} \begin{pmatrix} i \\ a \\ d \\ u \end{pmatrix} -$$

$$\begin{pmatrix} (1-\rho)\Lambda + [\beta s - \theta_1 - \Lambda + \alpha(a+d+u)]i \\ \theta_1 i + \theta_2 d + \theta_3 u - [\alpha + \omega + \Lambda - \alpha(a+d+u)]a \\ \psi\omega a - [\alpha + \theta_2 + \Lambda - \alpha(a+d+u)]d \\ (1-\psi)\omega a - [\alpha + \theta_3 + \Lambda - \alpha(a+d+u)]u \end{pmatrix}$$

$$\hat{N}(X,Z) = \begin{pmatrix} (-\theta_1 - \Lambda + \beta\rho)i \\ \theta_1 i - (\alpha+\Lambda+\omega)a + \theta_2 d + \theta_3 u \\ \psi\omega a - (\alpha+\theta_2+\Lambda)d \\ (1-\psi)\omega a - (\alpha+\theta_3+\Lambda)u \end{pmatrix} - \begin{pmatrix} (1-\rho)\Lambda + [\beta s - \theta_1 - \Lambda + \alpha(a+d+u)]i \\ \theta_1 i + \theta_2 d + \theta_3 u - [\alpha+\omega+\Lambda-\alpha(a+d+u)]a \\ \psi\omega a - [\alpha+\theta_2+\Lambda-\alpha(a+d+u)]d \\ (1-\psi)\omega a - [\alpha+\theta_3+\Lambda-\alpha(a+d+u)]u \end{pmatrix}$$

$$\hat{N}(X,Z) = \begin{pmatrix} -(1-\rho) - \alpha i(a+d+u) \\ -\alpha a(a+d+u) \\ -\alpha d(a+d+u) \\ -\alpha u(a+d+u) \end{pmatrix} = - \begin{pmatrix} (1-\rho) + \alpha i(a+d+u) \\ \alpha a(a+d+u) \\ \alpha d(a+d+u) \\ \alpha u(a+d+u) \end{pmatrix}$$

Hence, we observe that $\hat{N}(X,Z)$ is less than zero. Thus, H2 is not satisfied. Hence, E_0 may not be globally asymptotically stable. □

3.7. Existance of Endeimic Equilibrium. The endemic equilibrium point (E^*) is defined as a steady state solutions for the model (2.5), and this occurs when there is a persistence of the disease and it is obtained by equating the system of equation (2.5) to zero. Upon considering first equation of model (2.5) making s in terms of others and let $z^* = \Lambda - \alpha(a+d+u)$ gives:

$$s^* = \frac{1}{z}\left[\frac{\beta\Lambda \pm \sqrt{\left(\beta\Lambda(\rho-1) - \beta\rho\Lambda + z^2 + \theta_1 z\right)^2 - 4\beta\Lambda(\rho-1)z(\theta_1+z)} + z^2 + \theta_1 z}{2\beta}\right] \tag{3.14}$$

Similarly on considering second equation of model (2.5) and making i in terms of others becomes:

$$i^* = -\frac{-\beta\Lambda + \sqrt{(-\beta\Lambda + z^2 + \theta_1 z)^2 - 4\beta\Lambda(\rho-1)z(\theta_1+z)} + z^2 + \theta_1 z}{2\beta(\theta_1+z)} \tag{3.15}$$

Considering third equation from model (2.5) and making a in terms of others we have:

$$a^* = \frac{\theta_1 i(\alpha+\theta_2+z)(\alpha+\theta_3+z)}{\theta_2(\theta_3(\alpha+\psi\omega-\psi\omega+z)+(\alpha+z)(\alpha-\psi\omega+\omega+z))+(\alpha+z)(\theta_3(\alpha+\psi\omega+z)+(\alpha+z)(\alpha+\omega+z))} \tag{3.16}$$

Moreover upon considering fourth and fifth equation in model (2.5), we have

$$d^* = \frac{\theta_1 i\psi\omega(\alpha+\theta_3+z)}{-\theta_2(\theta_3(\alpha+\psi\omega-\psi\omega+z)+(\alpha+z)(\alpha-\psi\omega+\omega+z))-(\alpha+z)(\theta_3(\alpha+\psi\omega+z)+(\alpha+z)(\alpha+\omega+z))} \tag{3.17}$$

$$u^* = \frac{\theta_1 i(\psi-1)\omega(\alpha+\theta_2+z)}{\theta_2(\theta_3(\alpha+\psi\omega-\psi\omega+z)+(\alpha+z)(\alpha-\psi\omega+\omega+z))+(\alpha+z)(\theta_3(\alpha+\psi\omega+z)+(\alpha+z)(\alpha+\omega+z))} \tag{3.18}$$

Considering the system (2.5) with a force of infection $\lambda^* = \beta i^*$, where i^* is an endemic equilibrium given in equation (3.15). The polynomial will be written as:

$$2\beta(\theta_1+z)\lambda^* + \left(z^2+\theta_1 z-\beta\Lambda \pm \sqrt{(-\beta\Lambda+z^2+\theta_1 z)^2-4\beta\Lambda(\rho-1)z(\theta_1+z)}\right) = 0$$

$$p(\lambda^*) = H_0\lambda^* + H_1 = 0 \tag{3.19}$$

The normalized system of differential equation (2.5) have the endemic equilibrium E^* if $R_0^d > 1$ as satisfied by cases [3 and 4] in table (1). Also the ODE system (2.5) has more than one equilirium point if $R_0^d < 1$ as indicated in table (1) cases [1 and 3].

TABLE 1. Possible roots of polynomial (3.19) when $R_0^d > 1$ and $R_0^d < 1$

Cases	H_1	H_2	R_0^d	**No. of sign changes**	**No. of positive roots**
1	+	+	$R_0^d < 1$	0	0
3	+	-	$R_0^d > 1$	1	1
3	-	+	$R_0^d < 1$	1	1
4	-	-	$R_0^d > 1$	0	0

3.8. The global stability of the endemic equilibrium.

Theorem 3.5. If $R_0^d > 1$, the endemic equilibrium (E^*) of the model (2.5) is globally asymptotically stable.

Proof. To prove the GAS of the endemic equilibrium, we use the method of Lyapunov functions and choose the following Lyapunov function candidate

$$V(s,i,a,d,u) = \left(s-s^*-s^*\ln(\frac{s^*}{s})\right) + \left(i-i^*-i^*\ln(\frac{i^*}{i})\right) + \left(a-a^*-a^*\ln(\frac{a^*}{a})\right) + \left(d-d^*-d^*\ln(\frac{d^*}{d})\right) + \left(u-u^*-u^*\ln(\frac{u^*}{u})\right) \tag{3.20}$$

By direct calculating the time derivative of V along the solutions of the equation (2.1) gives:

$$\frac{\mathrm{d}V}{\mathrm{d}t} = \frac{\partial V}{\partial s}\frac{\mathrm{d}s}{\mathrm{d}t} + \frac{\partial V}{\partial i}\frac{\mathrm{d}i}{\mathrm{d}t} + \frac{\partial V}{\partial a}\frac{\mathrm{d}a}{\mathrm{d}t} + \frac{\partial V}{\partial d}\frac{\mathrm{d}d}{\mathrm{d}t} + \frac{\partial V}{\partial u}\frac{\mathrm{d}u}{\mathrm{d}t}$$

$$\frac{\mathrm{d}V}{\mathrm{d}t} = \left(\frac{s-s^*}{s}\right)\frac{\mathrm{d}s}{\mathrm{d}t} + \left(\frac{i-i^*}{i}\right)\frac{\mathrm{d}i}{\mathrm{d}t} + \left(\frac{a-a^*}{a}\right)\frac{\mathrm{d}a}{\mathrm{d}t} + \left(\frac{d-d^*}{d}\right)\frac{\mathrm{d}d}{\mathrm{d}t} + \left(\frac{u-u^*}{u}\right)\frac{\mathrm{d}u}{\mathrm{d}t}$$

$$\begin{aligned}\frac{\mathrm{d}V}{\mathrm{d}t} &= \left(\frac{s-s^*}{s}\right)(\rho\Lambda - [\beta i + \Lambda - \alpha(a+d+u)]s) \\ &+ \left(\frac{i-i^*}{i}\right)((1-\rho)\Lambda + [\beta s - \theta_1 - \Lambda + \alpha(a+d+u)]i) \\ &+ \left(\frac{a-a^*}{a}\right)(\theta_1 i + \theta_2 d + \theta_3 u - [\alpha + \omega + \Lambda - \alpha(a+d+u)]a) \\ &+ \left(\frac{d-d^*}{d}\right)(\psi\omega a - [\alpha + \theta_2 + \Lambda - \alpha(a+d+u)]d) \\ &+ \left(\frac{u-u^*}{u}\right)((1-\psi)\omega a - [\alpha + \theta_3 + \Lambda - \alpha(a+d+u)]u)\end{aligned}$$

$$\begin{aligned}\frac{\mathrm{d}V}{\mathrm{d}t} &= \left(\frac{s-s^*}{s}\right)(\rho\Lambda + \alpha(a+d+u)s) - \left(\frac{s-s^*}{s}\right)(\beta i + \Lambda)s + \\ &\left(\frac{i-i^*}{i}\right)(\Lambda + (\beta s + \alpha(a+d+u))i) - \left(\frac{i-i^*}{i}\right)(\rho\Lambda + (\theta_1 + \Lambda)i) + \\ &\left(\frac{a-a^*}{a}\right)(\theta_1 i + \theta_2 d + \theta_3 u + \alpha(a+d+u)a) - \left(\frac{a-a^*}{a}\right)(\alpha + \omega + \Lambda)a + \\ &\left(\frac{d-d^*}{d}\right)(\psi\omega a + \alpha(a+d+u)d) - \left(\frac{d-d^*}{d}\right)(\alpha + \theta_2 + \Lambda)d + \\ &\left(\frac{u-u^*}{u}\right)(\omega a + \alpha(a+d+u)u) - \left(\frac{u-u^*}{u}\right)(\psi\omega a + (\alpha + \theta_3 + \Lambda)u)\end{aligned}$$

$$\begin{aligned}\text{Let} \quad P &= \left(\frac{s-s^*}{s}\right)(\rho\Lambda + \alpha(a+d+u)s) + \left(\frac{i-i^*}{i}\right)(\Lambda + (\beta s + \alpha(a+d+u))i) + \\ &\left(\frac{a-a^*}{a}\right)(\theta_1 i + \theta_2 d + \theta_3 u + \alpha(a+d+u)a) + \left(\frac{d-d^*}{d}\right)(\psi\omega a + \alpha(a+d+u)d) + \\ &\left(\frac{u-u^*}{u}\right)(\omega a + \alpha(a+d+u)u) \quad \text{(Positive)}\end{aligned}$$

$$\begin{aligned}\text{Let} \quad Q &= -\left(\frac{s-s^*}{s}\right)(\beta i + \Lambda)s - \left(\frac{i-i^*}{i}\right)(\rho\Lambda + (\theta_1 + \Lambda)i) - \left(\frac{a-a^*}{a}\right)(\alpha + \omega + \Lambda)a - \\ &\left(\frac{d-d^*}{d}\right)(\alpha + \theta_2 + \Lambda)d - \left(\frac{u-u^*}{u}\right)(\psi\omega a + (\alpha + \theta_3 + \Lambda)u) \quad \text{(Negative)} \\ &\Longrightarrow \frac{\mathrm{d}V}{\mathrm{d}t} = P - Q\end{aligned}$$

Thus if $P-Q<0 \Longrightarrow P<Q$, then $\frac{\mathrm{d}V}{\mathrm{d}t}<0$ (Negative definite), and it follows that $\frac{\mathrm{d}V}{\mathrm{d}t}=0$ iff $s=s^*,i=i^*,a=a^*,d=d^* and u=u^*$. Therefore the largest compact invariant set in $\left\{(s^*,i^*,a^*,d^*,u^*)\in\Omega:\frac{\mathrm{d}V}{\mathrm{d}t}=0\right\}$ is the singleton E^*, where by E^* is the endemic equilibrium of the system (2.5). By LaSalles invariant principle [12], it implies that E^* is globally asymptotically stable in Ω if $P<Q$. □

3.9. Determination of Backward Bifurcation. To explore the possibility of backward or forward bifurcation of the model system (2.5) we use the centre manifold method which was introduce by Castillo Chavez [5] and is done by renaming the state variables as follows: Let $s=x_1,i=x_2,a=x_3,d=x_4,u=x_5 \Longrightarrow x=(x_1,x_2,x_3,x_4,x_5)$ It then follows that

$$\frac{\mathrm{d}x}{\mathrm{d}t}=F(x),\quad \text{where}\quad F(x)=(f_1,f_2,f_3,f_4,f_5)^T$$

the renamed eqution becomes:

$$\left\{\begin{array}{l} f_1=\dfrac{\mathrm{d}x_1}{\mathrm{d}t}=\rho\Lambda-[\beta x_2+\Lambda-\alpha(x_3+x_4+x_5)]x_1 \\ f_2=\dfrac{\mathrm{d}x_2}{\mathrm{d}t}=(1-\rho)\Lambda+[\beta x_1-\theta_1-\Lambda+\alpha(x_3+x_4+x_5)]x_2 \\ f_3=\dfrac{\mathrm{d}x_3}{\mathrm{d}t}=\theta_1 x_2+\theta_2 d+\theta_3 u-[\alpha+\omega+\Lambda-\alpha(x_3+x_4+x_5)]x_3 \\ f_4=\dfrac{\mathrm{d}x_4}{\mathrm{d}t}=\psi\omega x_3-[\alpha+\theta_2+\Lambda-\alpha(x_3+x_4+x_5)]x_4 \\ f_5=\dfrac{\mathrm{d}x_5}{\mathrm{d}t}=(1-\psi)\omega x_3-[\alpha+\theta_3+\Lambda-\alpha(x_3+x_4+x_5)]x_5 \end{array}\right. \tag{3.21}$$

where $x_1+x_2+x_3+x_4+x_5=1$ The Jacobian system of model (3.21) becomes:

$$\mathscr{J}=\begin{pmatrix} -\Lambda & -\beta x_1 & \alpha x_1 & \alpha x_1 & \alpha x_1 \\ 0 & -\theta_1-\Lambda+\beta x_1 & 0 & 0 & 0 \\ 0 & \theta_1 & -\alpha-\Lambda-\omega & \theta_2 & \theta_3 \\ 0 & 0 & \psi\omega & -\alpha-\theta_2-\Lambda & 0 \\ 0 & 0 & (1-\psi)\omega & 0 & -\alpha-\theta_3-\Lambda \end{pmatrix} \tag{3.22}$$

The Jacobian system of model at the disease free (3.21) becomes:

$$\mathscr{J}|_{(E_0=\rho)} = \begin{pmatrix} -\Lambda & -\beta\rho & \alpha\rho & \alpha\rho & \alpha\rho \\ 0 & -\theta_1-\Lambda+\beta\rho & 0 & 0 & 0 \\ 0 & \theta_1 & -\alpha-\Lambda-\omega & \theta_2 & \theta_3 \\ 0 & 0 & \psi\omega & -\alpha-\theta_2-\Lambda & 0 \\ 0 & 0 & (1-\psi)\omega & 0 & -\alpha-\theta_3-\Lambda \end{pmatrix} \tag{3.23}$$

Suppose that β is a bifurcation parameter and assume it takes place at $\beta = \beta^\star$, then the system (3.23) is linearized at the DFE point when reproduction number of HIV and AIDS model is at R_0^d=1.

$$R_0 = \frac{\beta\rho}{\theta_1+\Lambda} = 1 \Longrightarrow \beta^\star = \frac{\theta_1+\Lambda}{\rho} \tag{3.24}$$

The Jacobian of transformed system (3.21) has simple zero eigenvalue at $\beta = \beta^\star$. This gives us a way foward to study dynamics of system (3.21) and analyse the system near $\beta = \beta^\star$ by using Center Manifold theory by Carr and Muncaster [4]. The Jacobean matrix near $\beta = \beta^\star$ has a right eigenvector associated with the zero eigenvalue which is given by the component $\mathbf{w} = (w_1, w_2, w_3, w_4, w_5)^T$ and computed by using relation $\mathscr{J}_{(E_0=\rho)}.\mathbf{w} = 0$ which results into:

$$\begin{pmatrix} -\Lambda & -\beta\rho & \alpha\rho & \alpha\rho & \alpha\rho \\ 0 & -\theta_1-\Lambda+\beta\rho & 0 & 0 & 0 \\ 0 & \theta_1 & -\alpha-\Lambda-\omega & \theta_2 & \theta_3 \\ 0 & 0 & \psi\omega & -\alpha-\theta_2-\Lambda & 0 \\ 0 & 0 & (1-\psi)\omega & 0 & -\alpha-\theta_3-\Lambda \end{pmatrix} \begin{pmatrix} w_1 \\ w_2 \\ w_3 \\ w_4 \\ w_5 \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{3.25}$$

Then the eigen vector of the system (3.25) becomes,

$$\begin{cases} -\Lambda w_1 - \beta\rho w_2 + \alpha\rho w_3 + \alpha\rho w_4 + \alpha\rho w_5 & = 0 \\ (-\theta_1 - \Lambda + \beta\rho) w_2 & = 0 \\ \theta_1 w_2 - (\alpha + \Lambda + \omega) w_3 + \theta_2 w_4 + \theta_3 w_5 & = 0 \\ \psi\omega w_3 - (\alpha + \theta_2 + \Lambda) w_4 & = 0 \\ (1-\psi)\omega w_3 - (\alpha + \theta_3 + \Lambda) w_5 & = 0 \end{cases} \tag{3.26}$$

Solving system of equation (3.26) we get

$$w_1 = \frac{\alpha\rho}{\Lambda}\left\{\frac{\psi\omega}{(\alpha+\theta_2+\Lambda)} + \frac{(1-\psi)\omega}{(\alpha+\theta_3+\Lambda)} + \alpha\rho\right\} w_3 \tag{3.27}$$

$$w_2 = 0 \tag{3.28}$$

$$w_3 = \frac{\theta_2 w_4 + \theta_3 w_5}{(\alpha+\Lambda+\omega)} > 0 \quad \text{is free} \tag{3.29}$$

$$w_4 = \frac{\psi\omega w_3}{(\alpha+\theta_2+\Lambda)} \tag{3.30}$$

$$w_5 = \frac{(1-\psi)\omega w_3}{(\alpha+\theta_3+\Lambda)} \tag{3.31}$$

We then proceed on computing the components of vector $\mathbf{v} = (v_1, v_2, v_3, v_4, v_5)^T$ by considering

$$\mathscr{J}|^T_{(E_0=\rho)} \cdot \mathbf{v} = 0$$

$$\begin{pmatrix} -\Lambda & 0 & 0 & 0 & 0 \\ -\beta\rho & -\theta_1 - \Lambda + \beta\rho & \theta_1 & 0 & 0 \\ \alpha\rho & 0 & -\alpha - \Lambda - \omega & \psi\omega & (1-\psi)\omega \\ \alpha\rho & 0 & \theta_2 & -\alpha - \theta_2 - \Lambda & 0 \\ \alpha\rho & 0 & \theta_3 & 0 & -\alpha - \theta_3 - \Lambda \end{pmatrix} \begin{pmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \\ v_5 \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{3.32}$$

Then the eigen vector of the system (3.32) becomes,

$$\begin{cases} -\Lambda v_1 & = 0 \\ -\beta\rho v_1 + (-\theta_1 - \Lambda + \beta\rho)v_2 + \theta_1 v_3 & = 0 \\ \alpha\rho v_1 - (\alpha+\omega+\Lambda)v_3 + \psi\omega v_4 + (1-\psi)\omega v_5 & = 0 \\ \alpha\rho v_1 + \theta_2 v_3 - (\alpha+\theta_2+\Lambda)v_4 & = 0 \\ \alpha\rho v_1 + \theta_3 v_3 - (\alpha+\theta_2+\Lambda)v_5 & = 0 \end{cases} \tag{3.33}$$

Solving system of equation (3.26) we get

$$v_1 = 0 \tag{3.34}$$

$$v_2 = \frac{\theta_1}{(-\theta_1 - \Lambda + \beta\rho)} v_3 \tag{3.35}$$

$$v_3 = \frac{\psi\omega v_4 + (1-\psi)\omega v_5}{(\alpha+\omega+\Lambda)} > 0 \quad \text{is free} \tag{3.36}$$

$$v_4 = \frac{\theta_2}{(\alpha+\theta_2+\Lambda)} v_3 \tag{3.37}$$

$$v_5 = \frac{\theta_3}{(\alpha+\theta_3+\Lambda)} v_3 \tag{3.38}$$

To compute **a** and **b** we use a formula the formular

$$\mathbf{a} = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(s_0,0,0,0,0) \quad \text{and} \quad \mathbf{b} = \sum_{k,i,j=1}^{n} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta^\star}(s_0,0,0,0,0) \tag{3.39}$$

Since $v_1 = 0$, then we compute **a** for values of $k = 2,3,4$ and 5, then system of equations (3.21) becomes:

$$\begin{cases} f_2 = (1-\rho)\Lambda + [\beta x_1 - \theta_1 - \Lambda + \alpha(x_3+x_4+x_5)]x_2 \\ f_3 = \theta_1 x_2 + \theta_2 d + \theta_3 u - [\alpha+\omega+\Lambda-\alpha(x_3+x_4+x_5)]x_3 \\ f_4 = \psi\omega x_3 - [\alpha+\theta_2+\Lambda-\alpha(x_3+x_4+x_5)]x_4 \\ f_5 = (1-\psi)\omega x_3 - [\alpha+\theta_3+\Lambda-\alpha(x_3+x_4+x_5)]x_5 \end{cases} \tag{3.40}$$

By computing associated non zero second order partial derivatives at the DFE point at $\beta = \beta^\star$ we have;

$$\frac{\partial^2 f_2}{\partial x_1 \partial x_2} = \beta^\star, \frac{\partial^2 f_2}{\partial x_2 \partial x_3} = \frac{\partial^2 f_2}{\partial x_2 \partial x_4} = \frac{\partial^2 f_2}{\partial x_2 \partial x_5} = \alpha \tag{3.41}$$

$$\frac{\partial^2 f_3}{\partial x_3 \partial x_4} = \frac{\partial^2 f_3}{\partial x_3 \partial x_5} = \frac{\partial^2 f_4}{\partial x_3 \partial x_4} = \frac{\partial^2 f_4}{\partial x_3 \partial x_5} = \frac{\partial^2 f_5}{\partial x_3 \partial x_5} = \frac{\partial^2 f_5}{\partial x_4 \partial x_5} = \alpha \tag{3.42}$$

therefore

$$\mathbf{a} = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}$$

$$\mathbf{a} = v_2(\beta w_1 w_2 + \alpha w_2 w_3 + \alpha w_2 w_4 + \alpha w_2 w_5) +$$

$$v_3(\alpha w_3 w_4 + \alpha w_3 w_5) + v_4(\alpha w_3 w_4 + \alpha w_3 w_5) + v_5(\alpha w_3 w_5 + \alpha w_4 w_5)$$

$$\mathbf{a} = \beta^\star v_2 w_1 w_2 + \alpha[v_2(w_2 w_3 + w_2 w_4 + w_2 w_5) + v_3(\alpha w_3 w_4 + \alpha w_3 w_5)$$

$$+ v_4(\alpha w_3 w_4 + \alpha w_3 w_5) + v_5(\alpha w_3 w_5 + \alpha w_4 w_5)]$$

$$\mathbf{a} = \beta^\star v_2 w_1 w_2 + \alpha \mathscr{Q}$$

where

$$\mathscr{Q} = [v_2(w_2 w_3 + w_2 w_4 + w_2 w_5) + v_3(\alpha w_3 w_4 + \alpha w_3 w_5) + v_4(\alpha w_3 w_4 + \alpha w_3 w_5) + v_5(\alpha w_3 w_5 + \alpha w_4 w_5)]$$

Suppose, $\mathscr{Q} > 0$ and $w_2 \neq 0$, then $\mathbf{a} > 0$. Similarly, computing for b we need to find the second order partial derivatives of f_2, f_3, f_4 and f_5 with respect to x_i and $\beta^\star$ at the DFE point

$$\mathbf{b} = \sum_{k,i,j=1}^{n} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta^\star} \Longrightarrow \mathbf{b} = v_2 w_2 \rho > 0 \quad \text{if} \quad w_2 \neq 0$$

If $\mathbf{b}$ is positive, it follows that the sign of $\mathbf{a}$ determines the local dynamics around the DFE for $\beta = \beta^\star$ system (3.21) will undergo backward bifurcation.

Theorem 3.6. The HIV and AIDS model system (3.21) with viral load detectability exhibits backward bifurcation at $R_0^d = 1$ whenever $\mathbf{a}$ is positive otherwise it will exhibit a forward bifurcation at $R_0^d = 1$.

3.10. Sensitivity Analysis of the Model parameters. We carried out the sensitivity analysis to determine the model robustness to parameter values. This is to helpe us to identify the parameters that have a high impact on the reproductive number. he normalized forward sensitivity index of a variable to a parameter is a ratio of the relative change in the variable to the relative change in the parameter. Given that $R_0^d = \frac{\beta\rho}{(\theta_1+\Lambda)}$, then by using parameters in table (3), $(\Lambda = 0.8, \theta_1 = 0.6, \beta = 0.1, \rho = 0.7)$, then we have

$$S_\beta^{R_0^d} = \frac{\partial R_0^d}{\partial \beta} * \frac{\beta}{R_0^d} = 1 > 0 \tag{3.43}$$

$$S_\Lambda^{R_0^d} = \frac{\partial R_0^d}{\partial \Lambda} * \frac{\Lambda}{R_0^d} = -\frac{\Lambda}{\Lambda+\theta_1} = -0.5714 < 0 \tag{3.44}$$

$$S_{\theta_1}^{R_0^d} = \frac{\partial R_0^d}{\partial \theta_1} * \frac{\theta_1}{R_0^d} = -\frac{\theta_1}{\Lambda+\theta_1} = -0.4286 < 0 \tag{3.45}$$

$$S_\rho^{R_0^d} = \frac{\partial R_0^d}{\partial \rho} * \frac{\rho}{R_0^d} = 1 > 0 \tag{3.46}$$

TABLE 2. Sensitivity indices for basic reproduction number

Parameter	Descriptions	Sensitivity indices
β	The transmission rate, probability of getting infected	1
ρ	Proportion that joins Suceptible class	1
θ_1	Transfer rate from I(t) to A(t)	-0.4286
Λ	Recruitment rate	-0.5714

Table (2) shows the sensitivity indices of R_0^d to the parameters for the HIV and AIDS model with viral load detectability, evaluated at the baseline parameter values given in table (3). The parameters are ordered from most sensitive to least, the most sensitive parameter is the transmission rate β and ρ while the least sensitive parameter recruitment rateΛ and θ_1 . This result implies that, when the parameters β is increased keeping other parameters constant they increase the value of R_0^d thus, they increase the endemicity of the disease as they have positive indices then they lead to spreading of the diseases. Whilest the negative sensitive indices they are much more effective for disease control.

4. Numerical Simulations

In this section, we performed numerical simulation for HIV and AIDS with Viral Load (VL) detectability by using the parameter values given in table (3).

TABLE 3. Parameter values for HIV and AIDS model with viral load detectability

Parameter symbol	Values	Source
ρ	0.7	[6]
Λ	0.8	[13]
β	0.1	[8]
θ_1	0.6	[14]
θ_2	0.2	Assumed
θ_3	0.3	Assumed
α	0.33	Assumed
ω	0.4	Assumed
ψ	0.3	Assumed

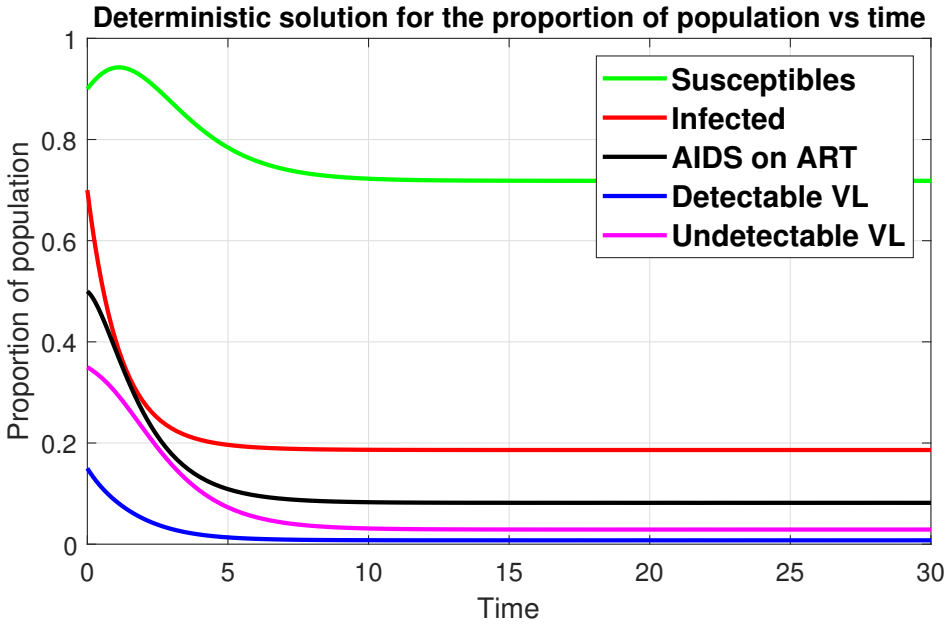

FIGURE 2. Variation of total number of population in five subclasses when $R_0^d = 0.0500 < 1$

4.1. Model solution. Figure (2) run the ODE model system (2.5) with parameters in table(3), initial conditions $(s_0, i_0, a_0, d_0, u_0 = 0.9, 0.7, 0.5, 0.15, 0.35)$ over 30 years. The Figure (2) shows

the long term variation of the total number population in all classes. It is clearly noted that the number of susceptible population decreases exponentially with time and then reaches its equilibrium position. This is due to fact that susceptible individuals interactig with Infective individuals they become Infected. Similarly number of infectives, AIDSs on ARVs, Undetectable viral load and detectable viral load population decreases with time and then reaches its equilibrium position. Therefore infection becomes less endemic in the population. The figure (2) clearly shows S(t) seems to outnumber all other classes of population, this is due to fact that the transmission rate is low and probaly the threshold parameter $R_0^d$is less tha unity. Considering figure (2), it is immediately clear that $R_0^d < 1$, means that each infected individual produces on average less than one new infected individuals, and therefore we predict that infectious will be fade out in a population. Using table (3) then we have

$$R_0^d = \frac{\beta\rho}{\theta_1 + \Lambda} = \frac{0.8 \times 0.7}{0.6 + 0.8} = 0.0500 \tag{4.1}$$

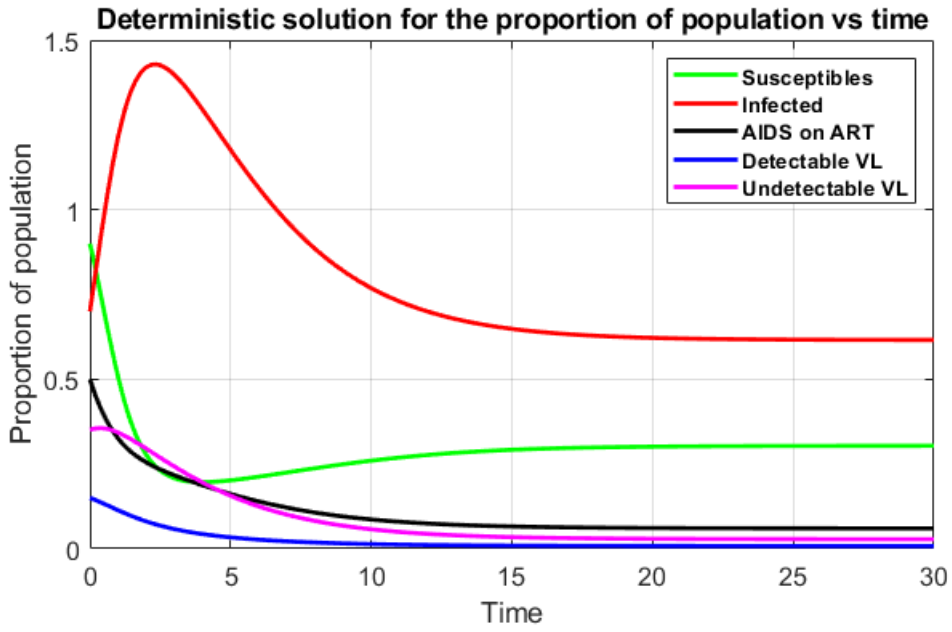

FIGURE 3. Variation of total number of population in five subclasses when $R_0^d = 1.2600 > 1$

Figure (3) shows the variation of total number of population when $R_0^d > 1$, it is when the infected population are able to invade the susceptible population. The figure clearly shows that the

Infected population (red color) outnumbers all other classes, indicating the increase in infected population. From table (3) when $\beta = 0.9$ and $\Lambda = 0.4$ gives the $R_0^d = 1.2600 > 1$.

4.2. Effects of varying transmission rate. Transimission rate (β) has much more impacts to susceptible individuals, Infected individuals and Individuals on treatment(ART).

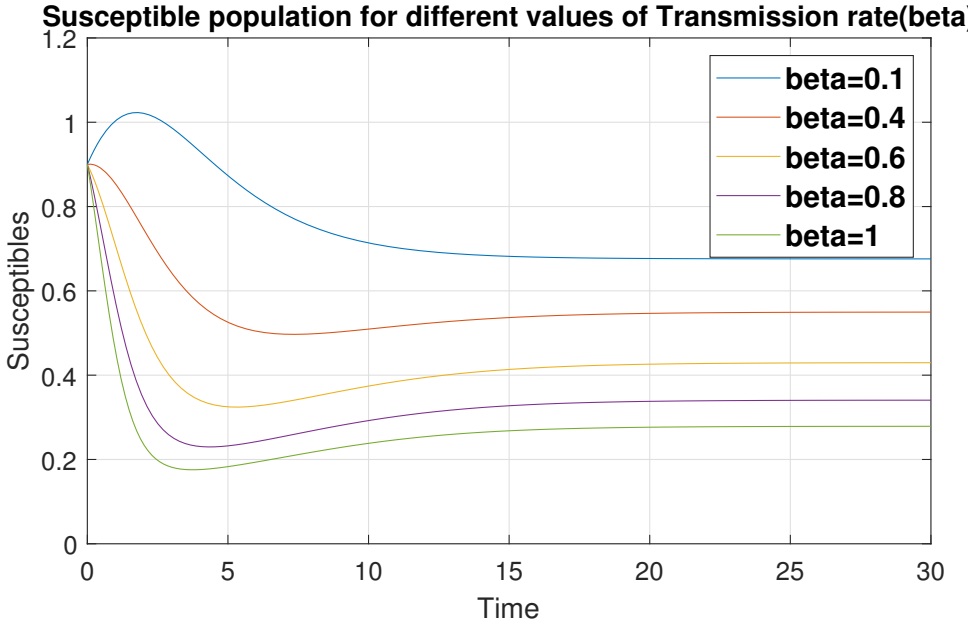

FIGURE 4. Effects of varying different values of β for S(t) population

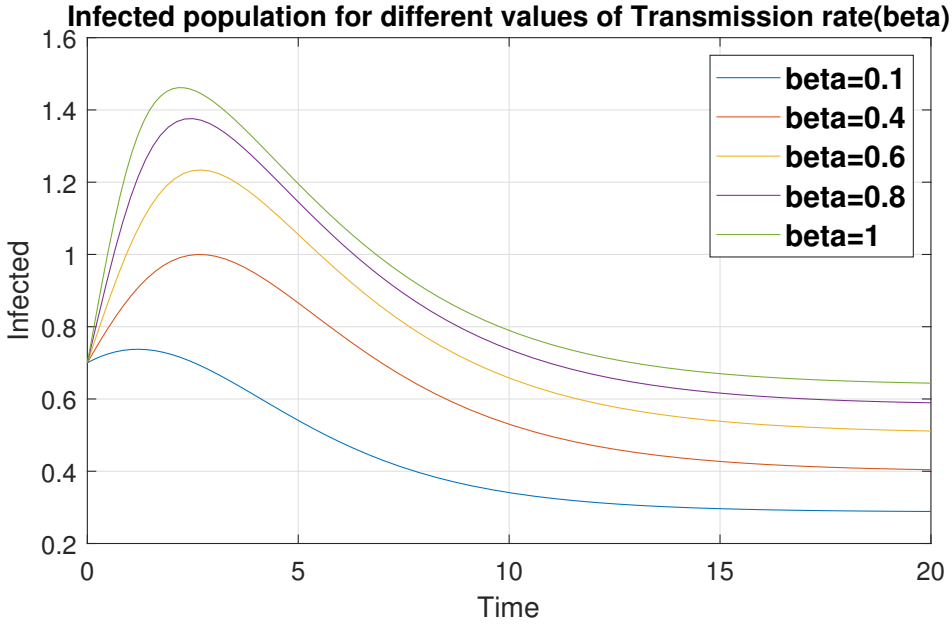

FIGURE 5. Effects of varying different values of β for I(t) population

Figure (4) and (5) illustrates the simulation of model (2.5) showing the effects of varying transmission rate β on S(t) and I(t) population over period of 20 years. The iniatial conditions used were ($s_0 = 0.9, i_0 = 0.7$) and parameter values used are from table (3).

In Figure (4), It is observed that, initially at $s(0) = 0.9$ we observed that when the rate of transmission is low say (β=0.1) then proportion of S(t) population is high as compared to when the rate of transmission is increasing say (β= 0.4, 0.6,0.8 and 1) then the proportion of S(t) population decrease exponentially to the constant equilibrium position. In Figure (5) it is observed that, when the rate transmission is high say ($\beta = 1, 0.8, 0.6, 0.4$) the Infected population increase and decreases when transmission rate $\beta = 0.1$.

4.3. Effects of varrying Viral Load rate. AIDS individuals on treatment can either join detectable VL class or Undetectable VL class if viral suppression rate (ω) is less than 1000 copies/ML. Therefore ψ indicate the proportion at which A(t) class joins D(t) class while $(1-\psi)$ indicates the proportion at which A(t) joins U(t) class.

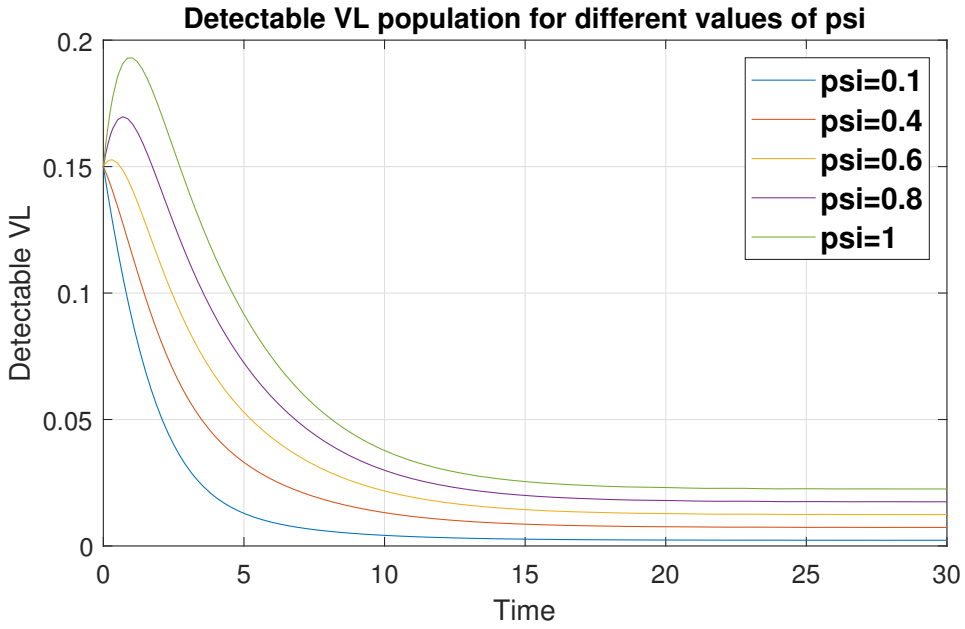

FIGURE 6. Time variation for different viral load rate ψ on D(t)

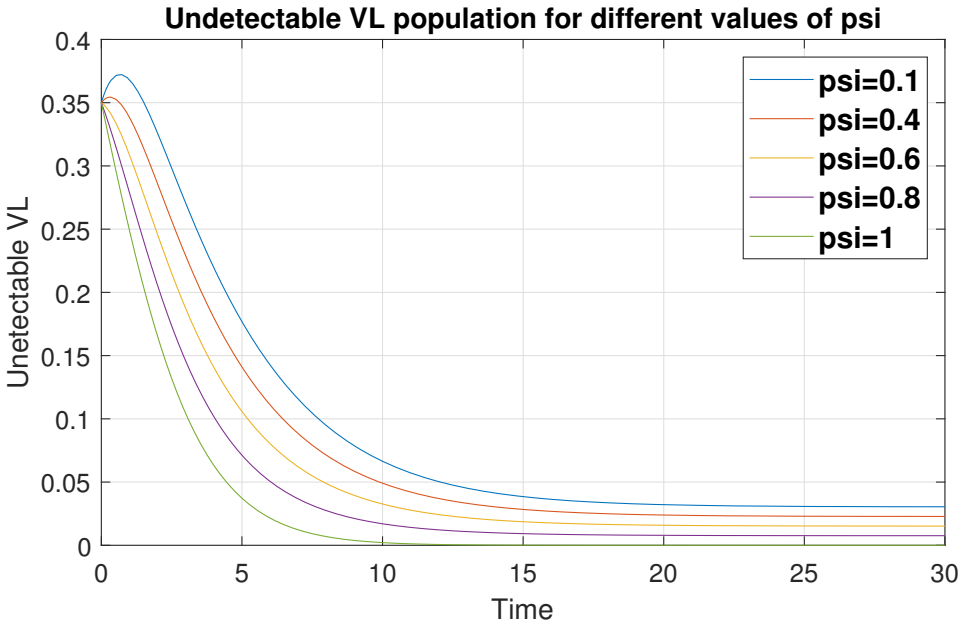

FIGURE 7. Time variation for different viral load rate ψ on U(t)

Figure (6) and (7) shows the variation of proportion of individuals onART joining Detectable and Undetectable classes respectively. The results revealed that when we increase the proportion of A(t) to join Detectable class with a viral load rate (say increase from ψ=0.4,0.6,0.8 to 1), then the D(t) will abruptly increase in number as compared to when the proportion is decreased(ψ=0.1). On other hand Figure (7) shows increasing value of ψ say ($\psi = 0.8 - 1$) decreases the number of U(t) and vise versa. Therefore when the viral load rate is high increases the D(t) while when the viral load rate is low increases the U(t).

5. CONCLUDING REMARKS

In this study, the deterministic nonlinear model for HIV and AIDS epidemic is developed using ODE and is subdivided into five compartments. In section (3) , the developed model of HIV and AIDS epidemic with viral load detectability is analyzed qualitatively i.e. invariant region of the models, positivity of the model solution, disease-free equilibrium, basic reproduction number, endemic equilibria, stability analysis of DFE, stability analysis of endemic equilibrium, bifurcation analysis is perfomed and model exhibits backward bifurcation. Similary sensitivity analysis of basic reproduction number was perfomed, the analysis shows that β and ρ are the most sensitive parameters in relation to reproduction number. In section (4), numerical simulation

is perfomed to confirm the analytical results, we investigated on the threshold parameter when it is less than unity ($R_0^d < 1$) as shown in Figure (2) and also when the threshold parameter is more than unity ($R_0^d > 1$) as shown in Figure (3). Moreover we analyzed the effects of variation of transmission rate (β) on S(t) and I(t) and effects of variation of viral load rate on D(t) and U(t). The results revealed that decreasing transmission rate (β) has a great contribution to bring down infection in the community whilest increasing transmission rate (β) leads to increasing infected in the community as in Figures [(4) and (5)]. Nevertheless, decreasing the viral load rate (ψ) has a contribution of decreasing the detectable viral load D(t) in the community whilest increasing viral load rate (ψ) leads to increase in detectable viral load individuals in the community as in Figures[(6) and (7)].

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CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

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