STABILITY ANALYSIS OF A STAGED PROGRESSION HIV/AIDS MODEL WITH SCREENING AND CONDOM USAGE

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Abstract

In this Paper, a staged-progression model for HIV/AIDS transmission dynamics is formulated and analyzed to study the impact of Screening, Condom usage and Condom compliance. The local stability for the disease free equilibrium (DFE) was proved for Rc < 1 and Kransnoselki sublinearity trick was used to show that the endemic equilibrium (EE) is locally asymptotically stable for a special case whenever Rc > 1. Numerical simulation was also carried out to investigate the effects of screening unaware (unscreened) asymptomatic individuals and Condom compliance. The result shows the influence of condom compliance and screening on the transmission dynamics of HIV/AIDS. The result clearly shows that increase in the compliance of Condom usage and increase of screening rate of HIV individuals reduces the total number of HIV/AIDS individuals. This point that increase in Condom usage and screening reduces HIV/AIDS burden.

Keywords: *HIV/AIDS, Staged progression, Screening, Condom*

1.0 Introduction

It is a well-known fact that the Human Immunodeficiency Virus (HIV) is a retroviral infection which leads to Acquired Immuno-Deficiency Syndrome (AIDS) is still a global public health problem since the first patients were identified in 1981. It is a deadly disease that essentially weakens the immune system by gradually infecting or killing the CD4+T−cells. This makes it difficult for the body to fight against opportunistic infections such as Cancer, Tuberculosis, Pneumonia and Meningitis. HIV has shown high degree of prevalence in population all over the world [12], since it was first identified in USA. Shortly after its detection AIDS became a global epidemic. About 90 percent of all HIV-infected people live in the developing countries [13].

The wide spread of HIV/AIDS continue to pose great threat to economic growth, through lowered productivity, reduced savings, overstretched of public expenditure exacerbated income inequality and increased poverty [3]. In view of all these, there are needs for HIV/AIDS to be controlled or eradicated. This study intend to show how awareness of HIV/AIDS status, condom

usage and condom compliance can be used to eliminate/reduce HIV/AIDS prevalence by improving the workdone by [1] by incorporating condom usage and condom compliance. This paper comprises 5 sections which are as follows: Section 1: Introduction, Section 2: Model Formulation, Section 3: Positivity of the Solution, Section 4: Equilibrium State and Stability Analysis of the Model, Section 5: Numerical Simulation and Discussion of Results and finally Section 6: Conclusion.

2.0 Model Formulation

The population of interest is with high HIV/AIDS prevalence due to heterosexual transmission. We classify the sexually active population into 7 classes. Susceptible S(t), Infected at asymptomatic stage but Unaware $I_{1A}(t)$, Infected at asymptomatic stage and aware $I_{2A}(t)$, Infected at symptomatic stage but unaware $I_{1S}(t)$, Infected at symptomatic stage and aware $I_{2S}(t)$, infected and receiving treatment $I_T(t)$, AIDS cases who are ill or showing AIDS symptoms $A(t)$ at time t. Thus the total sexually interacting adults' population is given by

$$N = S + I_{1A} + I_{2A} + I_{1S} + I_{2S} + I_T + A \quad (1)$$

It is assumed that at any moment in time, new recruits enter the sexually active population at a rate Q_0. Susceptible individuals acquire HIV infection following contact with HIV infected individuals at a rate given by

$$\lambda = \frac{(1-\varepsilon\alpha)[\beta_1(I_{1A} + \eta_1 I_{2A}) + \beta_2(I_{1S} + \eta_2 I_{2S})]}{N} \quad (2)$$

Table 2.1 Description of parameters

Parameters	Description	Nominal Value	References
Q_0	Recruitment rate	3,315,500	[10]
α_1	Rate of screening unaware (unscreened) asymptomatic individuals	(0,1)	Assumed
α_2	Rate of screening unaware (unscreened) symptomatic individuals	$q \propto_1$	Assumed
β_1	Effective contact rate for susceptible individuals asymptomatic	0.106	[6]
β_2	Effective contact rate for	0.5	[4]

	susceptible individuals symptomatic		
θ_1	Progression rate from unaware asymptomatic to unaware symptomatic stage	(0.14, 0.18)	[9]
θ_2	Progression rate from aware asymptomatic to aware symptomatic stage	0.01	[7]
η_1	Modification parameter associated to screened asymptomatic individuals	0.1	[7]
η_2	Modification parameter associated to screened symptomatic individuals	0.1	[7]
ϕ_1	Treatment rate for screened asymptomatic individuals	0.0655	[9]
ϕ_2	Treatment rate for screened symptomatic individuals	0.2	[11]
γ_1	Progression rate from unscreened symptomatic to full blown AIDS	0.7	[8]
γ_2	Progression rate from screened symptomatic to full blown AIDS	0.4	[2]
γ_3	Progression rate from treated compartment to full blown AIDS	0.13	[9]
μ	Natural death rate	0.02	[10]
δ	AIDS induced dead rate	0.333	[10]
ε	Condom efficacy	0.8	[5]
α	Condom compliance	(0,1)	[5]

q	Modification parameter associated with screening unaware (unscreened) asymptomatic individuals	[1,2]	Assumed

Table 2.2 Description of Variables

Variable	**Description**
S(t)	Susceptible Individuals
$I_{1A}(t)$	Infected at asymptomatic stage but Unaware
$I_{2A}(t)$	Infected at asymptomatic stage and aware
$I_{1S}(t)$	Infected at symptomatic stage but unaware
$I_{2S}(t)$	Infected at symptomatic stage and aware
$I_T(t)$	Infected and receiving treatment
$A(t)$	AIDS cases who are ill or showing AIDS symptoms.

Basic Assumptions for the model

The following assumptions were taken into account in the model construction

1. Individuals are only recruited into the susceptible class
2. The population varies with time and is homogenous
3. HIV individuals are aware of their status only when screened. Thus, it is logical to assume that treatment is administered to individuals only in I_{2A} and I_{2S}subpopulation.

Following the assumptions discussed above, the infection dynamics can be modelled by the following system of ODEs

$$\frac{ds}{dt} = Q_0 - \lambda S - \mu S$$

$$\frac{dI_{1A}}{dt} = \lambda S - (\mu + \theta_1 + \alpha_1) I_{1A}$$

$$\frac{dI_{2A}}{dt} = \alpha_1 I_{1A} - (\mu + \theta_2 + \phi_1) I_{2A}$$

$$\frac{dI_{1S}}{dt} = \theta_1 I_{1A} - (\mu + \alpha_2 + \gamma_1) I_{1S}$$

(3)

$$\frac{dI_{2S}}{dt} = \theta_2 I_{2A} + \alpha_2 I_{1S} - (\mu + \gamma_2 + \phi_2) I_{2S}$$

$$\frac{dI_T}{dt} = \phi_1 I_{2A} + \phi_2 I_{2S} - (\mu + \gamma_3) I_T$$

$$\frac{dA}{dt} = \gamma_1 I_{1S} + \gamma_2 I_{2S} + \gamma_3 I_T - (\mu + \delta) A$$

3.0 Positivity of the Solution

Since the model monitors changes in the human population, the variable and the parameter are assumed to be positive for all $t \geq 0$. System (3) will therefore be analyzed in a suitable region Ω of biological interest. We have the following lemma on the region system (3) is restricted to.

Lemma 3.1. The feasible region Ω defined by

$$\Omega = \left\{ (S, I_{1A}, I_{2A}, I_{1S}, I_{2S} I_T, I_A) \in \Re_+^z \middle| N \leq \frac{Q_0}{\mu} \right\}$$

With initial conditions $S(0) \geq 0,\ I_{1A}(0) \geq 0,\ I_{2A}(0) \geq 0,\ I_{1S}(0) \geq 0,\ I_{2S}(0) \geq 0,\ I_T(0) \geq 0,$ $I_A(0) \geq 0$, is positively invariant and attracting with respect to model (2) – (8) for all $t \geq 0$.

4.0 Equilibrium State and Stability Analysis of the Model

4.1 Existence of Equilibrium Point

At equilibrium,

$$\frac{dS}{dt} = \frac{dI_{1A}}{dt} = \frac{dI_{2A}}{dt} = \frac{dI_{1S}}{dt} = \frac{dI_{2S}}{dt} = \frac{dI_T}{dt} = \frac{dA}{dt} = \frac{dN}{dt} = 0$$

Thus system (3) becomes

$$0 = Q_0 - \lambda S - \mu S$$

$$
\begin{aligned}
0 &= \lambda S - K_1 I_{1A} \\
0 &= \alpha_1 I_{1A} - K_2 I_{2A} \\
0 &= \theta_1 I_{1A} - K_3 I_{1S} \\
0 &= \theta_2 I_{2A} + \alpha_2 I_{1S} - K_4 I_{2S} \\
0 &= \phi_1 I_{2A} + \phi_2 I_{2S} - K_5 I_T \\
0 &= \gamma_1 I_{1S} + \gamma_2 I_{2S} + \gamma_3 I_T - K_6 A \\
0 &= Q_0 - \mu N - \delta A
\end{aligned} \tag{4}
$$

Where

$$K_1 = \mu + \theta_1 + \alpha_1 \qquad K_2 = \mu + \theta_2 + \phi_1 \qquad K_3 = \mu + \alpha_2 + \gamma_1 \qquad K_4 = \mu + \gamma_2 + \phi_2$$

$$K_5 = \mu + \gamma_3 \qquad K_6 = \mu + \delta$$

4.2 Existence of Disease-free Equilibrium (DFE)

Let E_0 represent the equilibrium point at DFE. In the absence of infection and from (4). The model has its DFE given by

$$E_0 = (S^+, I_{1A}^+, I_{2A}^+, I_{1S}^+, I_{2S}^+, I_T^+, A^+) = \left(\frac{Q_0}{\mu}, 0, 0, 0, 0, 0, 0, 0 \right) \tag{5}$$

4.3 Effective Reproduction Number (R_c)

The effective reproduction number denoted by R_c of a model is defined as the total number of secondary infections caused by a typical infected individual in a completely susceptible population. Using the next generation matrix approach, on model (3) in the form of matrices F(non-negative) and V(non-singular). Where F denote the new infection terms

and V the transition term at E_0. Therefore the new infection and the transfer matrices of our model is given by

$$F=\begin{pmatrix} \beta_1(1-\varepsilon\alpha) & \beta_1(1-\varepsilon\alpha)\eta_1 & \beta_2(1-\varepsilon\alpha) & \beta_2(1-\varepsilon\alpha)\eta_2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V=\begin{pmatrix} K_1 & 0 & 0 & 0 & 0 & 0 \\ -\alpha_1 & K_2 & 0 & 0 & 0 & 0 \\ -\theta_1 & 0 & K_3 & 0 & 0 & 0 \\ 0 & -\theta_2 & -\alpha_2 & K_4 & 0 & 0 \\ 0 & -\phi_1 & 0 & -\phi_2 & K_5 & 0 \\ 0 & 0 & -\gamma_1 & -\gamma_2 & -\gamma_3 & K_6 \end{pmatrix}$$

We get R_c as follows

$$R_c=\rho(FV^{-1})=\frac{(1-\varepsilon\alpha)[\beta_1K_3K_4(K_2+\alpha_1\eta_1)+\beta_2[K_2K_4\theta_1+\eta_2(K_2\alpha_2\theta_1+K_3\alpha_1\theta_2)]]}{K_1K_2K_3K_4}$$

$$R_c=\frac{(1-\varepsilon\alpha)[\beta_1K_3K_4(K_2+\alpha_1\eta_1)+\beta_2(K_2K_4\theta_1+\eta_2B_1)]}{K_1K_2K_3K_4} \tag{6}$$

Where

$$B_1=K_2\alpha_2\theta_1+K_3\alpha_1\theta_2$$

4.4 Existence of Endemic Equilibrium Point (EEP)

In order to obtain the endemic equilibrium point of the model (3) (i.e, in the presence of infection, where at least one of the infected component of the model is non-zero). Let $E_1=(S^*, I_{1A}^*, I_{2A}^*, I_{1S}^*, I_{2S}^*, I_T^*, A^*)$ represents any arbitrary endemic equilibrium of the model (3). Solving equation (4) yield the following

$$S^*=\frac{Q_0(L_1-L_2)}{\mu L_1R_0-\mu L_2} \qquad \text{where} \quad L_1=K_1K_2K_3K_4K_5K_6 \qquad L_2=\delta B_3$$

$$I_{1A}^*=\frac{\mu Q_0L_1(R_0-1)}{K_1(\mu L_1R_0-\mu L_2)} \qquad I_{2A}^*=\frac{\mu Q_0L_1\alpha_1(R_0-1)}{K_1K_2(\mu L_1R_0-\mu L_2)} \tag{7}$$

$$I_{2S}^*=\frac{\mu Q_0L_1B_1(R_0-1)}{K_1K_2K_3K_4(\mu L_1R_0-\mu L_2)} \qquad I_T^*=\frac{\mu Q_0L_1B_2(R_0-1)}{K_1K_2K_3K_4K_5(\mu L_1R_0-\mu L_2)}$$

$$A^* = \frac{\mu Q_0 L_1 B_3 (R_0 - 1)}{K_1 K_2 K_3 K_4 K_5 K_6 (\mu L_1 R_0 - \mu L_2)}$$

Thus the component of E_1 are expressed by (7)

4.5 Local Stability at Disease Free Equilibrium (DFE)

Theorem 3:

The DFE of the model is locally asymptotically stable (LAS) if Rc < 1 and unstable if Rc > 1

Proof : The Jacobian matrix of the model evaluated at E_0 is obtain as

$$J(E_0) = \begin{pmatrix} -\mu & -\beta_1(1-\varepsilon\alpha) & -\beta_1\eta_1(1-\varepsilon\alpha) & -\beta_2(1-\varepsilon\alpha) & -\beta_2\eta_2(1-\varepsilon\alpha) & 0 & 0 \\ 0 & \beta_1(1-\varepsilon\alpha)-K_1 & \beta_1\eta_1(1-\varepsilon\alpha) & \beta_2(1-\varepsilon\alpha) & \beta_2\eta_2(1-\varepsilon\alpha) & 0 & 0 \\ 0 & \alpha_1 & -K_2 & 0 & 0 & 0 & 0 \\ 0 & \theta_1 & 0 & -K_3 & 0 & 0 & 0 \\ 0 & 0 & \theta_2 & \alpha_2 & -K_4 & 0 & 0 \\ 0 & 0 & \phi_1 & 0 & \phi_2 & -K_5 & 0 \\ 0 & 0 & 0 & \gamma_1 & \gamma_2 & \gamma_3 & -K_6 \end{pmatrix}$$

The characteristic equation of $J(E_0)$ is express as

$$(\lambda+\mu)(\lambda+K_5)(\lambda+K_6)[\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0] = 0 \quad (8)$$

Where

$$a_3 = K_1 + K_2 + K_3 + K_4 - \beta_1(1-\varepsilon\alpha)$$

$$a_2 = K_1(K_2+K_3+K_4) + K_2(K_3+K_4) + K_3K_4 - (1-\varepsilon\alpha)[\beta_1(K_2+K_3+K_4+\alpha_1\eta_1) + \beta_2\theta_1] \quad (9)$$

$$a_1 = K_1(K_2K_3 + K_2K_4 + K_3K_4) + K_2K_3K_4 - (1-\varepsilon\alpha)[\beta_1(K_3\alpha_1\eta_1 + K_4\alpha_1\eta_1 + K_3K_4 + K_2K_4 + K_2K_3) + \beta_2(\alpha_1\eta_2\theta_2 + \alpha_2\eta_2\theta_1 + K_2\theta_1 + K_4\theta_1)]$$

$$a_0 = K_1K_2K_3K_4 - (1-\varepsilon\alpha)[\beta_1K_3K_4(K_2 + \alpha_1\eta_1) + \beta_2[K_2K_4\theta_1 + \eta_2(K_2\alpha_2\theta_1 + K_3\alpha_1\theta_2)]]$$

Rewriting (6) as

$$R_0 = R_1 + R_2 + R_3 + R_4 + R_5 \quad (10)$$

Where

$$R_1 = \frac{\beta_1(1-\varepsilon\alpha)}{K_1} \qquad R_2 = \frac{\beta_1\alpha_1\eta_1(1-\varepsilon\alpha)}{K_1K_2} \qquad R_3 = \frac{\beta_2\theta_1(1-\varepsilon\alpha)}{K_1K_3} \quad (11)$$

$$R_4 = \frac{\beta_2\eta_2\alpha_2\theta_1(1-\varepsilon\alpha)}{K_1K_3K_4} \qquad R_5 = \frac{\beta_2\eta_2\alpha_1\theta_2(1-\varepsilon\alpha)}{K_1K_2K_4}$$

Using (11) into (9)

$$a_3 = K_2 + K_3 + K_4 + K_1(1-R_1)$$

$$a_2 = K_1K_2[1-(R_1+R_2)] + K_1K_3[1-(R_1+R_3)] + K_1K_4(1-R_1) + K_2(K_3+K_4) + K_3K_4 \quad (12)$$

$$a_1 = K_1K_2K_3[1-(R_2+R_4+R_1+R_3)] + K_1K_2K_4[1-(R_1+R_2+R_5)] + K_1K_3K_4[1-(R_1+R_3)] + K_2K_3K_4$$

$$a_0 = K_1K_2K_3K_4(1-R_0)$$

It is obvious from (8) that the first three eigenvalues are negative i.e

$$\lambda_1 = -\mu < 0, \lambda_2 = -K_5 < 0, \lambda_3 = -K_6 < 0$$

While the remaining four eigenvalues from

$$\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0$$

Will be negative if and only if a_3, a_2, a_1 and a_0 are all positives

Considering (11) we note that for $R_0 < 1$ the following inequalities holds

$1 > R_1$, $1 > R_1 + R_2$, $1 > R_1 + R_3$, $1 > R_1 + R_2 + R_3 + R_4$, $1 > R_1 + R_2 + R_5$ and $1 > R_1 + R_3$

Hence from (12) a_3, a_2, a_1 and a_0 are readily seen to be positive respectively. Then all the eigenvalues of (8) are negative for $R_0 < 1$. Thus concluding the proof.

4.6 Local Stability of Endemic Equilibrium points: Special Case

In this section, we shall investigate the local stability of the endemic equilibrium point for a special case where the disease induced death rate is absence or considered negligible (i.e δ=0) using the kranoselkii sub linearity technique.

For this special case (i.e δ=0), the derivative of the total population of model (9) becomes

$$\frac{dN}{dt} = Q_0 - \mu N$$

Thus $N \to \frac{Q_0}{\mu} = N^{\Delta}$ as $t \to \infty$ (13)

The endemic equilibrium for this special case denoted by E_2 is expressed as

$$E_1\big|_{\delta=0} = E_2$$

Thus

$$\lambda^{\Delta} = \mu(R_0 - 1)$$

$$S^{\Delta} = \frac{Q_0}{\mu R_0}$$

$$I_{1A}^{\Delta} = \frac{Q_0(R_0 - 1)}{K_1 R_0}$$

$$I_{2A}^{\Delta} = \frac{Q_0\alpha_1(R_0 - 1)}{K_1 K_2 R_0} \tag{14}$$

$$I_{1S}^{\Delta} = \frac{Q_0\theta_1(R_0 - 1)}{K_1 K_3 R_0}$$

$$I_{2S}^{\Delta} = \frac{Q_0 B_1(R_0 - 1)}{K_1 K_2 K_3 K_4 R_0}$$

$$I_T^{\Delta} = \frac{Q_0 B_2(R_0 - 1)}{K_1 K_2 K_3 K_4 K_5 R_0}$$

$$A^{\Delta} = \frac{Q_0 B_3(R_0 - 1)}{K_1 K_2 K_3 K_4 K_5 R_0}$$

Under the setting, (3) is reduced to

$$\left.\begin{aligned}
\frac{dI_{1A}}{dt} &= \lambda(N - I_{1A} - I_{2A} - I_{1S} - I_{2S} - I_T - A) - K_1 I_{1A} \\
\frac{dI_{2A}}{dt} &= \alpha_1 I_{1A} - K_2 I_{2A} \\
\frac{dI_{1S}}{dt} &= \theta_1 I_{1A} - K_3 I_{1S} \\
\frac{dI_{2S}}{dt} &= \theta_2 I_{2A} + \alpha_2 I_{1S} - K_4 I_{2S} \\
\frac{dI_T}{dt} &= \phi_1 I_{2A} + \phi_2 I_{2S} - K_5 I_T \\
\frac{dA}{dt} &= \gamma_1 I_{1S} + \gamma_2 I_{2S} + \gamma_3 I_T - \mu A
\end{aligned}\right\} \tag{15}$$

Theorem 4

The unique endemic equilibrium E_2 of (15) is locally asymptotically stable whenever$R_0 < 1$.

Proof

The theorem above will be established using the above mentioned technique which requires showing that the linearization of system (15), around E_2, has no solutions of the form

$$\bar{Y}(t) = \bar{Y}_0 e^{bt} \tag{16}$$

With $\bar{Y}_0 \in C^n \setminus \{0\},\ b \in C,\ Y_i \in C$ and $R_e(b) \geq 0$.

The jacobian matrix of (80) evaluated at E_2 is given by

$$\begin{pmatrix}
(m_2 - m_1) - K_1 & m_2\eta_1 - m_1 & m_3 - m_1 & m_3\eta_2 - m_1 & -m_1 & -m_1 \\
\alpha_1 & -K_2 & 0 & 0 & 0 & 0 \\
\theta_1 & 0 & -K_3 & 0 & 0 & 0 \\
0 & \theta_2 & \alpha_2 & -K_4 & 0 & 0 \\
0 & \phi_1 & 0 & \phi_2 & -K_5 & 0 \\
0 & 0 & \gamma_1 & \gamma_2 & \gamma_3 & -\mu
\end{pmatrix} \tag{17}$$

Where

$$m_1 = (1 - \varepsilon\alpha)\left[\frac{\beta_1(I_{1A}^{\Delta} + \eta_1 I_{2A}^{\Delta}) + \beta_2(I_{1S}^{\Delta} + \eta_2 I_{2S}^{\Delta})}{N^{\Delta}}\right]$$

$$m_2 = \frac{\beta_1(1-\varepsilon\alpha)S^{\Delta}}{N^{\Delta}}$$

$$m_3 = \frac{\beta_2(1-\varepsilon\alpha)S^{\Delta}}{N^{\Delta}}$$

Thus the linearization of (80) at E_2 gives

$$\left.\begin{aligned}
\frac{dI_{1A}}{dt} &= (m_2 - m_1 - K_1)I_{1A} + (m_2\eta_1 - m_1)I_{2A} + (m_3 - m_1)I_{1S} + (m_3\eta_2 - m_1)I_{2S} - m_1 I_T - m_1 A \\
\frac{dI_{2A}}{dt} &= \alpha_1 I_{1A} - K_2 I_{2A} \\
\frac{dI_{1S}}{dt} &= \theta_1 I_{1A} - K_3 I_{1S} \\
\frac{dI_{2S}}{dt} &= \theta_2 I_{2A} + \alpha_2 I_{1S} - K_4 I_{2S} \\
\frac{dI_T}{dt} &= \phi_1 I_{2A} + \phi_2 I_{2S} - K_5 I_T \\
\frac{dA}{dt} &= \gamma_1 I_{1S} + \gamma_2 I_{2S} + \gamma_3 I_T - \mu A
\end{aligned}\right\} \quad (18)$$

Substituting (16) into (18) to get

$$\left.\begin{aligned}
bZ_1 &= (m_2 - m_1 - K_1)Z_1 + (m_2\eta_1 - m_1)Z_2 + (m_3 - m_1)Z_3 + (m_3\eta_2 - m_1)Z_4 - m_1 Z_5 - m_1 Z_6 \\
bZ_2 &= \alpha_1 Z_1 - K_2 Z_2 \\
bZ_3 &= \theta_1 Z_1 - K_3 Z_3 \\
bZ_4 &= \theta_2 Z_2 + \alpha_2 Z_3 - K_4 Z_4 \\
bZ_5 &= \phi_1 Z_2 + \phi_2 Z_4 - K_5 Z_5 \\
bZ_6 &= \gamma_1 Z_3 + \gamma_2 Z_4 + \gamma_3 Z_5 - \mu Z_6
\end{aligned}\right\} \quad (19)$$

Simplifying (19) by moving all negative terms in the last five equations of (19) to their left hand sides. The resulting last five are expressed in terms of Y and substituted with the first equation of (19) and all other negative terms are moved to the left hand side to have

$$\left.\begin{aligned}
[1+G_1(b)]Z_1 &= (HY)_1 \\
1+G_2(b)]Z_2 &= (HY)_2 \\
1+G_3(b)]Z_3 &= (HY)_3 \\
1+G_4(b)]Z_4 &= (HY)_4 \\
1+G_5(b)]Z_5 &= (HY)_5 \\
1+G_6(b)]Z_6 &= (HY)_6
\end{aligned}\right\} \tag{20}$$

Where

$$G_1(b) = \frac{b + m_1(1 + T_1 + T_2 + T_3 + T_4 + T_5)}{K_1}, \quad G_2(b) = \frac{b}{K_2}, \quad G_3(b) = \frac{b}{K_3},$$

$$G_4(b) = \frac{b}{K_4}, \quad G_5(b) = \frac{b}{K_5}, \quad G_6(b) = \frac{b}{\mu},$$

With

$$H = \begin{pmatrix}
\frac{m_2}{K_1} & \frac{m_2\eta_1}{K_1} & \frac{m_3}{K_1} & \frac{m_3\eta_2}{K_1} & 0 & 0 \\
\frac{\alpha_1}{K_2} & 0 & 0 & 0 & 0 & 0 \\
\frac{\theta_1}{K_3} & 0 & 0 & 0 & 0 & 0 \\
0 & \frac{\theta_2}{K_4} & \frac{\alpha_2}{K_4} & 0 & 0 & 0 \\
0 & \frac{\phi_1}{K_5} & 0 & \frac{\phi_2}{K_5} & 0 & 0 \\
0 & 0 & \frac{\gamma_1}{\mu} & \frac{\gamma_2}{\mu} & \frac{\gamma_3}{\mu} & 0
\end{pmatrix}$$

The i^{th} coordinate of the vector $H(\bar{Y})$ is denoted by $H(\bar{Y})_i$ (with I = 1, 2, … 6) the equilibrium $E_2 = (I_{1A}^{\Delta}, I_{2A}^{\Delta}, I_{1S}^{\Delta}, I_{2S}^{\Delta}, I_T^{\Delta}, A^{\Delta})$ satisfies $E_2 = HE_2$ and it has non-negative entries. If $\bar{Y}$ is a solution of (20), then it is possible to find a minimal positive real number w such that

$$\left\| \bar{Y} \right\| \leq sE_2 \tag{21}$$

Where $\|Y\| = (\|Y_1\|, \|Y_2\|, \|Y_3\|, \|Y_4\|, \|Y_5\|, \|Y_6\|)$ with the lexicographic order, and $\|.\|$ is a norm in C. The aim is to show that $R_e(b) < 0,$ then the linearized system (18) has a solution of the form (16).

Now, we need to show that $R_e(b) \geq 0,$ is not satisfied which will then be sufficient to conclude that $R_e(b) < 0.$ then we have two general cases $b = 0 \; and \; b \neq 0.$

Case (1): $b = 0$

For $b = 0,$ then system (18) becomes a homogeneous linear system of the form

$$\bar{0} = J_{E_2} Y_i \qquad i = 1, 2, ...6$$

Then

$$\left| J_{E_2} \right| = B_1 \mu (R - 1) + \mu K_1 K_2 K_3 K_4 K_5 \left(1 - \frac{R_0 S^{\Delta}}{N^{\Delta}} \right) \tag{22}$$

By (71) and (73) we have that

$$\frac{S^{\Delta}}{N^{\Delta}} = \frac{1}{R_0} \tag{23}$$

Substituting (23) into (22) to get

$$\left| J_{E_2} \right| = B_4 \mu (R - 1) \tag{24}$$

Where

$$B_4 = \mu K_2 K_3 K_4 K_5 + \mu K_2 K_4 K_5 \theta_1 + \mu K_2 K_5 \alpha_2 \theta_1 + \mu K_2 \alpha_2 \phi_2 \theta_1 + \mu K_3 K_4 K_5 \alpha_1 + \mu K_3 K_4 \alpha_1 \phi_1 + \mu K_3 K_5 \alpha_1 \theta_2$$

$$+ \mu K_3 \alpha_1 \phi_2 \theta_2 + K_2 K_4 K_5 \gamma_1 \theta_1 + K_2 K_5 \alpha_2 \gamma_2 \theta_1 + K_2 \alpha_2 \gamma_3 \phi_2 \theta_1 + K_3 K_4 \alpha_1 \gamma_3 \phi_1 + K_3 K_5 \alpha_1 \gamma_2 \theta_2 + K_3 \alpha_1 \gamma_3 \phi_2 \theta_2$$

Thus, $\left| J_{E_2} \right| < 0,$ whenever $R_0 < 1.$ since the $\left| J_{E_2} \right|$ is negative it follows that the system (18) has a unique solution given by $Y = 0$ (which corresponds to the DFE (E_0)).

Case (2): $b \neq 0$

Since $R_e(b) > 0$ (by assumption), then $|1 + G_i(b)| > 1$ for all $i = 1, 2, ...6$

Define $G(b) = \min\{|1+G_i(b)|, i = 1,2,...6\},$ then $G(b) > 1$ and $\frac{s}{G(b)} < s.$ The minimality of s implies that

$$\left\|\bar{Y}\right\| > \frac{s}{G(b)} E_2 \tag{25}$$

Taking norm on both side of the second equation (25), and using the fact that the matrix H is non negative gives

$$\begin{aligned} G(b)\|Y_2\| &\le |1+G_2(b)|\|Y_2\| \\ &= \|(HY)_2\| \le H\|Y_2\| \le sH(E_2)_2 \\ &= s(E_2)_2 = sI_{2A}^{\Delta} \end{aligned} \tag{26}$$

It follows from (26) that $\|Y_2\| \le \frac{s}{G(b)} I_{2A}^{\Delta}$ which contradicts (25). Hence $R_e(b) < 0$. Thus, all eigenvalues of the characteristic equation associated with the linearized system (18) will have negative real part, so that the unique endemic equilibrium, E_2 is locally asymptotically stable whenever $R_0 > 1$.

Thus ends the proof.

5.0 Numerical Simulation and Discussion of Results

The role played by some important epidemiological parameters, are investigated with the aid of Maple software for the numerical simulation. Approximate solution of the model was also determined using Differential Transform Method (DTM). Numerical simulation was also carried out to investigate the effects of screening unaware (unscreened) asymptomatic individuals and Condom compliance.

Figure 1 and Figure 2 below shows the influence of Condom compliance and Screening on the transmission dynamics of HIV/AIDS. Figure 1 clearly shows that increase in the compliance of Condom usage, the total number of HIV/AIDS individuals reduces. This point that increase in Condom usage reduces HIV/AIDS burden.

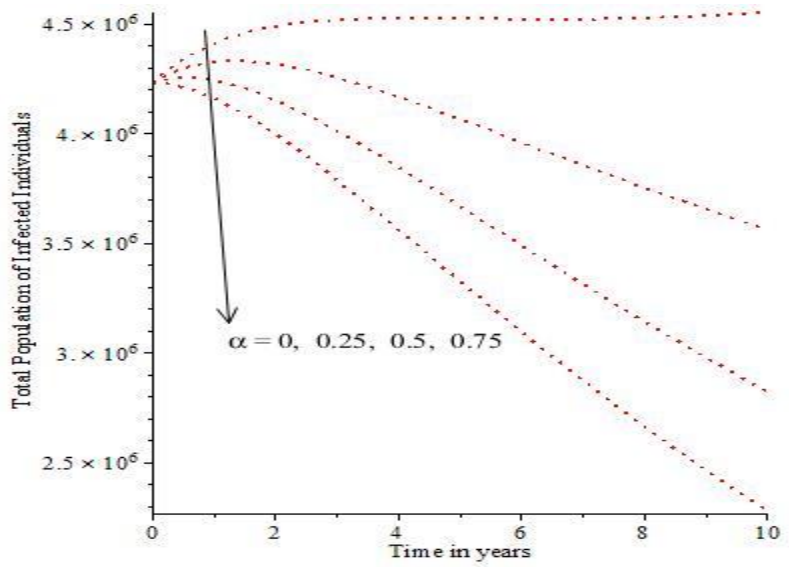

Figure 1: Variation of Condom compliance for $\alpha = 0.1,\ \alpha_1 = 0.015, \theta_1 = 0.14\ and\ q = 1$

Figure 2 below shows that the increase of screening rate of unaware HIV individuals decreases the total number of HIV/AIDS individual. Similarly screening of unaware HIV individual proffer some therapeutic benefit in reducing the burden of HIV/AIDS.

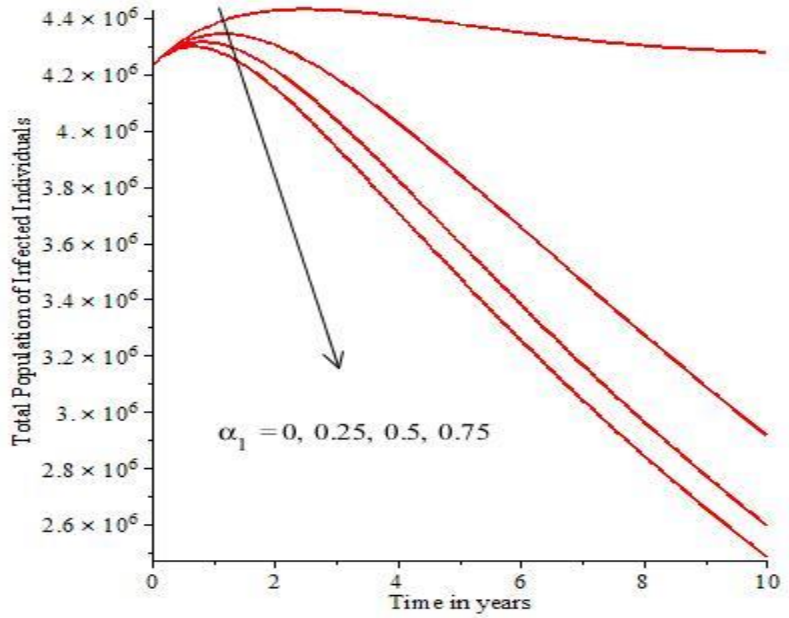

Figure 2: Variation of Screening for $\alpha = 0.1,\ \alpha_1 = 0.015, \theta_1 = 0.14\ and\ q = 1$

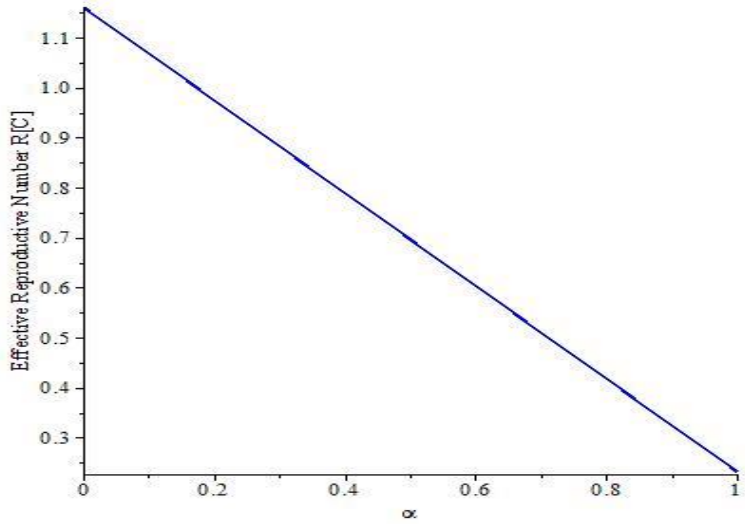

Figure 3: Effect of Condom compliance on Reproductive Number

As shown in figure 3, Increase of Condom compliance reduces Reproductive Number

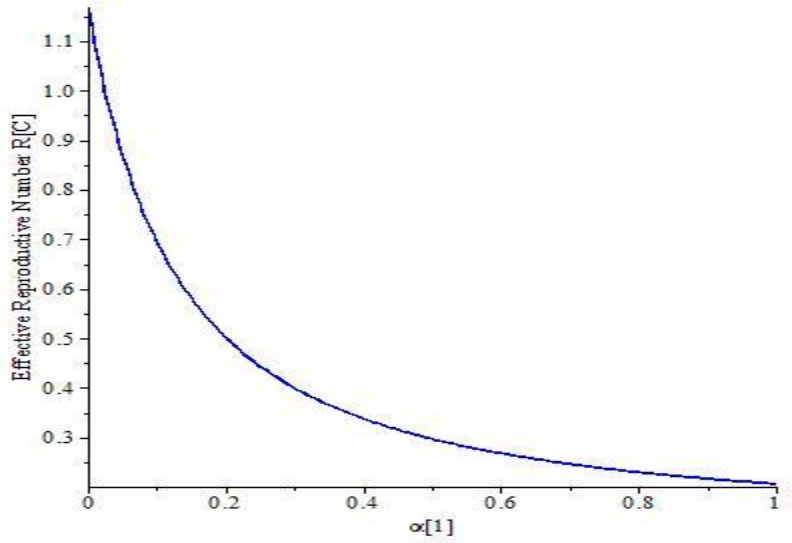

Figure 4: Effect of Screening on Reproductive Number

As shown in figure 4, Increase on Screening reduces Reproductive Number

6.0 Conclusion

In this study, a seven-dimensional, deterministic, staged progression HIV/AIDS model that extend and complement the models presented in Akinyemi *et al.*, 2016 is constructed and analyzed. Some of the main theoretical and epidemiological findings of the study are as follows.

(i) The model has a local asymptotically stability at DFE whenever $R_c < 1$.

(ii) Thus, this study shows that HIV/AIDS will be eliminated from the population whenever $R_c < 1$.

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