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Original Article

Stability Analysis of HIV/AIDS Model with Interaction Between Educated and Infected (Not Consuming ARV) Subpopulations

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Abstract *- We study stability analysis of HIV/AIDS model. The mathematical model of HIV/AIDS is constructed with seven compartments, S, E, I_1, I_2, A, T, and R. S is susceptible/uneducated individuals; E is educated individuals; I_1 is HIV-positive individuals consuming ARV; and I_2 is HIV-positive individuals not consuming ARV; A is full-blown AIDS not receiving treatment; T is individuals receiving ARV treatment; and R is recovered individuals who change and maintain their sexual habits for the rest of their lives. We consider multi-interaction between educated (E), uneducated (S) and infected (I_1 and I_2) subpopulations. We investigate local stability of the equilibrium points according to the basic reproduction number (R_0) as a threshold of disease transmission. The disease-free and endemic equilibrium points are locally asymptotically stable when $R_0 < 1$ and $R_0 > 1$ respectively. We conduct numerical simulation to support the analytical results.*

Keywords — *dynamical system, multi-interaction, local stability.*

I. INTRODUCTION

AIDS (Acquired Immune Deficiency Syndrome) is a disease of the immune system caused by HIV (human immunodeficiency virus). AIDS is a threat in the world because people infected with HIV can cause death. WHO seeks to campaign for the dangers of this disease and provide various controls including the use of condoms or consume ARV (Antiretroviral Treatment) [8].

To understanding the spread of HIV-AIDS infection, we establish mathematical model. Several mathematical model of HIV/AIDS have been studied by [1]-[4], [8], [10], [11]. The formulated model is including treatment compartment, stated in the SIATR model. Dynamical analysis of the HIV / AIDS epidemic model with different stages of infection and different stages of susceptible subpopulations respectively studied in [4], [5], [6], [7], [13]. In [6], they studied dynamical analysis of the model locally and globally. The results were locally and globally asymptotically stable. In [13], they constructed the mathematical model with seven compartments, S, E, I_1, I_2, A, T, and R, where they studied the stability analysis of the model by considering multi-interaction between uneducated (S) and infected (I_1 and I_2) subpopulations. The proposed model is more realistic.

In this research, we continue our study to analyze mathematical model of HIV/AIDS - SEI_1I_2ATR locally. We examine educated (E) subpopulation in the model such that we have the mathematical model including multi-interaction between educated (E), uneducated (S) and infected (I_1 and I_2) subpopulations. The first step is we determine the equilibrium points (disease-free and endemic points). Then, we determine the reproduction number (R_0) as a threshold of disease transmission. We apply the next generation matrix to get the reproduction number. Furthermore, we analyze the stability of equilibrium points locally. The disease-free equilibrium point is locally asymptotically stable when $R_0 < 1$. We used the Routh-Hurwitz criteria to determine the stability criteria of endemic equilibrium point, and the result is the endemic equilibrium point is locally asymptotically stable when $R_0 > 1$. The Runge-Kutta 4th order method is used to solve the HIV/AIDS numerically since the model is in the form of the system of differential equations with initial value problem. Numerical simulations are performed using values of selected parameters to support the analysis results. From the numerical simulation, we can see behavior of the model.

II. THE MODEL ANALYSIS

The mathematical model of HIV/AIDS is constructed using compartment diagram in Figure 1[15]. The model consists of seven compartments, S, E, I_1, I_2, A, T, and R. In this research, we study dynamical system of HIV/AIDS - SEI_1I_2ATR model by considering multi-interaction between educated (E), uneducated (S) and infected (I_1 and I_2) subpopulations

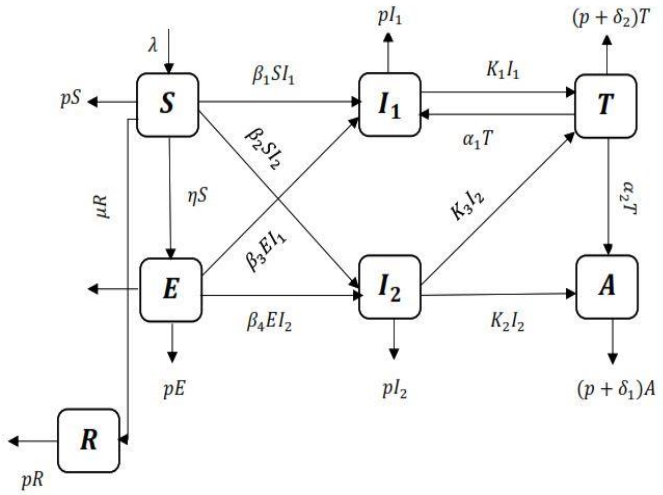


Fig. 1 The compartment diagram of HIV/AIDS model

The system of differential equations of HIV/AIDS model is

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \beta_1 SI_1 - \beta_2 SI_2 - aS,\\
\frac{dE}{dt} &= \eta S - \beta_4 EI_2 - dE,\\
\frac{dI_1}{dt} &= \beta_1 SI_1 + \alpha_1 T - bI_1,\\
\frac{dI_2}{dt} &= \beta_2 SI_2 + \beta_4 EI_2 + \alpha_1 T - cI_2,\\
\frac{dT}{dt} &= k_1 I_1 + k_3 I_2 - eT,\\
\frac{dA}{dt} &= k_2 I_2 + \alpha_2 T - fT,\\
\frac{dR}{dt} &= \mu S - dR.
\end{aligned} \tag{1}$$

where $a = \eta + \mu + d$, $b = k_1 + d$, $c = k_2 + k_3 + d$, $e = \alpha_1 + \alpha_2 + \delta_2 + d$, dan $f = \delta_1 + d$.

The description of the parameters that make up the system are given in the Table 1.

Table 1. Parameters of the HIV/AIDS - SEI₁I₂ATR epidemic model.

Parameter	Description
Λ	Recruitment rate
μ	The human natural death rate
β_1	Transmission coefficient of the infection from S to I_1
β_2	Transmission coefficient of the infection from S to I_2
β_3	Transmission coefficient of the infection from E to I_1
β_4	Transmission coefficient of the infection from E to I_2

η	Education rate
d	The human natural death rate
k_1	Progression rate from I_1 to T
k_2	Progression rate from I_2 to A
k_3	Progression rate from I_2 to T
α_1	Proportion of successful treatment
α_2	Proportion of treatment failure
δ_1	the disease-related death rate
δ_2	the disease-related death rate of being treated

A. Equilibrium points

The equilibrium points of system (1) are obtained when $\frac{dS}{dt}=0$, $\frac{dE}{dt}=0$, $\frac{dI_1}{dt}=0$, $\frac{dI_2}{dt}=0$, $\frac{dT}{dt}=0$, $\frac{dA}{dt}=0$, and $\frac{dR}{dt}=0$. The system (1) has two equilibrium points, called disease-free ($K_2{}^0$) and endemic ($K_2{}^*$) equilibrium points. Disease-free equilibrium point ($K_2{}^0$) is obtained when $I_1, I_2 = 0$, such that we have

$$K_2{}^0 = (S^0, E^0, I_1{}^0, I_2{}^0, T^0, A^0, R^0)$$
$$= \left(\frac{\Lambda}{a}, \frac{\eta\Lambda}{da}, 0, 0, 0, 0, \frac{\mu\Lambda}{da}\right).$$

The endemic equilibrium point ($K_2{}^*$) is obtained when $I_1, I_2 \neq 0$, such that we get

$$K_2{}^* = (S^*, E^*, I_1{}^*, I_2{}^*, T^*, A^*, R^*),$$

where

$$S^* = \frac{2\beta_4 c\Lambda}{\beta_4 c\beta_1 I_1{}^* + 2a\beta_4 c - J \pm \sqrt{(J+\beta_4 c\beta_1 I_1{}^*)^2 - 4\beta_2 c\beta_4(G + c\beta_1 I_1{}^* d)}} \quad \text{with } G = -\beta_2\Lambda d - \beta_4\beta_2\Lambda + dca \text{ and } J = -\beta_2 cd - \beta_4\beta_2\Lambda + \beta_4 ca$$

$$E^* = \left(\frac{2\eta\beta_4 c\Lambda}{\beta_4 c\beta_1 I_1{}^* + 2a\beta_4 c - J \pm \sqrt{(J+\beta_4 c\beta_1 I_1{}^*)^2 - 4\beta_2 c\beta_4(G + c\beta_1 I_1{}^* d)}}\right) \left(\frac{2\eta\beta_4 c\Lambda}{\beta_4 c\beta_1 I_1{}^* + 2a\beta_4 c - J \pm \sqrt{(J+\beta_4 c\beta_1 I_1{}^*)^2 - 4\beta_2 c\beta_4(G + c\beta_1 I_1{}^* d)}}\right)$$

$$(I_1{}^*)_{1,2} = \frac{-B \pm \sqrt{B^2 - 4AC}}{2A}, \text{ with}$$

$$A = c\beta_2\beta_3(\alpha_1\beta_2 k_1 + e\beta_1 c - \beta_1\alpha_1 k_3 - \beta_2 be),$$
$$B = \beta_2((\Lambda\beta_2 - ac)\beta_3\alpha_1 k_3 + \alpha_1\beta_2 k_1 cd + e\beta_1 ccd + e\beta_3\eta cc - c\beta_1\alpha_1 k_3 d - bec\beta_2 d,$$
$$C = (\Lambda\beta_2 - ac)\alpha_1\beta_2 k_3 d,$$

$$I_2{}^* = \frac{-\beta_1\beta_4 cI_1{}^* - J \pm \sqrt{\left(J+\beta_4 c\beta_1 I_1{}^*\right)^2 - 4\left(\beta_4 c\beta_2\right)\left(G + c\beta_1 I_1{}^* d\right)}}{2\left(\beta_4 c\right)\beta_2},$$

$$T^* = \left(\frac{(2\beta_4 c\beta_2 k_1 - k_3\beta_1\beta_4 c)I_1{}^* - k_3\left(J \pm \sqrt{\left(J+\beta_4 c\beta_1 I_1{}^*\right)^2 - 4\left(\beta_4 c\beta_2\right)\left(G + c\beta_1 I_1{}^* d\right)}\right)}{e2\left(\beta_4 c\right)\beta_2}\right) A^* = \left(\frac{\left(\alpha_2 k_1 2\left(\beta_4 c\right)\beta_2 - \beta_1\beta_4 c\left(ek_2 + \alpha_2 k_3\right)\right)I_1{}^*}{ef\,2\left(\beta_4 c\right)\beta_2}\right) + \frac{\alpha_2 k_1}{ef} I_1{}^* +$$

$$\frac{\left(ek_2 + \alpha_2 k_3\right)\left(-J \pm \sqrt{\left(J+\beta_4 c\beta_1 I_1{}^*\right)^2 - 4\left(\beta_4 c\beta_2\right)\left(G + c\beta_1 I_1{}^* d\right)}\right)}{ef\,2\left(\beta_4 c\right)\beta_2},$$

$$R^* = \left(\frac{2\mu\beta_4 c\Lambda}{\beta_4 c\beta_1 I_1{}^* + 2a\beta_4 c - J \pm \sqrt{(J+\beta_4 c\beta_1 I_1{}^*)^2 - 4\beta_2 c\beta_4(G + c\beta_1 I_1{}^* d)}}\right).$$

B. Reproduction number

In the epidemic model, there is a unique number, namely the basic reproduction number (R_0) which determines as a threshold of disease transmission whether an outbreak of an infectious disease occurs or not [12]. To determine the value of the basic reproduction number (R_0), we apply the next generation matrix method by following the steps in [13]. We get the basic reproduction number

$$R_0 = \frac{\beta_2 d\Lambda + \beta_4 \eta\Lambda}{acd}.$$

C. Stability analysis

The stability of the disease-free equilibrium point ($K_2{}^0$) is obtained by determining the eigenvalues of the Jacobian matrix system (1). The equilibrium point $K_2{}^0$ is locally asymptotically stable if all of the real parts of the eigenvalues are negative. The Jacobian matrix at $K_2{}^0$ is

$$J(K_2{}^0) = \begin{pmatrix} -a & 0 & -\frac{\beta_1\Lambda}{\alpha} & -\frac{\beta_2\Lambda}{\alpha} & 0 & 0 & 0 \\ \eta & -d & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{\beta_1\Lambda}{\alpha} - b & 0 & \alpha_1 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_2\Lambda}{\alpha} - c & 0 & 0 & 0 \\ 0 & 0 & k_1 & k_3 & -e & 0 & 0 \\ 0 & 0 & 0 & k_2 & \alpha_2 & -f & 0 \\ \mu & 0 & 0 & 0 & 0 & 0 & -d \end{pmatrix}.$$

According to the calculation of $\left|J\left(K_1{}^0\right) - rI\right| = 0$, we obtain $r_1 = -d, r_2 = -f, r_3 = -d, r_4 = -a, r_5 = \frac{\beta_2\Lambda}{a} - c$ where the value of $r_5 = \frac{\beta_2\Lambda}{a} - c = c(R_0 - 1)$ in the form of the reproduction number, and r_6, r_7 that meet

$$\begin{vmatrix} \frac{\beta_1\Lambda}{a} - b - r & \alpha_1 \\ k_1 & -e - r \end{vmatrix} = 0.$$

Then the value $r_6 r_7 = -ge - \alpha_1 k_1 > 0$ dan $r_6 + r_7 = -(e - g) < 0$, so that we get $r_{6,7} < 0$. Now, we get all of eigen values are negative if $R_0 < 1$ and the disease-free equilibrium point ($K_2{}^0$) is locally asymptotically stable if $R_0 < 1$.

Next, we analyze the stability of endemic equilibrium point ($K_2{}^*$) where is obtained by determining the eigenvalues of the Jacobian matrix system (1) at $K_2{}^*$. The Jacobian matrix at $K_2{}^*$ is

$$J(K_2{}^*) = \begin{pmatrix} -\beta_1 I_1 - \beta_2 I_2 - a & 0 & -\beta_1 S & -\beta_2 S & 0 & 0 & 0 \\ \eta & -\beta_3 I_1 - d & 0 & 0 & 0 & 0 & 0 \\ \beta_1 I & 0 & \beta_1 S - b & 0 & \alpha_1 & 0 & 0 \\ \beta_2 I_2 & 0 & 0 & \beta_2 S + \beta_4 E - c & 0 & 0 & 0 \\ 0 & \beta_4 I_2 & k_1 & k_3 & -e & 0 & 0 \\ 0 & 0 & 0 & k_2 & \alpha_2 & -f & 0 \\ \mu & 0 & 0 & 0 & 0 & 0 & -d \end{pmatrix}.$$

We define $H_1 = \beta_1 I_1 + \beta_2 I_2 + a$, $H_2 = -\beta_4 I_2 - d$, $H_3 = \beta_1 S - b$ and $H_4 = \beta_2 S + \beta_4 E - c$. The characteristic equation of matrix $J(K_2{}^*)$ is obtained by solving $\left|J\left(K_2{}^*\right) - rI\right| = 0$, such that we have

$$\begin{vmatrix} H_1 - r & 0 & -\beta_1 S & -\beta_2 S & 0 & 0 & 0 \\ \eta & H_2 - r & 0 & 0 & 0 & 0 & 0 \\ \beta_1 I & 0 & H_3 - r & 0 & \alpha_1 & 0 & 0 \\ \beta_2 I_2 & 0 & 0 & H_4 - r & 0 & 0 & 0 \\ 0 & \beta_4 I_2 & k_1 & k_3 & -e - r & 0 & 0 \\ 0 & 0 & 0 & k_2 & \alpha_2 & -f - r & 0 \\ \mu & 0 & 0 & 0 & 0 & 0 & -d - r \end{vmatrix} = 0,$$

where $r_1 = -d, r_2 = -f$, and r_3, r_4, r_5, r_6, r_7 . The characteristic equation of matrix $J(K_2^*)$ is

$$r^5 + b_1 r^4 + b_2 r^3 + b_3 r^2 + b_4 r + b_5 = 0, \tag{2}$$

where

$b_1 = e - H_1 - H_2 - H_3 - H_4$,

$b_2 = H_1H_2 + H_2H_3 + H_2H_4 + H_1H_3 + H_1H_4 + H_3H_4 + \beta_1 I_1 \beta_1 S + \beta_2 S \beta_2 I_2 - H_1 e - H_3 e - H_4 e - H_2 e$,

$b_3 = -H_1H_2H_3e - H_4H_2H_3e - \beta_1 I_1 \beta_1 SeH_2 - \beta_2 S \beta_2 I_2 eH_2 - H_4H_1H_2e \quad -H_4H_1H_3e - eH_4\beta_1 I_1 \beta_1 S - H_3 \beta_2 S \beta_1 I_2 e - H_2H_1H_3$,

$b_4 = \alpha_1 \eta \beta_1 S \beta_4 I_2 + \beta_1 S \beta_2 I_2 k_3 \alpha_1 - \beta_1 I_1 \beta_1 SeH_2 - \beta_2 S \beta_2 I_2 eH_2 - \quad eH_1H_3H_4 - H_4\beta_1 I_1 \beta_1 Se - H_3 \beta_2 S \beta_2 I_2 e + H_1H_2H_3H_4 +$
$H_4\beta_1 I_1 \beta_1 SH_2 + H_3 \beta_2 I_2 \beta_2 SH_2 - eH_1H_3H_2 - eH_1H_2H_4 \; -eH_2H_3H_4$,

$b_5 = -\alpha_1 \beta_1 SH_2 \beta_2 I_2 k_3 - \alpha_1 \eta \beta_1 SH_4 \beta_4 I_2 + H_1H_2H_3H_4e + \; H_2eH_4\beta_1 I_1 \beta_1 S + H_3 \beta_2 S \beta_2 I_2 H_2 e$.

Stability of the endemic equilibrium point (K_2^*) is obtained by using the Routh-Hurwitz criteria. Based on equation (2), the endemic equilibrium point K_2^* is asymptotically stable if only if $b_1 > 0$ and

1. $b_1 b_2 - b_3 > 0,$
2. $b_1 b_2 b_3 - b_3^2 - b_1^2 b_4 > 0,$
3. $b_1 b_2 b_3 b_4 + 2 b_1 b_4 b_5 + b_2 b_3 b_5 - b_1^2 b_4^2 - b_1 b_2^2 b_5 - b_3^2 b_4 - b_5^2 > 0$,
4. $b_5 > 0$.

We will show this stability using numerical simulation in next section.

III. NUMERICAL SIMULATION

In this section, we conduct the numerical simulation of HIV/AIDS model. We will show that by using parameters in Table 2, the HIV/AIDS model will converge to the disease-free and endemic equilibrium points when the condition in the analytical results is satisfied.

Table 2. Parameter values for numerical simulation.

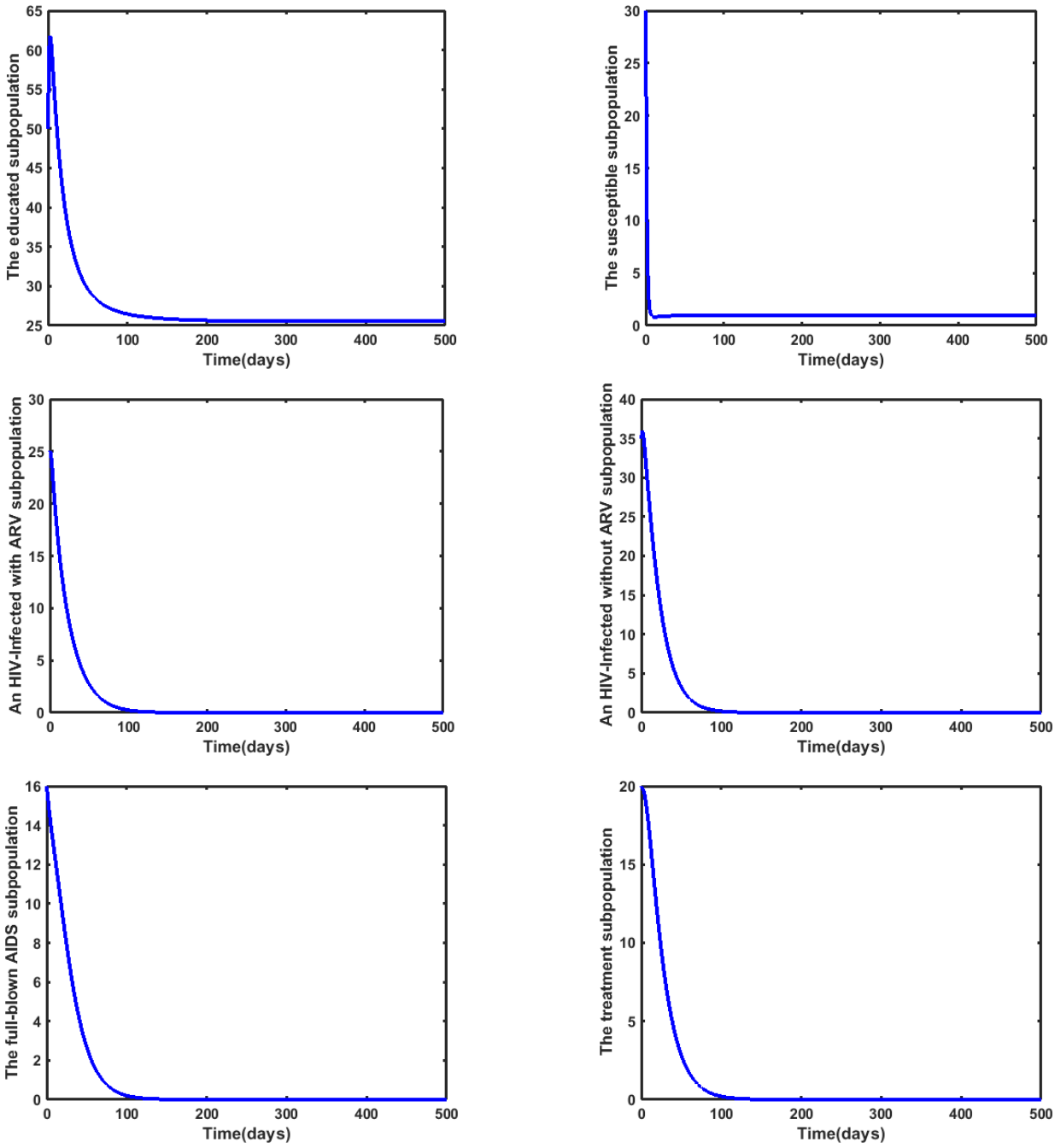
Symbol	value
Λ	0.55
μ	0.03
β_1	0.0023
β_2	0.0033
β_4	0.0019
η	0.3
d	0.0196
k_1	0.0498
k_2	0.008
k_3	0.05
α_1	0.02
α_2	0.05
δ_1	0.0909
δ_2	0.0667

The first simulation is we use parameters in Table 2 and get $R_0 = 0.5032 < 1$. Using initial values

$$NA = (30,10,25,35,20,16,50),$$

we have the solution of HIV/AIDS model as in Figure 2.

The results of this simulation show that with some initial values given, the solution leads to the disease-free equilibrium point (K_2^0), which means that after quite a long time, no infected individual. The numerical simulation results support the results of the analysis in Section 2 that said disease-free equilibrium (K_2^0) point is locally asymptotically stable when $R_0 < 1$.



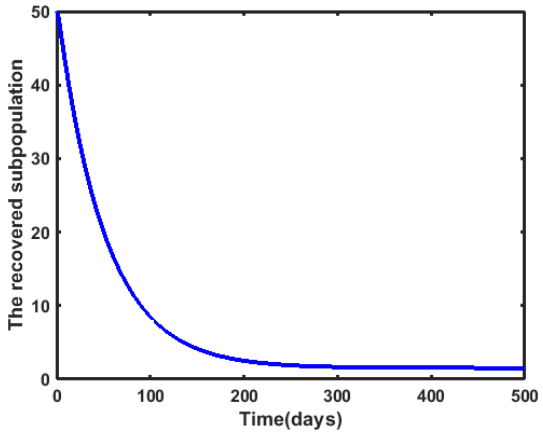


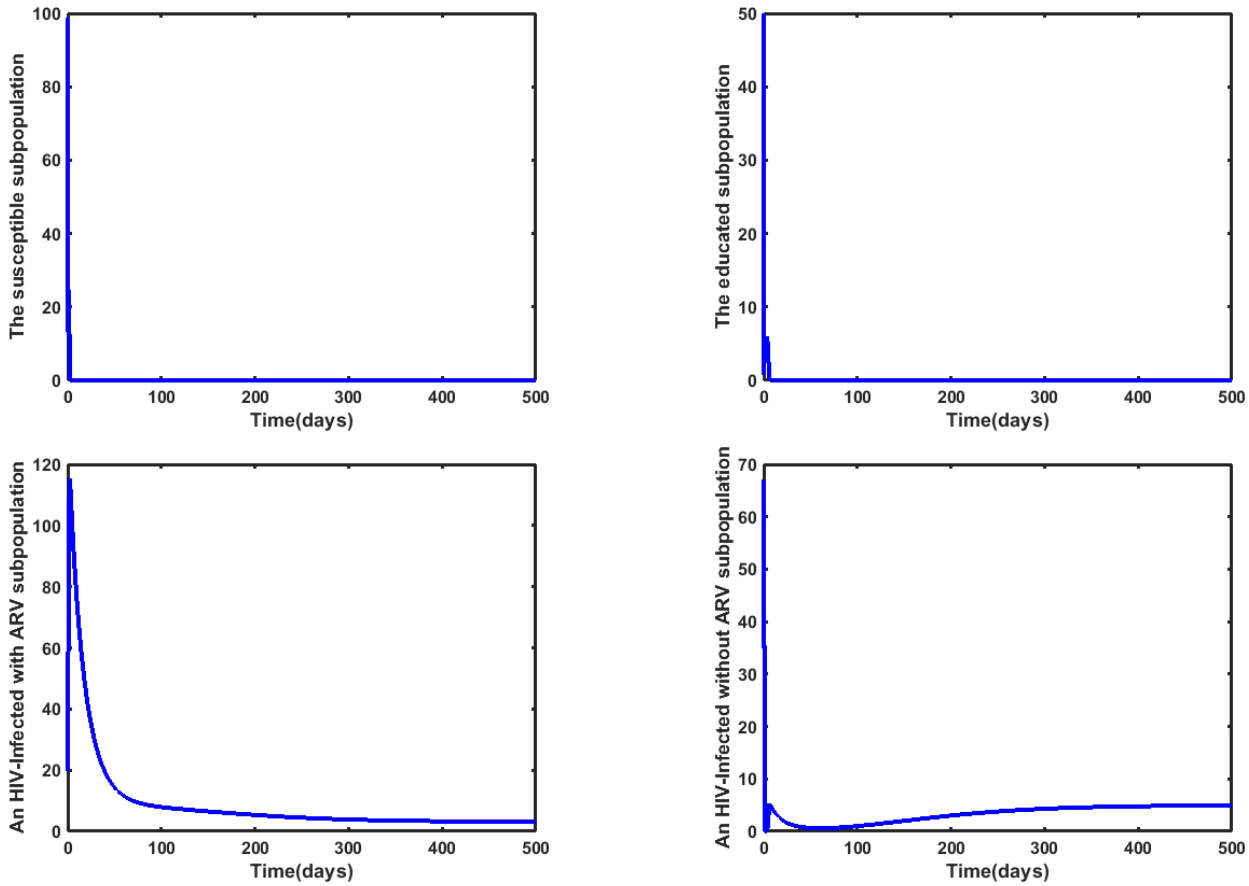
Fig. 2 The numerical solution of system (1) when $R_0 < 1$.

The second simulation is simulation of HIV/AIDS model with initial values,

$$NA = (30,10,25,35,20,16,50),$$

and $R_0 = 239.9441 > 1$. The solution of HIV/AIDS model is presented in Figure 3.

The results of this simulation show that with some initial values given, the solution leads to endemic equilibrium point (K_2^*), which means HIV/AIDS exist and spread in the populations. The numerical simulation results obtained support the analysis results in Section 2, so the endemic equilibrium point (K_2^*) is asymptotically stable if it meets the Routh-Hurwitz criteria.



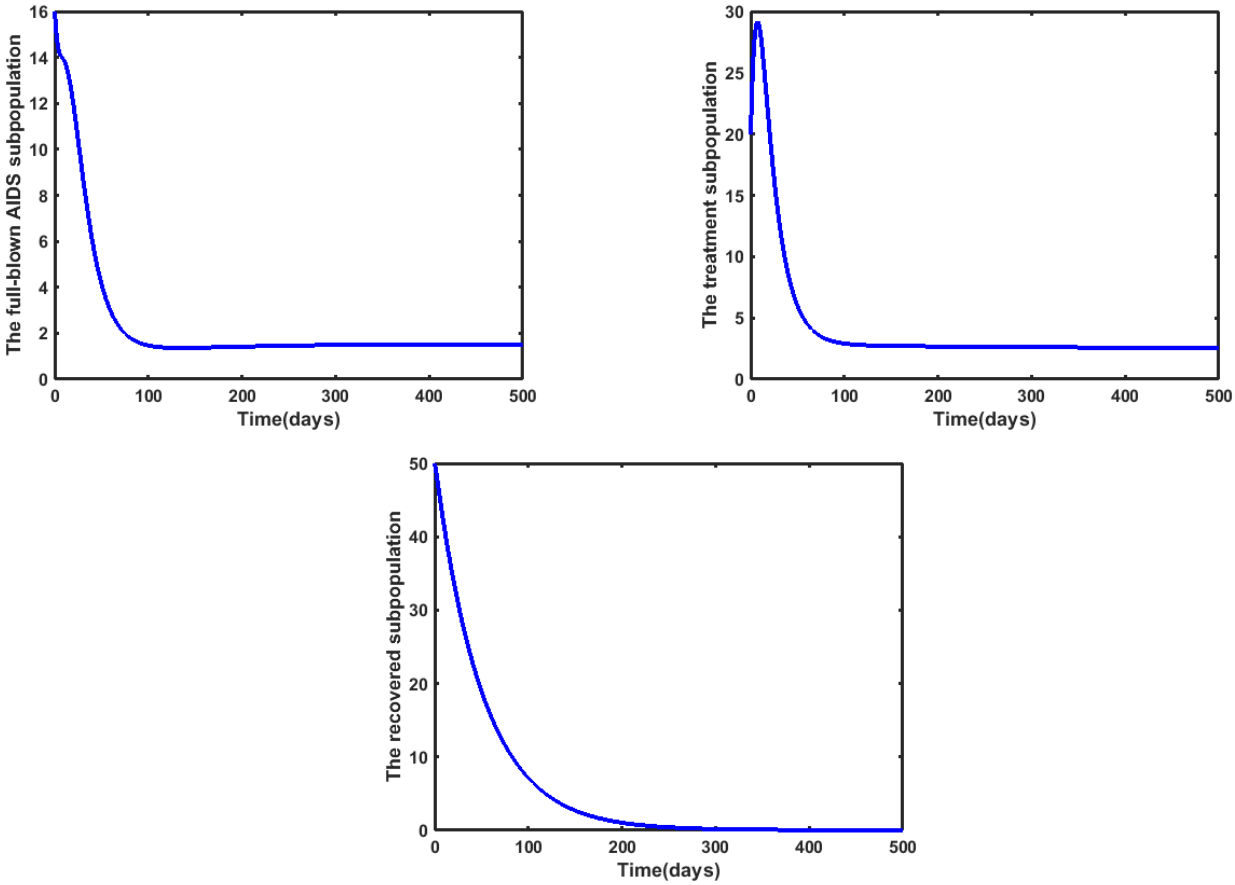


Fig 3. The numerical solution of system (1) when $R_0 > 1$.

IV. CONCLUSIONS

The dynamical analysis of HIV/AIDS model with multi-interaction between educated (E), uneducated (S) and infected (I_1 and I_2) subpopulations have been studied. The system has two equilibrium points, the disease-free and endemic equilibrium points. The stability analysis of HIV/AIDS model is determined according to the basic reproduction number. The disease-free equilibrium is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$. The endemic equilibrium is locally asymtotically stable when it meets the Routh-Hurwitz criteria. Numerical simulation are performed using values of selected parameters to support the analysis results.

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