

# Mathematical HIV/AIDS Model with Multi-Interaction Between Infected and Educated Subpopulations and Its Local Stability

Ummu Habibah<sup>1,2\*</sup> Trisilowati M. H. Muzaqi<sup>1</sup>

Tiara R. Tania<sup>1</sup> Labib U. AlFaruq<sup>1</sup>

<sup>1</sup>Department of Mathematics, Brawijaya University, Indonesia

<sup>2</sup>Research Group of Biomathematics, Brawijaya University, Indonesia

\*Corresponding author Email: [ummu\\_habibah@ub.ac.id](mailto:ummu_habibah@ub.ac.id)

## ABSTRACT

The mathematical formula of HIV/AIDS is governed by the ordinary differential equation with seven variables.  $S$  and  $E$  are susceptible/un-educated and educated individuals respectively,  $I_1$  and  $I_2$  are HIV-positive individuals consuming and not consuming ARV respectively;  $A$  and  $T$  are AIDS individuals not and receiving treatment; and  $R$  is a recovered individual. We study multi-interaction between infected and educated subpopulations. We analyze the local stability of the equilibrium points. The results are the disease-free is asymptotically stable when satisfying  $R_0 < 1$  and the endemic equilibrium point is asymptotically stable when satisfying  $R_0 > 1$ . The numerical solution supports the analytical results.

**Keywords:** Dynamical system, Multi-interaction, Local stability.

## 1. INTRODUCTION

HIV is a human immunodeficiency virus that causes AIDS (*Acquired Immune Deficiency Syndrome*), one of the immune system diseases. The study of the spread of AIDS gets attention from the researcher since HIV can cause death in the world. Mathematical models have made a significant contribution to know understanding the spread of HIV/AIDS disease. Mathematical formulas of HIV/AIDS have been investigated by [1-4] where they formulated the mathematical model of HIV/AIDS with the treatment stated in the SIATR. [4] and [5] studied the construction of the HIV/AIDS model with different levels of infection and susceptible subpopulations respectively. The theory of dynamical analysis and optimal control was applied to the problems. [6] studied the dynamic of the  $SI_1I_2ATR$  formula and the results were asymptotically stable, locally, and globally.

In this research, we propose a mathematical model of HIV/AIDS with an educated subpopulation. The proposed model is more realistic. From this study, we can get more understanding the spread of the HIV disease through the multi-interaction between subpopulations in the

constructed model. [6-8] studied the interaction between infected ( $I_2$ ) and educated ( $E$ ) subpopulations where in this research we consider multi-interaction between subpopulations, especially educated ( $E$ ) and infected ( $I_1$ ). The mathematical formulation is written in Section 2. Then in section 3, we show the stability analysis, locally. There are two equilibrium points, disease-free and endemic equilibrium points. The stability analysis of both equilibrium points said that the disease-free point is asymptotically stable when  $R_0 < 1$ , and when  $R_0 > 1$  is unstable. Furthermore, the endemic point is asymptotically stable when  $R_0 > 1$  and when  $R_0 < 1$  is unstable. In Section 4, we investigate the numerical simulation of the system of ordinary differential equation established in Section 2. We determine parameters for doing the simulation such that the result of the numerical simulations support the results of the analysis.

## 2. THE MATHEMATICAL FORMULA OF HIV/AIDS

The model formulation of HIV/AIDS in Figure 1 is from [6] HIV/AIDS mathematical formula with multi-interaction between educated ( $E$ ) and infected

( $I_1$  and  $I_2$ ) subpopulations then can be written as the system of differential equations as follows.

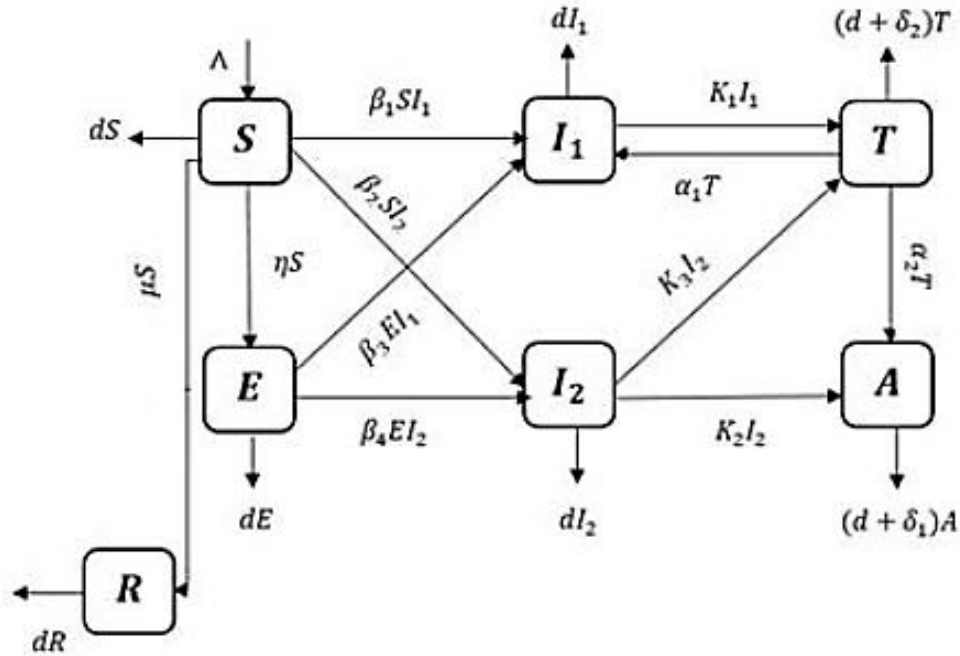


Figure 1 HIV/AIDS model with seven compartments.

$$\begin{aligned}
 \frac{dS}{dt} &= \Lambda - \beta_1 S I_1 - \beta_2 S I_2 - a S, \\
 \frac{dE}{dt} &= \eta S - \beta_3 E I_1 - d E, \\
 \frac{dI_1}{dt} &= \beta_1 S I_1 + \beta_3 E I_1 + \alpha_1 T - b I_1, \\
 \frac{dI_2}{dt} &= \beta_2 S I_2 + \alpha_1 T - c I_2, \\
 \frac{dT}{dt} &= k_1 I_1 + k_3 I_2 - e T, \\
 \frac{dA}{dt} &= k_2 I_2 + \alpha_2 T - f T, \\
 \frac{dR}{dt} &= \mu S - d R.
 \end{aligned}
 \tag{1}$$

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

description that we use in the system (1) is stated in following Table 1.

**Table 1.** Parameter’s description in the model

Symbol	Parameters
$\Lambda$	The rate of recruitment
$\mu$	The rate of recover
$\beta_1$	Coefficient of transmission from $S$ to $I_1$
$\beta_2$	Coefficient of transmission from $S$ to $I_2$
$\beta_3$	Coefficient of transmission from $E$ to $I_1$
$\beta_4$	Coefficient of transmission from $E$ to $I_2$
$\eta$	The rate of education
$d$	The rate of natural death
$k_1$	The rate of progression from $I_1$ to $T$
$k_2$	The rate of progression from $I_2$ to $A$
$k_3$	The rate of progression from $I_2$ to $T$
$\alpha_1$	Successful proportion of treatment
$\alpha_2$	Failure proportion of treatment
$\delta_1$	The rate of death because of AIDS
$\delta_2$	The rate of death because of AIDS being treated

**3. THE MODEL ANALYSIS**

Equilibrium points are determined by solving the system (1) when satisfies the following condition  $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI_1}{dt} = \frac{dI_2}{dt} = \frac{dT}{dt} = \frac{dA}{dt} = \frac{dR}{dt} = 0$ . By simple calculations, the ordinary differential equation of system (1) has two equilibrium points, we call them as disease-free ( $K_3^0 T^0$ ) and endemic ( $K_3^* T^*$ ) points. The disease-free equilibrium point ( $K_3^0 T^0$ ) is determined when the infected  $I_1, I_2 = 0$ , then we have

$$K_3^0 = (S^0, E^0, I_1^0, I_2^0, T^0, A^0, R^0) = \left( \frac{\Lambda}{a}, \frac{\eta\Lambda}{da}, 0, 0, 0, 0, \frac{\mu\Lambda}{da} \right).$$

Next, the endemic point ( $K_3^* T^*$ ) is yielded when  $I_1, I_2 \neq 0$  such that we get  $K_3^* = (S^*, E^*, I_1^*, I_2^*, T^*, A^*, R^*)$ . The values of endemic point ( $K_3^* T^*$ ) is determined by using numerical simulation. Before we analyze stability or the equilibrium points, we determine the basic reproduction number ( $R_0 T^*$ ) as a threshold of an outbreak of endemic occurs [9].

The basic reproduction number ( $R_0 T^*$ ) can be calculated using ( $R_0$ )next generation matrix method [5]. We find  $R_0 = \frac{\beta_1 d \Lambda + \beta_3 \eta \Lambda}{abd}$ .

The local stability analysis can be found by calculating the eigenvalues of the Jacobian matrix from equation (1). The disease-free point

$(K_3^0 T^0)$  is asymptotically stable when we get negative sign of all the eigen values (real part).

The Jacobian matrix of equation (1) at  $K_3^0$  is

$$J(K_3^0) = \begin{pmatrix} -a & 0 & \frac{\beta_1 \Lambda}{\alpha} & -\frac{\beta_2 \Lambda}{\alpha} & 0 & 0 & 0 \\ \eta & -d & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{\beta_1 \Lambda}{\alpha} - b & 0 & \alpha_1 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_2 \Lambda}{\alpha} - c & 0 & 0 & 0 \\ 0 & 0 & k_1 & k_3 & -e & 0 & 0 \\ 0 & 0 & 0 & k_2 & \alpha_2 & -f & 0 \\ \mu & 0 & 0 & 0 & 0 & 0 & -d \end{pmatrix}$$

According to the calculation of  $|J(K_3^0) - rI| = 0$ ,  $r_1 = -d, r_2 = -f, r_3 = -d, r_4 = -a, r_5 = \frac{\beta_2 \Lambda}{a} - c$  and  $r_6, r_7$  that meets

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

Then,  $r_5 = \frac{\beta_2 \Lambda}{a} - c = c(R_0 - 1)$  where  $r_5$  is negative if  $R_0 < 1$ . Furthermore,  $r_6, r_7 < 0$  if  $r_6, r_7 = -ge - \alpha_1 k_1 > 0$  and  $r_6 + r_7 = -(e - g) < 0$ . Finally, we get negative sign of all eigenvalues when

$R_0 < 1$  and we can state that the disease-free point ( $K_3^0 T^0$ ) is asymptotically stable when  $R_0 < 1$ .

Next, the stability analysis of endemic point ( $K_3^* T^*$ ) is determined by calculating the eigenvalues of the Jacobian matrix system (1) at  $K_3^*$  that can be expressed as follows

$$J(K_3^*) = \begin{pmatrix} -\beta_1 I_1 - \beta_2 I_2 - a & 0 & -\beta_1 S & -\beta_2 S & 0 & 0 & 0 \\ \eta & -\beta_3 I_1 - \beta_4 I_2 - d & 0 & -\beta_4 E & 0 & 0 & 0 \\ \beta_1 I & 0 & \beta_1 S + \beta_3 E - b & 0 & \alpha_1 & 0 & 0 \\ \beta_2 I_2 & \beta_4 I_2 & 0 & \beta_2 S + \beta_4 E - c & 0 & 0 & 0 \\ 0 & 0 & k_1 & k_3 & -e & 0 & 0 \\ 0 & 0 & 0 & k_2 & \alpha_2 & -f & 0 \\ \mu & 0 & 0 & 0 & 0 & 0 & -d \end{pmatrix}$$

If  $H_1 = \beta_1 I_1 + \beta_2 I_2 + a$ ,  $H_2 = \beta_3 I_1 + \beta_4 I_2 + d$ ,  $H_3 = \beta_1 S + \beta_3 E$ , dan  $H_4 = \beta_2 S + \beta_4 E$ , then

characteristic equation of  $J(K_3^*)$  is determined by getting the solution  $|J(K_3^*) - rI| = 0$

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

so that is obtained  $r_1 = -d, r_2 = -f$ , and  $r_3, r_4, r_5, r_6, r_7$  that meets

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

where

$$b_1 = H_1 - H_2 - H_3 - H_4 + b + c + e,$$

$$b_2 = \beta_1 I_1 \beta_1 S + I_2 \beta_2 S \beta_2 + H_1 b + H_1 c + H_1 e + H_2 H_3 + H_2 H_4 + H_3 H_4$$

$$+ bc + be + ce - H_1 H_2 - H_1 H_3 - H_1 H_4 - H_2 b - H_2 c - H_2 e - H_3 c - H_3 e - H_3 b - H_4 e - \alpha_1 k_1,$$

$$b_3 = \beta_1 I_1 \beta_1 S c + \beta_1 I_1 \beta_1 S e + \beta_2 S \beta_2 I_2 b + \beta_2 S \beta_2 I_2 e + \beta_2 S \beta_4 I_2 \eta + H_1 H_2 H_3$$

$$+ H_1 H_2 H_4 + H_1 H_3 H_4 + H_1 b c + H_1 b e + H_1 c e + H_2 H_3 c + H_2 H_3 e + H_2 H_4 b + H_2 H_4 e + H_2 \alpha_1 k_1 + H_3 H_4 e + H_4 \alpha_1 k_1 + b c e - \beta_1 I_1 \beta_1 S H_2 - \beta_2 S \beta_2 I_2 H_2 - \beta_2 S \beta_2 I_2 H_3 - \beta_1 I_1 \beta_1 S H_4 - H_1 H_2 b - H_1 H_2 c - H_1 H_2 e - H_1 H_3 c - H_1 H_3 e - H_1 H_4 e - H_1 H_4 b - H_1 \alpha_1 k_1 - H_2 H_3 H_4 - H_2 b c - H_2 b e - H_2 c e - H_3 c e - H_4 b e - \alpha_1 k_1 c,$$

$$b_4 = H_2 H_3 \beta_2 S \beta_2 I_2 + H_2 H_4 \beta_1 S \beta_1 I_1 + \beta_1 S \beta_1 I_1 c e + \alpha_1 k_3 \beta_1 S \beta_2 I_2 + \beta_2 S \beta_2 I_2 b e + \beta_2 S \beta_4 I_2 b \eta + \beta_2 S \beta_4 I_2 e \eta + H_1 H_2 H_3 c +$$

$$H_1 H_2 H_3 e + H_1 H_2 H_4 b + H_1 H_2 H_4 e + H_1 H_2 \alpha_1 k_1 + H_1 H_3 H_4 e + H_1 H_4 \alpha_1 k_1 + H_1 b c e + H_2 H_3 c e + H_2 H_4 b e + c H_2 \alpha_1 k_1 - H_2 I_2 S \beta_1 \beta_1 c - H_2 I_2 S \beta_1 \beta_1 e - H_2 I_2 S \beta_2 \beta_2 b - H_2 I_2 S \beta_2 \beta_2 e - H_3 I_2 S \beta_2 \beta_4 \eta - H_4 I_1 S \beta_1 \beta_1 e - I_2 S \beta_2 \beta_2 \alpha_1 k_1 - H_1 H_2 H_3 H_4 - H_1 H_2 b c - H_1 H_2 b e - H_1 H_2 c e - H_1 H_3 c e - H_1 H_4 b e - H_1 \alpha_1 k_1 c - H_2 H_4 H_4 e - H_2 H_4 \alpha_1 k_1 - H_2 b c e$$

$$b_5 = H_2 H_3 \beta_2 \beta_2 I_2 S e + H_2 H_4 \beta_1 \beta_1 I_1 S e + H_2 \beta_2 \beta_2 I_2 S \alpha_1 k_1 + I_2 S \alpha_1 k_3 \beta_1 \beta_4 \eta + I_2 S e b \beta_2 \beta_4 \eta + H_1 H_2 H_3 c e + H_1 H_2 H_4 b e$$

$$+ H_1 H_2 \alpha_1 c k_1 - H_2 I_1 S \beta_1 \beta_1 c e - H_2 I_2 S \beta_1 \beta_2 \alpha_1 k_3 - H_2 I_2 S b e \beta_2 \beta_2 - H_3 I_2 S \beta_2 \beta_4 e \eta - I_2 S \alpha_1 \eta k_1 \beta_2 \beta_4 - H_1 H_2 H_3 H_4 e - H_1 H_2 H_4 \alpha_1 k_1 - H_1 H_2 b c e.$$

Since it is rather complicated to find the eigenvalues from the characteristic equation (2), the stability analysis of the endemic point ( $K_3^*, T^*$ ) is yielded by applying the criteria of Routh-Hurwitz. The endemic

equilibrium  $K_3^*$  is asymptotically stable when satisfies  $b_1 > 0$  and

- i.  $b_1 b_2 - b_3 > 0,$
- ii.  $b_1 b_2 b_3 - b_3^2 - b_1^2 b_4 > 0,$
- iii.  $b_1 b_2 b_3 b_4 + 2 b_1 b_4 b_5 + b_2 b_3 b_5 - b_1^2 b_4^2 - b_1 b_2^2 b_5 - b_3^2 b_4 - b_5^2 > 0$
- iv.  $b_5 > 0$

4. NUMERICAL SIMULATION

In this part, we simulate numerically the equilibrium points by using the parameter values in Table 1. The disease-free point is presented in Figure 2, then we get the basic reproduction number  $R_0 = 0.1047 < 1$ . With initial values of each subpopulation  $NA = (30, 10, 25, 35, 20, 16, 50)$ , the

solutions converge to the disease-free point ( $K_3^0$ ). We can say that there is no infected individual in the population after quite a long time. This numerical simulation supports the analysis results in the previous section, that is asymptotically stable of the disease-free point ( $K_3^0$ ) when  $R_0 < 1$ .

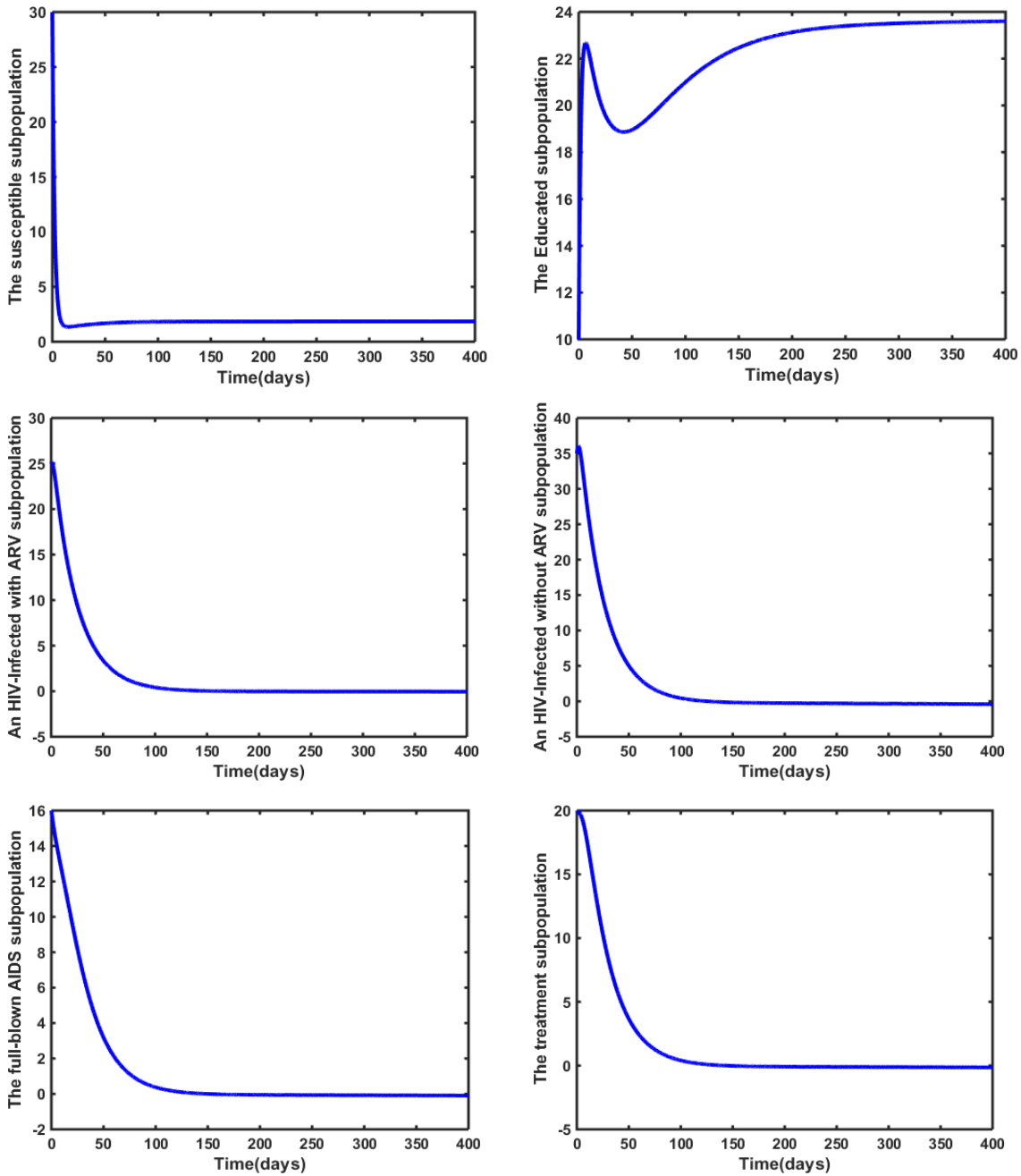
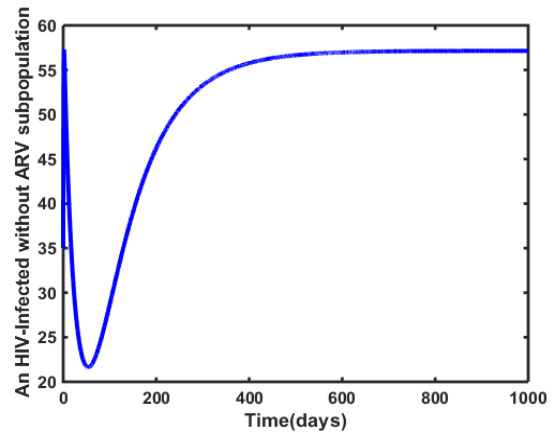
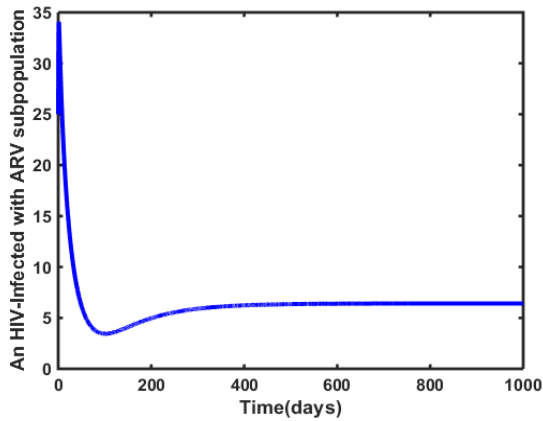
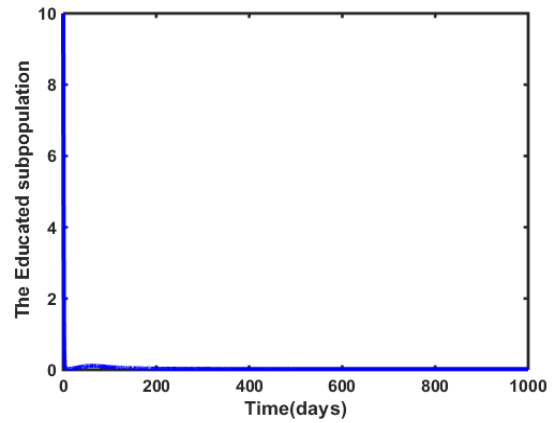
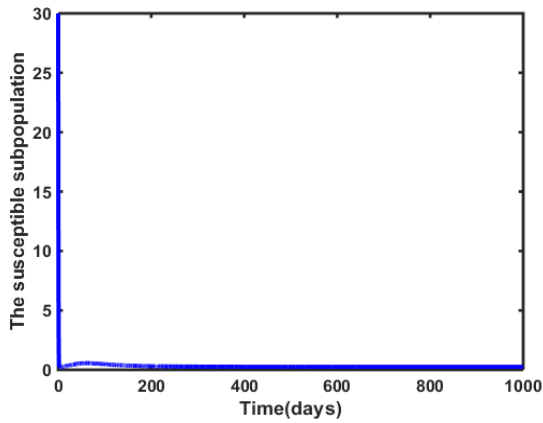


Figure 2 The solution of system (1) numerically when  $R_0 < 1$ .

Next, the numerical simulation of the endemic point is showed in Figure 3 by using the parameters in Table 1, and we get the basic reproduction number  $R_0 = 4.7321 > 1$ . Figure 3 presents the solution of system (1) with the same initial values as in the numerical simulation of the disease-free equilibrium point. We can see that by considering the interaction between educated and infected (consuming ARV), the educated subpopulation contributes small increase of infected subpopulation with consuming ARV when we compare to the result in [6]. It is

because even the educated has some knowledges about the spread of HIV/AIDS, when they interact each other, there is potential risk of the educated individual becomes infected individual. From Figure 3, the solution converges to endemic equilibrium ( $K_3^*$ ), that means disease of HIV spreads in the populations. This numerical simulation supports the analytical result that the endemic point ( $K_3^*$ ) is asymptotically stable when satisfies the criteria of Routh-Hurwitz.



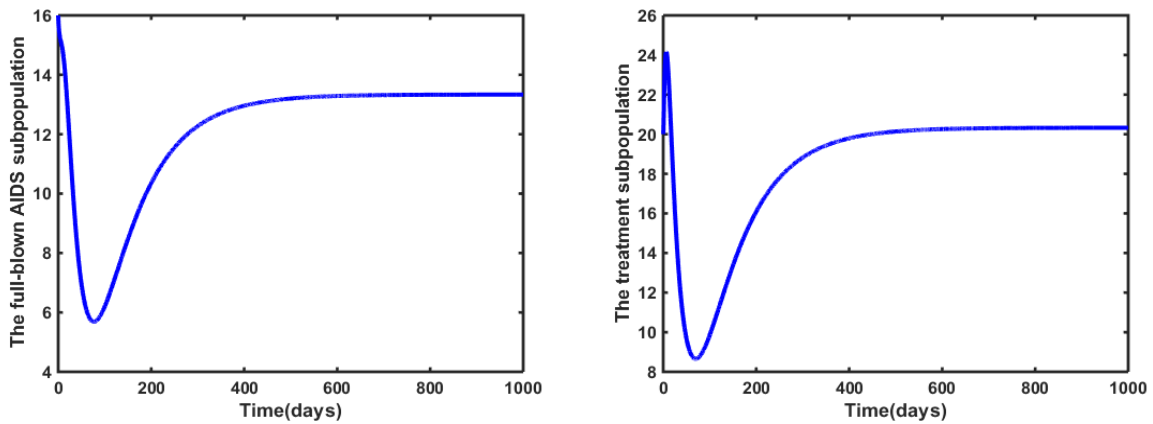


Figure 3 The solutions of system (1) numerically when  $R_0 > 1$ .

### 5. CONCLUSION

The study of dynamical system of constructed model of HIV/AIDS have been investigated. We consider with multi-interaction between subpopulations in the model, which is the interaction between educated (E) and infected ( $I_1$  and  $I_2$ ) subpopulations. The system has two equilibrium points, the disease-free and endemic points. The basic reproduction number has been obtained by applying the next generation matrix which is value can determine endemic occurs or not. The local stability analysis of equilibrium points of the model is conducted which gives the result asymptotically stable when  $R_0 < 1$  for the disease-free point and unstable otherwise. Furthermore, the endemic point is asymptotically stable when it satisfies the criteria of Routh-Hurwitz. The last result is the numerical simulations support the analysis results.

### AUTHORS' CONTRIBUTION

Habibah: designed the research and conceptualizing the manuscript. Trisilowati and Muzaqi: writing manuscript. Tania and AlFaruq: presenting and analysing the data.

### ACKNOWLEDGMENTS

The authors would like to express appreciation for the support of Brawijaya University, Project Number DIPA-023.17.2.677512/2021 and Agreement Hibah Penelitian Guru Besar dan Doktor 2021 Number 1629/UN10.F09/PN/2021

### REFERENCES

- [1] L. Cai, X. Li, M. Ghosh, B. Guo, Stability Analysis of an HIV/AIDS Epidemic Model with Treatment, *Journal of Computational and Applied Mathematics*, 229 (1) (2009) 313–323. DOI: <https://doi.org/10.1016/j.cam.2008.10.067>
- [2] L. Cai, S. Guo, S. Wang, Analysis of an extended HIV/AIDS epidemic model with treatment, *Applied Mathematics and Computation*, 236 (2014) 621–627. DOI: <http://dx.doi.org/10.1016/j.amc.2014.02.078>
- [3] H-F. Huo, R. Chen, X-Y Wang, Modelling and stability of HIV/AIDS Epidemic Model with Treatment, *Applied Mathematics Modelling*, 40(13–14) (2016) 6550–6559. DOI: <https://doi.org/10.1016/j.apm.2016.01.054>
- [4] H-F. Huo, R. Chen, Stability of an HIV/AIDS Treatment Model with Different Stages, *Discrete Dynamics in Nature and Society*, 2015 (2015) 1–9. DOI: <https://doi.org/10.1155/2015/630503>
- [5] B. Ulfa, T. Trisilowati, M. K. Wuryansari, Dynamical Analysis of HIV/AIDS Epidemic Model with Treatment, *The Journal of Experimental Life Science*, 8(1) 2018 23–29. DOI: <http://dx.doi.org/10.21776/ub.jels.2018.008.01.04>
- [6] U. Habibah, T. Trisilowati, Y. L. Pradana, W. Villadistyan, Mathematical Model of HIV/AIDS with Two Different Stages of Infection Subpopulation and Its Stability Analysis, *Engineering Letters*, 29(1) (2021)



- 1-9. Retrieved from [http://www.engineeringletters.com/issues\\_v29/issue\\_1/EL\\_29\\_1\\_01.pdf](http://www.engineeringletters.com/issues_v29/issue_1/EL_29_1_01.pdf)
- [7] H-F. Huo, L-X. Feng, Global Stability for an HIV/AIDS Epidemic Model with Different Latent Stages and Treatment, *Applied Mathematics Modelling*, 37(3) 2013 1480–1489. DOI: <https://doi.org/10.1016/j.apm.2012.04.013>
- [8] U. Habibah, R. A. Sari, The Effectiveness of an Antiretroviral Treatment (ARV) and a Highly Active Antiretroviral Therapy (HAART) on HIV/AIDS Epidemic Model, in *AIP Conference Proceedings*, 2018, pp. 1-6. DOI: <https://doi.org/10.1063/1.5062794>
- [9] A. Alshorman, X. Wang, M. J. Meyer, L. Rong, Analysis of HIV Models with Two Time Delays, *Journal of Biology Dynamics*, 11 (2017) 40–64. DOI: <https://doi.org/10.1080/17513758.2016.1148202>