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MODELING HIV/AIDS USING SHAT MODEL

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ABSTRACT

HIV/AIDS gets on the list of deadly infectious diseases, but there is no right medicine or vaccination for it until now. Indonesia is also inseparable from the spread of HIV/AIDS year by year number of people living with HIV/AIDS in Indonesia continues to grow. The peak of HIV cases over the last twelve years (starting from 2020) in Indonesia was 50,282 cases in 2019, then the peak of AIDS was 12,214 in 2013. The purpose of the study is to model the spread of HIV/AIDS and test it with data on the growth of HIV/AIDS in Indonesia from 2006 to 2018. The steps taken in conducting this research are to determine the equilibrium point, calculate the basic reproduction number, analyze the stability of the equilibrium point, and numeric simulation of the SHAT model with the Maple 18 tool. The numerical simulation produces a value of $R_0 = 0{,}899598817 < 1$. *Based on calculations using the Routh-Hurwitz table, we can find that the system will be asymptotically stable towards a disease-free equilibrium point, namely* $\varepsilon^0 = (229800000,0,0,0)$. *Based on the results obtained, it can conclude that HIV/AIDS will not become an epidemic in Indonesia.*

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1. INTRODUCTION

Human Immunodeficiency Virus (HIV) is a type of virus that infects white blood cells (leukocytes) which causes a decrease in human immunity. Meanwhile, Acquired Immune Deficiency Syndrome (AIDS) is a collection of symptoms that arise due to decreased immunity impacted by infection with HIV.[1] HIV/AIDS gets on the list of deadly infectious diseases, but there has not been found the right medicine and vaccination for it until now.

In 2020, 680,000 [480,000-1.0 million] people died from HIV-related causes and 1.5 million [1.0-2.0 million] people contracted HIV. HIV continues to be a global public health problem. It has been recognized by 36.3 million [27.2-47.8 million] lives so far [2]. Indonesia is also inseparable from the spread of HIV/AIDS year by year number of people living with HIV/AIDS in Indonesia continues to grow. In Indonesia, the peak of HIV cases over the last twelve years (starting from 2020) was 50,282 cases in 2019, then AIDS at 12,214 in 2013 [1].

The application of mathematics can be found in many daily activities. It can be modeled in mathematical form or could say it as a mathematical model. The role of Mathematics as the mother of all sciences also applies in the world of health. Many studies have been conducted in the world of health using mathematics. The process of mimicking reality by using the language of mathematics is known as mathematical modeling [3]. Then, from the process, we will lead to a mathematical model. Mathematical models are often used in solving the problem of the spread of infectious diseases. In the research of the spreading of diseases with a mathematical model, we will investigate whether the infectious disease will become an epidemic or disappear over time.

The SIR Epidemic Model divides the existing population into three sub-populations, namely Susceptible (S), Infected (I), and Recovered (R). Furthermore, Susceptible (S) is a susceptible individual, who is healthy and can contract the disease; Infected (I) is an infected individual, and, Recovered (R) is a recovered individual (R) who is immune to the disease [4]–[6]. The development of the SIR Epidemic Model in the modeling of HIV/AIDS resulted in the Susceptible-Infected-AIDS (SIA) Epidemic Model [7], [8]. The epidemic model continues to develop and produces several models, including the SEIR model [9], SJAT [10], SEIA[11], SICA[12].

There is no cure for HIV infection. But with access to effective HIV prevention, diagnosis, treatment, and care, including opportunistic infections, HIV infection has become a manageable chronic health condition, enabling people living with HIV to lead more fulfilling lives, long, and healthy [2]. People with HIV need treatment with antiretrovirals (ARVs) to reduce the amount of HIV in the body. With that, they don't enter the AIDS stage. People with AIDS need ARV treatment to prevent opportunistic infections with various complications [1]. Antiretroviral Therapy (ART) prevents people living with HIV/AIDS from transmitting HIV to their sexual partners. Thus, early treatment with ART and support for continuing care is urgent because it not only improves the health of people living with HIV but also prevents HIV transmission.

From the explanation in the previous paragraph, we can see that it is necessary to pay attention to the sub-populations receiving treatment for HIV/AIDS, then the authors examine a model that includes sub-populations both infected with HIV and infected who progress to AIDS and receive treatment. Emvudu, Y., Bongor, D., & Koïna entitle Mathematical analysis of HIV/AIDS stochastic dynamic models examines a Deterministic Model of HIV/AIDS with Treatment in their article [13]. The model in this study then becomes a reference to this study by adding new parameters that represent the displacement from compartment T to compartment H so that the SHAT model is formed. The SHAT epidemic model is used to model the infectious disease HIV/AIDS by dividing the population into four subpopulations, namely Susceptible (S), HIV infected (H), AIDS (A), and Treatment (T). It was further explained that Susceptible (S) is a sub-population that is healthy and can be transmitted disease. HIV-infected (H) is a sub-population infected with HIV. AIDS(A) is a sub-population affected by AIDS. Then, Treatment (T) is a sub-population receiving ARV treatment that they do not transmit HIV. The SHAT model simulation will be carried out using data and parameters obtained from the research of Khan, M. A., & Odinsyah [14] which this study uses data on the spread of HIV/AIDS in Indonesia from 2006 to 2018 as a basis for determining the parameters to be used in the numerical simulation.

2. RESEARCH METHODS

The steps taken in researching the spread of HIV/AIDS with the SHAT model are as follows:

2.1. Literature Review on the SHAT Model

Review the literature by understanding the theoretical model of the SHAT epidemic.

2.2. SHAT Modeling for HIV/AIDS

SHAT modeling for HIV/AIDS is obtained by modifying the existing model, which has a population of suspect individuals, HIV Infected, AIDS, and under ARV treatment. The model was modified by adding a migration factor from the sub-population under ARV treatment (T) into the HIV-infected sub-population (H).

2.3. Finding the Equilibrium Point in the SHAT Model

The disease-free equilibrium point is obtained with H = 0, A = 0, and T = 0. To find the endemic equilibrium point H ≠ 0, A ≠ 0 and T ≠ 0. After both points equilibrium are obtained, then evaluated using the Jacobian matrix.

2.4. Stability Analysis by Testing the Stability of the SHAT Model

Stability analysis was carried out by looking at the signs of the characteristic polynomial roots of the Jacobian matrix, which had been evaluated at the equilibrium point. Because the characteristic polynomial of the Jacobian matrix obtained is of a high degree, the Routh-Hurwitz criterion is used to make it easier.

2.5. Parameter Estimation

Estimation is done by examining the five populations and determining the influencing factors and determining the parameters (estimation). The parameters used in this study were taken from the Fractional model of HIV transmission with awareness effect by Khan, M. A., & Odinsyah.

2.6. Result Analysis

The analysis is carried out by looking at the value of the HIV and AIDS population, if it is not zero over time, the disease will become an epidemic in the population. Conversely, if the value is zero over time, the disease disappears and does not become an epidemic.

3. RESULTS AND DISCUSSION

The SHAT epidemic model is used to model the infectious disease HIV/AIDS by dividing the population into four subpopulations, namely Susceptible (S), HIV infected (H), AIDS (A), and Treatment (T). The SHAT model itself is formed by referring to the model that has been researched by Emvudu, Y., Bongor, D., & Koïna, then the model is modified by adding the parameter which is the displacement parameter from sub-population T to sub-population H.

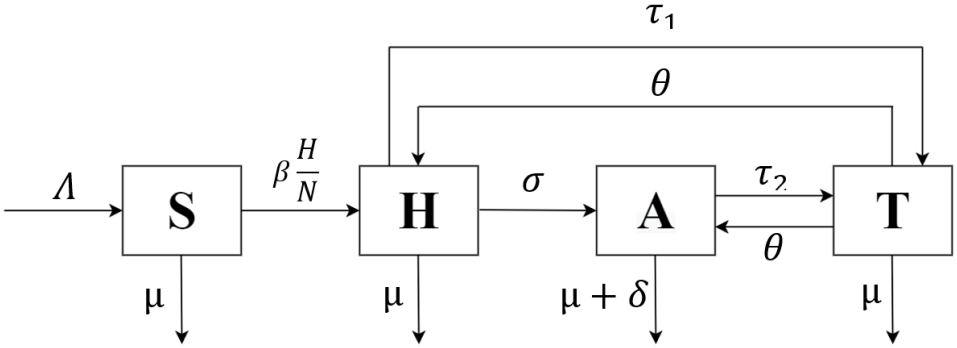

Figure 1. SHAT model schematic

In the form of a differential equation, the SHAT model can be written as follows,

$$\frac{dS}{dt} = \Lambda - \beta\frac{H}{N}S - \mu S$$

$$\frac{dH}{dt} = \beta\frac{H}{N}S - (\mu + \sigma + \tau_1)H + \theta T$$

$$\frac{dA}{dt} = \sigma H - (\mu + \delta + \tau_2)A + \theta T$$

$$\frac{dT}{dt} = \tau_1 H + \tau_2 A - (2\theta + \mu)T$$

The disease-free equilibrium point is the condition at which the population is free or not affected by a disease. When the disease does not exist, automatically, the sub-population infected with HIV (H), infected with AIDS (A), and undergoing treatment (T) is zero. Mathematically, it can be written as follows,

$$H = 0, A = 0, \text{and } T = 0.$$

Therefore, the vulnerable sub-population (S),

$$\begin{aligned} \frac{dS}{dt} &= 0 \\ \Lambda - \beta\frac{H^0}{N}S^0 - \mu S^0 &= 0 \\ \Lambda - \mu S^0 &= 0 \\ S^0 &= \frac{\Lambda}{\mu} \end{aligned}$$

Then the disease-free equilibrium point is obtained

$$\varepsilon^0 = (S^0, H^0, A^0, T^0) = \left(\frac{\Lambda}{\mu}, 0,0,0\right)$$

Next, the endemic equilibrium point will be calculated from the SHAT model. At this point, $H > 0, A > 0, T > 0$ which means the disease will spread and become an epidemic.

$$\begin{aligned} \frac{dS}{dt} &= 0 \\ \Lambda - \beta\frac{H^*}{N}S^* - \mu S^* &= 0 \\ \Lambda - \beta\frac{H^*}{N}S^* - \mu S^* &= 0 \\ S^* &= \frac{\Lambda}{\beta\frac{H^*}{N} + \mu} \end{aligned}$$

$$\begin{aligned} \frac{dH}{dt} &= 0 \\ \beta\frac{H^*}{N}S^* - (\mu + \sigma + \tau_1)H^* + \theta T^* &= 0 \\ H^* &= \frac{\theta T^*}{(\mu + \sigma + \tau_1) - \beta\frac{S^*}{N}} \end{aligned}$$

$$\begin{aligned} \frac{dA}{dt} &= 0 \\ \sigma H^* - (\mu + \delta + \tau_2)A^* + \theta T^* &= 0 \end{aligned}$$

$$A^* = \frac{\sigma H^* + \theta T^*}{(\mu + \delta + \tau_2)}$$

$$\frac{dT}{dt} = 0$$
$$\tau_1 H^* + \tau_2 A^* - (2\theta + \mu) T^* = 0$$
$$T^* = \frac{\tau_1 H^* + \tau_2 A^*}{(2\theta + \mu)}$$

After substitution several times in the above equations, the equilibrium point is generated as follows,

$$S^* = \frac{klm - \theta(\tau_1 l + \tau_2(\sigma + k))}{j(lm - \tau_2\theta)}$$

$$H^* = \frac{\Lambda(lm - \tau_2\theta)}{klm - \theta(\tau_1 l + \tau_2(\sigma + k))} - \frac{\mu}{j}$$

$$A^* = \left(\frac{m(\sigma + k) - km + \tau_1\theta}{lm - \tau_2\theta}\right)\left(\frac{\Lambda(lm - \tau_2\theta)}{klm - \theta(\tau_1 l + \tau_2(\sigma + k))} - \frac{\mu}{j}\right)$$

$$T^* = \frac{\tau_1 + \tau_2\left(\frac{m(\sigma+k) - km + \tau_1\theta}{lm - \tau_2\theta}\right)}{m}\left(\frac{\Lambda(lm - \tau_2\theta)}{klm - \theta(\tau_1 l + \tau_2(\sigma + k))} - \frac{\mu}{j}\right)$$

With $j = \frac{\beta}{N}, k = (\mu + \sigma + \tau_1), l = (\mu + \delta + \tau_2), m = (2\theta + \mu)$,

$$\varepsilon^* = (S^*, H^*, A^*, T^*)$$

As one of the factors used in determining whether a disease will become an epidemic or not, the basic reproduction number will be calculated. The basic reproduction number was calculated by taking into account the infected sub-population, namely $\frac{dH}{dt}, \frac{dA}{dt}, \frac{dT}{dt}$. With the differential equations of the three subpopulations, two F and V matrices will be constructed by linearizing the Fi and Vi matrices, respectively. Matrix F represents new infections and matrix V represents sub-populations that have been infected with HIV and AIDS. The matrices Fi and Vi are expressed as follows.

$$F_i = \begin{bmatrix} \beta \frac{H}{N} S \\ 0 \\ 0 \end{bmatrix}, V_i = \begin{bmatrix} (\mu + \sigma + \tau_1)H - \rho T \\ (\mu + \delta + \tau_2)A - \sigma H \\ (\mu + \rho)T - \tau_1 H - \tau_2 A \end{bmatrix}$$

Furthermore, it will be linearized with the Jacobian matrix to the matrix above, which results in

$$J(H, A, T) = F = \begin{bmatrix} \beta \frac{1}{N} S & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$J(H, A, T) = V = \begin{bmatrix} (\mu + \sigma + \tau_1) & 0 & -\theta \\ -\sigma & (\mu + \delta + \tau_2) & -\theta \\ -\tau_1 & -\tau_2 & (2\theta + \mu) \end{bmatrix}$$

Then by entering the value of the equilibrium point into the Jacobian matrix, we get

$$J\left(\frac{\Lambda}{\mu}, 0,0,0\right) = F = \begin{bmatrix} n & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$J\left(\frac{\Lambda}{\mu},0,0,0\right) = V = \begin{bmatrix} k & 0 & -\theta \\ -\sigma & l & -\theta \\ -\tau_1 & -\tau_2 & m \end{bmatrix}$$

with $n = \frac{\Lambda\beta}{\mu N}$. Then FV^{-1} will be calculated with the help of Maple 18, we get

$$FV^{-1} = \begin{bmatrix} \frac{n(lm-\tau_2\theta)}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta} & \frac{n\tau_2\theta}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta} & \frac{nl\theta}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Then we will look for the characteristic equation with $|FV^{-1} - \lambda I| = 0$

$$FV^{-1} - \lambda I = \begin{bmatrix} \frac{n(lm-\tau_2\theta)}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta} - \lambda & \frac{n\tau_2\theta}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta} & \frac{nl\theta}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta} \\ 0 & -\lambda & 0 \\ 0 & 0 & -\lambda \end{bmatrix}$$

Produced equation,

$$\lambda^2\left(\frac{n(lm-\tau_2\theta)}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta} - \lambda\right) = 0$$

Then,

$$\lambda_1 = 0, \qquad \lambda_2 = 0, \qquad \lambda_3 = \frac{n(lm-\tau_2\theta)}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta}$$

So, the largest eigenvalue is $\lambda_3 = \frac{n(lm-\tau_2\theta)}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta}$ then $R_0 = \frac{n(lm-\tau_2\theta)}{klm-k\tau_2\theta-l\tau_1\theta-\sigma\tau_2\theta}$. The basic reproduction number R_0 in population growth is a function of time t, R_0(t), as a result of the assumption that net transmission is directly proportional to the density of susceptible people multiplied by the density of infected persons **[15]**. The potential for the spread of a disease in a population can be seen with the parameter R_0. When $R_0 < 1$, the spread of the disease will stop immediately as the number of infected individuals decreases. On the other hand, when R_0>1, the disease will become an epidemic as a result of the increasing number of infected individuals **[16]**.

We will be checked by linearizing the differential equation of the SHAT model with the Jacobian matrix to determine the stability of the disease-free equilibrium point,

$$J(S,H,A,T) = M = \begin{bmatrix} -\frac{\beta H}{N} - \mu & -\frac{\beta S}{N} & 0 & 0 \\ \frac{\beta H}{N} & \frac{\beta S}{N} - (\mu+\sigma+\tau_1) & 0 & \theta \\ 0 & \sigma & -(\mu+\delta+\tau_2) & \theta \\ 0 & \tau_1 & \tau_2 & -(2\theta+\mu) \end{bmatrix}$$

$$J\left(\frac{\Lambda}{\mu},0,0,0\right) = M = \begin{bmatrix} -\mu & -\frac{\Lambda\beta}{\mu N} & 0 & 0 \\ 0 & \frac{\Lambda\beta}{\mu N} - (\mu+\sigma+\tau_1) & 0 & \theta \\ 0 & \sigma & -(\mu+\delta+\tau_2) & \theta \\ 0 & \tau_1 & \tau_2 & -(2\theta+\mu) \end{bmatrix}$$

Then the characteristic equation will be searched by calculating $|M - \lambda I| = 0$.

$$M-\lambda I=\begin{bmatrix} -\mu-\lambda & -\frac{\Lambda\beta}{\mu N} & 0 & 0 \\ 0 & \frac{\Lambda\beta}{\mu N}-(\mu+\sigma+\tau_1)-\lambda & 0 & \theta \\ 0 & \sigma & -(\mu+\delta+\tau_2)-\lambda & \theta \\ 0 & \tau_1 & \tau_2 & -(2\theta+\mu)-\lambda \end{bmatrix}$$

With the help of Maple 18, the characteristic equation is obtained,

$\frac{1}{\mu N}[(\lambda+\mu)(\mu N\lambda^3+(\mu N\delta+3\mu N\mu+2\mu N\theta+\mu N\sigma+\mu N\tau_1+\mu N\tau_2-\beta\Lambda)\lambda^2+(2\mu N\delta\mu+2\mu N\delta\theta+\mu N\delta\sigma+\mu N\delta\tau_1+3\mu N\mu^2+4\mu N\mu\theta+2\mu N\mu\sigma+2\mu N\mu\tau_1+2\mu N\mu\tau_2+2\mu N\sigma\theta+\mu N\theta\tau_2+\mu N\sigma\tau_2+\mu N\theta\tau_1+\mu N\tau_1\tau_2-\delta\beta\Lambda-2\mu\beta\Lambda-2\theta\beta\Lambda-\beta\Lambda\tau_2)\lambda+\mu N\delta\mu^2+\tau_1\theta\mu N\mu+\tau_1\theta\mu N\delta+2\mu N\delta\mu\theta+\mu N\delta\mu\sigma+\mu N\delta\mu\tau_1+2\mu N\delta\sigma\theta+\mu N\mu^3+2\mu N\mu^2\theta+\mu N\mu^2\sigma+\mu N\mu^2\tau_1+\mu N\mu^2\tau_2+2\mu N\mu\sigma\theta+\mu N\mu\theta\tau_2+\mu N\mu\sigma\tau_2+\mu N\mu\tau_1\tau_2-\delta\mu\beta\Lambda-2\delta\theta\beta\Lambda-\mu^2\beta\Lambda-2\mu\theta\beta\Lambda-\mu\beta\Lambda\tau_2-\theta\beta\Lambda\tau_2)]=0$ (**1**)

From **Equation 1**, we get $(\lambda+\mu)=0$ then $\lambda=-\mu$ and

$(\mu N)\lambda^3+(\mu N\delta+3\mu N\mu+2\mu N\theta+\mu N\sigma+\mu N\tau_1+\mu N\tau_2-\beta\Lambda)\lambda^2+(2\mu N\delta\mu+2\mu N\delta\theta+\mu N\delta\sigma+\mu N\delta\tau_1+3\mu N\mu^2+4\mu N\mu\theta+2\mu N\mu\sigma+2\mu N\mu\tau_1+2\mu N\mu\tau_2+2\mu N\sigma\theta+\mu N\theta\tau_2+\mu N\sigma\tau_2+\mu N\theta\tau_1+\mu N\tau_1\tau_2-\delta\beta\Lambda-2\mu\beta\Lambda-2\theta\beta\Lambda-\beta\Lambda\tau_2)\lambda+\mu N\delta\mu^2+\tau_1\theta\mu N\mu+\tau_1\theta\mu N\delta+2\mu N\delta\mu\theta+\mu N\delta\mu\sigma+\mu N\delta\mu\tau_1+2\mu N\delta\sigma\theta+\mu N\mu^3+2\mu N\mu^2\theta+\mu N\mu^2\sigma+\mu N\mu^2\tau_1+\mu N\mu^2\tau_2+2\mu N\mu\sigma\theta+\mu N\mu\theta\tau_2+\mu N\mu\sigma\tau_2+\mu N\mu\tau_1\tau_2-\delta\mu\beta\Lambda-2\delta\theta\beta\Lambda-\mu^2\beta\Lambda-2\mu\theta\beta\Lambda-\mu\beta\Lambda\tau_2-\theta\beta\Lambda\tau_2=0$ **(2)**

Equation 2 is an equation of a high degree, so Routh Hurwitz criteria will be used to analyze its stability. The Routh Hurwitz stability criterion tells whether or not there are unstable roots in a polynomial equation without actually solving them. A necessary and sufficient condition for a stable system is that all coefficients in the first column have a positive sign **[17]**. The first step is to determine the polynomial equation

$$a_n\lambda^n+a_{n-1}\lambda^{n-1}+\cdots+a_1\lambda+a_0=0$$

So that the following equation is obtained

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

Suppose that

$a_3=v=$ coefficient of $\lambda^3=\ \mu N$
$a_2=w=$ coefficient of $\lambda^2=\mu N\delta+3\mu N\mu+2\mu N\theta+\mu N\sigma+\mu N\tau_1+\mu N\tau_2-\beta\Lambda$
$a_1=x=$ coefficient of $\lambda^1=2\mu N\delta\mu+2\mu N\delta\theta+\mu N\delta\sigma+\mu N\delta\tau_1+3\mu N\mu^2+4\mu N\mu\theta+2\mu N\mu\sigma+2\mu N\mu\tau_1+2\mu N\mu\tau_2+2\mu N\sigma\theta+\mu N\theta\tau_2+\mu N\sigma\tau_2+\mu N\theta\tau_1+\mu N\tau_1\tau_2-\delta\beta\Lambda-2\mu\beta\Lambda-2\theta\beta\Lambda-\beta\Lambda\tau_2$
$a_0=y=$ coefficient of $\lambda^0=\mu N\delta\mu^2+\tau_1\theta\mu N\mu+\tau_1\theta\mu N\delta+2\mu N\delta\mu\theta+\mu N\delta\mu\sigma+\mu N\delta\mu\tau_1+2\mu N\delta\sigma\theta+\mu N\mu^3+2\mu N\mu^2\theta+\mu N\mu^2\sigma+\mu N\mu^2\tau_1+\mu N\mu^2\tau_2+2\mu N\mu\sigma\theta+\mu N\mu\theta\tau_2+\mu N\mu\sigma\tau_2+\mu N\mu\tau_1\tau_2-\delta\mu\beta\Lambda-2\delta\theta\beta\Lambda-\mu^2\beta\Lambda-2\mu\theta\beta\Lambda-\mu\beta\Lambda\tau_2-\theta\beta\Lambda\tau_2$

Then the equation will be arranged into the Routh Hurwitz array and we get

λ^3	a_3	a_1
λ^2	a_2	a_0
λ^1	b_1	
λ^0	c_1	

To fill the array, do the following calculations:

$$b_1 = -\frac{a_3a_0 - a_2a_1}{a_2} = -\frac{wx - \mu Ny}{w} = x - \frac{\mu Ny}{w}$$

$$c_1 = \frac{b_1a_0 - a_2b_2}{b_1} = \frac{\left(x - \frac{\mu Ny}{w}\right)y - x(0)}{x - \frac{\mu Ny}{w}} = y$$

The following array is obtained

λ^3	μN	x
λ^2	w	yN
λ^1	$x - \frac{\mu Ny}{w}$	
λ^0	y	

The next step is to analyze its stability by looking at the first column of the Routh Hurwitz array. Because $\mu N > 0$ to achieve local asymptotic stability, values of $w > 0, x - \frac{\mu Ny}{w} > 0,$ and $y > 0,$ are required. After calculating the value of these variables with the help of Maple 18, it was found that $w > 0, x - \frac{\mu Ny}{w} > 0,$ and $y > 0,$ it can be concluded that the disease-free equilibrium point is asymptotically stable.

Numerical simulations were calculated using data and parameters quoted from the Fractional model of HIV transmission with awareness effect **[14]**.

Table 1. Initial value

Variable	Value
$S(0)$	229789089
$H(0)$	7195
$A(0)$	3716
$T(0)$	0

Table 2. Parameter estimation

Parameter	Description	Value
Λ	Recruitment rate	$229800000/67.39$
μ	Natural Mortality rate	$1/67.39$
β	Transmission rate by HIV	0.1265
σ	Rate at which H leads to A	0.1882
θ	Rate T leave to H	0.2059
τ_1	Progression rate from H to T	0.00036523
τ_2	Progression rate from A to T	0.7661
δ	AIDS induced death rate	0.7012

The value of R_0 will be calculated with the initial values and parameter estimates above,

$$R_0 = \frac{n(lm - \tau_2\theta)}{klm - k\tau_2\theta - l\tau_1\theta - \sigma\tau_2\theta} = 0{,}899598817 \ < 1$$

Based on calculations using the Routh Hurwitz table, it is found that the system will be asymptotically stable towards a disease-free equilibrium point, namely $\varepsilon^0 = (229800000{,}0{,}0{,}0)$. Based on the results obtained, it can be concluded that HIV/AIDS will not become an epidemic. Numerical simulation was carried out with the help of Maple 18 then the result,

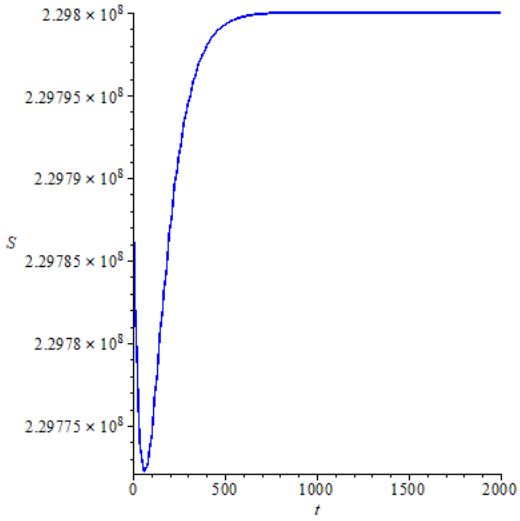

Figure 2. Susceptible sub-population (S)

In **Figure 2**, it can be seen that the vulnerable sub-population experienced a decrease from the initial value of S(0) = 229789089 due to the movement from the vulnerable sub-population to the HIV-infected sub-population. Furthermore, the chart has increased towards 229800000 as a result of continuous recruitment during the above timeframe.

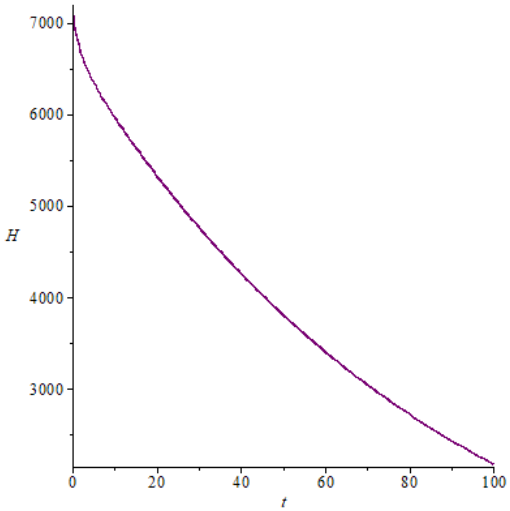

Figure 3. HIV-infected sub-population (H)

Figure 3 shows that the HIV-infected sub-population decreased from H(0) = 7195 to 0 due to the shift from this sub-population to the AIDS-infected sub-population and the sub-population undergoing ARV treatment as well as natural deaths.

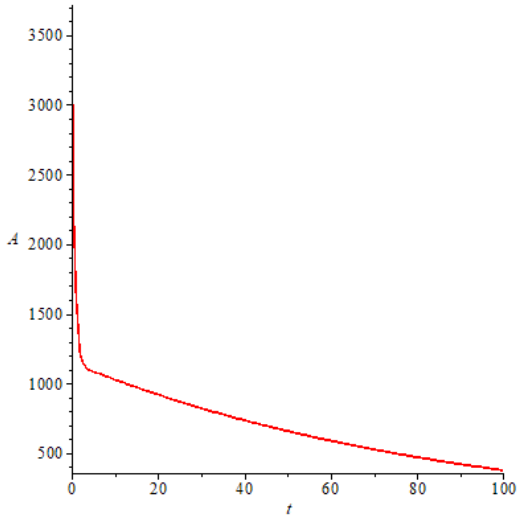

Figure 4 . AIDS infected sub-population (A)

Figure 4 shows that the graph has decreased from A(0) = 3716 to 0 due to the movement from this sub-population to the sub-population receiving care, natural deaths, and deaths by AIDS.

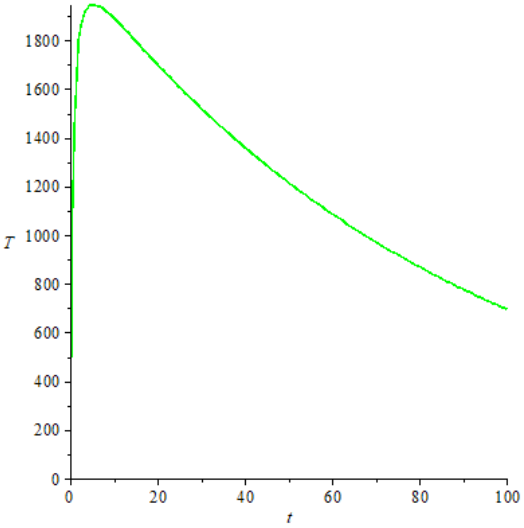

Figure 5. Sub-populations undergoing Treatment (T)

In **Figure 5**, it can be seen that the sub-population undergoing ARV treatment experienced an increase from the initial value of T(0) = 0 because the sub-population infected with HIV or AIDS received ARV treatment. Furthermore, the graph decreased to 0 as a result of the decline experienced by the HIV-infected sub-population and the AIDS-infected sub-population, the presence of individuals who stopped receiving treatment so that they returned to the infected sub-population, and natural deaths.

Based on the four graphs, it can be seen that the population will move towards a disease-free equilibrium point over time (t) toward infinity. Therefore, the numerical simulation on the SHAT Model shows that the disease will not become an epidemic in Indonesia.

4. CONCLUSION

The conclusion from this research is that with the SHAT model, it found that HIV/AIDS will not become an epidemic. It is known by the value of $R_0 = 0.899598817 < 1$and the stability of the model obtained by calculating the eigenvalues of the linearization. Then based on the numerical simulation of the SHAT model, a graph is generated that leads to a disease-free equilibrium point (where t goes to infinity).

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