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Numerical Simulation of SIA Model in HIV/AIDS Using Euler and 4th OrderRunge-Kutta Method

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Abstract

The HIV/AIDS epidemic remains a major public health issue, particularly in regions such as West Nusa Tenggara, Indonesia, where the number of reported cases continues to rise. To better understand and predict the spread of the disease, mathematical modeling provides a valuable analytical tool. This study employs the SIA (Susceptible-Infected-AIDS) compartmental model to describe the dynamics of HIV/AIDS transmission within the population. The model incorporates a latent phase, distinguishing it from simpler models and making it more suitable for diseases with long incubation periods such as HIV/AIDS. Two numerical methods, that is Euler and the 4th Order Runge–Kutta (RK4), are applied to solve the system of nonlinear differential equations derived from the model. Using official epidemiological data from 2023 in West Nusa Tenggara, the simulation tracks the evolution of the population across the three compartments over a 12-month period. The results indicate a consistent decline in the number of susceptible individuals and an increase in both infected and AIDS-diagnosed individuals. The basic reproduction number, $R_0 > 1$, suggesting that the disease is endemic in the region. Stability analysis further confirms that the disease-free equilibrium is unstable, while the endemic equilibrium is locally asymptotically stable. These findings highlight the urgency of targeted interventions and demonstrate the importance of mathematical models in guiding public health strategies for disease control.

Keywords: HIV/AIDS, SIA model, numerical simulation, Euler method, Runge-Kutta method

Abstrak

Epidemi HIV/AIDS tetap menjadi isu kesehatan masyarakat yang hangat, khususnya di usa Tenggara Barat, Indonesia, di mana jumlah kasus yang dilaporkan terus meningkat. Untuk memahami dan memprediksi penyebaran penyakit ini, diperlukan suatu pemodelan matematika yang mampu memberikan analisis yang tepat. Penelitian ini menggunakan model kompartemen SIA (Susceptible–Infected–AIDS) untuk menggambarkan dinamika penularan HIV/AIDS dalam populasi. Model ini memasukkan fase laten, yang membedakannya dari model yang lebih sederhana serta menjadikannya lebih sesuai untuk penyakit dengan masa inkubasi yang panjang, seperti HIV/AIDS. Dua metode numerik, Euler dan Runge–Kutta Orde Empat (RK4), digunakan untuk menyelesaikan sistem persamaan diferensial nonlinear yang diturunkan dari model. Simulasi dilakukan untuk melacak evolusi populasi pada tiga kompartemen selama periode 12 bulan dengan menggunakan data epidemiologi resmi tahun 2023 di Nusa Tenggara Barat. Hasil penelitian menunjukkan adanya penurunan secra konsisten jumlah individu rentan serta peningkatan jumlah individu yang terinfeksi dan terdiagnosis AIDS. Bilangan reproduksi dasar, $R_0 > 1$, mengindikasikan bahwa penyakit ini bersifat endemik di wilayah tersebut. Analisis kestabilan menunjukkan bahwa titik ekuilibrium bebas penyakit bersifat tidak stabil, sedangkan ekuilibrium endemik bersifat stabil asimtotik lokal. Hal ini menekankan pentingnya intervensi yang terarah serta menunjukkan pentingnya model matematika dalam mendukung strategi kesehatan masyarakat untuk pengendalian penyakit.

Kata Kunci: HIV/AIDS, Model SIA, Simulasi Numerik, Metode Euler, Metode Runge-Kutta.

1. INTRODUCTION

Human Immunodeficiency Virus and Acquired Immunodeficiency Syndrome, commonly referred to as HIV/AIDS, is one of the global health problems that is still a concern today because of its gradual spread and long incubation period, so it is often difficult to detect in the early stages (Mahuda & Rofiroh, 2024). In Indonesia, the spread of HIV/AIDS shows an alarming trend, including in West Nusa Tenggara (NTB) Province (Aryani, 2022). Throughout 2023, there was an increase number of HIV/AIDS cases in the NTB region (Fatmala et al., 2024). This condition shows the importance of better understanding the pattern of the spread of this disease through appropriate scientific approaches. Without adequate analysis, handling efforts can be less effective. One scientific approach that can be used is mathematical modeling (Akinwumi et al., 2021).

In the context of HIV/AIDS, mathematical models are often formulated in the form of systems of ordinary differential equations (ODEs), which describe the rate of change in each compartment over time (Seatlhodi, 2015). These models make it possible to estimate the basic reproduction number, R_0, determine the stability of equilibrium points, and analyze the long-term behavior of the epidemic within a population (Brauer et al., 2019). Such an approach, not only provides a theoretical framework for understanding the transmission dynamics, but also serves as a quantitative basis for evaluating the effectiveness of various intervention strategies.

The SIA model is one of the models used to describe the spread of HIV/AIDS by dividing the population into three groups, namely susceptible individuals (S), HIV-infected (I), and already in the AIDS stage (A) (Widyaningsih et al., 2019). Unlike the basic epidemiological model, the SIA model includes a latent phase so that it is considered more accurate for diseases that develop slowly such as HIV/AIDS (Nisa et al., 2024). This latent phase represents the time lag between a person being infected with HIV to the appearance of AIDS symptoms. With this structure, the model is able to show more realistic spread dynamics. The SIA model also allows researchers to explore how parameter changes affect the flow of spread (Apenteng, 2017). Therefore, this model is suitable for simulation purposes.

To analyze the SIA model mathematically, the system of nonlinear differential equations governing the transitions between compartments must be formulated. These equations describe how susceptible individuals become infected, how infected individuals progress to the AIDS stage, and how natural death or disease-induced mortality affects each group (Teklu & Mekonnen, 2021). Furthermore, stability analysis of the equilibrium points provides deeper insights into the long-term behavior of the epidemic and the potential effectiveness of intervention strategies (Lamwong & Pongsumpun, 2025).

However, despite the increasing number of HIV/AIDS cases in NTB, previous studies have not specifically applied or simulated the SIA model for this region. Most existing works focus on national data or other provinces, leaving a gap in region-specific modeling for NTB. Moreover, studies that compare numerical methods, particularly the Euler method and the 4th Order Runge-Kutta method, in the context of SIA model simulations for HIV/AIDS, are still limited. This lack of localized modeling and methodological comparison represents an important research gap that this study aims to address.

In this study, the SIA model is simulated using two numerical methods, namely the Euler method and the 4th Order Runge-Kutta method. Both methods were used to solve the system of nonlinear differential equations formed from the model (Iskandar & Tiong, 2022). The main objective of this simulation is to describe the behavior of the spread of HIV/AIDS in NTB based on predetermined parameters. The simulation results are expected to provide an overview of the dynamics of the spread of HIV/AIDS in the region.

2. METHOD

The data used in this quantitative research is secondary data obtained from the official report of the Ministry of Health Republic of Indonesia in 2023 regarding HIV/AIDS cases in Indonesia which includes the number of HIV cases, the number of infected individuals, and the number of AIDS cases.

The research begins with the determination of variables and model parameters, followed by the formulation of the model. The next stage is the analytical test, which includes determining the equilibrium points, conducting stability analysis, and calculating the basic reproduction number (R_0). After that, a simulation study is performed, which consists of parameter initialization, numerical solutions using the Euler and the 4th order Runge–Kutta method. The final step, we analyze the simulation results.

Among the 38 provinces in Indonesia, West Nusa Tenggara (NTB) Province was selected as the focus area of this study. The province of NTB was selected based on the availability of data and the significance of relevant cases to be analyzed. The corresponding data are presented in Table 1 (Ridho Ilham, 2025), (Wikipedia, 2025).

Table 1. Sample data of HIV/AIDS in NTB in 2023.

Variables	Description	Value
$S(t)$	Susceptible population	106.733
$I(t)$	Individuals infected with HIV	504
$A(t)$	Individuals with AIDS	148

The model used in this study is the SIA model. This model describes the dynamics of the spread of HIV/AIDS by considering three main compartments, namely S (vulnerable), I (HIV-infected), and A (AIDS). The model assumes that the number of population births and the number of natural deaths are in equilibrium; there are individuals who die naturally due to age or other diseases; HIV transmission occurs both from individuals who are in the HIV stage (I) and those who have entered the AIDS stage (A); and there is a progression from the HIV stage to the AIDS stage represented by the parameter γ. As a result of these assumptions and the flow of transmission, the compartment diagram of the HIV/AIDS spread model is obtained as follows:

The model employed in this study is the SIA model, which describes the dynamics of HIV/AIDS transmission by dividing the population into three main compartments, namely S (susceptible), I (HIV-infected), and A (AIDS). The model is formulated under several assumptions: (i) the birth rate and natural death rate of the population are in equilibrium; (ii) individuals may die naturally due to age or other causes; (iii) HIV transmission occurs from both I (HIV-infected individuals) and those in A (AIDS stage), and (iv) there is a progression from the HIV stage to the AIDS stage, represented by the parameter γ. Based on these assumptions and the transmission flow, the compartment diagram of the HIV/AIDS transmission model is presented in Figure 1.

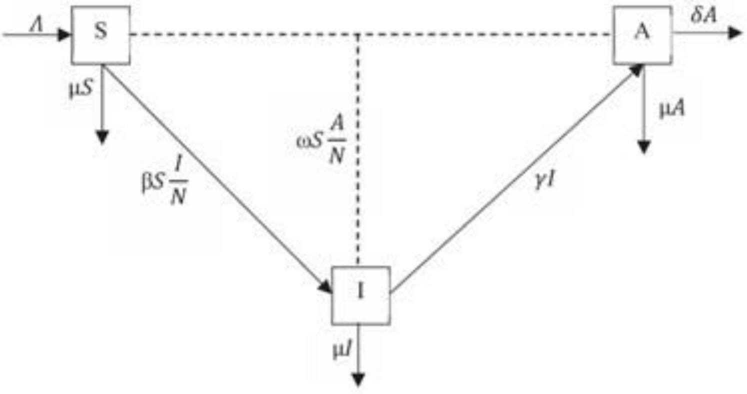

Figure 1. SIA Modelling Scheme.

The epidemiological model of HIV/AIDS transmission using the SIA model can be expressed as a system of dimensionless nonlinear differential equations, where the total population is normalized to unity, as in system (1) (Simangunsong & Mungkasi, 2021).

$$\begin{aligned}\frac{dS}{dt} &= \Lambda - \mu S - \beta S\frac{I}{N} - \omega S\frac{A}{N},\\ \frac{dI}{dt} &= \beta S\frac{I}{N} + \omega S\frac{A}{N} - \mu I - \gamma I,\\ \frac{dA}{dt} &= \gamma I - \mu A - \delta A,\end{aligned} \tag{1}$$

where the total number of population is

$$N(t) = S(t) + I(t) + A(t). \tag{2}$$

System (1) consists of eleven parameters, each with its corresponding description. The parameters and their values are summarized in Table 2.

Table 2. Description of each parameter and value.

Parameters	Description
$\boldsymbol{\Lambda}$	Recruitment (birth or inflow) rate of the population
$\boldsymbol{\beta}$	The rate transmission from HIV-infected persons to susceptible persons
$\boldsymbol{\omega}$	The rate transmission from persons with AIDS to susceptible persons
$\boldsymbol{\mu}$	Natural death rate
$\boldsymbol{\gamma}$	Progression rate from infected to AIDS
$\boldsymbol{\delta}$	Disease-induced death rate due to AIDS
$\boldsymbol{N}$	Total population
$\boldsymbol{t}$	Time in year

2.1 The Equilibrium Point

The point $a = (a_1, \dots, a_n) \in R^n$ is called the equilibrium point of $\dot{x} = f(x)$ if $f(a) = 0$, obtained by $\frac{df}{dt} = 0$ (Zeb et al., 2025). The equilibrium point of system (1) are

- the equilibrium point $a_1 = (1,0)$ known as the disease-free and
- the equilibrium point $a_2 = \left(\frac{\mu+\gamma}{\beta}, \frac{\beta-\mu-\gamma}{\beta(\mu+\gamma)}\right)$ known as the endemic.

2.2 The Stability Analysis

Stability analysis is needed to determine whether a disease will spread widely or disappear from a population. To evaluate the stability around the equilibrium point, the linearization method is used. In this case, the Jacobian matrix is obtained from the Taylor series approach to the system of differential equations.

2.3 Basic Reproduction Number (R_0)

One of the important parameters in disease epidemiology models is the basic reproduction number, that is R_0. The value of R_0 is obtained by finding the eigenvalues of the Jacobian matrix at the disease-free equilibrium point. The interpretation of R_0 reflects the conditions of disease spread. If $R_0 < 1$ then the disease-free equilibrium point is locally asymptotically stable which indicates the disease will not spread widely. In the opposite, if $R_0 > 1$ then the equilibrium point becomes unstable which means that the disease has the potential to spread. Meanwhile, if $R_0 = 0$ then the disease will not spread to other individuals and will remain in a constant amount.

2.4 Euler's Method

Given a system of first-order differential equations

$$\begin{aligned} \dot{x} &= \frac{dx}{dt} = f(x, y), \\ \dot{y} &= \frac{dy}{dt} = g(x, y). \end{aligned} \tag{3}$$

Suppose $x_i = x(t_i)$ dan $y_i = y(t_i)$ are the approximate values of x and y in t_i calculated by Euler's method. In this case, $t_i = t_0 + ih$ with $i = 0,1,2,3, \dots n$. System (3) states the Euler Method

$$\begin{aligned} x(t_{i+1}) &= x(t_i) + hf(x_i, y_i), \\ y(t_{i+1}) &= y(t_i) + hg(x_i, y_i), \end{aligned} \tag{4}$$

with $i = 0,1,2,3, \dots, n$.

2.4 The 4th Order Runge Kutta Method

One of the widely used techniques for solving differential equations is the 4th Order Runge-Kutta Method. The update formula to solve system (4) for x and y are

$$\begin{aligned} x_{i+1} &= x_i + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4), \\ y_{i+1} &= y_i + \frac{1}{6}(l_1 + 2l_2 + 2l_3 + l_4), \end{aligned} \tag{5}$$

where the intermediate terms are

$$\begin{gathered}
k_1 = hf(x_i, y_i),\\
k_2 = hf\left(t_i + \frac{1}{2}h, x_i + \frac{1}{2}k_1, y_i + \frac{1}{2}k_1\right),\\
k_3 = hf\left(t_i + \frac{1}{2}h, x_i + \frac{1}{2}k_2, y_i + \frac{1}{2}k_2\right),\\
k_4 = hf(t_i + h, x_i + k_3, y_i + k_3),
\end{gathered} \tag{6}$$

and

$$\begin{gathered}
l_1 = hf(x_i, y_i),\\
l_2 = hf\left(t_i + \frac{1}{2}h, x_i + \frac{1}{2}l_1, y_i + \frac{1}{2}l_1\right),\\
l_3 = hf\left(t_i + \frac{1}{2}h, x_i + \frac{1}{2}l_2, y_i + \frac{1}{2}l_2\right),\\
l_4 = hf(t_i + h, x_i + l_3, y_i + l_3).
\end{gathered} \tag{6}$$

3. RESULT AND DISCUSSION

The following section presents the results and discussion of our study.

3.1 Model Parameter Value

Figure 1 illustrates the mathematical model with initial conditions assigned to each variable in the subpopulation compartments of the HIV/AIDS transmission model in West Nusa Tenggara Province for 2023, as detailed in Table 3.

Table 3. The initial condition.

Variables	Description	Value
$S(t)$	Susceptible population	106.733
$I(t)$	Individuals infected with HIV	504
$A(t)$	Individuals with AIDS	148
N	Total	107.385

The value ofeach model parameters used can be seen in Table 4.

Table 4. Parameter Value.

Parameters	Description	Value	Units
$\boldsymbol{\Lambda}$	Recruitment (birth or inflow) rate of the population	500	per year
$\boldsymbol{\beta}$	The rate transmission from HIV-infected persons to susceptible persons	0,08	per year
$\boldsymbol{\omega}$	The rate transmission from persons with	0,0001	per year

	AIDS to susceptible persons		
$\boldsymbol{\mu}$	Natural death rate	0,015	per year
$\boldsymbol{\gamma}$	Progression rate from infected to AIDS	0,05	per year
$\boldsymbol{\delta}$	Disease-induced death rate due to AIDS	0,07	per year

3.2 Math Model Analysis

Assuming the initial population size of the population is N in system (1), the proportion of individuals within each group may be formally expressed as $x_1(t) = \frac{S(t)}{N}$, $x_2(t) = \frac{I(t)}{N}$, and $x_3(t) = \frac{A(t)}{N}$ so that system (1) can be reconstructed as in system (7) as follows

$$\begin{aligned} \frac{dx_1}{dt} &= \Lambda - \mu x_1 - \beta x_1 x_2 - \omega x_1 x_3, \\ \frac{dx_2}{dt} &= \beta x_1 x_2 + \omega x_1 x_3 - \mu x_2 - \gamma x_2, \\ \frac{dx_3}{dt} &= \gamma x_2 - \mu x_3 - \delta x_3. \end{aligned} \tag{7}$$

If $x = (x_1, x_2, x_3)$ then system (7) can be written as

$$\begin{aligned} \frac{dx_1}{dt} &= f_1(x) = \Lambda - \mu x_1 - \beta x_1 x_2 - \omega x_1 x_3, \\ \frac{dx_2}{dt} &= f_2(x) = \beta x_1 x_2 + \omega x_1 x_3 - \mu x_2 - \gamma x_2, \\ \frac{dx_3}{dt} &= f_3(x) = \gamma x_2 - \mu x_3 - \delta x_3. \end{aligned} \tag{8}$$

The next step is finding the equilibrium point. In system (8), two equilibrium points are obtained, namely

- The disease-free equilibrium point (E_0).
  This state describes a situation where there are no HIV-infected individuals in the population, or in other word $x_2 = 0$ and so automatically $x_3 = 0$. The equilibrium on this state is

$$E_0 = \left(\frac{\Lambda}{\mu}; 0; 0\right) = 33.333; 0; 0. \tag{9}$$

- The endemic equilibrium point (E_1).
  This state describes the situation when there are infected individuals in the population, or in other word $x_2 > 0$ and $x_3 > 0$. The equilibrium on this state is

$$E_1 = \left(\frac{\mu + \gamma}{\beta + \omega \cdot \frac{\gamma}{\mu + \delta}}; \frac{\Lambda - \mu x_1}{x_1\left(\beta + \omega \cdot \frac{\gamma}{\mu + \delta}\right)}; \frac{\gamma}{\mu + \delta} x_2\right) = (0{,}811903; 7692{,}12; 4524{,}78). \tag{10}$$

Once the equilibrium point has been identified, the subsequent step is to examine the stability of that equilibrium. By using linearization around the equilibrium point, the stability analysis will be obtained. The Jacobian matrix at the point $E_0 = \left(\frac{\Lambda}{\mu}; 0; 0\right)$ is

$$J_{E_0} = \begin{pmatrix} -\mu & -\beta\frac{\Lambda}{\mu} & -\omega\frac{\Lambda}{\mu} \\ 0 & \beta\frac{\Lambda}{\mu} - \mu - \gamma & \omega\frac{\Lambda}{\mu} \\ 0 & \gamma & -\mu - \delta \end{pmatrix} \tag{11}$$

and the eigenvalues were derived $\lambda_1 = -\mu$, $\lambda_2 = \frac{\beta\Lambda}{\mu} - \mu - \gamma$, and $\lambda_3 = -\mu - \delta$. The equilibrium point E_0 is said to be asymptotically stable if $\lambda < 0$ or $\frac{\beta\Lambda}{\mu} < \mu + \gamma$ and it will be unstable if $\lambda > 0$ or $\frac{\beta\Lambda}{\mu} > \mu + \gamma$. We conclude the eigen value that is $\lambda_1 = -0{,}015$, $\lambda_2 = 2666{,}6$, and $\lambda_3 = -0{,}085$. Because $\lambda_2 = 2666{,}6 > 0$ then E_0 is unstable.

We did the same thing on E_1 and the Jacobian matrix will be

$$J_{E_1} = \begin{pmatrix} -\mu - \beta x_2 - \omega x_3 & -\beta x_1 & -\omega x_1 \\ \beta x_2 + \omega x_3 & \beta x_1 - \mu - \gamma & \omega x_1 \\ 0 & \gamma & -\mu - \delta \end{pmatrix} \tag{12}$$

and we get the eigenvalue that is $\lambda_1 = -0{,}065$, $\lambda_2 = -615{,}722$, and $\lambda_3 = -0{,}085$. Ita can be seen that each $\lambda_1, \lambda_2, \lambda_3 < 0$. Therefore, E_2 is asymptotically stable.

The following step is obtaining Basic Reproduction Number or R_0 using NGM (Next Generation Matrix) method. The R_0 is determined using E_0 equilibrium point. The NGM method is defined as FV^{-1} with transmision matrix F and transition matrix F as $F = \begin{pmatrix} \beta & \omega \\ 0 & 0 \end{pmatrix}$ and $V = \begin{pmatrix} (\mu+\gamma) & 0 \\ -\gamma & (\mu+\delta) \end{pmatrix}$. Then, we get $NGM = FV^{-1} = \begin{pmatrix} \beta & \omega \\ 0 & 0 \end{pmatrix} \cdot V^{-1}$. Next, R_0 is the largest eigenvalue selected from $det(NGM - \lambda I)$, namely $R_0 = \frac{\beta}{\mu+\gamma} + \frac{\omega\cdot\gamma}{(\mu+\gamma)(\mu+\delta)} = \frac{0{,}08}{0{,}015+0{,}05} + \frac{0{,}0001\cdot 0{,}05}{(0{,}015+0{,}05)(0{,}015+0{,}07)} \approx 1{,}23$. Since $R_0 > 1$ then the HIV/AIDS disease will spread in the population.

3.3 Euler Method

Starting from system (1), we apply the Euler method to obtain the discretized sorm form in Equation (13).

$$S_1 = S_0 + \mathrm{h}\left(\Lambda - \mu S_0 - \beta S_0 \frac{I_0}{N} - \omega S_0 \frac{A_0}{N}\right),$$

$$I_1 = I_0 + h\left(\beta S_0 \frac{I_0}{N} + \omega S_0 \frac{A_0}{N} - \mu I_0 - \gamma I_0\right), \tag{13}$$

$$A_1 = A_0 + h(\gamma I_0 - \mu A_0 - \delta A_0).$$

By substituting the parameter values from Table 4 and the initial conditions from Table 3, the first iteration yields the following results.

$$dS_0 = 500 - (0{,}015 \cdot 106733) - \left(\frac{0{,}08 \cdot 106733 \cdot 504}{107385}\right) - \left(\frac{0{,}0001 \cdot 106733 \cdot 148}{107385}\right)$$
$$\approx -1141{,}07.$$

$$dI_0 = \left(\frac{0{,}08 \cdot 106733 \cdot 504}{107385}\right) + \left(\frac{0{,}0001 \cdot 106733 \cdot 148}{107385}\right) - (0{,}015 \cdot 504) - (0{,}05 \cdot 504)$$
$$\approx 7{,}3198.$$

$$dA_0 = (0{,}05 \cdot 504) - (0{,}015 \cdot 148) - (0{,}07 \cdot 148) \approx 12{,}62.$$

Hence, the population values after the first iteration are :

$$S_1 = 106733 + 1(-1141{,}07) = 105591{,}93,$$

$$I_1 = 504 + 1(7{,}3198) = 511{,}3198,$$

$$A_1 = 148 + 1(12{,}62) = 160{,}62.$$

We continue proceeding to the second iteration.

$$dS_1 = 500 - (0{,}015 \cdot 105591{,}93) - \left(\frac{0{,}08 \cdot 105591{,}93 \cdot 511{,}3198}{107385}\right)$$
$$- \left(\frac{0{,}0001 \cdot 105591{,}93 \cdot 160{,}62}{107385}\right) \approx -1124{,}1137.$$

$$dI_1 = \left(\frac{0{,}08 \cdot 105591{,}93 \cdot 511{,}3198}{107385}\right) + \left(\frac{0{,}0001 \cdot 105591{,}93 \cdot 160{,}62}{107385}\right) - (0{,}015 \cdot 511{,}3198)$$
$$- (0{,}05 \cdot 511{,}3198) \approx 6{,}9999.$$

$$dA_1 = (0{,}05 \cdot 511{,}3198) - (0{,}015 \cdot 160{,}62) - (0{,}07 \cdot 160{,}62) \approx 11{,}9133.$$

Thus, the population values after the second iteration are as follows.

$$S_1 = 105591{,}93 + 1(-1124{,}1137) = 104467{,}8163,$$

$$I_1 = 504 + 1(6{,}9999) = 510{,}999,$$

$A_1 = 148 + 1(11{,}9133) = 159{,}9133.$

This iterative process continues for the desired simulation duration (12 months). From the simulation results, we observe that the number of susceptible individuals (S) tends to decrease over time, while the number of infected individuals (I) and those with AIDS (A) increases. This trend is consistent with the natural progression of HIV/AIDS transmission and disease development in the absence of significant intervention strategies.

3.4 The 4th Order Runge-Kutta Method

In addition to the Euler method, the 4th Order Runge-Kutta Method (RK4) is also applied to solve the system of differential equations in the SIA model. This method provides more accurate approximation compared to the Euler method by considering intermediate slopes within each step. The general RK4 formula for each compartment are

$$\begin{aligned} S_{n+1} &= S_n + \frac{h}{6}\left(k_1{}^S + 2\left(k_2{}^S\right) + 2\left(k_3{}^S\right) + k_4{}^S\right),\\ I_{n+1} &= I_n + \frac{h}{6}\left(k_1{}^I + 2\left(k_2{}^I\right) + 2\left(k_3{}^I\right) + k_4{}^I\right),\\ A_{n+1} &= A_n + \frac{h}{6}\left(k_1{}^A + 2\left(k_2{}^A\right) + 2\left(k_3{}^A\right) + k_4{}^A\right). \end{aligned} \tag{14}$$

Using parameter values in Table 4 and the initial conditions in Table 3, we compute the following.

Step 1 : Compute k_1.

$k_1^S = \mathrm{h}\left(\Lambda - \mu S - \beta S\frac{I}{N} - \omega S\frac{A}{N}\right) = 1\left((500 - (0{,}015 \cdot 106733) - \left(\frac{0{,}08 \cdot 106733 \cdot 504}{107385}\right) - \left(\frac{0{,}0001 \cdot 106733 \cdot 148}{107385}\right)\right) \approx -1141{,}07.$

$$\begin{aligned} k_1^I &= h\left(\beta S\frac{I}{N} + \omega S\frac{A}{N} - \mu I - \gamma I\right)\\ &= 1\left(\left(\frac{0{,}08 \cdot 106733 \cdot 504}{107385}\right) + \left(\frac{0{,}0001 \cdot 106733 \cdot 148}{107385}\right) - (0{,}015 \cdot 504)\right.\\ &\quad \left. - (0{,}05 \cdot 504)\right) \approx 7{,}31. \end{aligned}$$

$k_1^A = h(\gamma I - \mu A - \delta A) = 1\big((0{,}05 \cdot 504) - (0{,}015 \cdot 148) - (0{,}07 \cdot 148)\big) \approx 12{,}62.$

Step 2 : Compute k_2 using intermediate values.

$S_{k_2} = S + \frac{1}{2}k_1^S = 106733 + \frac{1}{2}(-1141{,}07) = 106162{,}47.$

$I_{k_2} = I + \frac{1}{2}k_1^I = 504 + \frac{1}{2}(7{,}31) = 507{,}655.$

$A_{k_2} = A + \frac{1}{2}k_1^A = 148 + \frac{1}{2}(12{,}62) = 154{,}31.$

Then,

$$k_2^S = 1\left((500 - (0{,}015 \cdot 106162{,}47) - \left(\frac{0{,}08 \cdot 106162{,}47 \cdot 507{,}655}{107385}\right) - \left(\frac{0{,}0001 \cdot 106162{,}47 \cdot 154{,}31}{107385}\right)\right) \approx 7{,}1672,$$

$$k_2^I = 1\left(\left(\frac{0{,}08 \cdot 106162{,}47 \cdot 507{,}655}{107385}\right) + \left(\frac{0{,}0001 \cdot 106162{,}47 \cdot 154{,}31}{107385}\right) - (0{,}015 \cdot 507{,}655) - (0{,}05 \cdot 507{,}655)\right) \approx 7{,}1672,$$

$$k_2^A = 1\big((0{,}05 \cdot 507{,}655) - (0{,}015 \cdot 154{,}31) - (0{,}07 \cdot 154{,}31)\big) \approx 12{,}266.$$

Step 3 : Compute k_3 using the intermediate values.

$S_{k_3} = S + \frac{1}{2}k_2^S = 106162{,}47 + \frac{1}{2}(-1132{,}5952) = 105596{,}172.$

$I_{k_3} = I + \frac{1}{2}k_2^I = 507{,}655 + \frac{1}{2}(7{,}1672) = 511{,}239.$

$A_{k_3} = A + \frac{1}{2}k_2^A = 154{,}31 + \frac{1}{2}(12{,}266) = 160{,}443.$

Then,

$$k_3^S = 1\left(500 - (0{,}015 \cdot 105596{,}172) - \left(\frac{0{,}08 \cdot 105596{,}172 \cdot 511{,}239}{107385}\right) - \left(\frac{0{,}0001 \cdot 105596{,}172 \cdot 160{,}443}{107385}\right)\right) \approx -1124{,}1738,$$

$$k_3^I = 1\left(\left(\frac{0{,}08 \cdot 105596{,}172 \cdot 511{,}239}{107385}\right) + \left(\frac{0{,}0001 \cdot 105596{,}172 \cdot 160{,}443}{107385}\right) - (0{,}015 \cdot 511{,}239) - (0{,}05 \cdot 511{,}239)\right) \approx 7{,}0028,$$

$k_3^A = 1\big((0{,}05 \cdot 511{,}239) - (0{,}015 \cdot 160{,}443) - (0{,}07 \cdot 160{,}443)\big) \approx 11{,}924.$

Step 4 : Compute k_4 using intermediate values.

$S_{k_4} = S + \frac{1}{2}{k_3}^S = 105596{,}172 + \frac{1}{2}(-1124{,}1738) = 105034{,}0851.$

$I_{k_4} = I + \frac{1}{2}{k_3}^I = 511{,}239 + \frac{1}{2}(7{,}0028) = 514{,}7404.$

$A_{k_4} = A + \frac{1}{2}{k_3}^A = 160{,}443 + \frac{1}{2}(11{,}924) = 166{,}405.$

Then,

$$k_4^S = 1\left(500 - (0{,}015 \cdot 105034{,}0851\,) - \left(\frac{0{,}08\ \cdot\ 105034{,}0851\ \cdot\ 514{,}7404}{107385}\right) - \left(\frac{0{,}0001\ \cdot\ 105034{,}0851\ \cdot\ 166{,}405}{107385}\right)\right) \approx -1124{,}2343,$$

$$k_4^I = 1\left(\left(\frac{0{,}08\ \cdot\ 105034{,}0851\ \cdot\ 514{,}7404}{107385}\right) + \left(\frac{0{,}0001\ \cdot\ 105034{,}0851\ \cdot\ 166{,}405}{107385}\right) - (0{,}015 \cdot 514{,}7404) - (0{,}05 \cdot 514{,}7404)\right) \approx 6{,}8373,$$

$k_4^A = 1\big((0{,}05 \cdot 514{,}7404) - (0{,}015 \cdot 166{,}405) - (0{,}07 \cdot 166{,}405)\big) \approx 11{,}593.$

Final result, using the RK4 formula, we get

$S_1 = S_0 + \frac{1}{6}\big(k_1^S + 2\big(k_2^S\big) + 2\big(k_3^S\big) + k_4^S\big) = 106733 + \frac{1}{6}(-1141{,}07 + 2(-1132{,}5952) + 2(-1124{,}1738) + (-1124{,}2343)) = 105603{,}193,$

$$I_1 = I_0 + \frac{1}{6}(k_1^I + 2(k_2^I) + 2(k_3^I) + k_4^I) = 504 + \frac{1}{6}(7{,}31 + 2(7{,}1672) + 2(7{,}0028) + 6{,}8373) = 511{,}081,$$

$$A_1 = A_0 + \frac{1}{6}(k_1^A + 2\big(k_2^A\big) + 2\big(k_3^A\,\big) + k_4^A) = 148 + \frac{1}{6}(12{,}62 + 2(12{,}266) + 2(11{,}924) + 11{,}593) = 160{,}099,$$

From the calculations, it can be observed that, similar to the Euler method, the number of susceptible individuals (S) gradually declines while both infected (I) and AIDS-diagnosed individuals (A) increase steadily. This outcome reflects the intrinsic transmission dynamics of the disease within the framework of the SIA model.

3.4 Numerical Simulation

In this section, results from a 12-month numerical simulation of the HIV/AIDS SIA model are presented. The system of differential equations was solved using both the Euler and 4th Order Runge–Kutta (RK4) methods. The comparison aims to highlight differences in outcomes and evaluate the accuracy and stability of each method in capturing population dynamics. The graphs depict changes in each compartment over time and provide the foundation for further discussion.

The simulation in Figure 2 indicates that the number of infected individuals (I) and AIDS patients (A) steadily increased throughout the 12-month simulation period while the number of susceptible individuals (S) showed a consistent decline. This trend aligns with the theoretical analysis of the basic reproductive number (R_0), which was found to be greater than 1.

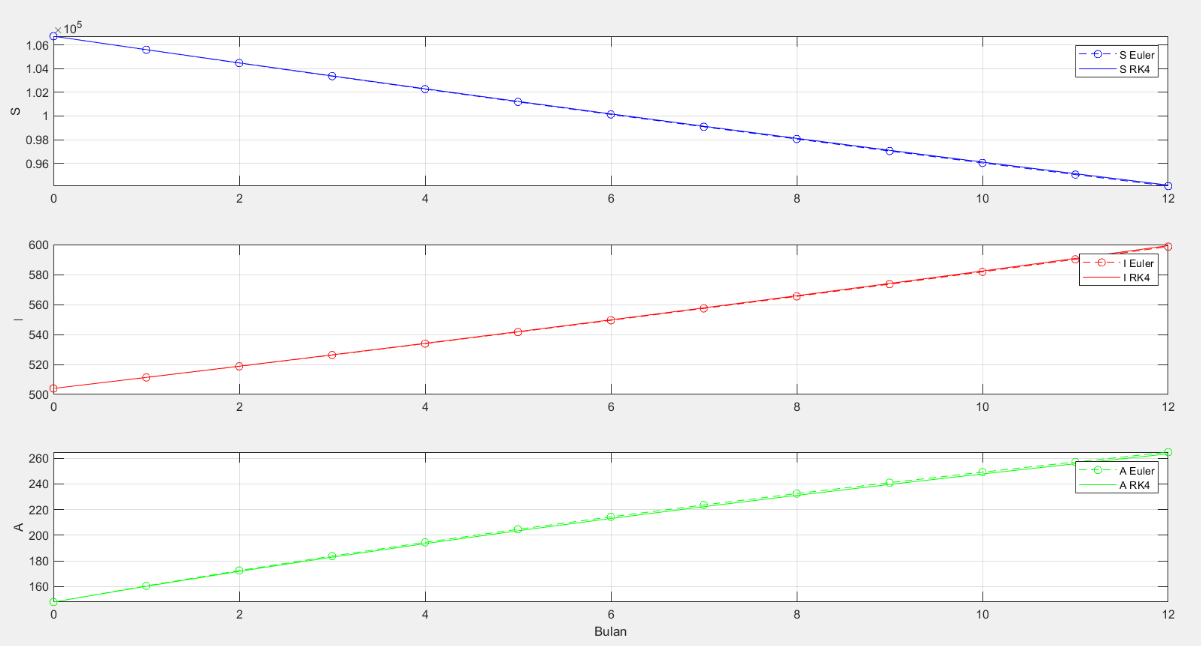

Figure 2. Numerical simulation result.

Since $R_0 > 1$, it can be signifies that each infected individual can transmit the disease to more than one susceptible individual. Consequently, the infection does not die out but instead persists and grows within the population. These findings reinforce the theoretical conclusion that under the given parameter settings, the HIV/AIDS epidemic remains endemic.

The consistency between the numerical results and the analytical threshold condition underscores the robustness of the SIA model in capturing the dynamics of disease transmission. Furthermore, the results highlight the urgent need for appropriate interventions, such as effective prevention strategies, early diagnosis, and treatment programs to reduce transmission spread.

4. CONCLUSION

The analytic analysis and simulation result demonstrate that the spread of HIV/AIDS in West Nusa Tenggara Province exhibits an endemic tendency. This is indicated by the basic reproduction number, $R_0 \approx 1{,}23 > 1$, which implies that each infected individual is capable of transmitting the disease to more than one susceptible individual.

The disease-free equilibrium (E_0) is shown to be unstable whereas the endemic equilibrium (E_1) is locally asymptotically stable. It is suggesting that the disease will persist within the population in the absence of adequate intervention measures.

Numerical simulations, conducted using the Euler and 4th Order Runge–Kutta methods, reveal a consistent pattern that is the number of susceptible individuals decreases while the number of infected individuals and AIDS patients increases. These results corroborate the theoretical findings and provide further evidence of the model's reliability.

Overall, this study underscores the critical role of mathematical modeling in capturing the dynamics of HIV/AIDS transmission and highlights its importance as a scientific foundation for developing effective prevention and control strategies in affected regions.

5. RECOMENDATION

It is strongly recommended that appropriate interventions such as the implementation of effective prevention strategies, early diagnosis, and comprehensive treatment programs, can be prioritized to reduce transmission and curb the spread of HIV/AIDS.

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