Analysis and Simulation of SIPA Model for HIV-AIDS Transmission

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Abstract. The aims of this study are: to build a SIPA model on the spread of HIV/AIDS; analyze and simulation of SIPA model and to predict the spread of HIV/AIDS. An applied mathematics for Analysis of the SIPA model in case of HIV/AIDS spreading using the Jacobi matrix method to obtain eigenvalues in two conditions, namely endemic and disease-free, while the simulation model uses Maple with initial value data in the form of assumptions represented in research. The research result are the mathematical SIPA model of HIV/AIDS spreading which is a system of differential equations. The analysis of the model gives the value of the disease-free equilibrium point and the asymptotically stable endemic equilibrium point. The results also found that the basic reproduction number was $R_0=0.0067$ for disease-free conditions and $R_0=2.7944$ for endemic conditions indicating the condition of HIV/AIDS spreading cases in the population. The simulation results found that there is a very significant difference between the numbers of AIDS populations when free from disease and during endemic conditions, so that attention is needed for the government to be able to tackle the spread of HIV/AIDS.

Keywords: Analysis, simulation, SIPA model, HIV-AIDS transmission

1. Introduction
Human Immunodeficiency Virus (HIV) is a type of virus that attacks or infects white blood cells which causes a decrease in human immunity. While AIDS or Acquired Immunodeficiency Syndrome is a collection of symptoms of disease that arise due to decreased immunity caused by HIV. Due to decreased immunity, the person is very susceptible to various infectious diseases (opportunistic infections) which are often fatal. Until 2017, there were 36.9 million people living with HIV worldwide with the number of new infections reaching 1.8 million people [1].

In 2012 to 2016, the highest pattern of HIV/AIDS transmission was through sexual transmission at 81.8%. In Indonesia, the strategic geographical location so that it is very good for the trade and tourism sectors is one of the factors accelerating the increase in HIV/AIDS cases. In addition, according to data from the Regional Office of the Ministry of Health of East Java, it shows that there is a continuous increase in HIV/AIDS cases among Indonesian workers who work abroad from year to year [2].
Research related to HIV/AIDS spreading cases concluded that the percentage of illiteracy, population density, human development index and regional development ratio had a significant influence on the number of HIV/AIDS cases in Indonesia [2]. In addition, the increase in urbanization that is known through the growth of built-up land area has a significant negative correlation with the increase in the number of HIV cases [3]. Other studies on HIV/AIDS spreading have been carried out by [4-5], then research on mathematical models on the transmission of covid-19, dengue fever, tuberculosis and social behavior has been carried out by [6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20], but focusing on disease transmission, has not discusses the issue of HIV/AIDS spreading cases. Then research on the mathematical model of HIV/AIDS spreading cases has been carried out by [1], [21] and [22], but in these studies they have not used the Suspected-Infected-Pre-AIDS-AIDS (SIPA) mathematical model when analyzing the spread of HIV cases/AIDS. This study uses the SIPA model to identify and predict HIV/AIDS spreading cases.

2. Research method
This research studying theories related to the problem of HIV/AIDS and then building a SIPA model. Further analysis of the model using the theory [7]. The SIPA model simulation on the problem of HIV/AIDS spreading cases with Maple uses assumption data which is divided into two cases, namely cases for $R_0 \leq 1$ and $R_0 > 1$. The simulation results can predict the spread of the number of cases of HIV/AIDS and the status of the spread that is free-disease or endemic.

3. Result
3.1. SIPA model SIPA for HIV/AIDS transmission.
Figure 1 interpret the changes in the population of the SIPA model on the spread of HIV/AIDS, while the parameters and variables definitions of the SIPA model are presented in Table 1.

![Figure 1. SIPA model schematic for HIV/AIDS transmission](image-url)
Table 1. Variables and parameters definition of the SIPA model for HIV/AIDS transmission

| Variable/Parameter | Definition                                                                 |
|--------------------|----------------------------------------------------------------------------|
| \( S(t) \)         | Suspected population number of HIV/AIDS                                    |
| \( I(t) \)         | Infected population number of HIV/AIDS                                     |
| \( P(t) \)         | Pre-AIDS population number                                                 |
| \( A(t) \)         | AIDS population number                                                     |
| \( N \)            | The total population                                                       |
| \( \alpha \)       | HIV infection rate                                                         |
| \( \mu \)          | Birth and death rate                                                       |
| \( \tau \)         | The probability of the population being infected with HIV but not yet in the Pre-AIDS period |
| \( \sigma \)       | The rate of the infected population with HIV becoming a pre-AIDS individual |
| \( \epsilon \)     | The population being infected with HIV and directly entering the population with AIDS rate |
| \( \omega \)       | Pre-AIDS population rate becoming AIDS sufferers                           |

The SIPA model for HIV/AIDS transmission in Figure 1 can be interpreted as a differential equations non-linear system and represented in Equation (1) to Equation (4).

\[
\begin{align*}
\frac{dS}{dt} &= \mu N - \left( \frac{\alpha \tau I}{N} + \frac{\alpha (1-\tau) I}{N} + \mu \right) S \\
\frac{dI}{dt} &= \frac{\alpha \tau SI}{N} - (\sigma + \epsilon + \mu) I \\
\frac{dP}{dt} &= \frac{\alpha (1-\tau) SI}{N} + \sigma I - (\omega + \mu) P \\
\frac{dA}{dt} &= \epsilon I + \omega P - \mu A
\end{align*}
\]

Let \( s = \frac{S}{N} \), \( i = \frac{I}{N} \), \( p = \frac{P}{N} \), \( a = \frac{A}{N} \) then the Equation (1)–(4) can be written in Equation (5) to Equation (8):

\[
\begin{align*}
\frac{ds}{dt} &= \mu - (\alpha \tau i + \alpha (1-\tau) i + \mu) s \\
\frac{di}{dt} &= \alpha \tau si - (\sigma + \epsilon + \mu) i \\
\frac{dp}{dt} &= \alpha (1-\tau) si + \sigma i - (\omega + \mu) p \\
\frac{da}{dt} &= \epsilon i + \omega p - \mu a
\end{align*}
\]

The equation (5)–(8) is a mathematical model of SIPA for HIV/AIDS transmission.

3.2. Analysis of the sipa model for HIV/AIDS transmission

3.2.1. The equilibrium point of the SIPA model for HIV/AIDS

The equilibrium point of the SIPA model for HIV/AIDS transmission is carried out by assuming \( \frac{ds}{dt} = \frac{di}{dt} = \frac{dp}{dt} = \frac{da}{dt} = 0 \) and obtained Equation (9) – (12).

\[
\begin{align*}
0 &= \mu - (\alpha \tau i + \alpha (1-\tau) i + \mu) s \\
0 &= \alpha \tau si - (\sigma + \epsilon + \mu) i \\
0 &= \alpha (1-\tau) si + \sigma i - (\omega + \mu) p \\
0 &= \epsilon i + \omega p - \mu a
\end{align*}
\]

Corolarly, we get Equation (13)-(16).
The first step in the equilibrium point stability analyzing of the SIPA model for HIV/AIDS transmission is to determine the Jacobi matrix Equation (5)–(8), namely:

\[
J = \begin{bmatrix}
-(\alpha ti + \alpha(1-\tau)i + \mu) & \alpha ti & \alpha(1-\tau)i & 0 \\
\alpha ti & \alpha ti + (\sigma + \varepsilon + \mu) & \alpha(1-\tau)i & 0 \\
\alpha(1-\tau)i & \alpha(1-\tau)i + \sigma & -(\omega + \mu) & 0 \\
0 & \varepsilon & \omega & -\mu
\end{bmatrix}
\]  

(24)
3.3.1. Analysis of stability of disease-free equilibrium point model SIPA for HIV/AIDS transmission

The stability analysis of the disease-free equilibrium point of the SIPA model for HIV/AIDS transmission is carried out by substituting the value of the disease-free equilibrium point into Equation (24) to obtain Equation (25).

\[
J = \begin{bmatrix}
-\mu & \alpha s + \sigma(1 - \tau)s & 0 & 0 \\
0 & \alpha s - (\sigma + \epsilon + \mu) & 0 & 0 \\
0 & \alpha(1 - \tau)s + \sigma & -(\omega + \mu) & 0 \\
0 & \epsilon & \omega & -\mu
\end{bmatrix}
\] (25)

Furthermore, determine the eigenvalues of Equation (25) with the formula \(0 = |\lambda I - J|\).

\[
0 = (\lambda + \mu)(\lambda - \alpha s + \sigma + \epsilon + \mu)(\lambda + \omega + \mu)(\lambda + \mu)
\] (26)

So that the characteristic equation is obtained as in Equation (27)

\[
0 = \lambda^4 + X_1\lambda^3 + X_2\lambda^2 + X_3\lambda + X_4
\] (27)

with

- \(X_1 = \omega + \sigma + \epsilon + 4\mu\)
- \(X_2 = \epsilon \sigma + 3\mu^2\sigma + 3\sigma\mu + 3\epsilon\mu + 3\mu\omega + 3\mu^2\omega + 6\mu^2 - 3\alpha\mu - \alpha\omega\)
- \(X_3 = 2\mu\omega + 2\mu\epsilon\omega + 3\mu^2\sigma + 3\mu^2\omega - 2\mu\alpha\omega - 3\mu^2\alpha\epsilon\)
- \(X_4 = 3\mu^2\omega + \mu^2\epsilon\omega + \mu^3\omega + \mu^3\sigma + \mu^3\epsilon + \mu^4 - \mu^3\alpha\epsilon - \mu^2\epsilon\omega\)

Based on Equation (27), the basic reproduction number \(R_0\) is obtained.

\[
R_0 = \frac{\alpha\tau}{\sigma + \epsilon + \mu}
\] (28)

Based on Equation (26), the eigenvalues of the matrix in Equation (25) are all negative if \(R_0 < 1\), so the equilibrium point of the disease-free case SIPA model is asymptotically stable.

3.3.2. Analysis of the stability of the endemic equilibrium point of the SIPA model for HIV/AIDS

The stability analysis of the endemic equilibrium point of the SIPA model for HIV/AIDS transmission was carried out by finding the eigenvalues of Equation (24) with the formula \(0 = |\lambda I - J|\).

\[
0 = \begin{vmatrix}
\lambda + (\alpha\tau i + \alpha(1 - \tau)i + \mu) & -\alpha i s - \alpha(1 - \tau)s & 0 & 0 \\
-\alpha i & \lambda - \alpha s + (\sigma + \epsilon + \mu) & 0 & 0 \\
-\alpha(1 - \tau)i & -\alpha(1 - \tau)s + \sigma & \lambda + (\omega + \mu) & 0 \\
0 & -\epsilon & -\omega & \lambda + \mu
\end{vmatrix}
\] (29)

Based on Equation (29), the eigenvalues of the SIPA model are obtained.

\[
\lambda_1 = -\mu
\] (30)

\[
\lambda_2 = -\mu - \omega
\] (31)

\[
\lambda_3 = -\mu - \frac{1}{2}(\sigma + \alpha\tau s + \alpha i + \epsilon)
\] (32)

\[
\lambda_4 = -\mu - \frac{1}{2}(\sigma + \alpha\tau s + \alpha i + \epsilon)
\] (33)

Based on Equation (30)–(33) the eigenvalue of the real part is negative, it is concluded that the endemic equilibrium point for HIV/AIDS transmission is asymptotically stable.

3.4. SIPA model simulation for HIV/AIDS transmission

Simulation of the SIPA model of HIV/AIDS transmission was carried out to predict the rate of addition of individuals in each compartment. The model simulation using Maple with the initial values variables and parameters of the model is presented in Table 2.
Table 2. Initial values of variables and parameters of the SIPA model for HIV-AIDS

| Variable | Values | Source | Parameter | Free-disease | Endemic | Source |
|----------|--------|--------|-----------|--------------|---------|--------|
| N        | 10000  | Assumption | γ        | 0.000003    | 0.00221 | Assumption |
| S₀       | 0.70   | Assumption | r         | 0.0092      | 0.085   | Assumption |
| I₀       | 0.15   | Assumption | ε         | 0.000525    | 0.00031 | Assumption |
| P₀       | 0.10   | Assumption | σ         | 0.0051      | 0.00171 | Assumption |
| A₀       | 0.05   | Assumption | α         | 0.0041      | 0.0741  | Assumption |
| Rₐ       |        |         | ω         | 0.000075    | 0.00188 | Assumption |

Substituting the disease-free parameter values in Table 2 into Equation (5)–(8), we get Equation (34) to Equation (37).

\[
\begin{align*}
\frac{ds}{dt} &= 0.000003 - (0.0041 i + 0.000003)s \\
\frac{di}{dt} &= 0.00003772 si - 0.005628 i \\
\frac{dp}{dt} &= 0.00406228 si + 0.0051 i - 0.000003 p \\
\frac{da}{dt} &= 0.000525 i + 0.000075 p - 0.000003 a \\
\end{align*}
\]

If Equation (34)–(37) is equal to zero, then the HIV/AIDS-free equilibrium point is obtained and the eigenvalues are:

\[
\lambda_1 = -0.000003, \quad \lambda_2 = -0.000078, \quad \lambda_3 = -0.005590, \quad \lambda_4 = -0.000003
\]

If the disease-free parameter values are substituting into Equation (24), the basic reproduction number value is obtained: \( R₀ = 0.0067 < 1 \) (38)

The simulation results for the disease-free parameter values are presented in Figure 2.

Figure 2. Simulation results of disease-free cases in the SIPA model for HIV/AIDS transmission

Based on the Figure 2, the number of suspected individuals infected with HIV/AIDS decreased from the beginning and then reached equilibrium at \( t=600 \). The number of individuals infected with the HIV virus decreased significantly from the start until it reached equilibrium at \( t=600 \). In addition, the number of individuals in the Pre-AIDS stage and those who have entered the AIDS stage both have increased since the beginning and are in a state of equilibrium starting at \( t=700 \).

Furthermore, substituting the endemic parameter values in Table 2 into Equation (5)–(8), we get Equation (39) to Equation (42).

\[
\begin{align*}
\frac{ds}{dt} &= 0.000221 - (0.0741 i + 0.000221)s \\
\frac{di}{dt} &= 0.0062985 si - 0.002262 i \\
\frac{dp}{dt} &= 0.0678015 si + 0.00171 i - 0.002101 p \\
\frac{da}{dt} &= 0.000331 i + 0.00188 p - 0.000221 a \\
\end{align*}
\]
If Equation (39)–(42) is equal to zero, then the HIV/AIDS endemic equilibrium point is obtained and the eigenvalues are:

\[ \lambda_1 = -0.000221, \quad \lambda_2 = -0.002101, \quad \lambda_3 = -0.000685, \quad \lambda_4 = -0.001301 \]

Substituting parameter values into Equation (24), the basic reproduction number value is obtained:

\[ R_0 = 2.7844 > 1 \] (43)

The simulation results for endemic parameter values are presented in Figure 3.

Figure 3. Simulation results of endemic parameter values of the SIPA model for HIV/AIDS transmission

| Table 3. Equilibrium point values and eigenvalues of the SIPA model for HIV-AIDS transmission |
|---------------------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| \( R_0 \) | \( S \) | \( I \) | \( P \) | \( \Lambda \) | \( \lambda_1 \) | \( \lambda_2 \) | \( \lambda_3 \) | \( \lambda_4 \) |
| 0.0067 | 1 | 0 | 0 | 0 | -0.000003 | -0.000078 | -0.005590 | -0.000003 |
| 2.7844 | 0.359133 | 0.005322 | 0.066013 | 0.569531 | -0.000221 | -0.002101 | -0.000685 | -0.001301 |

Figure 3 shown that the number of individuals who are suspected to HIV/AIDS has decreased drastically from the beginning then increased to \( t=500 \) and reached equilibrium. Figure 2 also shows that the number of the population infected with the HIV virus has decreased significantly since \( t=70 \) until it reaches a state of equilibrium at \( t=750 \). In addition, the number of individuals in the Pre-AIDS stage experienced a drastic increase from the beginning and decreased at \( t=200 \), then was in a state of equilibrium after \( t=750 \). A significant increase in the number of AIDS population also occurred since the beginning and was in a state of equilibrium at \( t = 750 \).

4. Discussion

The results of research by [1] shown that the decrease in the subpopulation infected with HIV/AIDS is influenced by the increasing in the number of subpopulation undergoing quarantine. Similar result, the increasing and decreasing in the subpopulation infected with HIV/AIDS is strongly influenced by the magnitude of the interaction rate between the Suscepted and Infected subpopulation so that, it can also be interpreted that the smaller the interaction between the susceptible and infected population, the individuals infected number with HIV/AIDS is also decreasing, so quarantine is needed so that the HIV/AIDS transmission does not increase. The results of the study [2] concluded that the percentage of illiteracy, the total population density, the human development index and the ratio of regional development have a significant influence on the number of HIV/AIDS cases in Indonesia, so that with such a large population density requires quarantine to suppress the HIV/AIDS transmission.

The results of research by [20] and [21] shown that the conditions for HIV/AIDS transmission were in two conditions, namely non-endemic and endemic conditions. The results [20] stated that the magnitude of the HIV/AIDS transmission rate was influenced by the interaction or use of needles by individuals in the population. Similar results can also be seen in the study by [21], the difference is in [21] a sensitivity analysis was carried out to determine the most influential parameter for HIV/AIDS transmission. Meanwhile, research shown that interactions between suspected individuals and other populations greatly affect the HIV/AIDS transmission number, so that some treatment is needed in the form of quarantine or education about HIV/AIDS ordinary people can take precautions early.
5. Conclusion
The conclusions of this study are: The SIPA model can be used to describe the HIV/AIDS transmission; Population dynamics of HIV/AIDS transmission in two different conditions, namely free of disease and endemic of HIV/AIDS, gave different results. A very clear difference can be seen in the condition of the AIDS population (A) in the two conditions where in disease-free conditions, the AIDS population (A) even though it has increased, the increase is quite small from time to time, while in endemic conditions the AIDS population (A) has increased which is very drastic from the beginning until it reaches the largest number compared to other variables.

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