BIOS : Jurnal Teknologi Informasi dan Rekayasa Komputer
Vol. 5, No. 2, September 2024, hlm. 150-160
ISSN: 2722-0850

Python Application to SEIR Model of the Spread of Malaria

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Keywords:

Python,
SEIRS model,
equilibrium point,
basic reproduction,
Malaria

ABSTRACT

Python is the next breakthrough in natural science computing because it enables users to do more and better science. Research on the Susceptible-Exposed-Infected-Recovered-Susceptible (SEIRS) disease spread model has received a lot of attention, but with different factors, and the article aims to apply Python in simulating SEIRS-type Malaria spread data with handling/treatment parameters in other classes. They are exposed to the assumption that individuals who recover from Malaria may become susceptible to transmission of the disease. The data processing simulation aims to see whether Malaria will develop into an epidemic. The use of Python code will make it easier to detect outbreaks. The model for spreading Malaria involves four classes: susceptible, infected but not yet active, infected, and recovered. The simulation data is the number of malaria sufferers in 2017 from the Mimika District Health Service, Indonesia. Mimika Regency is the region with the highest number of malaria cases at 29.12% of all malaria cases in Indonesia. The equilibrium point is determined using a SEIRS-type mathematical model. Data processing with simulations in the SEIRS model obtains a primary reproduction number (Ro) of 0.078 and R0 < 1, so the disease will not become an epidemic.

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Submitted : 15-08-2024; Accepted : 20-09-2024;
Published : 30-09-2024

1. INTRODUCTION

Python is the next breakthrough in natural science computing because it enables users to do more and better science. The natural sciences community has begun to realize Python's unique benefits, with the result that its user population continues to grow and is no longer limited to "early adopters" [1]. Python has concise syntax and prominent programs and is easy to read, such as determining executable pseudocode. Additionally, because the language is interpreted, development becomes more accessible. The characteristics of this language are as follows: ease of learning and use, extensibility, and the large number of software libraries have attracted the attention of educators and software developers [2]. However, Python is not a language without criticism from Quora [3].

Additionally, modern data structures and the object-oriented nature of the language make Python code more robust and less brittle. Python's unique strengths are the interconnectedness and completeness of its toolset and the ease of applying innovations from other communities and disciplines. Consider a typical geoscience computing workflow. However, Python also has real drawbacks, including that pure Python code runs much slower than compiled code, has fewer scientific libraries than Fortran, and has relatively sparse documentation and support for new science users. There are tools to overcome speed barriers, scientific library collections are growing, and science support resources are becoming more robust; however, this is a real problem. For most geoscience applications, Python's advantages outweigh its disadvantages [1]. As an advanced interpreted programming language, Python can support multiple platforms and programming paradigms [4].

Python is used as a requirement for parallel programming [5]. Saarela andjauhiainen have made a comparative study of several Python-based feature significance metrics [6]. According to Pawar et al. [7], Python can solve challenging problems such as viscous fluid dynamics. Python can simplify, find, and implement solutions [8,9]. Python is a high-level programming language widely used in various fields, including mathematical modelling. Python is a high-level programming language involving many functions to solve mathematical problems [10]. Due to its easy-to-understand syntax and ease of use, Python is very popular among beginners and experts. One of the benefits of Python in mathematical modelling is as follows:

1. Python's syntax is similar to English, making it easy to understand and use, especially for beginners.

2. Many Libraries: Python has many libraries that support mathematical modelling, such as NumPy, SciPy, and SymPy, which provide complete and efficient mathematical functions.
3. Interactive Python can be used interactively via IPython or Jupyter Notebook, making data exploration and mathematical modelling easier.
4. Open Source: Python is open source, so it can be used for free and has an active user community to support it.

This article discusses the application of Python in determining solutions to natural behaviour modelled in the form of a system of ordinary differential equations. Mathematical problems can arise from issues that investigate natural behaviour, and there are mathematical, logical relationships that explain everything. Natural behaviour can be modelled using linear and nonlinear differential equations [11]. Models can explain how the world system works. Describing and explaining real-world problems in mathematical statements is known as mathematical modelling. Mathematical modelling can explain how the world's patterns and rules work using the mathematics language. Some of the advantages of mathematical modelling include simplifying language with symbols and ideas in mathematical formulas and simulations [12]. One of the known mathematical models for the spread of disease is Susceptible, Exposed, Infectious, Recovered (SEIR). The SEIR epidemiological model is formulated through a compartmental model. The compartmental model is used to describe the spread of a disease [13]. The SEIR model is an appropriate epidemiological model to formulate the spread of Malaria.

The spread of Malaria in Mimika district, Indonesia, will be modelled using SEIR (Susceptible, Exposed, Infectious, Recovered), meaning that in this model, there are people who are susceptible to Malaria (S), people who are infected with Malaria (E), people who are infected with Malaria (I), and people who recovered from Malaria (R) [13]. Malaria is a dangerous disease that spreads to humans from several types of mosquitoes [14]. Parasites cause malaria infection and are not directly spread from person to person. Five species of Plasmodium can infect humans, namely, Plasmodium falciparum, Plasmodium malaria, Plasmodium vivax, Plasmodium ovale, Plasmodium knowlesi [15]. Symptoms of people affected by Malaria include fever and flu, seizures, headaches, muscle aches and fatigue, nausea and vomiting and diarrhea. One of the highest levels of malaria cases in Indonesia is in Mimika Regency, especially in Papua, with an average of more than 200 cases per thousand people per year. Data from 2017 showed that 92,342 people in Mimika were infected with malaria. Mimika Regency is the region with the highest number of malaria cases at 29.12% of all malaria cases in Indonesia. Health service data states that in 2017, Mimika Regency was the area with the highest number of malaria cases, namely 92,559 cases, and there was a decrease in 2018 with 64,640 cases, but there was an increase again in 2019 with 82,192 cases, 30 percent of which were cases of malaria relapse or relapse. Completion of a mathematical model of the spread of Malaria using Python programming to detect whether Malaria will become an epidemic. All calculations will be completed using Python. The novelty of this article is to determine the Python code of the essential reproduction (R_0) and the code for the SEIRS graph. The accuracy of these codes can be applied to the spread of Malaria in the future. Apart from that, these codes were created to solve the system of differential equations, which are presented to provide a research overview for other research on the SEIR Epidemic Model

Mathematical approaches to epidemiology are carried out through compartment models. The compartment model is used to describe the transmission of a disease. In the compartment model, the population that is the object of research is divided into several groups. Each group consists of individuals who have similar characteristics. The compartment model is formulated based on assumptions about the nature and movement rate from one compartment to another [16]. The compartment model has time (t) as the independent variable. The rate of movement between compartments is modelled as the derivative of compartment size versus time. Therefore, the compartment model forms a system of differential equations [16].

In developing compartment models to understand the transmission of a disease, the exposed or exposed compartment was added to represent conditions where an individual is not yet fully infected with the disease and, therefore, cannot transmit the disease in the population.

Adding the Exposed or exposed compartment creates the SEIR model [16]. The classic SEIR model consists of four elements dividing the population into four sub-populations or groups: Susceptible, Exposed, Infected, and Recovered. Susceptible is a group vulnerable to disease. Vulnerable groups who have contact with infected individuals so that they have been exposed to the virus that causes the disease but have not been able to transmit the disease are included in Exposed. Infected contains individuals who have been infected with a disease-causing virus so that they can transmit the disease they suffer from to individuals who are included in the vulnerable group. Individuals who recover from the disease will be included in the Recovered group. N is the total population where $N = S + E + I + R$ [17]. The SEIR epidemic model compartment diagram can be seen in the following figure:

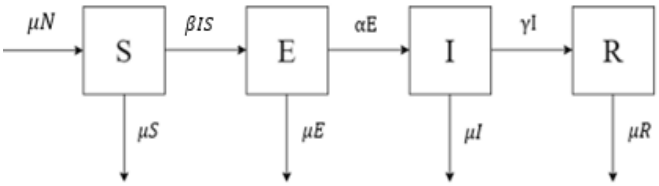

Figure 1. Classical SIR Model Compartment Diagram

The system of equations formed from the compartment diagram above is as follows:

$$\frac{dS}{dt} = \mu N - \beta IS - \mu S$$
$$\frac{dE}{dt} = \beta IS - \alpha E - \mu E$$
$$\frac{dI}{dt} = \alpha E - \gamma I - \mu I$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

β is an interaction parameter between susceptible or susceptible individuals and infected or infected individuals so that they become exposed or exposed individuals. α is a parameter for changing an exposed individual into an infected individual. The recovery parameter for an infected individual so that they become recovered is symbolized by γ. In this model, the population is considered constant so that the natural birth and death parameters symbolized by μ are assumed to be the same [18].

The information for the system of equations obtained from the compartment diagram in Figure 1 is as follows:

1. Changes in the number of vulnerable subpopulations (S) over time (t) are modelled in the equation

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

The number of individuals in the vulnerable subpopulation (S) increases due to births that occur in the population (N) with birth parameters (μ) so that (μN) is obtained. The number of individuals in the susceptible subpopulation (S) decreases due to interactions that occur between the susceptible subpopulation (S) and the infected subpopulation (I) with parameters (β), causing changes in susceptible individuals to exposed individuals (βIS). In addition, natural death in the susceptible subpopulation (S) with the mortality parameter (μ) thus obtained (μS) also causes a reduction in the number of individuals in the susceptible subpopulation (S).

2. Changes in the number of exposed subpopulations (E) over time (t) are modelled using the equation.

$$\frac{dE}{dt} = \beta IS - \alpha E - \mu E$$

The number of individuals in the exposed subpopulation (E) increases due to interactions that occur between the susceptible subpopulation (S) and the infected subpopulation (I) with parameters (β), thereby causing changes in susceptible individuals to exposed individuals (βIS). Meanwhile, the exposed subpopulation (E) is fully infected after going through the virus incubation period with the change parameter (α) so that it is obtained (αE) and natural death in the exposed subpopulation (E) with the death parameter (μ) so that it is obtained (μE) causes a reduction number of individuals in the exposed subpopulation (E).

3. Changes in the number of infected subpopulations (I) over time (t) are modelled using the equation.

$$\frac{dI}{dt} = \alpha E - \gamma I - \mu I$$

The number of individuals in the infected subpopulation (I) increases due to the exposed subpopulation (E) changing to become infected with the change parameter (α) resulting in (αE). The number of individuals in the infected subpopulation (I) decreases with the recovery of the infected subpopulation (I) with the recovery parameter (γ), thus obtaining (γI) and deaths occurring in the infected subpopulation (I) with the death parameter (μ) thereby obtaining (μI).

4. Changes in the number of recovered subpopulations (R) over time (t) are modelled using the equation.

$$\frac{dR}{dt} = \gamma I - \mu R$$

The number of individuals in the recovered subpopulation (R) increases with the recovery that occurs in the infected subpopulation (I) with parameters (γ) to obtain (γI). The number of individuals in the recovered

subpopulation (R) decreases with the occurrence of death in the recovered subpopulation (R) with the death parameter (μ) so that (μR) is obtained.

The model above can be used to analyze the spread of diseases, one of which is Malaria. The form of the model used will adjust depending on the intervention measures taken to suppress the spread of the disease and adapt to the availability of data to be used [19]. Malaria is a disease that attacks humans and animals by mosquitoes caused by protists of the genus Plasmodium. Malaria comes from the bite of a female mosquito, which enters the body's circulation. The following is the life cycle of Plasmodium.

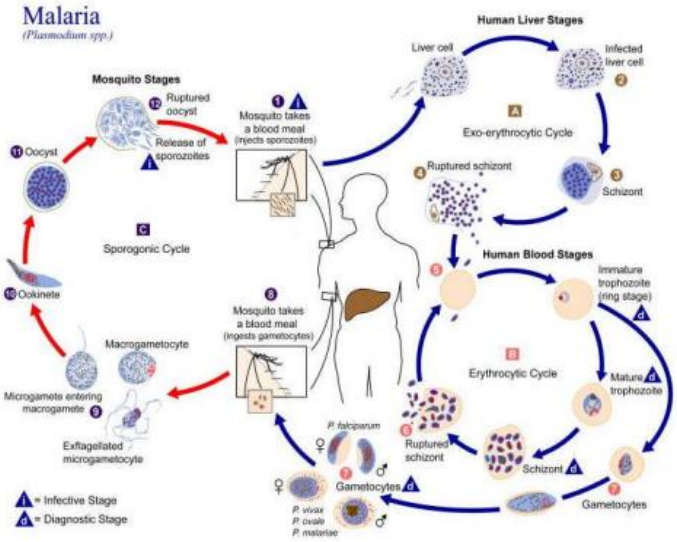

Figure 2. Plasmodium life cycle

In the SEIRS model, the human population (N) has four variables, namely, humans who may be infected with the virus (susceptible), humans who show symptoms of the virus (exposed), humans who have been infected (infected), and humans who have recovered [20]. Mathematically the SEIRS mathematical model is a system of ordinary differential equations. Next, determine the equilibrium point, which is a point that does not change over the years. Consider a system of differential equations given the form,

$$\left.\begin{aligned}\frac{dx}{dt} &= f(x,y)\\ \frac{dy}{dt} &= g(x,y)\end{aligned}\right\} \qquad (1)$$

The point (x_0, y_0) is said to be the equilibrium point of system (1) if it satisfies $f(x_0, y_0) = 0$ and $g(x_0, y_0) = 0$. The equilibrium point is a system solution (1) with a constant value because $\frac{dx}{dt} = 0$ and $\frac{dy}{dt} = 0$ at point (x_0, y_0). The stability of the model through the balance point is analyzed using the Jacobian matrix in the form of eigenvalues. In general, the balance point has two behaviours: (1) Stable if the eigenvalue is negative and each component of the eigenvalue has a complex value less than or equal to zero. (2) Unstable if the new eigenvalue is positive and every eigenvalue has a complex value greater than zero [21]. Next, the primary reproduction number (R_0), a fundamental concept in epidemiology, is determined. R_0 is a quantity that represents the number of secondary infections resulting from one primary infection in a susceptible population. Following the development of mathematical modelling approaches in epidemiology in the last century, R_0 has become a key concept in preventing the emergence of epidemics [22]. Three R_0 conditions will appear, namely (1) If $R_0 < 1$, then the disease will disappear; (2) If $R_0 = 1$, then the disease will remain; and (3) If $R_0 > 1$, then the disease will develop into an epidemic.

2. RESEARCH METHODS

The processing of research data follows the following steps: (1) The research subjects are divided into several groups that have similar characteristics. (2) The compartment model is formulated based on the assumption that individuals who recover from Malaria can be susceptible to transmission of the disease and the rate of change from one compartment to another. (3) Constructing a SEIR model for the spread of Malaria to analyze the relationship between variables. (4) Determining the Equilibrium Point with the condition f(x)=0. The SEIR model formed has two types of equilibrium points, namely the disease-free equilibrium point and the endemic equilibrium point. (5) Determining the Basic reproduction number (R0) by linearizing the infected subsystem around the disease-free

equilibrium point. (6) Analyzing the stability of the equilibrium point to find a qualitative solution to the SEIR model. (7) Determining the estimated parameter value using secondary data as a simulation of research results using Python and formulating it in graphical form.

3. RESULTS AND ANALYSIS

This research used data on malaria sufferers at the Mimika District Health Service, Indonesia, for model simulations 2018. The steps in solving this model problem include (1) making assumptions to simplify the model, (2) creating an SEIRS model related to disease characteristics, (3) creating a mathematical model in the form of a system of differential equations, and (4) analyzing the stability of the SEIRS model by identifying its fixed points, namely the endemic disease fixed point and the disease-free fixed point. Several assumptions are used to model the spread of Malaria, namely:

1) There are births and deaths in a population.
2) Death can occur in classes S, E, I, and R.
3) Diseases can be cured (people who have been cured have a temporary immune system)
4) Everyone has the same chance of being infected
5) No treatment is carried out, only on exposed individuals.

Figure 3 below is a SEIRS compartment diagram of the spread of Malaria.

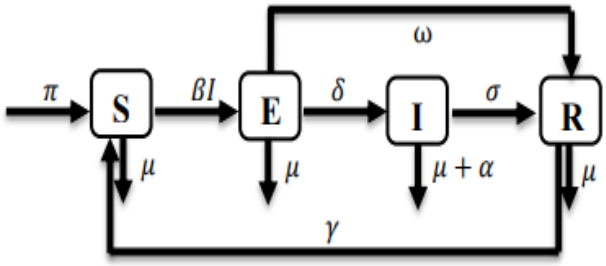

Figure 3. SEIRS Malaria compartment diagram

Figure 3 can be translated into a mathematical model to form a system of differential equations, which appears in the equation below.

$$\left.\begin{aligned} \frac{dS(t)}{dt} &= \pi + \gamma R - (\mu + \beta I)S \\ \frac{dE(t)}{dt} &= \beta IS - (\mu + \omega + \delta)E \\ \frac{dI(t)}{dt} &= \delta E - (\mu + \alpha + \sigma)I \\ \frac{dR(t)}{dt} &= \sigma I + \omega E - (\mu + \gamma)R \end{aligned}\right\} \quad (2)$$

From Table 1, Table 2, and Table 3, the balance point occurs at

$$\left(\frac{dS}{dt}, \frac{dE}{dt}, \frac{dl}{dt}, \frac{dR}{dt}\right) = (0,0,0,0)$$

Table 1. Variable description

Variable	Description
S	Number of susceptible individuals
E	The number of individuals experiencing symptoms but not yet infected
I	Number of infected individuals
R	Number of individuals who recovered
π	Birth rate
δ	Individual pace
βI	The rate at which an individual becomes a latent individual
μ	Death rate
α	Death from Malaria
γ	Constant rate of loss of immunity after recovery
ω	Effectiveness of treatment in humans
σ	Recovery rate

Table 2. SEIR Simulation Data

Variable	Amount	Source
N	219501	public health Office
S	118983	public health Office
E	42653	public health Office
I	49503	public health Office
R	8362	Assumption

Table 3. SEIR Parameter Values

Parameter	Parameter values
π	0.045
δ	0.358
β	0.416
μ	0.045
α	0.831
γ	0.001
ω	1
σ	0.5

The system of equations OF Figure 3 has two balance points: the disease-free equilibrium point denoted E_0, and the disease-endemic equilibrium point denoted E_1. The disease-free equilibrium point is obtained when E = 0 and I = 0, meaning that the population has no spread of infectious diseases. Based on the system of equations (2), a disease-free equilibrium point is obtained

$$E_0 = (S, E, I, R) = \left(\frac{\pi + \gamma R}{\mu}, 0,0,0\right)$$

Let E_1 (S*, E*, I*, R*). Assume S*, E*, I*, R* ≠ 0 so that,

$$S^* = \frac{\pi+\gamma R}{(\mu+\beta I)},$$

$$E^* = \frac{\beta IS}{(\mu+\omega+\delta)} = \frac{\beta I \dfrac{\pi+\gamma R}{(\mu+\beta I)}}{(\mu+\omega+\delta)} = \frac{\beta I(\pi+\gamma R)}{(\mu+\omega+\delta)(\mu+\beta I)}$$

$$I^* = \frac{\delta}{(\mu+\alpha+\sigma)} \frac{\beta I(\pi+\gamma R)}{(\mu+\omega+\delta)(\mu+\beta I)}$$

$$R^* = \frac{\sigma I + \omega E}{(\mu+\gamma)}$$

The Jacobian matrix can be used to determine the equilibrium point.

$$J(E_0) = \begin{bmatrix} -\mu & 0 & -\dfrac{\beta\pi}{\mu} & \gamma \\ 0 & -(\mu+\omega+\delta) & \dfrac{\beta\pi}{\mu} & 0 \\ 0 & \delta & -(\mu+\alpha+\sigma) & 0 \\ 0 & \omega & \sigma & -(\mu+\gamma) \end{bmatrix}$$

$$det\left(\lambda\begin{bmatrix}1&0&0&0\\0&1&0&0\\0&0&1&0\\0&0&0&1\end{bmatrix}-\begin{bmatrix}-\mu & 0 & -\frac{\beta\pi}{\mu} & \gamma\\ 0 & -(\mu+\omega+\delta) & \frac{\beta\pi}{\mu} & 0\\ 0 & \delta & -(\mu+\alpha+\sigma) & 0\\ 0 & \omega & \sigma & -(\mu+\gamma)\end{bmatrix}\right)=0$$

$$det\left(\begin{bmatrix}\lambda+\mu & 0 & \frac{\beta\pi}{\mu} & -\gamma\\ 0 & \lambda+\mu+\omega+\delta & -\frac{\beta\pi}{\mu} & 0\\ 0 & -\delta & \lambda+\mu+\alpha+\sigma & 0\\ 0 & -\omega & -\sigma & \lambda+\mu+\gamma\end{bmatrix}\right)=0$$

The eigenvalues obtained, namely$\lambda_1, \lambda_2, \lambda_3, \lambda_4$, are negative so that the accessible balance point E_0 is stable. The primary reproduction number of Malaria is obtained by determining the eigenvalues of the Jacobian matrix of the system of equations calculated at the disease-free equilibrium point.

$$\mu\gamma\alpha\delta + \mu\gamma\alpha\omega + \mu^2\gamma\alpha\omega + \mu\gamma\delta\sigma + \mu\gamma\delta\sigma + \mu^2\gamma\omega + \mu^2\gamma\sigma = \gamma\delta\beta\pi$$

The primary reproduction number of the above equation is obtained by equating the positive and negative parts.

$$R_0 = \frac{\gamma\delta\beta\pi}{\mu\gamma\alpha\delta + \mu\gamma\alpha\omega + \mu^2\gamma\delta + \mu\gamma\delta\sigma + \mu\gamma\sigma\omega + \mu^2\gamma\omega + \mu^2\gamma\sigma}$$

The following is the Python code used to determine R0 or the primary reproduction number and its eigenvalues

```
: import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
from scipy.optimize import fsolve

# Initial Value
N = 219501
S = 118983
E = 42653
I = 49503
R = 8362
# Parameter
phi = 0.045
delta = 0.358
beta = 0.416
miu = 0.045
alpha = 0.831
gamma = 0.001
omega = 1
sigma=0.5

# Function to find the equilibrium point
def equilibrium_point (phi,delta,beta, miu, alpha, gamma, omega,sigma):
    # Equations that must be solved to find the equilibrium point
    def equation (e):
        S, E, I, R = e
        return [
          phi+gamma*R-(miu+beta*I)*S,
```

```
            beta*I*S-(miu+omega+delta)*E,
            delta*E-(miu+alpha+sigma)*I,
            sigma*I+omega*E-(miu+gamma)*R

        ]

    # Initial guess
    initial_guess = [S/N, E/N, I/N, R/N]

    # Looking for a numerical solution
    equilibrium = fsolve(equation, initial_guess)

    return equilibrium



# Jacobian matrix of a system of differential equations
def jacobian_matrix(S, E, I, R):
    N = S + E + I + R
    J = np.array([[-miu, 0, -beta*phi/miu, gamma],
                  [0, -(miu+omega+delta), beta*phi/miu, 0],
                  [0, delta, -(miu+alpha+sigma), 0],
                  [0, omega, sigma, -(miu+gamma)]])
    return J

# Call a function to find the equilibrium point
solution_ equilibrium = point_ equilibrium (phi,delta,beta, miu, alpha,
gamma, omega,sigma)
S_eq, E_eq, I_eq, R_eq = solution_equilibrium

# Calculating the Jacobian matrix at the equilibrium point
J_eq = jacobian_matrix(S_eq, E_eq, I_eq, R_eq)

# Calculating eigenvalues
Value_Eigen = np.linalg.eigvals(J_eq)
# R0
R0 = (gamma*delta*beta*phi)/(miu*gamma*alpha*delta + miu*gamma*alpha*omega
+ (miu**2)*gamma*delta +
miu*gamma*delta*sigma+miu*gamma*sigma*omega+(miu**2)*gamma*omega+(miu**2)*
gamma*sigma)
# Print results
print("Eigen Value:")
print(Value_Eigen)
print(f"Value R0 = {R0}")
```

The result is a value of $R_0 = 0.078751<1$, so Malaria will disappear in the coming year. The complete picture is shown in Figure 4.

```
Eigen Values:
[-0.045      -0.046      -1.18541158 -0.59458842]

Reproduction basic number (R0)
0.0787517159252671
```

Figure 4. Eigenvalues and Basic Reproducibility

Here is the code for the SEIRS chart

```
: import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import solve_ivp

# Initial Value
N = 219501
S = 118983
E = 42653
I = 49503
R = 8362
# Parameter
phi = 0.045
delta = 0.358
beta = 0.416
miu = 0.045
alpha = 0.831
gamma = 0.001
omega = 1
sigma=0.5

# Functions for SEIR models
def SEIR_model(t, y, phi,delta,beta, miu, alpha, gamma, omega,sigma):
    S, E, I, R = y
    N = S + E + I + R
    dSdt=phi+gamma*R-(miu+beta*I)*S
    dEdt = beta*I*S-(miu+omega+delta)*E
    dIdt=delta*E-(miu+alpha+sigma)*I
    dRdt=sigma*I+omega*E-(miu+gamma)*R
    return np.array([dSdt, dEdt, dIdt, dRdt])

# Initial values and parameters
y0 = np.array([S, E, I, R])
# Period
t_span = (0, 100)
t_eval = np.linspace(0, 100, 1000)  # To produce smoother curves

# Solution need scipy.integrate.solve_ivp
sol = solve_ivp(lambda t, y: SEIR_model(t, y, phi,delta,beta, miu, alpha,
gamma, omega,sigma), t_span, y0, t_eval=t_eval)

# Plot the results
plt.figure(figsize=(10, 6))
```

```
plt.plot(sol.t, sol.y[0], label='Susceptible')
plt.plot(sol.t, sol.y[1], label='Exposed')
plt.plot(sol.t, sol.y[2], label='Infectious')
plt.plot(sol.t, sol.y[3], label='Recovered')
plt.xlabel('Time')
plt.ylabel('Total Population)
plt.title('Model SEIRS')
plt.legend()
plt.grid(True)
plt.show()
```

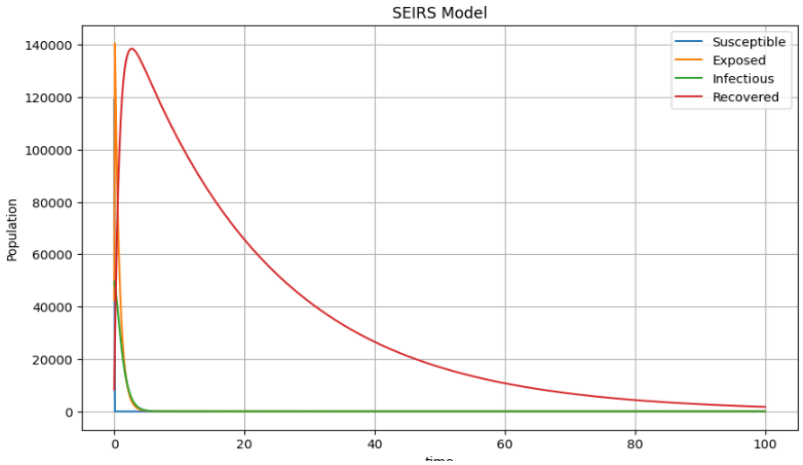

Figure 5. Graph of parameter values

Figure 5 above results from a numerical simulation of the disease-free equilibrium point from the SEIR model of Malaria's spread. It shows that Malaria's spread is decreasing and will not become an epidemic.

4. CONCLUSIONS

The research results show that the SEIRS mathematical model regarding the spread of Malaria in Mimika Regency was built with the assumption that there are births and deaths in a population, deaths occur in classes S, E, I, and R, every baby will be susceptible, the disease can be cured, all people have the same chance of being infected, and there are people who get the disease again.

$$\frac{dS(t)}{dt} = \pi + \gamma R - (\mu + \beta I)S$$
$$\frac{dE(t)}{dt} = \beta IS - (\mu + \omega + \delta)E$$
$$\frac{dI(t)}{dt} = \delta E - (\mu + \alpha + \sigma)I$$
$$\frac{dR(t)}{dt} = \sigma I + \omega E - (\mu + \gamma)R$$

For the spread of Malaria in Mimika Regency, the stability of the primary reproduction number (R0) of the SEIRS model was calculated using Python, and a value of 0.078, each lower than one, was obtained. Based on stability analysis and numerical simulation of the disease-free equilibrium point, the disease-free equilibrium point is locally asymptotically stable if R0 <1. This can mean that Malaria will disappear from the population under certain conditions that cause R0 <1. The Python code in this research can be used to make it easier to detect the spread of Malaria.

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