JTAM (Jurnal Teori dan Aplikasi Matematika)
http://journal.ummat.ac.id/index.php/jtam
p-ISSN 2597-7512 | e-ISSN 2614-1175
Vol. 6, No. 3, July 2022, pp. 777-788

The Effect of Susceptible Immigrants in a System Dynamic on the Spread of Malaria in Indonesia

Euis Aprianti[1], Jaharuddin[2], Endar H. Nugrahani[3]
[1,2,3]Department of Mathematics, IPB University, Indonesia
apriantieuis@apps.ipb.ac.id[1], jaharuddin@apps.ipb.ac.id[2], e_nugrahani@apps.ipb.ac.id[3]

Article History:
Received : 30-04-2022
Revised : 16-06-2022
Accepted: 22-06-2022
Online : 16-07-2022

Keywords:
Basic Reproduction Number;
Bifurcation;
Malaria;
Stability;
Susceptible Immigrants;

ABSTRACT

The spread of malaria is a serious public health problem, including in Indonesia. The mathematical model is formulated to describe the dynamic nature of the spread of malaria. The model used in this article is the SIR-SI model. This article discusses the stability of the fixed point analyzed using the Jacobian matrix and Routh-Hurwitz criteria, bifurcation analysis using the Castillo-Chaves and Song Theorem, and numerical simulation of the effect of the rate of susceptible immigrants on the dynamics of the malaria by using data on malaria cases in Indonesia. The results of the analysis show that the stability of the fixed point is related to the basic reproduction number determined by the next-generation matrix, and bifurcation occurs when the basic reproduction number is equal to one. The results of numerical simulations show that in order to suppress the spread of malaria, it is necessary to reduce the rate of susceptible immigrants.

https://doi.org/10.31764/jtam.v6i3.8630

A. INTRODUCTION

Malaria is an infectious disease transmitted by the bite of a female Anopheles mosquito infected with the malaria parasite. When sucking blood, the infected mosquito transmits sporozoites into the human body. Sporozoites reproduce in liver cells to become merozoites. After the liver cells rupture, the merozoites infect red blood cells and reproduce asexually. Symptoms of malaria will appear 4–8 days after the red blood cells are infected (Phillips et al., 2017). The spread of this disease has become a public health problem in the world, WHO estimates that there 229 million cases of malaria with 409,000 deaths in 2019 (World Health Organization, 2020) . While in Indonesia, The Indonesian Ministry of Health noted that there were 250,644 malaria cases in 2019 (Nurhakim, 2021) , with 49 deaths (Triyudha, 2020) .

Mathematically, the spread of malaria can be modelled based on several assumptions that can occur in the spread of malaria. This mathematical model was used to determine the dynamic nature of the spread of malaria. It is important to know this as a consideration for making decisions or policies in malaria control and eradication programs. The first mathematical model that describes the dynamics of the spread of malaria was introduced by Ronald Ross in 1911. In this model, the human population is divided into two groups, namely

the susceptible human population (S_h) and the infected human population (I_h), assuming that humans who are infected can become susceptible again. The mosquito population is also divided into two groups, namely the susceptible mosquito population (S_v) and the infected mosquito population (I_v) (Wedajo et al., 2018). The SIR (Susceptible, Infectious, and Recovered) model to describe the spread of malaria was first introduced by Kermack and McKendrick in 1927 (Brauer & Castillo-Chavez, 2012). Various mathematical models have been developed to describe the dynamics of the spread of malaria. (Tumwiine et al., 2007) studied the malaria spread model, which consisted of the SIR compartment for the human population and the SI compartment for the mosquito population, assuming that recovered individuals could be re-infected. In this model, population migration factors are ignored, while in (Martens & Hall, 2000), it is stated that population migration factors have the potential to have an impact on the spread of malaria. Such as Geleta Wedajo et al. (2018) investigated the model of malaria spread that allow migration factor.

Therefore, this article aims to determine the influence of susceptible immigrants on the spread of malaria in Indonesia using the SIR-SI model from Wedajo et al. (2018) modified by adding the effect of vaccination referring to (Putri et al., 2014) and the effect of using the long-lasting insecticidal net, the use of long-lasting insecticidal nets while sleeping is effective in avoiding mosquito bites because Anopheles mosquitoes actively bite and suck human blood at night (Rahmawati et al., 2014). This research was carried out by determining the fixed point and basic reproduction number for the model, then stability and bifurcation analysis. Then perform a numerical simulation using data on malaria cases in Indonesia.

B. METHODS

Suppose the human population is divided into three groups, namely: the susceptible human population is denoted S_h, the infected human population is denoted I_h, and the human population recovered from infection is denoted R_h. The mosquito population is divided into two groups, namely the susceptible mosquito population, denoted S_v, and the infected mosquito population, denoted I_v. In the formulation of the model, the following assumptions are made:

On human:

1. Every individual who is born is susceptible to infection.
2. There are immigrants who enter into the susceptible population.
3. The effectiveness of the malaria vaccine can provide permanent immunity to susceptible individuals (who have been vaccinated) against the disease and recovery.
4. Susceptible individuals can become infected by being bitten by an infected mosquito.
5. Infected individuals may recover from the infection or die from the disease.
6. Individuals who have recovered from infection have permanent immunity, so recovered humans cannot become susceptible again.
7. Any individual can leave any group due to natural death.

On mosquitoes:

1. Every mosquito that is born is susceptible to infection.
2. The mosquito birth rate is assumed to be the same as the mosquito death rate.

3. Susceptible mosquitoes can die by natural death or can become infected by biting infected individuals.
4. Infected mosquitoes end in natural death due to the relatively short life cycle of mosquitoes. The period of spread of mosquitoes ending in death means never recovering from infection.

From the assumptions above, the spread of malaria can be illustrated in the compartment diagram in Figure 1.

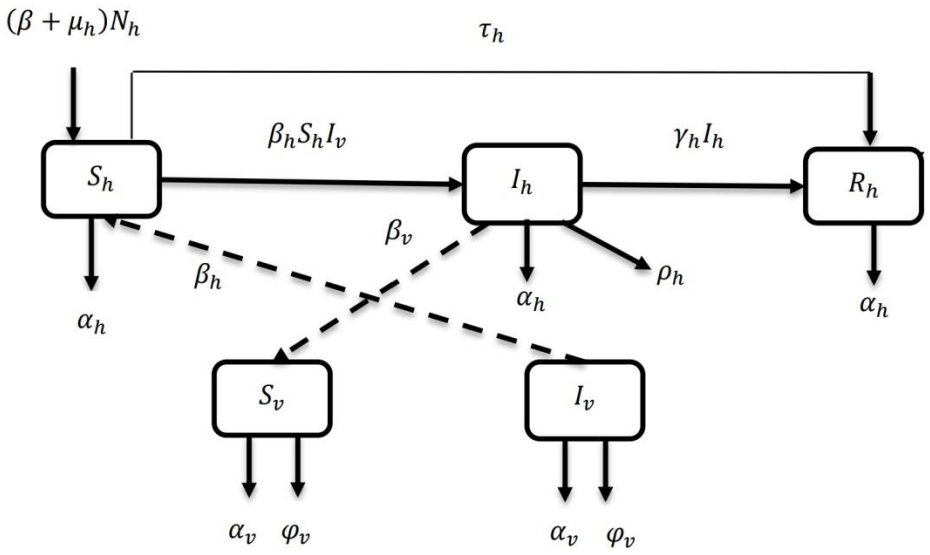

Figure 1. Compartment Diagram of the Spread of Malaria

Based on Figure 1, the mathematical model that describes the spread of malaria takes the form:

$$\frac{dS_h}{dt} = (\beta + \mu_h)N_h - \beta_h S_h I_v - \alpha_h S_h - \tau_h S_h \quad (1)$$

$$\frac{dI_h}{dt} = \beta_h S_h I_v - \rho_h I_h - \gamma_h I_h - \alpha_h I_h \quad (2)$$

$$\frac{dR_h}{dt} = \gamma_h I_h - \alpha_h R_h + \tau_h S_h \quad (3)$$

$$\frac{dS_v}{dt} = \mu_v N_v - \beta_v S_v I_h - \alpha_v S_v - \varphi_v S_v \quad (4)$$

$$\frac{dI_v}{dt} = \beta_v S_v I_h - \alpha_v I_v - \varphi_v I_v \quad (5)$$

With positive constans $\mu_h, \beta, \beta_h, \gamma_h, \alpha_h, \tau_h, \rho_h, \mu_v, \beta_v, \alpha_v, \varphi_v$. The total population of humans and mosquitoes is expressed by $N_h = S_h + I_h + R_h$ and $N_v = S_v + I_v$.

The descriptions of variables and parameters used in equations $(1) - (5)$ are given in the, as shown in Table 1 and Table 2.

Table 1. Description of Variables Used in the Model

Variable	Description	Unit
S_h	The number of susceptible humans at the time	People
I_h	The number of infected human at the time	People
R_h	The number of humans recovered from infection at the time	People
N_h	The total human population at the time	People
S_v	The number of susceptible mosquitoes at the time	Mosquito
I_v	The number of infected mosquitoes at the time	Mosquito
N_v	The total mosquito population at the time	Mosquito

Table 2. Description of Parameters Used in the Model

Parameter	Description	Unit
μ_h	The human birth rate	1/time
β	The human migration rate	1/time
β_h	The rate of disease transmission by contact between susceptible humans and infected mosquitoes	1/(mosquito × time)
γ_h	The human recovery rate	1/time
α_h	The natural death rate of humans	1/time
τ_h	The effectiveness of the malaria vaccine	1/time
ρ_h	The death rate due to human disease	1/time
μ_v	The mosquito birth rate	1/time
β_v	The rate of disease transmission by contact between susceptible mosquitoes and infected humans	1/(people × time)
α_v	The natural death rate of mosquito	1/time
φ_v	The effectiveness of the long-lasting insecticidal nets	1/time

C. RESULT AND DISCUSSION

1. Dynamic Characteristics

In the following, the dynamic characteristics of the malaria distribution model are discussed in equations (1) – (5). For this purpose, the following dimensionless variables are introduced:

$$s_h = \frac{S_h}{N_h}, i_h = \frac{I_h}{N_h}, r_h = \frac{R_h}{N_h}, s_v = \frac{S_v}{N_v}, i_v = \frac{I_v}{N_v}, t^* = t\,\mu_h.$$

If these dimensionless variables are substituted into equations (1) – (5), the following mathematical model of the spread of malaria is obtained, where the role of the notation t^* is replaced by t.

$$\frac{ds_h}{dt} = 1 + \xi - Bs_h i_v - (\alpha + \sigma)s_h \tag{6}$$

$$\frac{di_h}{dt} = Bs_h i_v - (\alpha + \gamma)i_h \tag{7}$$

$$\frac{di_v}{dt} = \frac{1}{\epsilon}(\nu(1 - i_v)i_h - \delta i_v - \theta i_v) \tag{8}$$

with the positive constants $\xi, B, \alpha, \sigma, \gamma, \epsilon, \nu, \delta, \theta$ which are stated as follows:

$$\xi = \frac{\beta}{\mu_h}, B = \frac{\beta_h N_v}{\mu_h}, \alpha = \frac{\alpha_h}{\mu_h}, \sigma = \frac{\tau_h}{\mu_h}, \gamma = \frac{\rho_h + \gamma_h}{\mu_h}, \epsilon = \frac{\mu_v}{\mu_h}, \nu = \frac{\beta_v N_h}{\mu_v}, \delta = \frac{\alpha_v}{\mu_v}, \theta = \frac{\varphi_v}{\mu_v}.$$

The stability of the disease-free fixed point and the endemic fixed point was determined based on the basic reproduction number. The basic reproduction number is defined as the average number of susceptible individuals that can be infected by one infected individual during the transmission period.This number can provide information about a condition that indicates whether a disease has spread or not (Giesecke, 2017). The disease-free fixed point of equations (6) – (8) is: $E_0(s_h, i_h, i_v) = \left(\frac{1+\xi}{\alpha+\sigma}, 0, 0\right)$, while the endemic fixed point is: $E_1(s_h, i_h, i_v) = (s_h^*, i_h^*, i_v^*)$ with

$$\begin{aligned}
s_h^* &= \frac{\alpha(\delta+\theta) + \gamma(\delta+\theta) + \nu(1+\xi)}{\nu(B+\alpha+\sigma)}, \\
i_h^* &= -\frac{\alpha^2(\delta+\theta) - B\nu(1+\xi) + \gamma(\delta+\theta)\sigma + \alpha(\delta+\theta)(\gamma+\sigma)}{(\alpha+\gamma)\nu(B+\alpha+\sigma)}, \\
i_v^* &= -\frac{\alpha^2(\delta+\theta) - B\nu(1+\xi) + \gamma(\delta+\theta)\sigma + \alpha(\delta+\theta)(\gamma+\sigma)}{B\big(\alpha(\delta+\theta) + \gamma(\delta+\theta) + \nu(1+\xi)\big)}.
\end{aligned}$$

Then the basic reproduction number is derived using the next-generation matrix (van den Driessche & Watmough, 2002). Based on equations $(7) - (8)$, the rate of emergence of new infective individuals in compartment i is:

$$F_i = \begin{pmatrix} Bs_h i_v \\ \frac{\nu}{\epsilon} i_h - \frac{\nu}{\epsilon} i_h i_v \end{pmatrix}$$

and the disease movement rate in compartment i is:

$$V_i = \begin{pmatrix} \left(\frac{\delta+\theta}{\epsilon}\right)(\alpha+\gamma) i_h \\ i_v \end{pmatrix}$$

so that it is obtained

$$F = \begin{pmatrix} \frac{\partial F_1}{\partial i_h} & \frac{\partial F_1}{\partial i_v} \\ \frac{\partial F_2}{\partial i_h} & \frac{\partial F_2}{\partial i_v} \end{pmatrix}\Bigg|_{E_0} = \begin{pmatrix} 0 & Bs_h \\ \frac{\nu}{\epsilon} - \frac{\nu}{\epsilon} i_v & -\frac{\nu}{\epsilon} i_h \end{pmatrix}\Bigg|_{E_0} = \begin{pmatrix} 0 & \frac{B(1+\xi)}{\alpha+\sigma} \\ \frac{\nu}{\epsilon} & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} \frac{\partial V_1}{\partial i_h} & \frac{\partial V_1}{\partial i_v} \\ \frac{\partial V_2}{\partial i_h} & \frac{\partial V_2}{\partial i_v} \end{pmatrix}\Bigg|_{E_0} = \begin{pmatrix} \alpha+\gamma & 0 \\ 0 & \frac{\delta+\theta}{\epsilon} \end{pmatrix}\Bigg|_{E_0} = \begin{pmatrix} \alpha+\gamma & 0 \\ 0 & \frac{\delta+\theta}{\epsilon} \end{pmatrix},$$

and the next-generation matrix:

$$FV^{-1} = \begin{pmatrix} 0 & \frac{B\epsilon(1+\xi)}{(\delta+\theta)(\alpha+\sigma)} \\ \frac{\nu}{(\alpha+\gamma)\epsilon} & 0 \end{pmatrix}.$$

The basic reproduction number, R_0 is the largest non-negative eigenvalue of the next-generation matrix, which is:

$$R_0 = \sqrt{\frac{B\nu(1+\xi)}{(\alpha+\gamma)(\delta+\theta)(\alpha+\sigma)}}.$$

The following is the stability theorem of the disease-free fixed point and the endemic fixed point based on the value of the basic reproduction number.

Theorem 1: The disease-free fixed point E_0 in equations $(6)-(8)$ is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$.

Proof.

Based on equations (6) – (8) defined $f_1 = 1 + \xi - Bs_h i_v - (\alpha+\sigma)s_h$, $f_2 = Bs_h i_v - (\alpha+\gamma)i_h$, $f_3 = \frac{1}{\epsilon}(\nu(1-i_v)i_h - \delta i_v - \theta i_v)$, so the Jacobian matrix at E_0 is:

$$J_0 = \begin{bmatrix} \frac{\partial f_1}{\partial s_h} & \frac{\partial f_1}{\partial i_h} & \frac{\partial f_1}{\partial i_v} \\ \frac{\partial f_2}{\partial s_h} & \frac{\partial f_2}{\partial i_h} & \frac{\partial f_2}{\partial i_v} \\ \frac{\partial f_3}{\partial s_h} & \frac{\partial f_3}{\partial i_h} & \frac{\partial f_3}{\partial i_v} \end{bmatrix}_{E_0} = \begin{bmatrix} -\alpha-\sigma & 0 & -\frac{B(1+\xi)}{\alpha+\sigma} \\ 0 & -\alpha-\gamma & \frac{B(1+\xi)}{\alpha+\sigma} \\ 0 & \frac{\nu}{\varepsilon} & \frac{-\delta-\theta}{\varepsilon} \end{bmatrix}.$$

The eigenvalues of Jacobian matrix J_0 are obtained from the following characteristic equation: $|\lambda \boldsymbol{I} - J_0| = 0$ or

$$(\lambda+\alpha+\sigma)\left[\lambda^2 + \left(k + \frac{\delta+\theta}{\varepsilon}\right)\lambda + \frac{k(\delta+\theta)}{\epsilon}(1-\mathcal{R}_0^2)\right] = 0, \tag{9}$$

with $k = \alpha + \gamma$. Based on equation (9), obtained three eigenvalues namely:

$$\lambda_1 = -\alpha - \sigma$$

$$\lambda_2 = \frac{-\left(k + \frac{\delta+\theta}{\varepsilon}\right) - \sqrt{\left(k + \frac{\delta+\theta}{\varepsilon}\right)^2 - 4\frac{k(\delta+\theta)}{\epsilon}(1-\mathcal{R}_0^2)}}{2}$$

$$\lambda_3 = \frac{-\left(k + \frac{\delta+\theta}{\epsilon}\right) + \sqrt{\left(k + \frac{\delta+\theta}{\varepsilon}\right)^2 - 4\frac{k(\delta+\theta)}{\epsilon}(1-\mathcal{R}_0^2)}}{2}.$$

The eigenvalues of λ_1 and λ_2 are negative, while λ_3 is negative if $\mathcal{R}_0 < 1$. This shows that the disease-free fixed point E_0 is locally asymptotic, meaning that malaria will disappear from the population. If $\mathcal{R}_0 > 1$, then λ_3 is positive, indicating that the disease-free fixed point E_0 is unstable if $\mathcal{R}_0 > 1$. ■

Theorem 2: The endemic fixed point E_1 in equations (6) − (8) is locally asymptotically stable if $\mathcal{R}_0 > 1$.

Proof.

The Jacobian matrix at E_1 is

$$J_1 = \begin{bmatrix} j_{11} & 0 & j_{13} \\ j_{21} & -\alpha-\gamma & j_{23} \\ 0 & j_{32} & j_{33} \end{bmatrix}$$

with

$$j_{11} = -\frac{\nu(1+\xi)(B+\alpha+\sigma)}{(\alpha+\gamma)(\delta+\theta)+(1+\xi)\nu},$$
$$j_{21} = \frac{B\nu(1+\xi)-(\delta+\theta)(\alpha+\sigma)(\alpha+\gamma)}{(\alpha+\gamma)(\delta+\theta)+(1+\xi)\nu},$$
$$j_{32} = \frac{\nu(\delta+\theta)(\alpha+\gamma)(B+\alpha+\sigma)}{B\epsilon\big((\alpha+\gamma)(\delta+\theta)+(1+\xi)\nu\big)},$$
$$j_{13} = -\frac{B\big(\nu(1+\xi)+(\delta+\theta)(\alpha+\gamma)\big)}{\nu(B+\alpha+\sigma)},$$
$$j_{23} = \frac{B\big(\nu(1+\xi)+(\delta+\theta)(\alpha+\gamma)\big)}{\nu(B+\alpha+\sigma)},$$
$$j_{33} = -\frac{B\big(\nu(1+\xi)+(\delta+\theta)(\alpha+\gamma)\big)}{\epsilon(B+\alpha+\sigma)(\alpha+\gamma)}.$$

So the characteristic equation is obtained as follows:

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

with

$$a_1 = \alpha+\gamma+\frac{B\big(\nu(1+\xi)+(\delta+\theta)(\alpha+\gamma)\big)}{\epsilon(B+\alpha+\sigma)(\alpha+\gamma)}+\frac{\nu(1+\xi)(B+\alpha+\sigma)}{(\alpha+\gamma)(\delta+\theta)+(1+\xi)\nu},$$
$$a_2 = \frac{B\big(\nu(1+\xi)+(\delta+\theta)(\alpha+\gamma)\big)}{\epsilon(B+\alpha+\sigma)}+\frac{\nu(1+\xi)(B+\alpha+\sigma)(\alpha+\gamma)}{(\alpha+\gamma)(\delta+\theta)+(1+\xi)\nu} + \left(\frac{(\delta+\theta)(\alpha+\sigma)}{\epsilon}\right)\left(\mathcal{R}_0^2-\frac{\alpha+\gamma}{\alpha+\sigma}\right),$$
$$a_3 = \frac{(\alpha+\gamma)(\delta+\theta)(\alpha+\sigma)}{\epsilon}(\mathcal{R}_0^2-1).$$

Because $a_1 > 0$, and for $\mathcal{R}_0 > 1$, $a_3 > 0$ and applies $a_1a_2 - a_3 > 0$, then according Routh-Hurwitz criteria (Edelstein-Keshet, 2005) , the endemic fixed point E_1 locally asymptotically stable. In other words, the disease of malaria will spread within the population. ■

Based on the above theorem, it is found that the stability of a fixed point depends on the basic reproduction number. Furthermore, an analysis will be carried out to determine the effect of changing which parameters can change the condition of the stability of the fixed point, in other words, change the condition of $\mathcal{R}_0 > 1$ to $\mathcal{R}_0 < 1$.

2. Bifurcation Analysis

The following is an analysis of the bifurcation that occurs when $\mathcal{R}_0 = 1$. For that, suppose $\varphi = B$ is selected as the bifurcation parameter and $x_1 = s_h; x_2 = i_h; x_3 = i_v$. The Jacobian matrix of equations (6) – (8) is evaluated at E_0 to find the eigenvalues and obtain equation (9). When $\mathcal{R}_0 = 1$, three eigenvalues are obtained, namely $\lambda_1 = -\alpha-\sigma, \lambda_2 = -\left(\alpha+\gamma+\frac{\delta+\theta}{\varepsilon}\right)$,

and $\lambda_3 = 0$. So that the first assumption of the Castillo-Chaves and Song Theorem is fulfilled, that is, it has one simple zero eigenvalue and the other has negative real values.

In addition, the zero eigenvalues are related to the J_0 matrix, which has a right eigenvector and a left eigenvector. The right eigenvector, which corresponds to $\lambda_3 = 0$ is obtained as follows.

$$u = \begin{bmatrix} u_1 \\ u_2 \\ u_3 \end{bmatrix} = \begin{bmatrix} -\left(\frac{B(1+\xi)}{(\alpha+\sigma)^2}\right)u_3 \\ \frac{\delta+\theta}{\nu}u_3 \\ u_3 > 0 \end{bmatrix}.$$

The left eigenvector corresponding to $\lambda_3 = 0$ is

$$v = \begin{bmatrix} v_1 \\ v_2 \\ v_3 \end{bmatrix} = \begin{bmatrix} 0 \\ \frac{\nu}{(\alpha+\gamma)\varepsilon}v_3 \\ v_3 > 0 \end{bmatrix}.$$

Furthermore, the values of a and b are obtained as follows.

$$a = \sum_{k,i,j=1}^{3} v_k u_i u_j \frac{\partial^2 f_k(E_0,0)}{\partial x_i \partial x_j} = v_2 u_1 u_3 \frac{\partial^2 f_2(E_0,0)}{\partial x_1 \partial x_3} = v_2 u_1 u_3 B < 0$$

and

$$b = \sum_{k,i,j=1}^{3} v_k u_i \frac{\partial^2 f_k(E_0,0)}{\partial x_i \partial B} = v_2 u_3 \frac{\partial^2 f_2(E_0,0)}{\partial x_3 \partial B} = v_2 u_3 \left(\frac{1+\xi}{\alpha+\sigma}\right) > 0.$$

The value of a and b obtained correspond to case 4 of the Castillo-Chaves and Song Theorem (Castillo-Chavez & Song, 2004). This shows that the bifurcation that occurs when $\mathcal{R}_0 = 1$ is a trans-critical bifurcation (Ndii, 2022). Next, the bifurcation simulation will be carried out to see the compatibility between the results of the analysis and the numerical results.

3. Bifurcation Simulation

In this section, a numerical simulation is carried out to see the bifurcation that occurs with the parameter values used, which are presented in Table 3.

Table 3. Parameter Values Used in Simulation

Parameter	Parameter Value	Reference
ξ	6.77	(Rosiana et al., 2020)
B	15	(Wedajo et al., 2018)
α	0.36	(Jayani, 2019)
σ	18.2	(Juliawan, 2019)
γ	2.34	(KEMENKES RI, 2018, 2020)
ϵ	1	(Jayani, 2019)
ν	10	(Wedajo et al., 2018)
δ	1	Asumsi
θ	21.84	(Nurmaliani & Arisanti, 2021)

Based on the parameter values in Table 3, the following bifurcation curve is obtained. As shown in Figure 2.

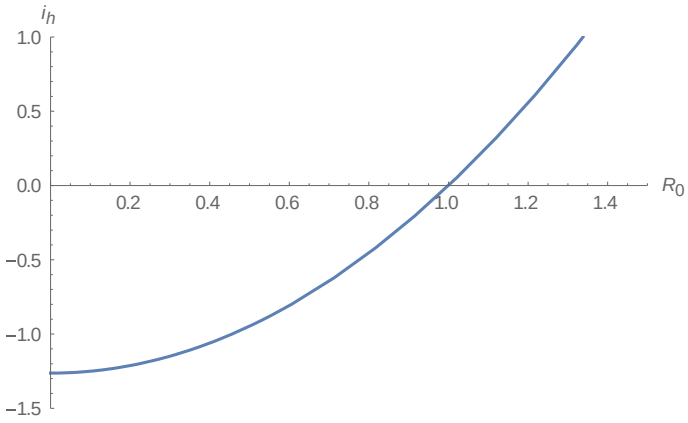

Figure 2. Trans-critical Bifurcation Curve

Based on Figure 2, The red curve is not an endemic fixed point because it gives a value of $i_h < 0$ meaning that the endemic fixed point is unstable and the disease-free fixed point is stable, while the blue curve gives a value of $i_h > 0$ meaning the endemic fixed point is stable and the disease-free fixed point is unstable. The simulation results show that there is a change in the stability of the disease-free fixed point and the endemic fixed point when $\mathcal{R}_0 = 1$, each changing from stable to unstable and vice versa, from unstable to stable.

So the results of the analysis and numerical simulation give the same result, namely bifurcation occurs when $\mathcal{R}_0 = 1$, so that changes in the value of a parameter will result in changes in the stability of the fixed point, one of which is a change in the value of the human migration rate. Furthermore, numerical simulations will be carried out to see the effect of changes in the value of the migration rate on the dynamycs of the spread of malaria.

4. Simulation of the Effect of Susceptible Immigrants on Population Dynamics

Furthermore, to determine the effect of the migration rate on the dynamics of the spread of malaria, a simulation was carried out by changing the parameter value ξ because the parameter depends on the migration rate of humans (β). Simulations were carried out using Mathematica 11.0 software.

In this case, it will be shown that there will be a decrease in the value of $\mathcal{R}_0$ if the value of the parameter ξ is decreased by the value of another parameter being fixed. The simulation is carried out with the parameter values presented in Table 3 by assuming the initial values are $s_{h0} = 0.9$, $i_{h0} = 0.1$, and $i_{v0} = 0.1$. The changes in the parameter value ξ used are presented in Table 4.

Table 4. The Effect of Changing the Value of Parameter $\boldsymbol{\xi}$ on the Value of the Basic Reproduction Number

Value of Parameter ξ	Value of $\mathcal{R}_0$
6.77	1.008
5	0.885
3	0.723

The following is an image that illustrates the dynamics of each population due to changes in the value of ξ. As shown in Figure 3.

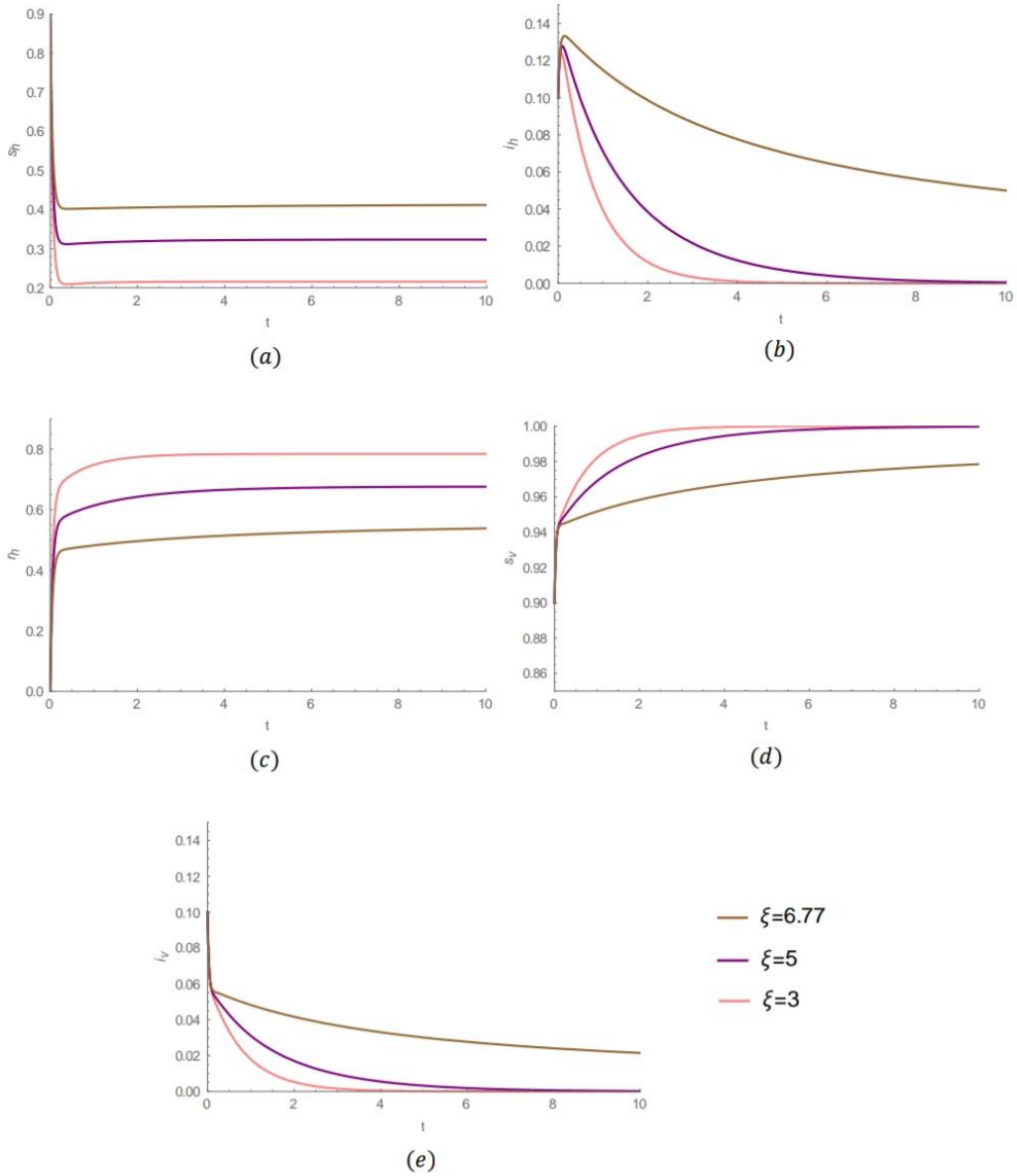

Figure 3. The Dynamics of Each Population Due to Changes in the Value of ξ

Figure 3 shows that the change in the value of ξ affects the dynamics of each population. Figures 3a-c show that if the value of ξ is lowered, the proportion of the susceptible human population will decrease due to a decrease in immigrants entering the susceptible population, and the proportion of the infected human population will also decrease and even become extinct when $\xi = 5$ and $\xi = 3$. The proportion of the recovering human population has increased. Figure 3d-e shows that if the value of ξ is lowered, the proportion of the infected mosquito population decreases and even experiences extinction when $\xi = 5$ and $\xi = 3$ so that the remaining population of susceptible mosquitoes.

The simulation results show that if the value of ξ is reduced, the proportion of infected human populations and infected mosquitoes will decrease. Since the value of ξ is directly proportional to the rate of human migration (β), a decrease in the value of β can reduce the proportion of infected human populations and infected mosquitoes and even cause them to become extinct. Thus, efforts that can be made to suppress the spread of malaria is to reduce the rate of human migration.

D. CONCLUSION AND SUGGESTIONS

The SIR-SI model was applied to the spread of malaria to predict the dynamics of malaria outbreaks. This model consists of a SIR compartment for the human population and an SI compartment for the mosquito population. The assumption made in this model is that it allows the recruitment of individuals through migration. Before performing the analysis, the model was simplified by non-dimensionalizing the variables in a system of differential equations that described the dynamics of the spread of malaria. The results of the analysis show that the model has two fixed points, namely the disease-free fixed point and the endemic fixed point. The disease-free fixed point is locally asymptotically stable, if the basic reproduction number is less than one, it means that the disease will die within a certain time. The endemic fixed point is locally asymptotically stable, if the basic reproduction number is more than one, it means that the disease will spread in the population. The result of further analysis shows that bifurcation occurs in the system when the basic reproduction number is equal to one, meaning that there is a change in the stability of the fixed point due to changes in parameters, one of which is a change in migration parameters.

Based on the simulation results, changes in the migration rate have a directly proportional effect on changes in the basic reproduction number. If the migration rate is reduced, the value of the basic reproduction number will decrease, so that it can reduce the rate of malaria spread. Therefore, the best thing that can be done to minimize the malaria outbreak caused by the human population and infected mosquitoes is to reduce the rate of population migration. Suggestions for further research are to consider the possibility of recovered individuals being infected with malaria again so that the SIR-SI model becomes SIRS-SI model.

REFERENCES

Brauer, F., & Castillo-Chavez, C. (2012). *Mathematical Models in Population Biology and Epidemiology* (2nd ed., Vol. 40). Springer. https://doi.org/10.1007/978-1-4614-1686-9

Castillo-Chavez, C., & Song, B. (2004). Dynamical Models of Tuberculosis and Their Applications. *Mathematical Biosciences and Engineering*, *1*(2), 361–404. https://doi.org/10.3934/mbe.2004.1.361

Edelstein-Keshet, L. (2005). *Mathematical Models in Biology*. SIAM.

Giesecke, J. (2017). *Modern infectious disease epidemiology* (3rd ed.). CRC Pr.

Jayani, D. H. (2019). *2015-2045: Angka Kematian Terus Naik, Angka Kelahiran Relatif Stabil | Databoks*. Databoks. https://databoks.katadata.co.id/datapublish/2019/07/18/2015-2045-angka-kematian-terus-naik-angka-kelahiran-relatif-stabil#

Juliawan, K. D. (2019). RTS, S/AS01 sebagai Vaksin Malaria Generasi Pertama. *Jurnal Ilmiah Kesehatan Sandi Husada*, *10*(2), 275–280. https://doi.org/10.35816/jiskh.v10i2.170

KEMENKES RI. (2018). *Laporan Nasional RISKESDAS 2018*. KEMENKES RI.

KEMENKES RI. (2020). *Rencana Aksi Keiatan (RAK) 2020-2024* (p. 91). KEMENKES RI.

Martens, P., & Hall, L. (2000). Malaria on the Move: Human Population Movement and Malaria Transmission. *Emerging Infectious Diseases*, *6*(2), 103–109. https://doi.org/10.3201/eid0602.000202

Ndii, M. Z. (2022). *Pemodelan Matematika*. Penerbit NEM.

Nurhakim, F. (2021). *Kasus Malaria Masih Jadi Persoalan di Propinsi ini*. Gatra.Com. https://www.gatra.com/detail/news/510015/kesehatan/kasus-malaria-masih-jadi-persoalan-di-propinsi-ini

Nurmaliani, R., & Arisanti, M. (2021). Efektivitas Kelambu Berinsektisida dalam Pengendalian Vektor Malaria di Indonesia. *SPIRAKEL*, *13*(2), 70–77. https://doi.org/10.22435/spirakel.v13i2.5616

Phillips, M. A., Burrows, J. N., Manyando, C., van Huijsduijnen, R. H., Van Voorhis, W. C., & Wells, T. N. C. (2017). Malaria. *Nature Reviews Disease Primers*, *3*(1), 1–24. https://doi.org/10.1038/nrdp.2017.50

Putri, R. G., Jaharuddin, & Bakhtiar, T. (2014). Sirs-Si Model of Malaria Disease with Application of Vaccines, Anti-Malarial Drugs, and Spraying. *IOSR Journal of Mathematics*, *10*(5), 66–72. https://doi.org/10.9790/5728-10526672

Rahmawati, E., Hadi, U., & Soviana, S. (2014). Keanekaragaman jenis dan perilaku menggigit vektor malaria (Anopheles spp.) di Desa Lifuleo, Kecamatan Kupang Barat, Kabupaten Kupang, Nusa Tenggara Timur. *Jurnal Entomologi Indonesia*, *11*(2), 53–64. https://doi.org/10.5994/jei.11.2.53

Rosiana, N., Soblia, H. T., Prabawa, P. D., & Firdaus, P. I. (2020). *Profil Migran Hasil Survei Sosial Ekonomi Nasional 2019*. Badan Pusat Statistik.

Triyudha, A. (2020). *Mengatasi Ancaman Malaria*. Harnas.Co. http://www.harnas.co/2020/05/01/mengatasi-ancaman-malaria

Tumwiine, J., Mugisha, J. Y. T., & Luboobi, L. S. (2007). A mathematical model for the dynamics of malaria in a human host and mosquito vector with temporary immunity. *Applied Mathematics and Computation*, *189*(2), 1953–1965. https://doi.org/10.1016/j.amc.2006.12.084

van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*, *180*(1–2), 29–48. https://doi.org/10.1016/S0025-5564(02)00108-6

Wedajo, A. G., Bole, B. K., & Koya, P. R. (2018). The Impact of Susceptible Human Immigrants on the Spread and Dynamics of Malaria Transmission. *American Journal of Applied Mathematics*, *6*(3), 117–127. https://doi.org/10.11648/j.ajam.20180603.13

World Health Organization. (2020). *World malaria report 2020: 20 years of global progress and challenges*. WHO.