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Transmission of Dengue Virus With and Without Vaccination Using SIR Model

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Abstract: Dengue is a mosquito-borne aggressive disease. The Susceptible-Infected-Recovered (SIR) model for the transmission of dengue virus is discussed. This project focused the dengue transmission into three compartments, namely: susceptible, infected and recovered for dengue transmission. The focus was to deduce the SIR model to find the base reproductive number R_0 analytically. The SIR model was used to investigate the stability analysis of disease free and endemic for dengue transmission with and without vaccination by solving the Ordinary Differential Equation (ODE). In addition, SIR model was also used to analyze and predict the spread of dengue virus with and without vaccination. The transmission of dengue was studied using data taken from Thailand by observing the graph of population of dengue versus time in years for all three compartments of the SIR model. The graph will be plotted using MAPLE software. As a result of the stability analysis, it shows that the transmission of the dengue virus without vaccination will make the system unstable because not all of the roots are negative and the transmission of dengue with vaccination for both disease free and endemic will make the system stable.

Keywords: Dengue, Disease Free, Endemic Equilibrium, SIR model, Vaccination

1 Introduction

Dengue fever is a viral infectious disease spread through the bite of an infected Aedes mosquito. It can cause a severe illness and death in some cases. In recent decades, the global occurrence of dengue fever has risen significantly. Dengue fever is spread through a human-to-mosquito-to-human transmission cycle. The virus spread to humans through a bite from the female mosquito of the Aedes aegypti and Aedes al-bopictus. Female Aedes aegypti mosquito bites and ingests blood that contains the dengue virus. According to Lestari et al. [1]. There are four serotypes of dengue virus which are dengue virus type 1 (DEN-1), dengue virus type $2(\text{DEN}-2)$, dengue virus type 3 (DEN-3), dengue virus type 4 (DEN-4).

Besides transmission through mosquito bites, dengue virus can also spread from a pregnant woman to her baby. A pregnant woman who is infected with dengue will spread the infection to her fetus during pregnancy or at the time of birth. However, the dengue virus can rarely be transmitted by blood transfusion, organ transplantation or by injury from a needle stick.

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Since there is no specific effective treatment for the disease, Deng et al. [2] stated that vaccinations to prevent infection and illness development are urgently needed. According to Nealon et al. [3], the first dengue vaccine, Dengvaxia has been developed by Sanofi Pasteur and approved in December 2015. Based on the research of da Silveira et al. [4], it was stated that dengue vaccines are in various phases of development in Brazil, and only one commercial formulation (CYD-TDV) manufactured by Sanofi Pasteur is available.

According to The Lancet Infectious Diseases [5], in comparison to without vaccinated controls, recipients who were seronegative before vaccination had a greater risk of severe dengue sickness and hospital admission. MAPLE software was used for constructing the graph of SIR model by taking Thailand's data which was the parameter value that was used by Chauhan et al. [6] in their research.

According to Yu et al. [7], the SIR model can be used to forecast the spread of the disease in areas and time. It gives a satisfying result of dimensional dispersal of the dengue fever outbreak. The model grants health officials with a useful note to manage and counter the spread of the dengue virus. Syafruddin et al. [8] researched on a system of differential equations that models dengue transmission vector SIR population dynamics. There were two populations, a human population (N_h) and a vector population, are defined by the SIR model(N_v). The human population (N_h) is divided into three groups which are people who may potentially get infected with the dengue virus(S_h), people who are infected with dengue (I_h) and people who have recovered(R_h). The vector population of mosquitoes (N_v) is divided into two groups which are mosquitoes that may potentially become infected with dengue virus (S_v) and mosquitoes that are infected with dengue virus(I_e).

According to Angstmann et al. [9], they conducted a study using a stochastic process, to create an SIR model that demonstrates how a fractional order may be included into the disease of infection rate. They also stated that for a person to be contagious by the disease at time t, they must have been affected for some time already and they have not been evacuated into the removed cubicle or die. The outbreak of dengue virus is wondrous, but under several methods, the spread of dengue virus can be controlled. By using a mathematical model on the SIR model, it will help to control the spread of the disease instead of increasing the prospect of surviving from the disease in the future.

In this project, the transmission of the dengue virus among human populations will be investigated. This research will show the stability analysis of disease free and endemic by using equilibrium points of with and without vaccination. For the researcher, it allows us to understand and predict the effects of different strategies for disease control. It will also help the government to increase awareness on vaccine benefits.

Therefore, this study focused on the effect of dengue virus on the disease-free equilibrium point and endemic equilibrium point with and without vaccination and to compare the number of people infected by the dengue virus before and after vaccination.

2 Methodology

A The General Solution of SIR Model.

i. Description of SIR Model of Dengue without Vaccination

The model has three compartments which are Susceptible (S), Infected (I) and Recovered (R). Susceptible class is for individuals who are still free from dengue virus. Infected class is for individuals who are currently infected and able to transmit the dengue virus to others. Recovered class is for individuals who have recovered from dengue infection. Below is the system of ordinary differential equation by Chauhan et al. [6]

$$\frac{\mathrm{dS}}{\mathrm{dt}} = \mu N - \frac{\beta \mathrm{I(t)S(t)}}{\mathrm{N}} - \mu \mathrm{S}(t) \quad (1)$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = \frac{\beta \mathrm{I(t)S(t)}}{\mathrm{N}} - \gamma I(t) - \mu \bar{I}(t) \quad (2)$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} = \gamma I(t) - \mu R(t) \quad (3)$$

where,
$S(t)$ is number of susceptible individuals at time t
I(t) is number of infected individuals at time t
R(t) is number of recovered individuals at time t
N is total population size
β is transmission of disease from an infected person in a time period
μ is death and birth rate which are assumed to be equal
γ is recovery rate

ii. Description of SIR Model of Dengue with Vaccination

Vaccination has a significant impact on the existence of disease-free and endemic equilibrium points. As a result, the model below was generated with the assistance of induced vaccination by Chauhan et al. [6].

$$\frac{\mathrm{dS}}{\mathrm{dt}} = (1-p)\mu N - \frac{\beta \mathrm{I(t)S(t)}}{\mathrm{N}} - \mu \mathrm{S}(t) \quad (4)$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = \frac{\beta \mathrm{I(t)S(t)}}{\mathrm{N}} - \gamma I(t) - \mu I(t) \quad (5)$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} = \gamma I(t) - \mu R(t) \quad (6)$$

$$\frac{\mathrm{dV}}{\mathrm{dt}} = p\mu - \mu V(t) \quad (7)$$

where:
S(t) is the susceptible population
I(t) is infected population

R(t) is the recovered population
V(t) the group to which vaccination is given
μ is the mortality rate
p is the vaccination rate
γ is the recovery rate

B Deducing SIR Model to find R_0 of Dengue Transmission

R_0, pronounced "R naught" is a mathematical term that indicates how contagious an infectious disease is. It is also referred to as the basic reproduction number. As an infection is transmitted to new people, it reproduces itself. R_0 tells you the average number of people who will contract a contagious disease from a person with that disease. It specifically applies to a population of people who were previously free of infection and have not been vaccinated. If R_0 is less than 1, each existing infection causes less than one new infection. In this case, the disease will decline and eventually die out. If R_0 equals 1, each existing infection causes a new infection. The disease will stay alive and stable, but there will not be an outbreak or an epidemic. If R_0 is more than 1, each existing infection causes more than one new infection. The disease will be transmitted between people, and there may be an outbreak or epidemic.

i. Basic Reproductive Ratio of Dengue Transmission without Vaccination

By solving the matrix from ODE (10,11,12) using Next Generation Matrix Approach, basic reproductive ratio was from Chauhan et al. [6] below:

$$R_0 - \frac{\beta}{\gamma+\mu} \tag{8}$$

ii. Basic Reproductive Ratio of Dengue Transmission with Vaccination

After the induction of vaccination in the model, the basic reproductive ratio is from Chauhan et al. [6] below:

$$R_e = R_0(1-p) \tag{9}$$

C To Investigate the Stability Analysis of Disease Free

The stability analysis can be investigated. Firstly, linearize the SIR model. Secondly, form Jacobian Matrix from ODE. Then, substitute the disease-free equilibrium point into Jacobian matrix ($s = 1, I = 0, v = p$). Lastly, find the roots, λ by solving det (J-λI) $= 0$. The system can be determined whether it is stable or unstable by focus on the sign of the roots, λ. The system is stable when all the roots give the negative sign.

D To Investigate the Stability Analysis Endemic Equilibrium Point

For endemic equilibrium point, it also used the same method with disease free. The endemic equilibrium point only exists if $R_v > 1$. The system is considered stable if all the roots are negative. Otherwise, it is considered unstable.

E Parameter Values

The standard values for ODE parameters utilized in this research were obtained from Chauhan et al. [6]. The simulations and analysis were conducted using the standard values shown in Table 1 below.

Table 1: Parameter values

Parameter	Description	Value
γ	recovery rate	0.5
μ	mortality rate	0.5
β	effective contact rate between susceptible and infected individual	1.98
p	vaccination rate	0.6

F Basic Reproduction Number

The matrix $G = FV^{-1}$ is known as the next generation matrix. Ro can be obtained from $G = FV^{-1}$ where F represents new infections that will arise and V^{-1} represents transmittal from one comportment to another.

i. Basic Reproductive Ratio of Dengue Transmission without Vaccination

In this case, if $R_0 > 1$, each current infection results in the formation of many new infections. The disease will be spread by human contact and an outbreak or epidemic may occur. For simplicity, we can consider the prevalence of the proportions by redefining $s = \frac{S}{N}, i = \frac{1}{N}$ and $r = \frac{R}{N}$ and substituting into equation (1,2,3) will get:

$$\frac{\mathrm{ds}}{\mathrm{dt}} = \mu - \beta is - \mu s \tag{10}$$

$$\frac{\mathrm{di}}{\mathrm{dt}} = \beta is - \gamma i - \mu i \tag{11}$$

$$\frac{\mathrm{dr}}{\mathrm{dt}} = \gamma i - \mu r \tag{12}$$

According to the elimination rule in general form: Column 1 represent S, column 2 represent I and column 3 represent R.

$$G = \begin{bmatrix} a & b & c \\ d & e & f \\ g & h & i \end{bmatrix}$$

Therefore, from the equation(10,11,12), the next generation matrix G can be built:

$$G = \begin{bmatrix} -\beta i - \mu & -\beta s & 0 \\ \beta i & \beta s - \gamma - \mu & 0 \\ 0 & \gamma & -\mu \end{bmatrix}$$

The element in the left submatrix G is said to be F − V and lower submatrix is termed by J_1 and J_2

$$G = \begin{bmatrix} F - V & 0 \\ J_1 & J_2 \end{bmatrix}$$

Therefore, from the submatrix G,

$$F - V = \begin{bmatrix} -\beta i - \mu & -\beta s \\ \beta i & \beta_8 - \gamma - \mu \end{bmatrix}$$

when i = 0, s = 1, F − V will get:

$$F - V = \begin{bmatrix} -\mu & -\beta \\ 0 & \beta - \gamma - \mu \end{bmatrix}$$

From matrix F − V, we need to identify the matrix F and the matrix V :

$$F - V = \begin{bmatrix} 0 & 0 \\ 0 & \beta \end{bmatrix} - \begin{bmatrix} \mu & \beta \\ 0 & \gamma + \mu \end{bmatrix}$$

$$V = \begin{bmatrix} \mu & \beta \\ 0 & \gamma + \mu \end{bmatrix}$$

From matrix V, the inverse of the matrix V will be:

$$V^{-1} = \frac{1}{\mu(\gamma + \mu)} \begin{bmatrix} \gamma + \mu & 0 \\ -\beta & \mu \end{bmatrix}$$

$$= \begin{bmatrix} \frac{1}{\mu} & 0 \\ \frac{-\beta}{\mu(\gamma + \mu)} & \frac{1}{\gamma + \mu} \end{bmatrix}$$

Therefore, to find $R_0 - FV^{-1}$ will get:

$$FV^{-1} = \begin{bmatrix} 0 & 0 \\ 0 & \beta \end{bmatrix} \begin{bmatrix} \frac{1}{\mu} & 0 \\ \frac{-\beta}{\mu(\gamma+\mu)} & \frac{1}{\gamma+\mu} \end{bmatrix}$$

$$= \begin{bmatrix} 0 & 0 \\ 0 & \frac{\beta}{\gamma+\mu} \end{bmatrix}$$

$$R_0 = \frac{\beta}{\gamma+\mu}$$

By substituting the value of parameter,

$$R_0 = \frac{(1.98)}{0.5+0.5}$$
$$= 1.98$$

Therefore, the epidemic occurs since R_0 is more than 1.

ii. Basic Reproductive Ratio of Dengue Transmission with Vaccination

After the induction of vaccination in the model, the new reproduction number is:

$$R_{\mathrm{e}} = R_0(1 - \mathrm{p})$$

By substituting the value of parameter in Table 3.1.

$$R_e = 1.98(1 - 0.6)$$
$$= 0.792$$

Therefore, the epidemic does not occur since R_0 is less than 1.

G Stability Analysis of Disease Free

i. Stability Analysis of Disease Free without Vaccination

Linearizing the model equation of dengue transmission without vaccination will get:

$$\frac{\mathrm{ds}}{\mathrm{dt}} = \mu - \beta is - \mu s \quad (13)$$

$$\frac{\mathrm{di}}{\mathrm{dt}} = \beta is - \gamma i - \mu i \quad (14)$$

$$\frac{\mathrm{dr}}{\mathrm{dt}} = \gamma i - \mu r \quad (15)$$

The ODE above gives the Jacobian matrix:

$$J(s,i) = \begin{bmatrix} -\beta i - \mu & -\beta s \\ \beta i & \beta s - \gamma - \mu \end{bmatrix}$$

Let the disease free equilibrium point $(s = 1, i = 0)$:

$$J(1,0) = \begin{bmatrix} -\mu & -\beta \\ 0 & \beta - \gamma - \mu \end{bmatrix}$$
$$J - \lambda I = \begin{bmatrix} -\mu & \beta \\ 0 & \beta - \gamma - \mu \end{bmatrix} - \lambda \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$
$$= \begin{bmatrix} -\mu - \lambda & \beta \\ 0 & \beta - \gamma - \mu - \lambda \end{bmatrix}$$

In order to find the roots, then the determinant of $J - \lambda I$ will be set equal to zero:

$$\det(I - \lambda I) = \begin{bmatrix} -\mu - \lambda & \beta \\ 0 & \beta - \gamma - \mu - \lambda \end{bmatrix} = 0$$
$$\det(J - \lambda I) = (-\mu - \lambda)(\beta - \gamma - \mu - \lambda) = 0$$
$$= -\mu\beta + \mu\gamma + \mu^2 + \mu\lambda - \lambda\beta + \lambda\gamma + \lambda\mu + \lambda^2 = 0$$
$$= -\mu\beta + \mu\gamma + \mu^2 + 2\mu\lambda - \lambda\beta + \lambda\gamma + \lambda^2 = 0$$

By substituting the value of the parameter into the above equation:

$$\det(J - \lambda I) = -(0.5)(1.98) + (0.5)(0.5) + (0.5)^2 + 2(0.5)\lambda - 1.98\lambda + 0.5\lambda + \lambda^2 = 0$$
$$= \lambda^2 - 0.48\lambda - 0.49 = 0$$
$$= (0.98 - \lambda)(0.5 + \lambda) = 0$$

where,

$$\lambda_1 = 0.98$$
$$\lambda_2 = -0.5$$

Since not all the roots are negative the system is said to be unstable.

ii. Stability Analysis of Disease Free with Vaccination

By considering the total population density:

$$s(t) + i(t) + r(t) + v(t) = 1$$
$$= 1 - s(t) - i(t) - v(t)$$

Therefore, it is enough to consider:

$$\frac{\mathrm{ds}}{\mathrm{dt}} = (1 - p)\mu - \beta is - \mu 8 \quad (16)$$

$$\frac{\mathrm{di}}{\mathrm{dt}} = \beta is - \gamma i - \mu i \quad (17)$$

$$\frac{\mathrm{dv}}{\mathrm{dt}} = p\mu - \mu v \tag{18}$$

The ODE above gives the Jacobian matrix:

$$J = \begin{bmatrix} -\beta i - \mu & -\beta s & 0 \\ \beta i & \beta s - \gamma - \mu & 0 \\ 0 & 0 & -\mu \end{bmatrix}$$

Since the disease free equilibrium ($s = 1 - p, i = 0, v = p$) therefore,

$$J = \begin{bmatrix} -\mu & -\partial(1-p) & 0 \\ 0 & \beta(1-p) - \gamma - \mu & 0 \\ 0 & 0 & -\mu \end{bmatrix}$$

Next,

$$\begin{aligned} J - \lambda I &= \begin{bmatrix} -\mu & -\beta(1-p) & 0 \\ 0 & \beta(1-p) - \gamma - \mu & 0 \\ 0 & 0 & -\mu \end{bmatrix} - \lambda \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} \\ &= \begin{bmatrix} -\mu - \lambda & -\beta(1-p) & 0 \\ 0 & \beta(1-p) - \gamma - \mu - \lambda & 0 \\ 0 & 0 & -\mu - \lambda \end{bmatrix} \end{aligned}$$

To solve the determinant of $J - \lambda I$, it will be set equals to zero:

$$\det(J - \lambda I) = (-\mu - \lambda) \begin{bmatrix} \beta(1-p) - \gamma - \mu - \lambda & 0 \\ 0 & -\mu - \lambda \end{bmatrix} = 0$$

$$\begin{aligned} &= (-\mu - \lambda)[\beta(1-p) - \gamma - \mu - \lambda][-\mu - \lambda] = 0 \\ &= (\mu + \lambda)[\beta(1-p) - \gamma - \mu - \lambda][\mu + \lambda] = 0 \\ &= (\mu + \lambda)[\beta\mu(1-p) + \beta\lambda(1-p) - \gamma\mu - \gamma\lambda - \mu^2 - \mu\lambda - \lambda\mu - \lambda^2] = 0 \\ &= (\mu + \lambda)[\beta\mu(1-p) + \beta\lambda(1-p) - \gamma\mu - \gamma\lambda - \mu^2 - 2\lambda\mu - \lambda^2] = 0 \\ &= \beta\mu^2(1-p) + \beta\mu\lambda(1-p) - \gamma\mu^2 - \mu\gamma\lambda - \mu^3 - 2\lambda\mu^2 - \mu\lambda^2 + \\ &\beta\mu\lambda(1-p) + \beta\lambda\text{^}2\,(1-p) - \gamma\mu\lambda - \gamma\lambda^2 - \mu^2\lambda - 2\lambda^2\mu - \lambda^3] = 0 \end{aligned}$$

By substituting the value of the parameter into above equation will get:

$$\begin{aligned} &0.198 + 0.396\lambda - 0.125 - 0.25\lambda - 0.125 - 0.5\lambda^2 - 0.5\lambda + 0.396\lambda + \\ &0.792\lambda^2 - 0.25\lambda - 0.5\lambda^2 - 0.25\lambda - \lambda^3 - \lambda^2 = 0 \end{aligned}$$

Using the factorization into quadratics method, we will get:

$$-\lambda^3 - 1.208\lambda^2 - 0.458\lambda - 0.052 = 0$$
$$(\lambda_1 + 0.208)(\lambda_2 + 0.5)(\lambda_3 + 0.5) = 0$$

where,

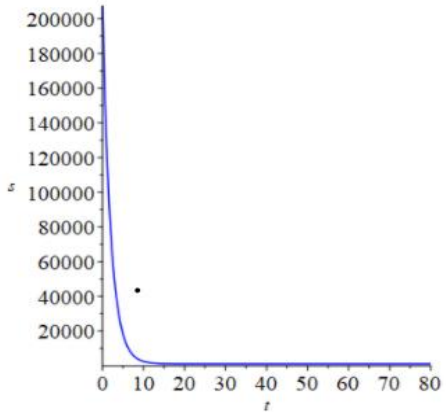
$$\lambda_1 = -0.208$$
$$\lambda_2 = -0.5$$
$$\lambda_3 = -0.5$$

Since all the roots of the equation are negative, then the system is said to be stable.

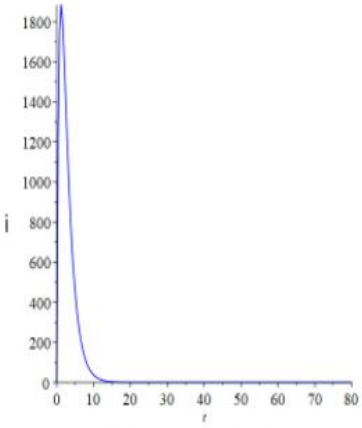
3 Results and Discussion

A Discussion on the Graph of SIR Model of Dengue without Vaccination

The discussion in this section covers susceptible and infection compartment of the SIR model for without vaccination. The Maple software was used and proceeded to stimulate the model using the parameter values in Table 1. The number of dengue cases that occurred in Thailand was taken from Chao et al. [10]. Data was taken from Thailand because Thailand is one of the countries that introduced vaccine for dengue while other countries like Malaysia do not distribute the dengue vaccine, either in the government or private sector.



a) Susceptible without vaccination



b) Infection without vaccination

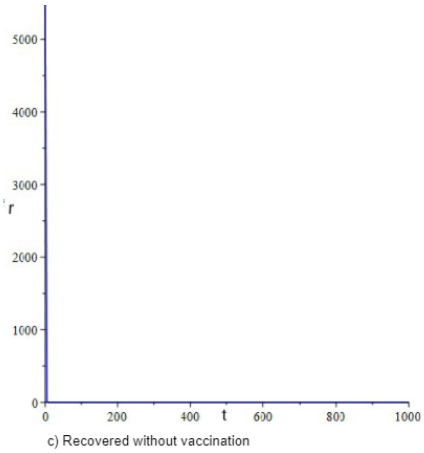
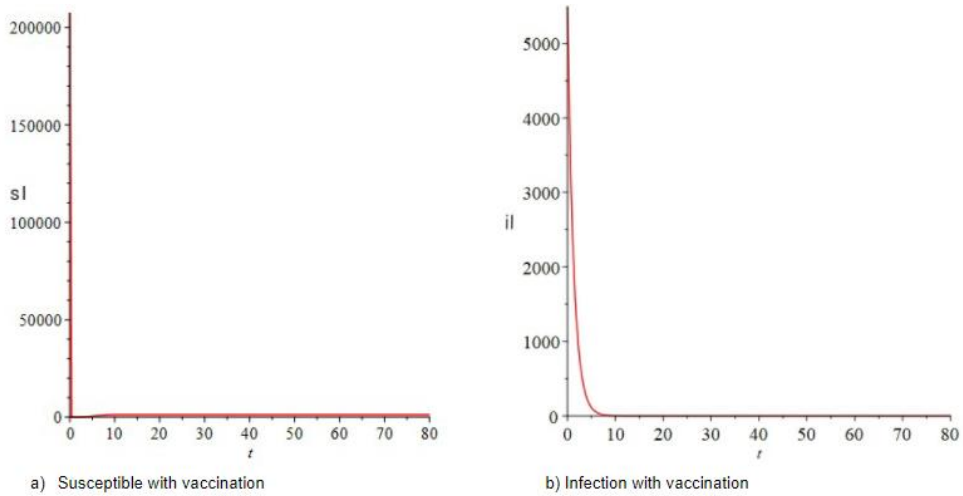


Figure 1: Graph of SIR Model without Vaccination

From Figure 1(a), the graph shows the susceptible class for humans where they are still free of dengue fever and have not been vaccinated. The initial population of susceptible class is 207,591 people. For the number of susceptible humans without vaccination remains at 207,591 people. Figure 1(b) shows the infected class for humans who were infected with the disease and have a high risk of not recovering from it and can lead to death. The number of infected people as shown in Figure 1(b) decreases gradually from 5,027 to 427 people in the beginning without vaccination. From Figure 1 (c), it shows that the recovered class for human rose steadily on the axis. This is because the number of infected humans have not recovered from the disease yet since there is no specific treatment or vaccine provided in this state.

B Discussion on the Graph of SIR model of Dengue with Vaccination

All the compartments of the SIR model for vaccination are discussed in this section. The Maple software is being used and the model was then stimulated with the data in Table 1. Dengue fever cases in Thailand, based on data from Chao et al.[10].



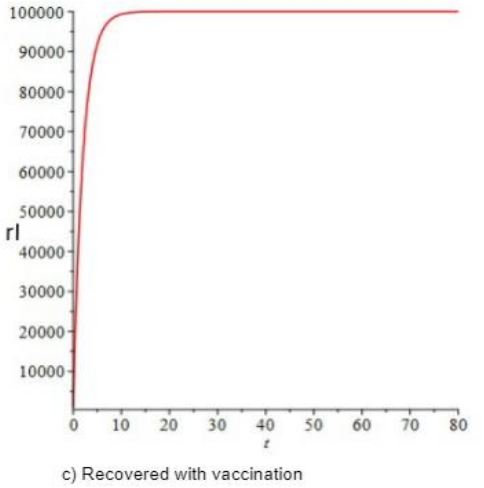


Figure 2: Graph of SIR model with vaccination

Figure 2(a) shows the number of susceptible humans with vaccination reached zero because vaccination has been provided at the rate of 0.6. As shown in Figure 2(b), the curve of the graph was smaller than the curve of the graph from human infected class without vaccination. The number of people infected after getting vaccinated decreased gradually from 2,562 to 969 and it will take several years to reach zero infected humans. The article from Chanprasopchai et al. [11] shows that the graph result of infected class for with vaccination decreased steadily. From that, it can be agreed that for this project, the same result will also be achieved.

From Figure 2(c), it shows that the recovered class for humans increased rapidly. This is because the number of infected humans recovered from the disease also increased. Assuming that the result of the human population for this class will not be infected by the disease again or capable to transmit the disease to others because of the effect of vaccination.

4 Conclusion

Based on the study, the parameter value of the basic reproductive value, R_0 for dengue virus transmission without vaccination $R_0 = 1.98$ which suggests that an epidemic will occur. In contrast, the basic reproductive number of dengue transmission with vaccination is $R_0 = 0.792$ where $R_0 < 1$. As we can see, the basic reproductive number has decreased. Thus, we can say that vaccination helps to reduce the transmission of the dengue virus. Moreover, the stability analysis of disease-free equilibrium point of dengue transmission were determined by the root of the system. Stability analysis of disease-free equilibrium of dengue transmission without vaccination has one positive root and another one with negative roots. This implies that the system is unstable since not all of their roots are negative. Consequently, the stability analysis of disease-free equilibrium of dengue transmission with vaccination has three negative roots which means that the system is stable.

Furthermore, stability analysis of the endemic equilibrium point of dengue transmission was also determined by finding the root of the system. The stability analysis of endemic equilibrium point of dengue transmission without vaccination has two negative roots indicating that the system is stable. Whereas the stability analysis of endemic equilibrium of dengue

transmission with vaccination has one positive value and two negative values. Thus, the system is said to be unstable.

Broadly speaking, dengue fever is one of the diseases that have taken so many lives. In order to prevent and reduce the spread of the disease, people play an important role in being aware of their surroundings and make sure there is no mosquito breeding especially around their house. People could also use mosquito repellents before going outside to avoid Aedes mosquito bites. Despite significant efforts, the government must spread the knowledge about the importance of the vaccination and urge people to get vaccinated. Researchers have been surprised by the development of an efficient vaccination. Finally, the study also recommends raising the awareness on the importance of the dengue virus knowledge in all countries especially for those who live in higher-risk locations. It will help to prevent the dengue virus from spreading.

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