MODELING THE SPREAD OF DENGUE FEVER BY USING SIR MODEL

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Abstract

The establishment and spread of dengue fever is a complex phenomenon with many factors that interact with each other. This report present a study on a mathematical model, the SIR (Susceptible, Infected and Recovered) that serve as a framework for understanding the spread of the infectious dengue fever. We begin with a brief discussion of the origin and historical development of the disease. This is followed by a review on the relation between the three compartments, susceptible, infected and recovered. The modeling steps that lead to the SIR model using ordinary differential equation is explained in detail. The solution gives the basic reproduction number R_0, and this basic reproduction number is use to determine whether the dengue fever will dies out or persists in human population in the long run. The disease-free equilibrium point is determined and R_0 is used to determine whether the disease free equilibrium is stable or unstable. Establishing the endemic equilibrium point determines when the dengue fever will become calm.

Keywords: SIR model, Basic reproduction number, disease free equilibrium, endemic equilibrium

Introduction

Dengue fever is a dangerous disease having huge social, economic and health burden. It is predominantly present in the tropical countries. Even though the disease has been checked out for long time ago, it still remains a major public health issue. Many researchers had model the dengue fever to investigate the spread of the disease. There are a lot of model that described the dengue fever, such as SIR model, SEIR model, MSIR model, and MSEIR model. The most important thing to build a model is identify the variable involve in the model. So, the variable must be determined correctly. In order to investigate the spread of disease, the most important aspect that we need to find out is basic reproduction number. Basic reproduction number is to determine whether the disease will die out or not. Moreover, basic reproduction number can use to find the disease free equilibrium point and endemic equilibrium point.

In this report, we study how a system of differential equation is used to model the spread of dengue fever. The main purpose of this study are, identify a deterministic dynamics model to represent the transmission of the disease in different compartments, study the dynamics of dengue fever in a deterministic model involving ordinary differential equations, explore the relation of basic reproduction number (R_0), disease free equilibrium (E_0), and endemic equilibrium (E_1).

Literature Review

We will review the studies of the researchers related to the dengue fever. The researches that were presented are SIA model, SEIR model, MSEIR model, SIS model, and statistically presented method. In modeling a model for spread of dengue fever, it is necessary to determine the variables involve in the system and understand the basic reproduction number. The variables are determined base on the situation of the system. Basic reproduction number

is to determine whether the disease is stable or not stable. Both the variables and basic reproduction number are important to study the spread of dengue fever.

A study about SIS model was carried out by Helmersson, Jing (2012) on Mathematical Modeling of Dengue -Temperature Effect on Vectorial Capacity. This research is aims at finding the best way to incorporate temperature effect on dengue transmission. Another research is carried out by Kiyeny, Silas Kipchirchir (2014) on SIA model. A 5-dimensional system of ordinary differential equations (ODEs) is use to model the malaria disease. This is because the model contained of 5 different variables. The model was analyzed for the disease free equilibrium and endemic equilibrium. A research about modeling the spread of dengue in Singapore was done by K.C.Ang and Z.Li. In this research, they developed a model that describes the spread of dengue in Singapore. They considered S-E-I-R (susceptible→exposed→infectious→recovered) model for human population, while S-E-I (susceptible→exposed→infectious) model for mosquito population. Besides that, a model of dengue fever has been published by M Derouich, A Boutayeb, and EH Twizell. In this paper, they consider an S-I-R model. It is about medical research in terms of vaccination and antibiotics of dengue fever.

Methodology

In this report, we will emphasize on the SIR model, which the model is the easiest to understand. First, we need to identify the variables and parameters that need to take into consideration. Such as the birth rate, death rate, recovery rate, and so on. After that, we need to analyse the model to check whether it is adequate or not. If the dimension of the model is too large, then model order reduction is to be applied. Basic reproduction number is a must to find out for every modelling of infectious disease. With the basic reproduction number, we can determine the seriousness of the disease. The basic reproduction number can be use to find the disease free equilibrium point and endemic equilibrium point.

` Generally, modelling consists of four steps. First of all, a flow diagram that describes the whole process is a must in order to do the modelling. Flow diagram represents the natural history and transmission of infection. After that, move to second step. Second step is to write a set of mathematical equations to express the transmission process based on the flow diagram that construct in first step. Then, the third step is to find proper values for the parameters used in the equations and make sure that the variable use is appropriate. Finally, we need to solve the equations algebraically or numerically with help of computer simulation programs since some of the equations are very complicated and need the help of computer programming.

The population can be classified into three compartments:

- Susceptible to the disease (Susceptible)– S,
- Currently Infectious (Infectious or Infective) – I,
- Recovered and immune (Recovered or Removals) – R.

Susceptible state means a person is under identify likely or liable to be influenced or harmed by dengue fever but not yet confirm that person is infected. Infectious state means a person is confirmed infected by dengue fever. Recovered state means a person is recovered from infectious. As stated above, every process needs a flow diagram to represent and describe the particular situation. Therefore, at here S, I, R, represent the number of individuals in each compartment. The total host population is $N = S + I + R$.

Each arrow in the flow diagram represents the flow rate at which individuals enter or leave a compartment per unit time, which is called the incidence rate.

Model order reduction is a technique for reducing the complexity of mathematical models in numerical simulation. In the real life process, many modern mathematical models are complicated when process in numerical simulation. This is due to the large size of the mathematical model's dimension. The purpose of reduce the order of the model is to lower down the computational complexity of that model.

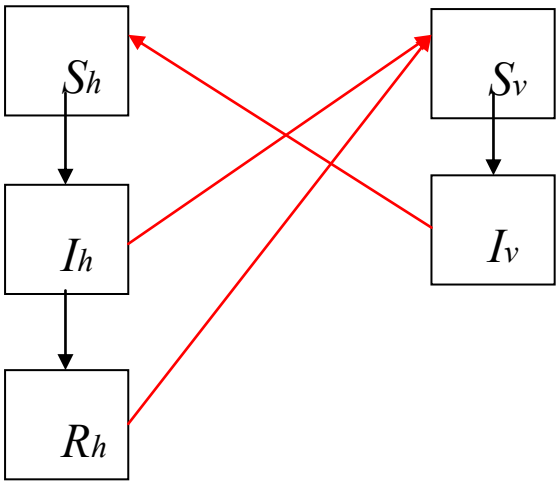
The basic reproduction number is useful because it helps determine whether or not an infectious disease can spread through a population. When $R_0 < 1$, the infection will slowly die out in the long time. When $R_0 > 1$, the infection will be able to spread in a population. Therefore, in generally, the larger the value of R_0, the harder it is to control the epidemic.

Disease free equilibrium is to see whether the epidemic is stable or unstable when there is no more diseases presence. Disease free equilibrium point is a point where there is no more disease appears. The disease free equilibrium point is depends on the basic reproduction number, R_0 . When $R_0 < 1$, then the disease free equilibrium point is stable. It is, however if the basic reproduction number, $R_0 > 1$, then the disease free equilibrium point is unstable. Thus, R_0 is a threshold parameter for the model.

Endemic equilibrium point is a point where the disease is at the steady state. The endemic equilibrium is to determine whether the epidemic is stable or unstable when the disease is at the steady state. Similarly, endemic equilibrium is also depending on the basic reproduction number, R_0. When $R_0 < 1$, the endemic equilibrium point is unstable, whereas the endemic equilibrium point is stable if $R_0 > 1$.

Findings and Discussion

Our model is a mathematical simulation of transmission of dengue virus between host and vector (human and mosquito) where humans and mosquitoes interact and infect each other. Basically, the model is considered only on the susceptible, infectious and recovered or immune (SIR model). In the model, we let the notation of total population sizes of human and mosquito as N_h and N_v respectively. In the model of human population, it is divided into three classes; the Susceptible (S_h), the Infectious (I_h), and Recovered (R_h). In the model of mosquito population, it is divided into two classes; the Susceptible (S_v), the Infectious (I_v).



The equations representing the relationship between the population of host and vector are given as:

$$\frac{dS_h}{dt} = \lambda_h - ab_1 I_v \frac{S_h}{N_h} - \mu_h S_h + \gamma(I_h + R_h)$$
$$\frac{dI_h}{dt} = ab_1 I_v \frac{S_h}{N_h} - (\mu_h + \alpha + \delta + \gamma) I_h$$
$$\frac{dR_h}{dt} = \delta I_h - (\mu_h + \gamma) R_h$$
$$\frac{dS_v}{dt} = \lambda_v - ab_2 S_v \frac{I_h}{N_h} - ab_3 S_v \frac{R_h}{N_h} - \mu_v S_v$$
$$\frac{dI_v}{dt} = ab_2 S_v \frac{I_h}{N_h} + ab_3 S_v \frac{R_h}{N_h} - \mu_v I_v$$

After that we analyse the model to test whether the equation is adequate or not.

For human population;

$N_h(t) = \frac{\lambda_h}{\mu_h} + Ce^{-\mu_h t}$

When t is equal to 0, $N_h(0) = \frac{\lambda_h}{\mu_h} + C$

When t are approaches to infinity, $N_h(\infty) = \frac{\lambda_h}{\mu_h}$

From the above, it implies that the human population is constant in the absence of the disease. Also implies that in the long time, the human's population will become constant.

For mosquito population;

$N_v(t) = \frac{\lambda_v}{\mu_v} + De^{-\mu_v t}$

When t is equal to 0, $N_v(0) = \frac{\lambda_v}{\mu_v} + D$

When t are approaches to infinity, $N_v(\infty) = \frac{\lambda_v}{\mu_v}$

From the above, it implies that the population of mosquito is a constant and would not go to infinity.

Since there are 5 differential equations, then we reduce the model to 4 equations. From the equation $\frac{dN_v}{dt} = \lambda_v - \mu_v N_v$, we can see that the N_v is only the one variable. That is mean the equation only depends on N_v . Hence, by using Vidyasagar theorem, we can reduce the system to four equations.

$$\frac{dI_h}{dt} = ab_1 I_v \frac{S_h}{N_h} - (\mu_h + \alpha + \delta + \gamma) I_h \quad (1)$$

$$\frac{dR_h}{dt} = \delta I_h - (\mu_h + \gamma) R_h \quad (2)$$

$$\frac{dI_v}{dt} = ab_2 S_v \frac{I_h}{N_h} + ab_3 S_v \frac{R_h}{N_h} - \mu_v I_v \quad (3)$$

$$\frac{dN_h}{dt} = \lambda_h - \mu_h N_h - \alpha I_h \quad (4)$$

After reduce the model order, now we can find the basic reproduction number by transform the differential equation to matrix form.

$$\begin{bmatrix} \frac{dI_h}{dt} \\ \frac{dR_h}{dt} \\ \frac{dI_v}{dt} \\ \frac{dN_h}{dt} \end{bmatrix} = \begin{bmatrix} -(\mu_h + \alpha + \delta + \gamma) & 0 & ab_1 \frac{S_h}{N_h} & 0 \\ \delta & -(\mu_h + \gamma) & 0 & 0 \\ ab_2 \frac{S_v}{N_h} & ab_3 \frac{S_v}{N_h} & -\mu_v & 0 \\ -\alpha & 0 & 0 & -\mu_h \end{bmatrix} \begin{bmatrix} I_h \\ R_h \\ I_v \\ N_h \end{bmatrix}$$

$$\begin{bmatrix} \frac{dI_h}{dt} \\ \frac{dR_h}{dt} \\ \frac{dI_v}{dt} \\ \frac{dN_h}{dt} \end{bmatrix} = \left\{ \begin{bmatrix} 0 & 0 & ab_1 \frac{S_h}{N_h} & 0 \\ 0 & 0 & 0 & 0 \\ ab_2 \frac{S_v}{N_h} & ab_3 \frac{S_v}{N_h} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} - \begin{bmatrix} (\mu_h + \alpha + \delta + \gamma) & 0 & 0 & 0 \\ -\delta & (\mu_h + \gamma) & 0 & 0 \\ 0 & 0 & \mu_v & 0 \\ \alpha & 0 & 0 & \mu_h \end{bmatrix} \right\} \begin{bmatrix} I_h \\ R_h \\ I_v \\ N_h \end{bmatrix}$$

$$\begin{bmatrix} \frac{dI_h}{dt} \\ \frac{dR_h}{dt} \\ \frac{dI_v}{dt} \\ \frac{dN_h}{dt} \end{bmatrix} = [F - V] \begin{bmatrix} I_h \\ R_h \\ I_v \\ N_h \end{bmatrix}$$

With the matrices F and V at above, we can use this matrices to find the reproduction number, R_0. The reproduction number, $R_0 = \lambda^2$, where λ is the eigenvalue of FV^{-1}.

$$R_0 = \lambda^2 = \frac{a^2 b_1 N_v [b_2(\mu_h + \gamma) + \delta b_3]}{(\mu_v N_h)(\mu_h + \gamma)(\mu_h + \alpha + \delta + \gamma)}$$

The disease free equilibrium point is $E_0 = (0,0,0,\frac{\lambda_h}{\mu_h})$. The purpose of doing this analysis is to determine if the disease free equilibrium point is stable. First of all, we analyze the stability of the disease free equilibrium by linearize the above differential equations (1), (2), (3), and (4) to a Jacobian matrix.

$$J_{DFE} = \begin{bmatrix} -\mathrm{A} & 0 & ab_1 & 0 \\ \delta & -(\mu_h + \gamma) & 0 & 0 \\ \frac{ab_2 \lambda_v \mu_h}{\mu_v \lambda_h} & \frac{ab_3 \lambda_v \mu_h}{\mu_v \lambda_h} & -\mu_v & 0 \\ -\alpha & 0 & 0 & -\mu_h \end{bmatrix}$$

Next, we want to determine the eigenvalues of this Jacobian matrix. The eigenvalues of this Jacobian matrix can determine whether the disease free equilibrium point, E_0 is stable.

$$P(\lambda) = |J_{DFE} - \lambda I| = \begin{vmatrix} -(\mathrm{A} + \lambda) & 0 & ab_1 & 0 \\ \delta & -(\mu_h + \gamma + \lambda) & 0 & 0 \\ \frac{ab_2 \lambda_v \mu_h}{\mu_v \lambda_h} & \frac{ab_3 \lambda_v \mu_h}{\mu_v \lambda_h} & -(\mu_v + \lambda) & 0 \\ -\alpha & 0 & 0 & -(\mu_h + \lambda) \end{vmatrix} = 0$$

$$\lambda^3 + \lambda^2[2(\mu_h + \gamma) + \alpha + \delta + \mu_v] + \lambda\left[\mathrm{A}(\mu_h + \gamma + \mu_v) + (\mu_h + \gamma)\mu_v - \frac{a^2 b_1 b_2 \lambda_v \mu_h}{\mu_v \lambda_h}\right] + \left[(\mu_h + \gamma)\mu_v \mathrm{A} - \frac{a^2 b_1 \lambda_v \mu_h [(\mu_h + \gamma)b_2 + b_3 \delta]}{\mu_v \lambda_h}\right] = 0$$

We can write the equation into third order polynomial, which is equivalent to the above equation.

$$C_1\lambda^3 + C_2\lambda^2 + C_3\lambda + C_4 = 0$$

$$C_1 = 1 > 0$$
$$C_2 = 2(\mu_h + \gamma) + \alpha + \delta + \mu_v > 0$$
$$C_3 = \mathrm{A}(\mu_h + \gamma + \mu_v) + (\mu_h + \gamma)\mu_v - \frac{a^2 b_1 b_2 \lambda_v \mu_h}{\mu_v \lambda_h}$$
$$= \mathrm{A}(\mu_h + \gamma) + (\mu_h + \gamma)\mu_v + \mathrm{A}\mu_v - \frac{a^2 b_1 b_2 \lambda_v \mu_h (\mu_h + \gamma)}{\mu_v \lambda_h (\mu_h + \gamma)} - \frac{a^2 b_1 b_3 \delta \lambda_v \mu_h}{\mu_v \lambda_h (\mu_h + \gamma)} + \frac{a^2 b_1 b_3 \delta \lambda_v \mu_h}{\mu_v \lambda_h (\mu_h + \gamma)}$$

$$= (\mu_h + \gamma)(\mathrm{A} + \mu_v) + \frac{a^2 b_1 b_3 \delta \lambda_v \mu_h}{\mu_v \lambda_h (\mu_h + \gamma)} + \mathrm{A}\mu_v \left[1 - \frac{a^2 b_1 \lambda_v \mu_h [b_2(\mu_h + \gamma) + \delta b_3]}{(\mu_v^2 \lambda_h)(\mu_h + \gamma)\mathrm{A}}\right]$$

$$= (\mu_h + \gamma)(\mathrm{A} + \mu_v) + \frac{a^2 b_1 b_3 \delta \lambda_v \mu_h}{\mu_v \lambda_h (\mu_h + \gamma)} + \mathrm{A}\mu_v [1 - R_0]$$

C_3 is always greater than zero when R_0 is less than 1.

$$C_4 = (\mu_h + \gamma)\mu_v \mathrm{A} - \frac{a^2 b_1 \lambda_v \mu_h [(\mu_h + \gamma) b_2 + b_3 \delta]}{\mu_v \lambda_h}$$

$$= (\mu_h + \gamma)\mu_v \mathrm{A}\left[1 - \frac{a^2 b_1 \lambda_v \mu_h [(\mu_h + \gamma) b_2 + b_3 \delta]}{(\mu_v^2 \lambda_h)(\mu_h + \gamma)\mathrm{A}}\right]$$

$$= (\mu_h + \gamma)\mu_v \mathrm{A}[1 - R_0]$$

C_4 is always greater than zero when R_0 is less than 1.

Therefore, the disease free equilibrium point E_0 is stable if $R_0 < 1$. If $R_0 > 1$, then the disease free equilibrium point E_0 is unstable.

The endemic equilibrium point is $E_1 = (\overline{I_h}, \overline{R_h}, \overline{I_v}, \overline{N_h})$. When the disease has reached its equilibrium point, then the differential equations are equal to zero. Therefore, we can write the differential equation into;

$$ab_1 \overline{I_v}(\overline{N_h} - \overline{I_h} - \overline{R_h}) - (\mu_h + \alpha + \delta + \gamma)\overline{I_h}\,\overline{N_h} = 0 \quad (5)$$

$$\delta \overline{I_h} - (\mu_h + \gamma)\overline{R_h} = 0 \quad (6)$$

$$ab_2(N_v - \overline{I_v})\overline{I_h} + ab_3(N_v - \overline{I_v})\overline{R_h} - \mu_v \overline{I_v}\,\overline{N_h} = 0 \quad (7)$$

$$\lambda_h - \mu_h \overline{N_h} - \alpha \overline{I_h} = 0 \quad (8)$$

Solve $\overline{I_h}$, $\overline{R_h}$, $\overline{I_v}$, *and* $\overline{N_h}$ in terms of $\overline{I_h}$ by using the above equations, equation (5), (6), (7), and (8). Hence we get:

$$\overline{I_h} = \frac{-B \pm \sqrt{B^2 - 4AC}}{2A}$$

$$\overline{R_h} = \frac{\delta}{(\mu_h + \gamma)}\overline{I_h}$$

$$\overline{I_v} = \frac{(\mu_h + \alpha + \delta + \gamma)(\lambda_h - \alpha \overline{I_h})(\mu_h + \gamma)\overline{I_h}}{ab_1[\lambda_h(\mu_h + \gamma) - [(\mu_h + \gamma)(\alpha + \mu_h) + \mu_h \delta]\overline{I_h}]}$$

$$\overline{N_h} = \frac{\lambda_h - \alpha \overline{I_h}}{\mu_h}$$

Conclusion and Recommendation

We have studied the modeling of dengue disease in a 5-dimentional system of ordinary differential equations. We analyzed the differential equations, and showed that the model that we use is adequate because the population of human and mosquito are both converge to

a constant. The system was then reduced to 4-dimentional system of ordinary differential equation. This is due to by solving the 5-dimentional system of ordinary differential equation has a very tedious computation.

After that, we have defined the basic reproduction number, R_0 in terms of parameters. R_0 must be find correctly because it is greatly use in finding the disease free equilibrium and endemic equilibrium. We also established that if the basic reproduction number $R_0 < 1$, the disease free equilibrium point is stable and the disease will dies out after some period of time. However, if the $R_0 > 1$, the disease free equilibrium point is unstable and the disease will become more serious and continuously spread. We also establish the endemic equilibrium point.

From the results above, the basic reproduction number we obtained is $R_0 = 1.9689$, which the $R_0 > 1$. This number is quite high because it is greater than one. This meaning that in the long run, the dengue fever will not dies out, but it will continuously spread. Such number is not ideal in the future. We can describe the situation from the graph (figure 4.2). It is clearly showed that in the long period of time, the population of human will keep decreasing. Therefore, we need to do change the parameters to reduce the R_0 . For example we can reduce the mosquito birth rate by killing the mosquito, and create a better vaccine to increase the recovery rate.

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