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Modeling dengue transmission in Singapore

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Abstract. Dengue fever is a widespread epidemic that transmits between the vector mosquitoes and the host humans. It has long remained a threat to the public health for many countries since there is no effective treatment for it currently. Therefore, it is practically valuable to conduct research on the transmission of Dengue Fever virus to help combat Dengue Virus. Out of this purpose and to bridge the gap in the research of Dengue Fever, this paper took use of parameters such as susceptible humans and carrier humans to construct a differential equations model that reasonably depicts the host-to-vector and vector-to-host transmission of Dengue Fever Virus. Especially, in this model, by computing out the spectral radius of the matrix FV^{-1} at the disease-free equilibrium (DFE) point, we could get the basic reproductive number of the dengue fever virus, which is of great practical importance (where the detailed interpretation of notation F and V will be given in the second chapter in this paper). Besides, we conducted empirical analysis with the data of cases of Dengue Fever in Singapore at the year of 2019 to show that our method is valid in the real world. Also, we made an extensive prediction with the data of 2022.

Keywords: epidemic models, differential equations, matrix differentiation.

1. Introduction

1.1. Background

Dengue fever is serious mosquito-borne tropical disease as a direct result of the dengue virus. It has become a significant global public health issue, a main cause of illness and death in tropical and subtropical regions. A growing trend of cases persists despite various interventions by the Ministry of Health Singapore. Every year, millions of dengue cases are reported worldwide by the World Health Organization (WHO). [1-5]

As a result of mosquito bites from infective mosquitoes such as aedes, dengue fever symptoms typically appear within 3 to 14 days. Symptoms can vary from a mild fever to a severe high fever with headaches, rashes, and muscles and joint pain. Dengue fever does not have any specific treatments at the present time. Instead, most of the control and prevention measures are focused on combating vector mosquitoes [6-9].

1.2. Literature review

For understanding the infectious disease transmission dynamics, it is important to model the underlying biological interactions mathematically. In the recent years, various mathematical models have been used to investigate dengue transmission. Joseph et.al [10] considers an SIR epidemiological

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model describing the host-to-vector and vector-to-host transmission dynamics. Shakoor Ahmad et.al [11] conducted fractional order SIR Dengue model, and concludes that Dengue disease transmission can be evaluated more accurately by fractional order equations than by integer order equations. Chai Jian Tay [12] et.al constructed a transmission model of type SI-SIR based on the dengue incidence data in Malaysia−Kuala Lumpur and Selangor−from the year 2011 to 2014. All of the former research employed classical transmission models such as SIR to construct models; however, they did not pay enough attention to detailed problems such as issues related with carriers. Also, many of them did not dive deeper in respect of matrix differentiation and try to compute the reproduction number of the Dengue Fever virus by calculating the spectral radius of specific derivative matrices.

Based on these papers and real-world evidence, we constructed a differential equations model, which carefully considers the transmission between the vector mosquitoes and the host human. Taking various variables such as the number of carrier humans and the number of susceptible humans into consideration, this paper tried to depict both transmission from vector to host and transmission from host to vector precisely. Different from previous research, we considered some detailed problems such as the mortality rate in the vector-to-host transmission and host-to-vector transmission and the difference in transmission rate for mosquitos and humans. Through solving our equations with data at a specific time, we can obtain the value of parameters of interest. For instance, in the second chapter, we let $I_h = C_h = I_m = 0$ and obtained the number of recovered people in the transmission process through solving differential equations. Besides, we could obtain the reproduction number of Dengue Fever Virus by computing the spectral radius of the matrix FV^{-1}, which is of great practical significance, where the detailed definition of F and V is given in the second chapter.

1.3. Paper structure

This paper consists of four chapters in total. The first chapter is introduction, in which we introduced the background knowledge of Dengue Fever Virus, made a literature review in terms of epidemic models and virus transmission, briefly introduced our model and states the advantages of our method and model. In the second chapter, we explained the detailed construction of our model, the parameters interpretation in our model and how to obtain our parameters of interest through solving differential equations. Also, by calculating the spectral radius of the specific matrix FV^{-1}, we could obtain the reproduction number of Dengue Fever Virus in this chapter. The third chapter is about empirical analysis, we employed the data in the year of 2019 to show that our model and method is of practical value. In the fourth chapter, we made a brief conclusion of our research, concluded the limitations of our research and put forward prospective research topics in the future.

2. Epidemic model

In this chapter, we focus on the core model of this paper, and we will demonstrate the detailed construction of our differential equations model that depicts the vector-to-host and host-to-vector transmission. Besides, in this chapter we will clearly demonstrate detailed information that is important to understand our model, such as model settings, model assumptions, parameter interpretation. Finally, at the end of the chapter, we will show how to obtain the reproduction number of Dengue Fever Virus by computing the spectral radius of the specific matrix FV^{-1}.

2.1. Model settings and assumptions

Based on previous research, literature and related expert knowledge, we rationally set and assumed that:

1) A two-way transmission can happen between the vector mosquitos and the host human. However, there is no transmission from human to human.
2) There is no carrier stage for mosquitos, while infectious humans can transform into carrier stage.
3) All of the humans living in an area are thought to be susceptible to Dengue fever due to the strong infectious possibility.

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4) The infectious humans and carrier humans of Dengue Fever Virus could be fully cured.

2.2. Model construction

In this paper, we constructed a differential equations model that depicts the transmission from the vector to host and the host to vector. To better illustrate the construction of our model and show the transmission process clearly, we drew some straightforward figures shown as below.

The transmission happening on humans is shown in Figure 1.

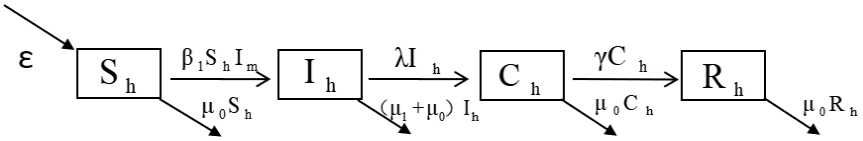

Figure 1. Transmission happening on humans.

The transmission happening on mosquitoes is shown in Figure 2.

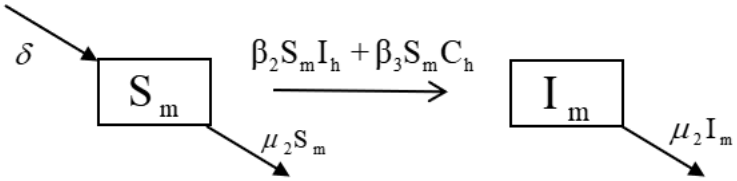

Figure 2. Transmission happening on mosquitos.

The meanings of the parameters involved in Figure 1 and Figure 2 above are shown in Table 1.

Table 1. Representation of parameters.

Parameter	Interpretation
S_h	Susceptible humans
I_h	Infectious humans
C_h	Carrier humans
R_h	Recovered humans
S_m	Susceptible mosquitoes
I_m	Infectious mosquitoes
β_1	Rate of transmission from infectious mosquitoes to susceptible humans
β_2	Rate of transmission from infectious humans to susceptible mosquitoes
β_3	Rate of transmission from carrier humans to susceptible mosquitoes
λ	Rate of infectious humans entering carrier stage
γ	Recovery rate for carrier humans
ε	Natural birth rate of humans
μ_0	Natural mortality rate of humans
μ_1	The additional mortality rate of infectious humans
δ	Natural birth rate of mosquitoes
μ_2	Natural death rate of mosquitoes

The transmission process in Figure 1 and Figure 2 are represented with differential equations shown as below. These differential equations constitute our model.

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$$\begin{cases} \dfrac{dS_h(t)}{dt} = \varepsilon - \mu_0 S_h - \beta_1 S_h I_m \\ \dfrac{dI_h(t)}{dt} = \beta_1 S_h I_m - \lambda I_h - (\mu_0 + \mu_1) I_h \\ \dfrac{dC_h(t)}{dt} = \lambda I_h - \mu_0 C_h - \gamma C_h \\ \dfrac{dR_h(t)}{dt} = \gamma C_h - \mu_0 R_h \\ \dfrac{dS_m(t)}{dt} = \delta - \mu_2 S_m - \beta_2 S_m I_h - \beta_3 S_m C_h \\ \dfrac{dI_m(t)}{dt} = \beta_2 S_m I_h + \beta_3 S_m C_h - \mu_2 I_m \end{cases}$$

2.3. Differential equations computation and parameter estimation

We assume that I_h, C_h, and I_m are infected compartments and S_h, R_h, and S_m are uninfected compartments.

Let

$$F=\begin{pmatrix} \beta_1 S_h I_m \\ 0 \\ \beta_2 S_m I_h + \beta_3 S_m C_h \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

and

$$V=\begin{pmatrix} \lambda I_h + (\mu_0 + \mu_1) I_h \\ -\lambda I_h + (\mu_0 + \gamma) C_h \\ \mu_2 I_m \\ -\varepsilon + \mu_0 S_h + \beta_1 S_h I_m \\ \mu_0 R_h - \gamma C_h \\ -\delta + \mu_2 S_m + \beta_2 S_m I_h + \beta_3 S_m C_h \end{pmatrix}$$

where F denotes the transition from uninfected compartments to infected compartments, and (F- V) represents all the model differential equations.

The disease-free equilibrium (DFE) point $x_0 = (I_h, C_h, I_m, S_h, R_h, S_m,)$ can be calculated by letting $I_h = C_h = I_m = 0$ and all the differential equations above equal to 0. Then we got

$$x_0 = (0,0,0,\frac{\varepsilon}{\mu_0},0,\frac{\delta}{\mu_2})$$

Then, we find DF ,the derivative of matrix F at x_0:

$$DF=\begin{pmatrix} F_{3\times3} & 0_{3\times3} \\ 0_{3\times3} & 0_{3\times3} \end{pmatrix}, \text{ where } F=\begin{pmatrix} 0 & 0 & \beta_1 S_h \\ 0 & 0 & 0 \\ \beta_2 S_m & \beta_3 S_m & 0 \end{pmatrix}$$

and DV, the derivative of matrix V at x_0:

$$DV=\begin{pmatrix} V_{3\times3} & 0_{3\times3} \\ J_3 & J_3 \end{pmatrix}, \text{ where } V=\begin{pmatrix} \lambda + \mu_0 + \mu_1 & 0 & 0 \\ -\lambda & \mu_0 + \gamma & 0 \\ 0 & 0 & \mu_2 \end{pmatrix}$$

We find V^{-1}, the inverse of matrix V,

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$$V^{-1} = \begin{pmatrix} \frac{1}{\lambda+\mu_0+\mu_1} & 0 & 0 \\ \frac{\lambda}{(\mu_0+\gamma)(\lambda+\mu_0+\mu_1)} & \frac{1}{\mu_0+\gamma} & 0 \\ 0 & 0 & \frac{1}{\mu_2} \end{pmatrix}$$

and

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \frac{\beta_1 S_h}{\mu_2} \\ 0 & 0 & 0 \\ \frac{\beta_2 S_m(\mu_0+\gamma)+\lambda\beta_3 S_m}{(\mu_0+\gamma)(\lambda+\mu_0+\mu_1)} & \frac{\beta_3 S_m}{\mu_0+\gamma} & 0 \end{pmatrix}$$

Afterwards, we can calculate R_0, the basic reproduction number according to document [1]

$$R_0 = \rho(FV^{-1}) = \sqrt{\frac{\beta_1 S_h \beta_2 S_m(\mu_0+\gamma)+\beta_1 S_h \lambda \beta_3 S_m}{\mu_2(\mu_0+\gamma)(\lambda+\mu_0+\mu_1)}}$$

where $\rho(FV^{-1})$ represents the spectral radius of matrix (FV^{-1}).

3. Empirical analysis

In this chapter, we combine our theoretical model with practical data to find out whether our differential equations model is valid and accurate in depicting the transmission of Dengue Fever virus between the vector mosquitoes and the host humans. To be more specific, we employed the data of the cases of Dengue Fever in Singapore in 2019 to calculate R0, and make an extensive prediction of the transmission of Dengue Fever virus in 2022.

3.1. Data

From sources such as Statista and the official website of National Environmental Agency of Singapore, we acquired the data of the parameters that we needed to compute out the value of the parameters of our interest in our differential equations model. We mainly used the data of the cases of Dengue Fever virus at Singapore at the year of 2019 to further conduct our empirical analysis to test the validity and accuracy of our differential equations model. However, since it is hard to obtain the data of some specific parameters in our model, such as the data related with carriers and mosquitoes, we are forced to estimate such data based on other parameters and indicators. We also mentioned this point in the section that discusses the limitations of our paper in the last chapter.

To better illustrate the data we employed, we drew out a bar chart to demonstrate the cases of Dengue Fever virus in Singapore from the year of 2011 to 2019. The bar chart is shown as below. In the next two sections, we conducted empirical analysis and an extensive prediction with the data of Dengue Fever cases in Singapore at the year of 2019. The results of our empirical analysis and extensive prediction are highly consistent with the data in the real world, which proves the validity and accuracy of our differential equations model in terms of depicting the transmission of Dengue Fever virus from the vector mosquitoes to the host humans and from the host humans to the vector mosquitoes.

3.2. Empirical analysis

To minimise the impact of COVID-19 on various parameters, this paper uses the data in 2019, before the outbreak of COVID-19 pandemic. The table 2 which is below this paragraph shows the basic situation of data in 2019. More detailed information about the data could be seen in the endnote of this paper.

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Table 2. Value of parameters in empirical analysis.

Parameter	Value (per year)
S_h	5.703×10^{7}[2]
S_m	2.5×10^{8}(assumption)
β_1	2.805×10^{-4}
β_2	2.4×10^{-9}
β_3	2.4×10^{-9}
λ	0.9989
γ	1
ε	0.008584 [3]
μ_0	0.004600[4]
μ_1	0.001125
μ_2	20 (assumption)

To get μ_1, the additional mortality rate of infectious humans, we divide the number of death cases, 18[5] by the total dengue cases, 15998[6] in 2019. Since dengue is not a chronic disease, all dengue cases except for death cases will recover in one year. Hence, we consider γ, the recovery rate for carrier humans as 1, and λ, the rate of infectious humans entering carrier stage as $(1 - \mu_1) = 0.9989$.

By putting the data of the cases of Dengue Fever in Singapore at the year of 2019 into our differential equations model described in Chapter 2, we could compute out the value of the parameters of interest. For instance, by letting $I_h = C_h = I_m = 0$, we could obtain that at the equilibrium,

Afterwards, we can calculate R_0, the basic reproduction number according to document [1]

$$R_0 = \rho(FV^{-1}) = \sqrt{\frac{\beta_1 S_h \beta_2 S_m(\mu_0 + \gamma) + \beta_1 S_h \lambda \beta_3 S_m}{\mu_2(\mu_0 + \gamma)(\lambda + \mu_0 + \mu_1)}} = 30.865 \approx 31$$

where $\rho(FV^{-1})$ denotes the spectral radius of matrix (FV^{-1}).

Finally, the value of R_0 that we obtained through putting the data of cases of Dengue Fever in the year of 2019 is kind of consistent with the data in the real world, ranging from 0.16 to 65[13]. Therefore, it can be believed that our differential equations model has strong practical meaning and can be applied to the analyze the Dengue Fever transmission in reality.

3.3. Extensive prediction

In this section, we employ the latest data of the cases of Dengue Fever at the year of 2022 to make an extensive prediction of the transmission of Dengue Fever in the future.

Similar with our methods and steps in the last section Empirical Analysis, we considered to use the data of cases of Dengue Fever in Singapore at the year of 2022 to make a prediction of the value of the parameters of our interest in the future. However, because we did not take into account the potential impact brought by COVID-19 pandemic to our differential equations model, such a prediction is not completely rigorous.

By using the value of R0 calculated in section 3.2, we substituted the values of parameters in 2022 back to the formula for R0, the spectral radius of the matrix FV^{-1} .Finally, we computed out the value of the number of cases of Dengue Fever virus at the year of 2022, which is 26436. According to the tendency in the recent years, such a number is reasonable.

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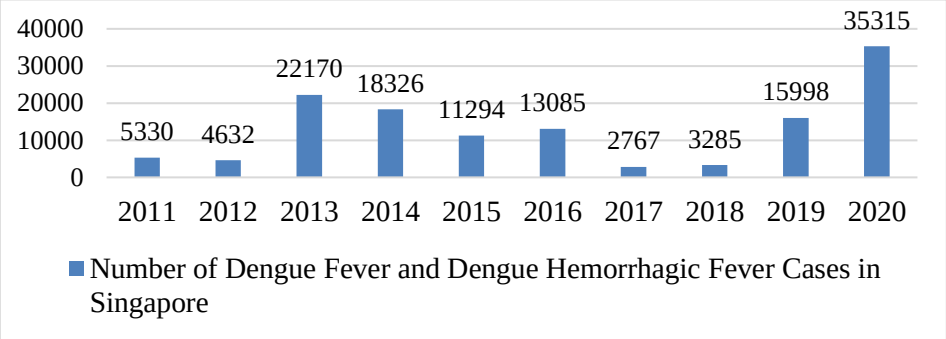

Figure 3. Number of dengue fever and dengue hemorrhagic fever cases in Singapore from 2011 to 2020.

4. Conclusions and limitations

4.1. Conclusions

In order to fill the gap in the research of the transmission of Dengue Fever virus between the vector mosquitoes and the host humans, we constructed a differential equations model that describes the vector-to-host and host-to-vector transmission of Dengue Fever. We clearly state the model settings and presumptions and make an interpretation of parameters to help the readers to understand our epidemiological model. By putting the value of parameters collected at different time during the transmission of the epidemic, we can obtain the value of specific parameters through solving the differential equations. For instance, to figure out the number of people recovered throughout the outbreak of the Dengue Fever virus, by letting $I_h = C_h = I_m = 0$, we get

$$x_0 = (0,0,0,\frac{\varepsilon}{\mu_0},0,\frac{\delta}{\mu_2})$$

Then, we calculated the spectral radius of the matrix FV^{-1} to acquire the reproduction number of the Dengue Fever virus. However , the reproduction number of the Dengue Fever virus is about 31,which is considerably high. This explains the significant increase in Dengue cases in Singapore in recent years very well. Since the death rate of mosquitoes, μ_2,is in the denominator of the formula for basic reproduction number, one effective to mitigate the Dengue Fever virus is to implement mosquito killing and control in order to raise the value of μ_2.

By putting the data of cases of Dengue Fever in Singapore at the year of 2019, we made an empirical analysis to test the validity and accuracy of our differential equations model. Besides, we used the latest data of the cases of Dengue Fever at the year of 2022 to make an extensive prediction of the transmission of Dengue Fever virus. The result is that our differential equations model is valid in terms of illustrating the two-way transmission of Dengue Fever virus between the vector mosquitoes and the host humans.

4.2. Limitations

An obstacle to our research is the vagueness of data. For instance, the number of carriers and the number of mosquitoes are hard to find. Although sometimes we can find such data of a specific time period, those data that we find can be inaccurate or vague. Due to the lack of data that we need, we cannot obtain the value of specific parameters of our interest.

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