

A SIR Model for Spread of Dengue Fever Disease (Simulation for South Sulawesi, Indonesia and Selangor, Malaysia)*

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(Received April 9 2012, Revised July 25 2012, Accepted April 14 2013)

Abstract. In this paper, we study a system of differential equations that models the population dynamics of Susceptible, Infected, and Removed (SIR) vector transmission of dengue fever. The model studied re-breeding value based on the number of reported cases of dengue fever in South Sulawesi, Indonesia and Selangor, Malaysia. Using the SIR model and based on the rate of infection of humans, the spread of the dengue virus in both countries reached maximum levels in only a very short time. Theoretical and empirical calculations using the model were found to be suitable, and application of the SIR model showed similarities between the countries. However, the SIR model simulation indicated that dengue fever has not become endemic in either country.

Keywords: dengue fever, endemic, SIR model, stability, threshold parameter

1 Introduction

Dengue fever is regarded as a serious infectious disease threatening about 2.5 billion people all over the world, especially in tropical countries. In 2009 the World Health Organization (WHO)^[21] estimated 50 to 100 million reported cases worldwide. Around 500,000 people are estimated to be infected by hemorrhagic dengue fever each year. Dengue fever has become a major epidemic disease in Southeast Asia. Such an epidemic arises from climate change and is made worse by the population's lack of knowledge about and awareness of dengue fever, so that dengue fever may become endemic.

Mathematical models for dengue fever have investigated compartment dynamics using Susceptible, Infected, and Removed (SIR) models^[3, 6, 14, 15, 17, 22]; these models have only scrutinized the formulation of the model. Our paper has modified the models in [14] and [22] and applied the collected real data reported by the Ministry of Health in South Sulawesi, Indonesia (KKRI)^[10] and by the Ministry of Health (KKMa) in Selangor, Malaysia^[8]. The purpose of this study was to match the empirical data with the model simulation. Hence, the SIR model presented in this paper is intended to be a trusted reference and as a control tool in dealing with dengue fever in both countries. The first part of this paper formulates a SIR model for transmission of dengue fever, the second part analyzes the model, and the last section simulates the model for both countries. The simulation is compared to a theoretical calculation generation by ODESOLVE.

* The authors would like to thank Skim Zamalah Pasca Siswazah (UKM-OUP-ICT-34-174/2010) for financial support. The authors also thank Alena Lee Sanusi for helpful editorial comments on the manuscript.

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1.1 Dengue fever

Dengue fever is caused by four closely related virus serotypes: dengue virus 1 (DEN1), dengue virus 2 (DEN2), dengue virus 3 (DEN3) and dengue virus 4 (DEN4); two of the serotypes are hemorrhagic and often fatal while the other two are not and often not fatal. The disease is spread by the bite of *Aedes aegypti* mosquitoes infected with the virus. Although *Aedes albopictus* can transmit the dengue virus and has been detected in Asia in recent years^[21], the *Aedes aegypti* mosquito is still the principal vector of dengue virus transmission. Interestingly, while dengue fever previously has been known to attack mainly children of primary school age, now everybody is vulnerable to the fever^[16].

1.2 Dengue fever in South Sulawesi, Indonesia and Selangor, Malaysia

Indonesia stands as the Southeast Asian country with the second largest number of cases of dengue fever in Southeast Asia after Thailand. South Sulawesi is one of the Indonesian provinces with the greatest number of sufferers of dengue fever. In 2008, the highest number of dengue fever cases were found in the cities like Bone, Bulukumba, Pinrang, Makassar and Gowa (between 217 and 668 cases), while in the cities of North Luwu, Tator, Enrekang, Maros, Jeneponto and Selayar no cases were found, as reported by The Division of Disease Control, Public Health Department (DPH).

Malaysia is not exempt from this disease; in fact, the first dengue fever case in Malaysia was reported in 1902^[4]. A spokesman for the Malaysian Ministry of Health said in 2008 that the highest numbers of dengue cases were reported in the state of Selangor (2,391 cases with 5 deaths). Until June 2010, deaths from dengue fever increased to 90 cases and overall 41034 cases were reported in 2010. About 10,318 cases of dengue have been reported since January 2010 with the metropolitan area of Kajang in Selangor state reporting the most cases, totaling 1,930. However, the Selangor state government has said that 32 people died of dengue fever in the state, with both Shah Alam and Subang Jaya urban areas reporting six deaths, whereas Kajang recorded only one severe case not ending in death^[9, 15].

2 The SIR model for dengue fever disease

The SIR mathematical model simulates the spread of serotypes 1 of dengue virus between host and vector. The model is based on the Susceptible, Infected, and Removed (SIR) model of infectious disease epidemiology, which was adopted by [14, 22]. The SIR model identifies two populations, a human population (N_h) and a vector population (N_v). The human population (N_h) is divided into three groups: people who may potentially get infected with dengue virus (susceptible; S_h), people who are infected with dengue (infected; I_h), and people who have recovered (removed; R_h). The vector population of mosquitoes (N_v) is divided into two groups: mosquitoes that may potentially become infected with dengue virus (susceptible; S_v) and mosquitoes that are infected with dengue virus (infected; I_v).

In this paper, it is assumed that a number of people in the population have already been infected by the virus while others have not. It is also assumed that the transmission of the virus continues in the population, but the number of mosquitoes is constant. The number of mosquitoes as the vector is assumed to be constant. Both people and mosquitoes are categorized in one group at a time. The rate of change in the total host population which may easily be infected over the time due to host population birth rate is $(\mu_k N_k)$; people in category S_h have the probability of being infected with dengue virus at a rate $\frac{\beta_h b I_v}{N_h}$, where $\beta_h b$ is sufficient rate of correlation of vector population to human population. β_h represents the probability of infection from an infected individual to a mosquito that is susceptible to infection, while b represents the average number of bites per infected mosquito. Deaths of the susceptible host are represented by $(\mu_h S_h)$.

The rate of change in the number of the infected host depends on the host infected population. A death among the infected host population is represented by $(\mu_h I_h)$, while members of the host population that recover their health after infection is $(\gamma_h I_h)$. In addition, the total host population that has recovered (R_h) will change according to changing times. The rate changes for a healthy population of the total time is the difference of the host recovers from infection $(\gamma_h I_h)$ with total mortality in healthy host $(\mu_h R_h)$.

Changes for the group S_v show that each individual in the susceptible population has a probability of being bitten by mosquitoes infected with dengue virus at a rate $\left(\frac{\beta_v b I_h}{N_h}\right)$, where $\beta_v b$ is the sufficient rate of correlation of human to vector, including the probability of transmission from infected humans to potentially infected mosquitoes (β_v). The number of deaths among the susceptible mosquito population is $\mu_v S_v$ at any given time, and total mortality of the population of infected mosquitoes is $(\gamma_v I_v)$. Changes that occur in all groups of people and of mosquitoes can be defined in a mathematical model of host-vector interaction comprising non-linear differential equations as follows:

$$\frac{d}{dt} S_h = \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \mu_h S_h, \quad (1)$$

$$\frac{d}{dt} I_h = \frac{\beta_h b}{N_h} I_v S_h - (\mu_h + \gamma_h) I_h, \quad (2)$$

$$\frac{d}{dt} R_h = \gamma_h I_h - \mu_h R_h. \quad (3)$$

Vector population

$$\frac{d}{dt} S_v = \mu_v N_v - \frac{b\beta_v}{N_h} I_h S_v - \mu_v S_v, \quad (4)$$

$$\frac{d}{dt} I_v = \frac{\beta_v b}{N_h} I_h S_v - \mu_v I_v, \quad (5)$$

with the condition

$$S_h + I_h + R_h = N_h \Rightarrow R_h = N_h - S_h - I_h, \quad (6)$$

$$S_v + I_v = N_v = \frac{A}{\mu_v} \Rightarrow S_v = N_v - I_v = \frac{A}{\mu_v} - I_v. \quad (7)$$

Thus, the model for the human and mosquito populations can be simplified as follows:

$$\frac{d}{dt} S_h = \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \mu_h S_h, \quad (8)$$

$$\frac{d}{dt} I_h = \frac{\beta_h b}{N_h} I_v S_h - (\mu_h + \gamma_h) I_h, \quad (9)$$

$$\frac{d}{dt} I_v = \frac{\beta_v b}{N_h} I_h S_v - \mu_v I_v. \quad (10)$$

The model can be simplified by assuming the following fractions:

$$x = \frac{S_h}{N_h}, y = \frac{I_h}{N_h} \text{ and } z = \frac{I_v}{N_v} = \frac{I_v}{A/\mu_v}. \quad (11)$$

Thus, the model for the human and mosquito populations can be simplified as follows:

$$\frac{dx}{dt} = \mu_h(1 - x(t)) - \alpha x(t)z(t), \quad (12)$$

$$\frac{dy}{dt} = \alpha x(t)z(t) - \beta y(t), \quad (13)$$

$$\frac{dz}{dt} = \gamma(1 - z(t))y(t) - \delta z(t), \quad (14)$$

with the value $\alpha = \frac{b\beta_h A}{\mu_v N_h}$, $\beta = \gamma_h + \mu_h$, $\gamma = b\beta_v$, $\delta = \mu_v$.

A critical point will occur when the value of

$$\frac{dx}{dt} = \frac{dy}{dt} = \frac{dz}{dt} = 0. \quad (15)$$

Insert Eqs. (12), (13) and (14) into Eq. (15) yielding:

$$\mu_h(1 - x(t)) - \alpha x(t)z(t) = 0, \quad (16)$$

$$\alpha x(t)z(t) - \beta y(t) = 0, \quad (17)$$

$$\gamma(1 - z(t))y(t) - \delta z(t) = 0. \quad (18)$$

Inserting Eqs. (16) and (17) into Eq. (18) indicates that the equilibrium points of the system are: $F_1 = (1, 0, 0)$ and $F_2 = (x_0, y_0, z_0)$ with the values

$$x_0 = \frac{\mu_h\gamma + \beta\delta}{\gamma(\mu_h + \alpha)}, \quad y_0 = \frac{\mu_h(\gamma\alpha + \beta\delta)}{\beta\gamma(\mu_h + \alpha)} \quad \text{and} \quad z_0 = \frac{\mu_h(\gamma\alpha + \beta\delta)}{\alpha(\gamma\mu_h + \beta\delta)}. \quad (19)$$

Linearization of Eqs. (12), (13) and (14) on the equilibrium point (1,0,0) yields the following equation:

$$\begin{pmatrix} \frac{dx}{dt} \\ \frac{dy}{dt} \\ \frac{dz}{dt} \end{pmatrix} = \begin{pmatrix} -\mu_h & 0 & -\alpha \\ 0 & -\beta & \alpha \\ 0 & \gamma & -\delta \end{pmatrix} \begin{pmatrix} x \\ y \\ z \end{pmatrix}. \quad (20)$$

Using MAPLE, Eq. (20) leads to three eigen value equations as follows:

$$\lambda^3 + (\mu_h + \beta + \delta)\lambda^2 + (\mu_h\beta + \mu_h\delta + \beta\delta - \alpha\gamma)\lambda + (\mu_h\beta\delta - \mu_h\alpha\gamma) = 0, \quad (21)$$

with eigenvalues

$$\lambda_1 = -\mu_h, \quad \lambda_2 = -\frac{\beta + \delta + \sqrt{\beta^2 - 2\beta\delta + \delta^2 - 4\alpha\gamma}}{2} \quad \text{and} \quad \lambda_3 = -\frac{\beta + \delta - \sqrt{\beta^2 - 2\beta\delta + \delta^2 - 4\alpha\gamma}}{2}. \quad (22)$$

Linearization of Eqs. (12), (13) and (14) on the equilibrium point (x_0, y_0, z_0) yields the following equation:

$$\begin{pmatrix} \frac{dx}{dt} \\ \frac{dy}{dt} \\ \frac{dz}{dt} \end{pmatrix} = \begin{pmatrix} -\mu_h - \alpha\left(\frac{\mu_h(\alpha\gamma + \beta\delta)}{\alpha(\mu_h\gamma + \beta\delta)}\right) & 0 & -\alpha\left(\frac{\mu_h + \beta\delta}{\gamma(\mu_h + \alpha)}\right) \\ \alpha\left(\frac{\mu_h(\alpha\gamma + \beta\delta)}{\alpha(\mu_h\gamma + \beta\delta)}\right) & -\beta & \alpha\left(\frac{\mu_h + \beta\delta}{\gamma(\mu_h + \alpha)}\right) \\ 0 & \gamma\left(1 - \left(\frac{\mu_h(\alpha\gamma + \beta\delta)}{\alpha(\mu_h\gamma + \beta\delta)}\right)\right) & -\gamma\left(\frac{\mu_h(\alpha\gamma + \beta\delta)}{\beta\gamma(\mu_h + \alpha)}\right) - \delta \end{pmatrix} \begin{pmatrix} x \\ y \\ z \end{pmatrix}. \quad (23)$$

2.1 SIR model equilibrium point for South Sulawesi, Indonesia, and Selangor, Malaysia

Parameters in this model are variously determined. Some of the parameter values are taken from the Annual Health Facts published by KKM^[8] and KKRI^[10] supplemented by data from a previous study by Derouich and Boutayeb^[3] where there is a gap in the KKMa data. In addition, the model also used parameter values from Singapore. Lee's^[12] study found that infection rate of the mosquito population is around 10 percent. According to Lee^[11], life expectancy for the female *Aedes aegypti* is between 12 and 56 days, averaging 34 days. The findings of this study on Singapore cases were used in this model because Singapore, Indonesia and Malaysia are geographic neighbors, hence the three countries have a similar environment and climate, with similar values of the parameter estimates for mosquito infection rates in Indonesia and Malaysia. The following table gives parameters, values and sources of parameter data.

The equilibrium points were determined using the SIR model with set parameters for the state of South Sulawesi. Then, to determine the critical point, Eqs. (16), (17) and (18) were set equal to zero, as shown below.

$$0.000046(1 - x) - 0.2925xz = 0, \quad (24)$$

$$0.2925xz - (0.328833 + 0.000046)y = 0, \quad (25)$$

$$0.375(1 - z)y - 0.0323z = 0. \quad (26)$$

Table 1. Parameter values

Name of Parameter	Notation	Value (INA and MY)	Sources
Infected rate of host to recover	r_h	0.3288330	KKRI (2008) [10] & KKM (2007) [8]
Effective contact rate, human to vector	$b\beta_v$	0.3750000	Derouich & Boutayeb (2006) [3]
Effective contact rate, vector to human	$b\beta_h$	0.7500000	Derouich & Boutayeb (2006) [3]
Human life span	μ_h	0.0000460 & 0.0045000	KKRI (2008) [10] & KKM (2007) [8]
Vector life span	μ_v	0.0323000 & 0.0294100	KKRI (2008) [10] & Lee (2000) [11]

The equilibrium points for the SIR model are

$$(x, y, z) = (S_h, I_h, I_v) = (1, 0, 0)$$

and

$$(S_h, I_h, I_v) = (0.096988, 0.000126, 0.00148).$$

Use of the MAPLE software identified eigen values of λ as follows:

At the equilibrium point (1,0,0), eigen values $\lambda = -0.000046$, $\lambda = -0.543463$ and $\lambda = 0.182284$.

At equilibrium point (0.096988, 0.000126, 0.00148), eigen values $\lambda = -0.000244 + 0.003563i$, $\lambda = -0.000244 - 0.003563i$ and $\lambda = -0.361218$

Equilibrium points were determined using the SIR model with set parameters for the state of Selangor. Then, to determine the critical point, Eqs. (16), (17) and (18) were set equal to zero, as shown below:

$$0.0045(1 - x) - 0.006xz = 0, \tag{27}$$

$$0.006xz - (0.328833 + 0.0045)y = 0, \tag{28}$$

$$0.375(1 - z)y - 0.02941z = 0. \tag{29}$$

The equilibrium points for the SIR model for South Sulawesi were found to be:

$$(x, y, z) = (S_h, I_h, I_v) = (1, 0, 0)$$

and

$$(S_h, I_h, I_v) = (2.918184, -0.025896, -0.493004).$$

The equilibrium points (2.918184, -0.025896, -0.493004) were not suitable for study because only the value of S_h is positive while the other values are negative, which is illogical.

Use of the MAPLE software obtained eigen values of λ as follows:

At the equilibrium point (1,0,0) eigen values were $\lambda = -0.0045$, $\lambda = -0.340564$ and $\lambda = -0.022179$.

At equilibrium point (2.918184, -0.025896, -0.493004), eigen values were $\lambda = -0.006746$, $\lambda = 0.013928$ and $\lambda = -0.361756$.

2.2 SIR model for stability analysis in South Sulawesi and Selangor

Results of the SIR model solution in search of equilibrium points and eigen values are shown in Tab. 2.

Referring to the obtained equilibrium points, the results in Tab. 2 shows two equilibrium points that are saddle points. The equilibrium point for the state of South Sulawesi is a saddle point, indicating no occurrence of dengue virus infection since there are no infected humans or infected mosquitoes. Every human in the population is healthy and not infected with the virus. The second equilibrium point (0.096988, 0.000126, 0.00148) shows that if the number of people in South Sulawesi were to reach 0.097 of the total suspect population and if the number of infected people were infected at a rate of 0.0001 of the human population, the focus of dengue

Table 2. Equilibrium points and stability analysis model

Equilibrium points (S_v, I_v, R_v)	Eigen values	Stability Analysis
(1,0,0)	Real and opposite sign	saddle point
(0.096988,0.000126,0.00148)	Complex and all negative signs	focus stable asymptotically
(1,0,0)	Real and all negative signs	Node Stable

fever would be stable and present no significant concerns, except as in certain areas infection would start to increase again. Therefore, precautionary measures for areas that are the focus of dengue fever in South Sulawesi have been taken to prevent the occurrence of dengue virus infection, so the equilibrium point $(1, 0, 0)$ for those states is stable. This indicates that all human populations are healthy as there is no occurrence of dengue virus infection and no infected mosquitoes.

3 Results and discussion

Several investigations have been conducted using the SIR model. The particular SIR model which proves most suitable for the states of South Sulawesi and Selangor is the model in [14] and [22] because the results obtained are appropriate for the data reported by the Ministry of Health in each country. In this section, we describe the results of the SIR model for both countries.

3.1 SIR model for South Sulawesi, Indonesia

A simulation was carried out using ODESOLVE, MATLAB. Data on the number of dengue fever cases in the state of South Sulawesi, Indonesia, are given in Fig. 1, and results for the SIR model for the state of South Sulawesi are described in Fig. 2, where the x-axis is time (months) and the y-axis is the fraction of the variables. SIR model simulation for the state of South Sulawesi using MATLAB $S_h(0) = \frac{7675406}{7675893}$, $I_h(0) =$

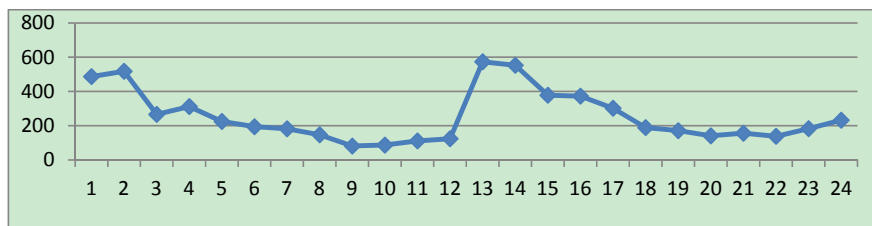


Fig. 1. Number of cases reported to the South Sulawesi, Indonesia, in 2007 and 2008 by month

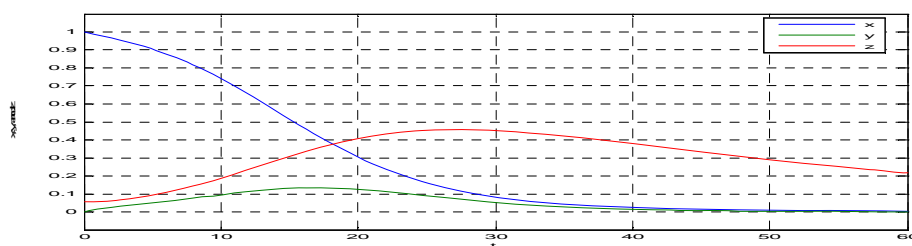


Fig. 2. Transmission of dengue fever with initial condition

$\frac{487}{7675893}$ and $I_v(0) = 0.056$ with parameter $\mu_k = 0.000046$, $C_{vh} = 0.75$, $C_{hv} = 0.375$, $\gamma_h = 0.328833$ and $\mu_v = 0.0323$.

The data in Fig. 2, generated using MATLAB, can be compared with the data obtained from the Indonesian Ministry of Health (KKRI) for South Sulawesi, as shown in Fig. 1. The product of the SIR model diagram is compatible with the diagram product of real data.

According to Fig. 1, the number of dengue virus cases (in SIR terms, virus-infected humans) will reach the maximum level within the next 12 months, while Fig. 2 shows that the number of infected people takes 14 months to reach its highest level of 10% of the human population, and the number of people infected will be reduced to close to zero for the next 35 months. This is because the parameters used were inappropriate, although the determination of these parameters meet the requirements of the SIR model that recovery rate must be smaller than the rate of infection [19]. Meanwhile, the number of infected mosquitoes (Fig. 2) takes about 23 months to reach its peak at 40% of the population of mosquitoes. In addition, the number of infected mosquitoes takes more than 60 months to approach zero point. This indicates that the vector mosquito population takes more time to eliminate than does the number of infected people. A graph of the SIR model using MATLAB and data from Ministry of Health (KKRI) is presented in Fig. 5.

3.2 The SIR model for Selangor, Malaysia

A simulation was carried out using ODESOLVE and MATLAB. Data on the number of dengue fever cases in the state of Selangor, Malaysia, are given in Fig. 3, and the results from each model are described in Fig. 4, where the x-axis is a time series (in months) and the y-axis is the fraction of the variables. Result

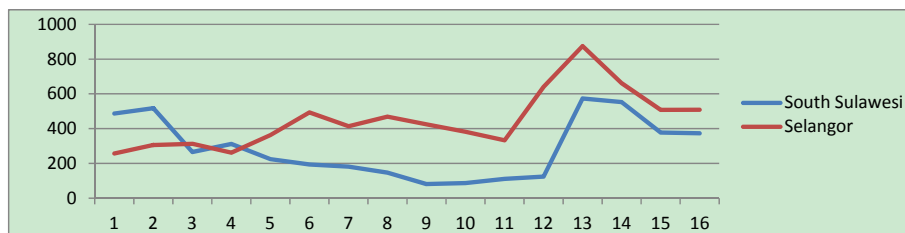


Fig. 3. Number of dengue cases reported in Selangor, Malaysia and South Sulawesi, Indonesia in 2008 by month

of SIR model simulation for the state of Selangor using MATLAB $S_h(0) = \frac{5070822}{5071126}$, $I_h(0) = \frac{304}{5071126}$ and

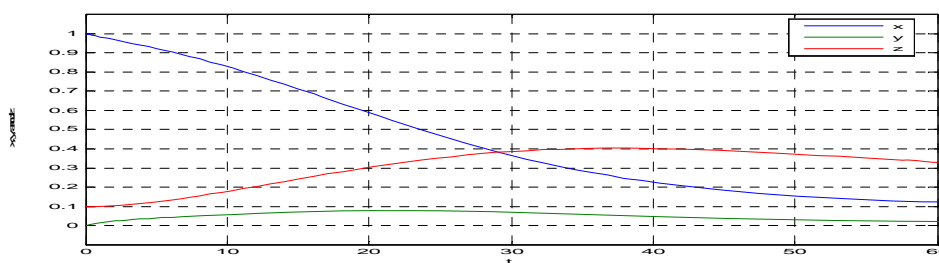


Fig. 4. Transmission of dengue fever with initial condition

$I_v(0) = 0.1$ with parameter $\mu_k = 0.0045$, $C_{vh} = 0.75$, $C_{hv} = 0.375$, $\gamma_h = 0.15$ and $\mu_v = 0.02941$.

Data from Fig. 4, generated from the MATLAB simulation, can be compared with the data obtained from the Malaysian Ministry of Health (KKMa) shown in Fig. 3 and outcomes from Fig. 4 based on SIR model results. According to Fig. 3, the number of dengue fever cases (virus-infected humans) will reach the maximum level within the next 12 months. However, Fig. 4 shows that the number of infected people takes 14 months to reach its highest level of 10% of the human population and the number of infected people will be reduced to close to zero for the next 35 months. Again, this finding arises because the parameters used were inappropriate, although the determination of these parameters met the requirements of the SIR model that recovery rate must be smaller than the rate of infection. Meanwhile, the number of infected mosquitoes

from Fig. 4 takes approximately 23 months to reach its peak of 40% of the population of mosquitoes. In addition, the number of infected mosquitoes takes more than 60 months to approach zero level. This indicates that it takes longer to eliminate the mosquito population than to eliminate infections among the human host population.

Noting the number of dengue cases reported during 2007 and 2008, the occurrence of dengue fever had not reached a very serious level in either of these two countries in general and for the states under study in particular. The number of reported dengue fever cases was as high as 10% of the population both in South Sulawesi and in Selangor. A graph of the SIR model generated using MATLAB, data from the Malaysian Ministry of Health (KKMa) and the Indonesian Ministry of Health (KKRI) is presented in Fig. 5.

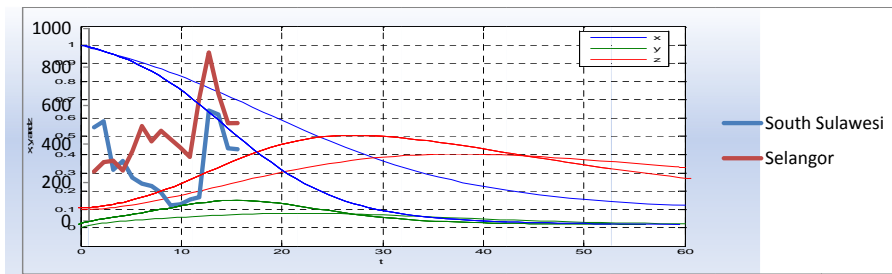


Fig. 5. Graph of SIR model and data from Indonesian and Malaysian Ministries of Health (KKRI and KKMa respectively)

3.3 Breeding rates, r_0

Searching for the re-breeding rate $R_0 = \frac{C_{hv}I_v/N_h}{\gamma_h} S(0)$ is important because this rate shows how many infections will occur among humans as a result of an infection by a mosquito. If an infection can go on to infect more than one other ($R_0 > 1$), then dengue fever becomes epidemic. Determination of the re-breeding rate has been introduced by [13].

The impetus for determining the value of is to predict the infection rate of humans who have the potential to be infected ($C_{hv}I_v/N_h$) and rates for humans who have recovered (γ_h). A simulation was carried out using ODESOLVE, MATLAB. Stability analysis was carried out for the epidemic and values of the threshold were obtained. Illustration of the dynamics of each epidemic is given in Fig. 6 and Fig. 7.

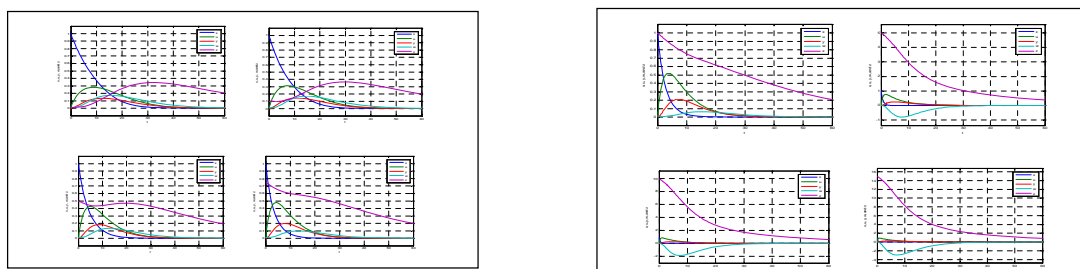


Fig. 6. Illustration of the dynamics system with $R_0 \leq 1$ (Convergence) **Fig. 7.** Illustration of the dynamics system with $R_0 > 1$ (Oscillation)

Fig. 6 shows the typical behavior of the solutions, indicating that the rate of SIR approaches, asymptotically, the trivial state of the system (the ideal state) to the case where all the population will remain healthy (in this case $R_0 \leq 1$).

Fig. 7 illustrates an oscillatory behavior near the neighborhood of the endemic equilibrium point. This behavior can be justified if $R_0 > 1$ and if the initial value I_h satisfies the solution. Using the initial values and

parameter values from data in both countries, the obtained result of threshold parameter value R_0 for South Sulawesi and for Selangor can be rewritten in mathematical form as follows:

$$R_0 \text{ for the state of South Sulawesi is } R_0 = \frac{C_{hv}I_v/N_h}{\gamma_h} S(0) = 1.1403I_v,$$

$$R_0 \text{ for the state of Selangor is } R_0 = \frac{C_{hv}I_v/N_h}{\gamma_h} S(0) = 1.1403I_v.$$

The reproductive rate depends on the number of infected mosquitoes (I_v). Determination of value R_0 depends on the value of I_v by replacing some of the different values shown in Tab. 3, the difference between these values is very significant.

Table 3. Determination of the re-breeding value R_0 of infected mosquitoes

I_v value	R_0 value
0.056	0.0639
0.1	0.11403
1	1.1403
5	5.7015

Tab. 3 shows that, if the number of infected mosquitoes is less than one ($I_v < 1$), then the value $R_0 < 1$. This applies to the cases from both states. Thus, cases of dengue fever in the state of South Sulawesi and the state of Selangor are not worrying since the obtained results show that the dengue virus infection is low as an infected individual will give rise to less than one individual with the potential to infect others. If the number of infected mosquitoes is more than one ($I_v > 1$), then the value $R_0 > 1$, so the transmission of dengue virus caused more than one person to be infected with dengue virus.

4 Conclusions

The SIR model results show that the danger of dengue fever is not worrisome for cities in both South Sulawesi and Selangor. However, precautions must be taken, especially for some cities in South Sulawesi. Moreover, the study also found that the dengue fever virus for both countries spreads rapidly if the transmission rate between humans and mosquitoes is high. In fact, the number of infected people will reach a very high level of cases before it declines. In addition, dengue fever requires a very long time to reach the point where the number of infected people has zero value since dengue virus infection occurs when there is a continuous relationship between human and mosquito populations.

The results of the SIR model for reproduction/re-breeding for the two states showed that all mosquitoes infected with dengue virus have the potential to infect more than one person. As a whole, where the mosquito population in general and the infected mosquito population in particular can be controlled or eliminated, the dengue virus will be less transmissible or non-transmissible. Dengue virus infects humans whose potential to be infected depends largely on the number of infected mosquitoes. However, it must be noted that it is difficult to eliminate the population of *Aedes aegypti* as this mosquito prefers to lurk in dark and hidden places.

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