Journal of Quality Measurement and Analysis *JQMA* 19(2) 2023, 45-56
e-ISSN: 2600-8602 *http://www.ukm.my/jqma*

ESTIMATING THE TRANSMISSION DYNAMICS OF DENGUE FEVER IN SUBTROPICAL MALAYSIA USING SEIR MODEL

(Menganggarkan Dinamik Penularan Demam Dengi di Subtropika Malaysia Menggunakan Model SEIR)

SABASTINE EMMANUEL, SARATHA SATHASIVAM*, MAJID KHAN MAJAHAR ALI, TAN JIN KEE & YAP SZE LING

ABSTRACT

In this study, we utilized the SEIR model in conjunction with Heun's predictor-corrector method to analyze the transmission dynamics of dengue fever over time in subtropical Malaysia. Our main focus was on estimating the recovery rate of the infected population and gaining insights into the patterns of disease spread. By applying Heun's method to the SEIR model, we were able to provide more accurate estimations and a comprehensive understanding of the dynamics of dengue fever. We examined the population dynamics of susceptible, exposed, infectious, and recovered individuals, and analyzed the effectiveness of intervention measures.Through our analysis, we not only uncovered the patterns of disease transmission but also shed light on the impact of various control measures. Our findings contribute to the existing knowledge and offer valuable insights into managing and controlling the spread of dengue fever in subtropical regions like Malaysia.

Keywords: mathematics modelling; dengue fever; Heun's predictor corrector method

ABSTRAK

Dalam kajian kami, kami menggunakan model SEIR bersempena dengan kaedah pembetulan peramal Heun untuk menganalisis dinamik penularan demam denggi dari masa ke masa di subtropika Malaysia. Fokus utama kami adalah untuk menganggarkan kadar pemulihan penduduk yang dijangkiti dan mendapatkan pandangan mengenai corak penyebaran penyakit. Dengan menggunakan kaedah Heun kepada model SEIR, kami dapat memberikan anggaran yang lebih tepat dan pemahaman yang komprehensif mengenai dinamik demam denggi. Kami mengkaji dinamik populasi individu yang mudah terdedah, terdedah, berjangkit, dan pulih, dan menganalisis keberkesanan langkah intervensi. Melalui analisis kami, kami bukan sahaja mendedahkan corak penularan penyakit tetapi juga memberi penerangan tentang kesan pelbagai langkah kawalan. Penemuan kami menyumbang kepada pengetahuan sedia ada dan menawarkan pandangan berharga dalam mengurus dan mengawal penyebaran demam denggi di kawasan subtropika seperti Malaysia.

Kata kunci: pemodelan matematik; demam denggi; kaedah pembetulan peramal Heun

1. Introduction

Dengue fever is caused by four closely related dengue serotypes (DEN1-4). These viruses are transmitted by the bite of two species of female mosquitoes, Aedes aegypti and Aedes albopictus. The primary vector responsible for transmitting the disease is Aedes aegypti as recognized by the (World Health Organizations 2021). Dengue can lead to a range of illnesses, varying from mild flu-like symptoms to severe disease. Proper treatment is essential for severe dengue, as it carries a higher risk of mortality.

Dengue fever is the most prevalent viral illness transmitted by arthropod-borne among humans (Kyle & Harris 2008). Dengue infects around 45-50 million individuals in both tropical, subtropical and semi-urban settings every year, with up to 500,000 developing

potentially fatal complications known as dengue hemorrhagic fever/dengue shock syndrome (Nuraini *et al.* 2008). Due to its high prevalence, absence of a registered vaccine or effective preventive measures, and lack of specific treatment options, dengue fever poses a significant public health challenge worldwide (Lei *et al.* 2002).

As a nation in Southeast Asia, Malaysia is not an exception to this disease. Skae published the earliest recorded account of a dengue outbreak in Malaya on November 15, 1902. He stated that an outbreak of dengue fever occurred in the northern state of Penang between December 1901 and March 1903. Dengue Haemorrhagic Fever (DHF), a severe form of dengue, was originally discovered in Georgetown, Penang, in November 1962. Dengue fever instances started to appear in Penang and Kuala Lumpur's metropolitan regions in the 1960s. Dengue Haemorrhagic Fever (DHF) spread over all of Malaysia by the early 1970s, placing a heavy burden on the nation's public health.

The incidence of dengue has significantly grown because of a number of factors, including urban population development, waste disposal practices that are careless and ineffective, and the increased and effective movement of dengue viruses in infected people via contemporary transportation (Esteva & Vargas 2000). Dengue virus transmission is illustrated in the diagram below.

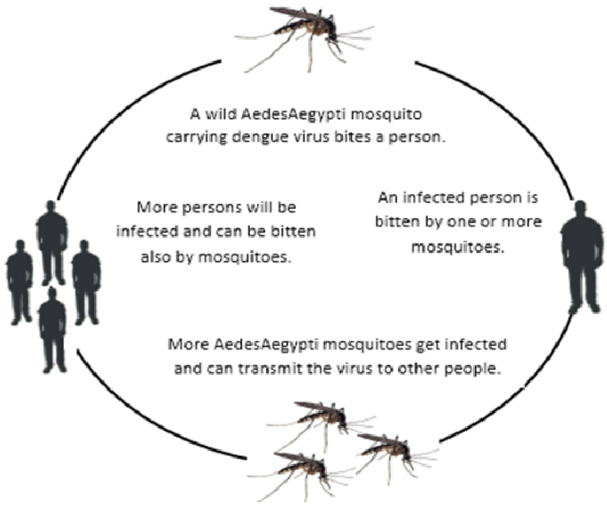

Figure 1: Pictorial representation of Dengue virus transmission process

Following World War II, dengue fever emerged as a perilous infectious disease that posed a significant threat to approximately 2.5 billion people worldwide, primarily in tropical regions, with Southeast Asia being notably affected. Outbreak of dengue fever typically reach their peak during and after wet seasons (Wu *et al*. 2009; Yang *et al.* 2009). The World Health Organization (WHO) recognizes dengue fever as one of the top ten public health threats (Fine 1993 & Heesterbeek 2002). Since dengue fever is transmitted by mosquitoes, mathematical models often incorporate vector dynamics to capture the mosquito population and its interactions with humans. Vector dynamics models include parameters such as mosquito biting rates, lifespan and reproduction rates (Derouich *et al.* 2003; Dietz 1993). These models help understand the impact of mosquito control measures on dengue transmission. The aim of this study is to develop and refine mathematical models to simulate and predict the transmission dynamics of dengue fever (Esteva & Vargas 1998), including the impact of intervention, climate factors and population movements, in order to provide insight into the

dynamics and control of the disease, enabling policy makers and public health officials to make informed decision and develop effective strategies for prevention and control.

2. Mathematical Model

Mathematical modelling of dengue fever found compartmental dynamics such as Susceptible, Infected and Removed (SIR), and Susceptible, Exposed, Infected and Removed (SEIR). In comparison with SIR model (Altmann 1995), SEIR model considers the latent period as an additional vectors variable for examining the spread of dengue fever. With unpredictable climate change being one of the consequences of global warming nowadays, latent period is critical.

In our investigation into the SEIR model, we intend to analyze and observe the transmission of dengue fever by applying different initial conditions under varying time. Distinct scenarios of transmission of dengue fever under varying time are considered with the differential equations as follows:

$$\begin{aligned}
\frac{dx}{dt} &= \mu_h(1-x) - px - \alpha xz \\
\frac{du}{dt} &= (az+p)x - (\mu_h + \varphi_h)u \\
\frac{dy}{dt} &= \varphi_h u - (\mu_h + \gamma_h + \alpha_h)y \\
\frac{dw}{dt} &= \gamma_v(1-z-w)y - (\mu_v + \delta_v)w \\
\frac{dz}{dt} &= \delta_v w - \mu_v z
\end{aligned} \tag{1}$$

2.1. *Methodology*

In this research, we choose Heun's Predictor corrector method as the numerical method to solve the SEIR model.

2.1.1. *SEIR model*

The SEIR model is a mathematical model used to simulate the transmission of the dengue virus serotype between the human host population and the vector population (mosquitoes). In this study, we consider a scenario where a group of individuals has already been infected by the virus, and the dengue virus continues to spread within the population, while the number of vectors (mosquitoes) remains constant.

In our model, we assume that individuals who have been infected receive treatment, which grants them lifelong immunity and prevents reinfection. Over time, the population of both humans and mosquitoes is expected to naturally decline. Furthermore, individuals infected with dengue fever may face the risk of mortality resulting from the infection. To represent the changes that occur within each group (humans and mosquitoes), we can use the following mathematical model under the specified conditions:

$$N_h = S_h + E_h + I_h + R_h \Rightarrow R_h = N_h - S_h - E_h - I_h, \tag{2}$$

$$N_v = \frac{A}{\mu_v} = S_v + E_v + I_v \Rightarrow S_v = \frac{A}{\mu_v} - E_v - I_v \tag{3}$$

and the following assumptions of fractions

$$x = \frac{S_h}{N_h}, u = \frac{E_h}{N_h}, y = \frac{I_h}{N_h}, w = \frac{E_v}{N_v}, z = \frac{I_v}{N_v} = \frac{I_v}{\frac{A}{\mu_v}} \tag{4}$$

SEIR model for the transmission of dengue fever is represented as follows:

$$\begin{aligned}
\frac{dx}{dt} &= \mu_h (1-x) - px - \alpha xz \\
\frac{du}{dt} &= (az + p)x - (\mu_h + \varphi_h)u \\
\frac{dy}{dt} &= \varphi_h u - (\mu_h + \gamma_h + \alpha_h)y \\
\frac{dw}{dt} &= \gamma_v (1 - z - w)y - (\mu_v + \delta_v)w \\
\frac{dz}{dt} &= \delta_v w - \mu_v z
\end{aligned} \tag{5}$$

where

$$\alpha = \frac{\beta_h bA}{N_h \mu_v}, \tag{6}$$

Table 1: Parameters of the vector population

Population vector (N_v)	
S_v	Potential infected mosquitoes with dengue virus.
E_v	Mosquitoes that are exposed to dengue virus infection.
I_v	Infected mosquitoes.
β_v	Probability of transmission from infected person to the potential mosquitoes.
δ_v	Proportional rates of mosquitoes exposed to the human virus infection.
μ_v	Natural death rate of mosquitoes.
p	Percentage of infected mosquitoes
b	Average bite of potentially infected mosquitoes.

Table 2: Parameters of the human population

Human Population (N_h)	
S_h	Potential infected person with dengue virus.
E_h	Individual who are exposed to dengue virus infection.
I_h	Infected person.
R_h	Recovered person.
β_h	Probability of transmission from an infected mosquitoes to potentially infected person.
φ_h	Proportional rate of people who are exposed to dengue virus infection.
γ_h	Healing rate from virus infection.
μ_h	Natural death rate of human.
α_h	Death rate caused by dengue

2.2. *Heun's predictor corrector*

Heun's Method is an improvement over Euler's method in numerical approximation, offering increased accuracy. This method addresses some of the errors encountered in Euler's method and provides more reliable results. To illustrate the advantages of Heun's Method, consider the following scenario.

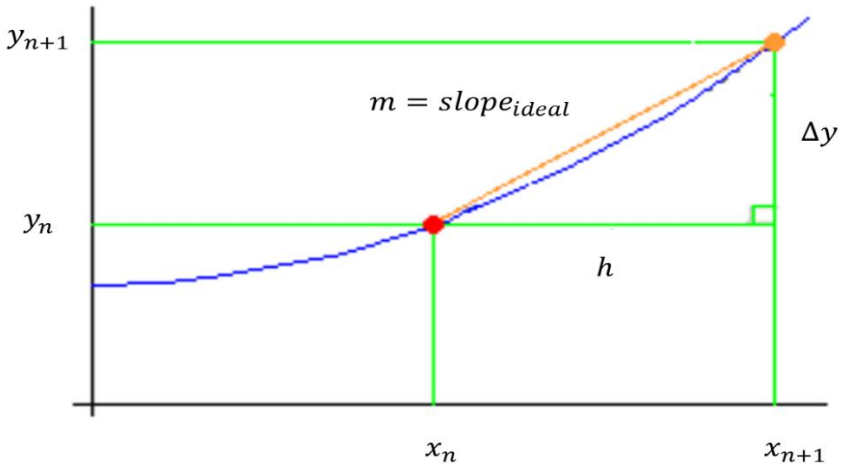

Figure 2: The slope of the tangent

From Figure 2, The slope of the tangent line at the left end point is

$$slope_{left} = f(x_n, y_n) \tag{7}$$

Euler's rough estimate of the next coordinate gives us an estimate of the slope of the tangent line at the right endpoint. Thus, the slope of ideal prediction line is the average of the slope .i.e.

$$slope_{ideal} = \frac{1}{2}\left(slope_{left} + slope_{right}\right) \tag{8}$$

Using the basic idea, we derive the formula

$$slope_{ideal} = \frac{\Delta y}{h} \tag{9}$$

From Figure 2 in which it can be rearranged to give us $\Delta y = hslope_{ideal}$. Then, we can predict the coordinates of the next point where $x_{n+1} = x_n + h$

$$slope_{right} = f\left(x_n + h, y_n + hf\left(x_n, y_n\right)\right) \tag{10}$$

By replacing Δy with the value we had found before, it yields

$$\begin{aligned} y_{n+1} &= y_n + hslope_{ideal} \\ &= y_n + \frac{1}{2}h\left(slope_{left} + slope_{right}\right) \\ &= y_n + \frac{h}{2}\left(f\left(x_n, y_n\right) + f\left(x_n + h, y_n + hf\left(x_n, y_n\right)\right)\right) \end{aligned} \tag{11}$$

Since it is a predictor-corrector method, hence it has two stages were

Predictor: $y_{n+1}^{p} = y_n + hf\left(x_n, y_n\right)$ (12)

Corrector: $y_{n+1}^{c} = y_n + \frac{h}{2}\left(f\left(x_n, y_n\right) + f\left(x_{n+1}, y_{n+1}^{p}\right)\right)$ (13)

3. Algorithm and Flow Chart of the Model

(1) Initialize the parameters and initial population values for the susceptible (S), exposed (E), infected (I), and recovered (R) compartments.
(2) Set the total simulation time, step size, and create an empty matrix to store the output.
(3) Define the system of differential equations representing the SEIR model.
(4) Implement the Heun's predictor-corrector method:
  (i) Set the initial time and population values.
  (ii) While the current time is less than the total simulation time:
    a. Use the predictor step to estimate the population values at the next time step.
    b. Use the corrector step to refine the estimates by averaging the predictor and current values.
    c. Update the population values with the corrected estimates.
    d. Append the current time and population values to the output matrix.

e. Increment the current time by the step size.

(5) Display or save the output matrix with the time and population values for each compartment.

(6) Visualize the results using plots or graphs to observe the population dynamics over time.

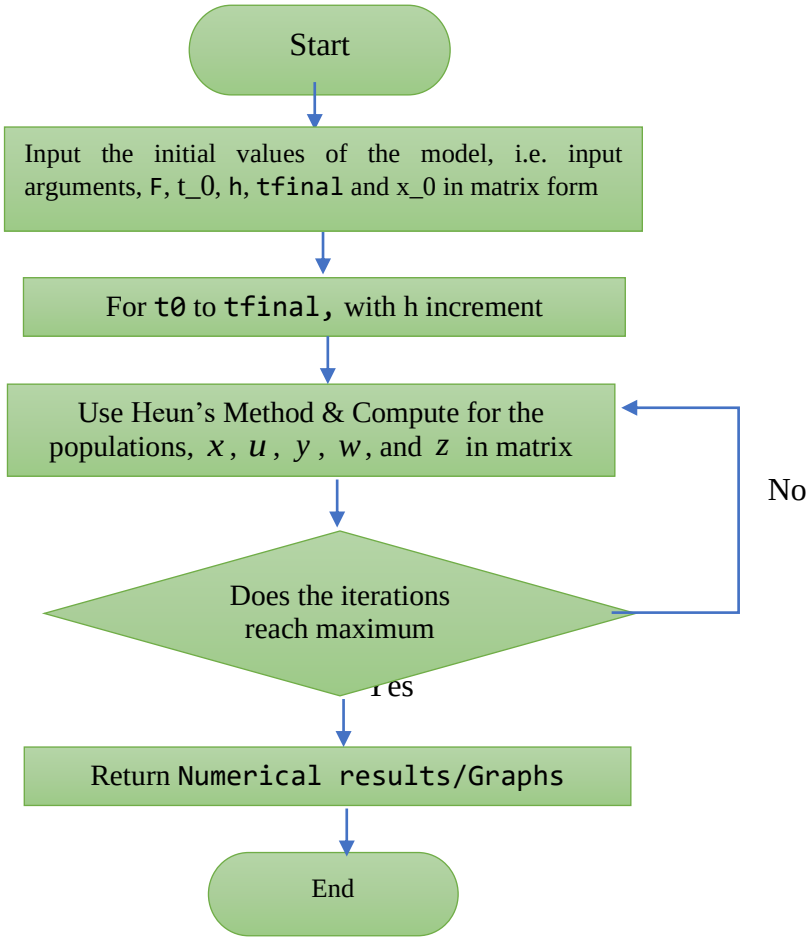

Figure 3: Flow chart of Heun's method

4. Numerical Results and Simulation

Data were gathered from Lee *et al.* (2000), Derouich *et al.* (2006) and Side & Noorani (2013) sources and incorporated into the model as functions of (t) and I(t). The parameters h is assume to be equal to 3.0, parameters values from sources are $\mu_h = 0.0045$, $p = 0.09$, $\alpha = 0.006$, $\varphi_h = 0.1667$, $\gamma_h = 0.328833$, $\alpha_h = 0.0000002$, $\gamma_v = 0.375$, $\mu_v = 0.02941$, and $\delta_v = 0.1428$ respectively, with the initial populations $x_0 = 0.9999$, $u_0 = 0.0100$, $y_0 = 0.0001$, $w_0 = 0.0100$ and $z_0 = 0.1000$ at $t = 0$.

The MATLAB code produce the following results presented in Tables 3 and 4, along with the corresponding graphs, illustrating the population dynamics with a total period of 60 months and step size of 3 months, where $\gamma_h = 0.1$ and $\gamma_h = 0.5$.The output is a matrix that consists of 6 columns, which are the time t, and the populations involved i.e. x, u, y, w, and z respectively.

Table 3: Populations of each compartment in the model when the parameter $\gamma_h = 0.1$

Time, t	Susceptible Human, x	Exposed Human, u	Infected Human, y	Exposed Mosquitoes, w	Infected Mosquitoes, z
0	0.9999	0.0100	0.0001	0.0100	0.1000
3.0000	0.7670	0.1712	0.0709	0.0087	0.0946
6.0000	0.5910	0.2328	0.1545	0.0857	0.1045
9.0000	0.4579	0.2424	0.2221	0.1727	0.1515
12.0000	0.3570	0.2268	0.2657	0.2298	0.2265
15.0000	0.2804	0.2009	0.2865	0.2512	0.3109
18.0000	0.2225	0.1725	0.2890	0.2469	0.3899
21.0000	0.1787	0.1455	0.2786	0.2291	0.4561
24.0000	0.1456	0.1216	0.2600	0.2062	0.5073
27.0000	0.1207	0.1014	0.2371	0.1832	0.5441
30.0000	0.1020	0.0847	0.2126	0.1623	0.5685
33.0000	0.0879	0.0713	0.1884	0.1442	0.5829
36.0000	0.0774	0.0607	0.1657	0.1289	0.5892
39.0000	0.0695	0.0524	0.1451	0.1159	0.5893
42.0000	0.0636	0.0459	0.1270	0.1050	0.5845
45.0000	0.0591	0.0409	0.1114	0.0957	0.5761
48.0000	0.0558	0.0371	0.0981	0.0879	0.5649
51.0000	0.0534	0.0341	0.0869	0.0812	0.5517
54.0000	0.0515	0.0319	0.0777	0.0754	0.5372
57.0000	0.0502	0.0302	0.0701	0.0706	0.5217
60.0000	0.0492	0.0289	0.0639	0.0665	0.5056

Table 4: Populations of each compartment in the model when the parameter $\gamma_h = 0.5$

Time, t	Susceptible Human, x	Exposed Human, u	Infected Human, y	Exposed Mosquitoes, w	Infected Mosquitoes, z
0	0.9999	0.0100	0.0001	0.0100	0.1000
3.0000	0.7670	0.1712	0.0679	0.0087	0.0946
6.0000	0.5910	0.2328	0.0939	0.0458	0.1039
9.0000	0.4580	0.2423	0.0979	0.0797	0.1280
12.0000	0.3573	0.2266	0.0914	0.0991	0.1597
15.0000	0.2811	0.2005	0.0806	0.1052	0.1922
18.0000	0.2235	0.1720	0.0688	0.1023	0.2211
21.0000	0.1800	0.1449	0.0576	0.0944	0.2442
24.0000	0.1472	0.1211	0.0478	0.0842	0.2610
27.0000	0.1224	0.1010	0.0395	0.0736	0.2717
30.0000	0.1038	0.0844	0.0327	0.0636	0.2770
33.0000	0.0897	0.0712	0.0272	0.0546	0.2779
36.0000	0.0791	0.0606	0.0229	0.0468	0.2751
39.0000	0.0711	0.0524	0.0195	0.0403	0.2697
42.0000	0.0651	0.0459	0.0168	0.0349	0.2622
45.0000	0.0606	0.0410	0.0148	0.0305	0.2534
48.0000	0.0572	0.0372	0.0132	0.0270	0.2437
51.0000	0.0547	0.0342	0.0120	0.0242	0.2335
54.0000	0.0528	0.0320	0.0111	0.0220	0.2232
57.0000	0.0514	0.0303	0.0104	0.0203	0.2130
60.0000	0.0503	0.0290	0.0099	0.0190	0.2030

Fractions in the model represent the proportions of the total population in each compartment, providing precise insights into the relative sizes of susceptible, exposed, and infected individuals, enabling tracking of population changes, evaluating intervention impacts, and understanding compartment interactions for effective dengue control and outbreak prediction.

For example, the initial value of 0.9999 for "Susceptible Human" at a specific time point means that almost the entire population is susceptible to dengue infection, with only a very

small fraction being immune or already infected. Similarly, a value of 0.0100 for "Exposed Human" suggests that a small proportion of the population has been exposed to the virus but has not yet developed symptoms or become infectious.

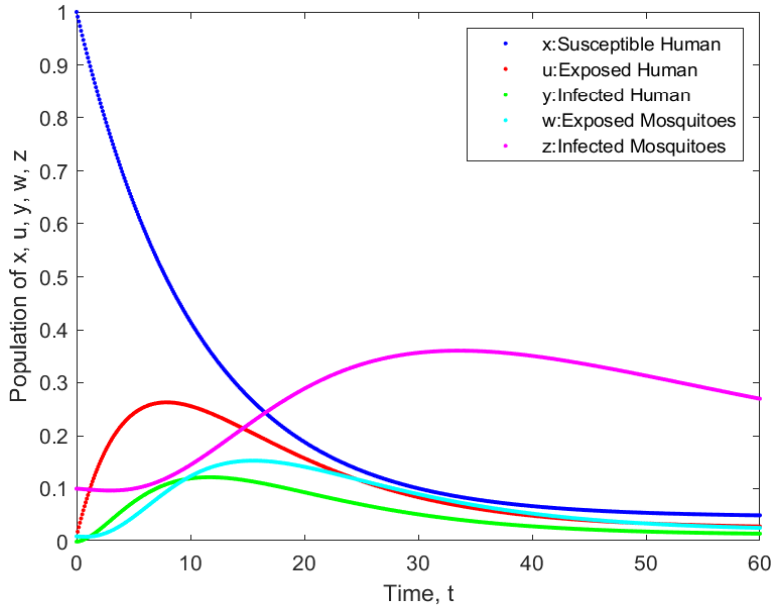

Figure 4: Populations of each compartment in the model when the parameter $\gamma_h = 0.328833$

When the healing rate from virus infection, γ_h decreases from 0.328833 in the previous graph to 0.1, the graph is shown as below:

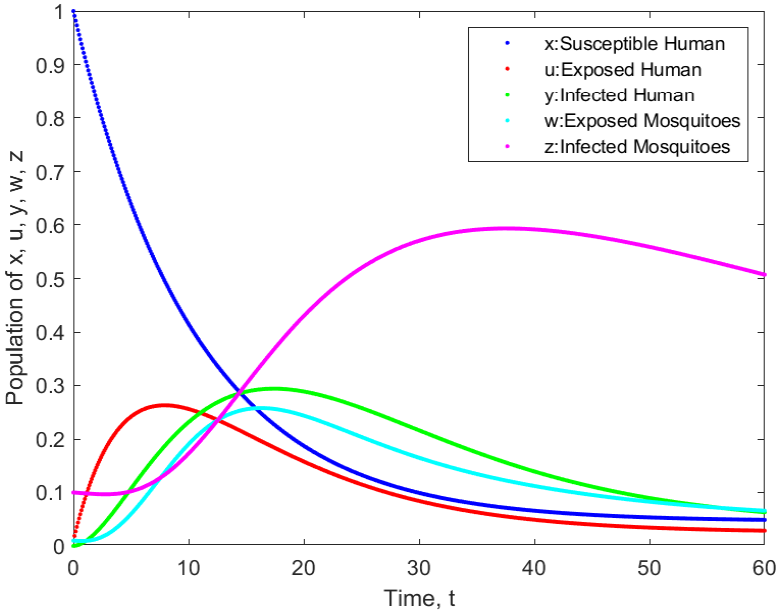

Figure 5: Populations of each compartment in the model when the parameter $\gamma_h = 0.1$

Then, when the recovery rate from virus infection, γ_h increases to 0.5, the graph is shown as below:

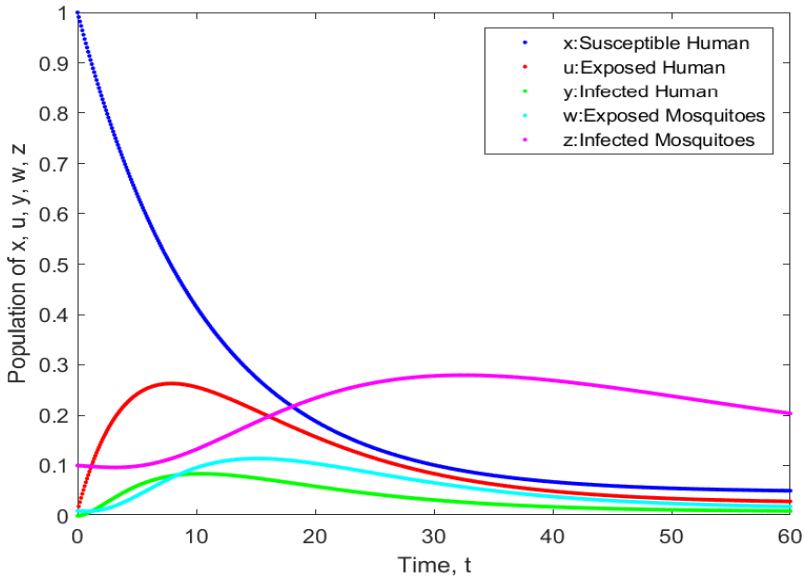

Figure 6: Populations of each compartment in the model when the parameter $\gamma_h = 0.5$

5. Discussion of Results

We have increased the human's healing rate from virus infection, γ_h to 0.5 and decreased it to 0.1 from the estimated value of 0.328833. The effects of varying the parameter value can be seen from the results shown from the graphs and tables in the previous section. The initial populations of the 5 compartments in the SEIR model remain unchanged to investigate the direct changes in the graphs while varying the parameter value. From Figures 3, 4 and 5, it can be seen that the curvatures of the graphs for the elements of infected human y, exposed mosquitoes w, and infected mosquitoes z have slight changes where the peak values of the graphs have changed. At about $t = 10$ months, the populations of the infected human and the exposed mosquitoes (green and light blue graphs) reach the highest level when $\gamma_h = 0.1$, and the lowest level when $\gamma_h = 0.5$.

On the other hand, at about $t = 30$ months, the population of the infected mosquitoes (magenta graph) reaches the highest level when $\gamma_h = 0.1$, and the lowest level when $\gamma_h = 0.5$. At the final $t = 60$ months, it can also be noticed that the population for the infected human, the exposed mosquitoes, and the infected mosquitoes has a significant decrease as γ_h increases.

Table 5: Rate of increase and decrease of compartments

γ_h	Susceptible Human x	Exposed Human u	Infected Human y	Exposed Mosquitoes w	Infected Mosquitoes z
0.1	0.0492	0.0289	0.0639	0.0665	0.5056
0.328833	0.0500	0.0290	0.0153	0.0265	0.2690
0.5	0.0503	0.0290	0.0099	0.0190	0.2030

Therefore, it can be said that γ_h is closely related to the basic reproductive rate, R_0. From the above statements, the relationship between γ_h and R_0 can be deduced:

$$R_0 \propto \frac{1}{\gamma_h} \tag{14}$$

where γ_h is inversely proportional to R_0.

6. Conclusion

In this study, we have applied numerical techniques in computational analysis to successfully and effectively complete our investigation. The plot function available in MATLAB software has been instrumental in visualizing the population dynamics of each compartment in the SEIR model, considering different initial conditions. Additionally, the utilization of various 'M' files and function definitions has facilitated a simple and efficient process of inputting variables, parameters, and data.

Through the application of Heun's predictor-corrector method, we have estimated the future populations of compartments within the SEIR model for dengue fever transmission in Malaysia. By considering the given parameter values, we have predicted the dynamics of susceptible individuals, exposed individuals, infectious cases, and recovered individuals over time.

Furthermore, we have examined the impact of varying the recovery rate of humans from virus infection. Employing the predictor-corrector method, we have explored the relationship between this parameter and the basic reproductive number (R_0). Our analysis has provided insights into how changes in the recovery rate can influence the transmission dynamics of dengue fever and its overall spread.

As a conclusion, to reduce the basic reproductive rate (R_0), it is crucial to increase the healing rate of infected individuals. This emphasizes the importance of government initiatives in providing healthcare services and allocating suitable clinical care for dengue fever patients before their conditions worsen. Additionally, individuals should take preventive measures against dengue fever to minimize their exposure to the dengue viruses. By collectively addressing these factors, we can effectively combat the transmission and impact of dengue fever in Malaysia.

Acknowledgments

This research is supported by Research University Grant (RUI) (1001/PMATHS/8011131) by Universiti Sains Malaysia.

References

Altmann M. 1995. Susceptible-infected-removed epidemic models with dynamic partnerships. *Journal of Mathematical Biology* **33**(6): 661-675.

Derouich M. & Boutayeb A. 2006. Dengue fever: Mathematical modelling and computer simulation. *Applied Mathematics and Computation* **177**(2): 528–544.

Derouich M., Boutayeb A. & Twizell E.H. 2003. A Model of dengue fever. *Biomedical Engineering Online* **2**: 4.

Dietz K. 1993. The estimation of the basic reproduction number for infectious diseases. *Statistical Methods in Medical Research* **2**(1): 23-41.

Esteva L. & Vargas C. 2000. Influence of vertical and mechanical transmission on the dynamics of dengue disease. *Mathematical Biosciences* **167**(1): 51–64 .

Esteva L. & Vargas, C. 1998. Analysis of dengue disease transmission model. *Mathematical Biosciences* **150**(2): 131–135.

Fine P.E. 1993. Herd immunity: history, theory, practice. *Epidemiologic Reviews* **15**(2): 265-302.

Heesterbeek J.A.P. 2002. A brief history of R0 and a recipe for its calculation. *Acta Biotheoretica* **50**(3): 189-204.
Kyle J.L. & Harris E. 2008. Global spread and persistence of dengue. *Annual review of microbiology* **62**: 71–92.
Lei H.Y., Huang J.H., Huang K.J. & Chang C. 2002. Status of dengue control programme in Taiwan – 2001. *Dengue Bulletin* **26**: 14–23.
Bakar M.R.A., Mohammed S.G., Ibrahim N.A. & Monsi M. 2008. Deterministic models in dengue transmission dynamics. *Research Bulletin Institute for Mathematical Research* **2**(1): 21–33.
Nuraini N., Soewono, E. & Sidarto K.A. 2008. Mathematical model of dengue disease transmission with severe DHF compartment. *Bulletin of the Malaysian Mathematical Sciences Society* **30**(2): 143–157.
Side S. & M.S.M. Noorani. 2013. A SIR model for spread of dengue fever disease (simulation for South Sulawesi, Indonesia and Selangor, Malaysia). *World Journal of Modelling and Simulation* **9**(2): 96–105.
World Health Organization. 2021. Poliomyelitis (polio). https://www.who.int/health-topics/poliomyelitis#tab=tab_1 (11 June 2022).
Wu P.C., Lay J.G., Guo H.R., Lin C.Y., Lung S.C. & Su H.J. 2009. Higher temperature and urbanization affect the spatial patterns of dengue fever transmission in subtropical Taiwan. *Science of The Total Environment* **407**(7): 2224–2233.
Yang H.M., Macoris M.L.G., Galvani K.C., Andrighetti M.T.M. & Wanderley D.M.V. 2009. Assessing the effects of temperature on the population of Aedes aegypti, the vector of dengue. *Epidemiology and Infection* **137**(8): 1188–1202.

School of Mathematical Sciences,
Universiti Sains Malaysia,
11800 USM
Pulau Pinang, MALAYSIA.
E-mail: sabastine.emmanuel@fulokoja.edu.ng, saratha@usm.my,majidkhanmajaharali@usm.my, tanjinkee0909@student.usm.my, yapszeling@student.usm.my*

Received: 2 May 2023
Accepted: 15 June 2023

*Corresponding author