UNIVERSITI TEKNOLOGI MARA

MATHEMATICS LETTERS
https://sites.google.com/tmsk.uitm.edu.my/mathematicsletters

A Deterministic SIR–SI Dengue Model With Seasonal Transmission Intensity

[1]Harith Hafizi Hamdi, & [2,*]Nur `Izzati Hamdan
[1&2] Faculty of Computer and Mathematical Sciences, Universiti Teknologi MARA, 40450 Shah Alam, Selangor, Malaysia
[1]2023239998@student.uitm.edu.my
[*2] izzatihamdan@uitm.edu.my
*Corresponding author

Received: 5/10/2026 Revised: 24/10/2026 Accepted: 26/10/2026 Published: 31/10/2026

ABSTRACT

Dengue fever remains a major mosquito-borne disease in tropical countries, including Malaysia, where environmental variation can influence mosquito activity and transmission. This study develops a deterministic SIR–SI mathematical model with seasonal transmission intensity to describe dengue transmission between human and mosquito populations. Humans are divided into susceptible, infected, and recovered compartments, while mosquitoes are divided into susceptible and infected compartments. Seasonal variation is represented through a periodic transmission function, allowing the model to reflect changes in transmission intensity over time while retaining an analytically tractable structure. The model is analysed through the disease-free equilibrium, endemic equilibrium, basic reproduction number, and local stability using the next generation matrix and Jacobian approaches. Numerical simulations are conducted in MATLAB to examine the temporal behaviour of the five compartments and the effects of selected parameters. The simulations show that higher baseline transmission rates produce earlier and larger epidemic peaks, while stronger seasonal transmission intensity increases outbreak magnitude. Conversely, increasing the mosquito natural death rate reduces and delays the epidemic peak. These findings demonstrate that seasonality and mosquito survival are important determinants of dengue transmission dynamics and indicate that a relatively simple deterministic model can provide useful insight for dengue surveillance and vector-control planning.

Keywords: Dengue fever, deterministic model, SIR–SI, seasonal transmission, vector-borne disease

INTRODUCTION

Dengue fever is a major mosquito-borne viral disease in tropical and subtropical regions and continues to create substantial public-health challenges in Malaysia. The disease is transmitted through interactions between infected mosquitoes and susceptible humans, so its dynamics depend on both host and vector populations. Mathematical models are useful for representing these interactions because they provide a structured way to study disease persistence, epidemic thresholds and the consequences of changes in epidemiological parameters. Deterministic compartmental models are particularly useful when the objective is to obtain interpretable mathematical conditions for equilibrium and stability, because the same initial conditions and parameter values produce the same model trajectory (Brauer &

Castillo-Chávez, 2012). Host–vector models have therefore become an established approach for analysing dengue transmission and for examining the contribution of mosquito dynamics to epidemic behaviour (Andraud et al., 2012; Esteva & Vargas, 1998).

An important feature of dengue transmission is its temporal variation. Rainfall, temperature and other environmental conditions can alter mosquito abundance, survival, biting behaviour and the efficiency of virus transmission. Consequently, assuming a constant transmission rate throughout the year may not adequately represent the periodic behaviour of dengue outbreaks. Previous mathematical studies have incorporated seasonal variation into dengue transmission models and have shown that seasonal forcing can influence the timing, magnitude and persistence of outbreaks (Abidemi & Adekunle, 2022; Hamdan et al., 2020). Systematic reviews have also highlighted the wide range of deterministic structures used to represent dengue transmission and vector control, with increasing model complexity often introduced to capture additional biological or intervention mechanisms (Ogunlade et al., 2023). While additional compartments may improve biological detail, excessive complexity can make equilibrium and stability analysis more difficult to interpret.

The SIR–SI framework offers a useful balance between biological representation and mathematical tractability. In the human population, the SIR structure distinguishes susceptible, infected and recovered individuals, whereas the mosquito population is represented by an SI structure because infected mosquitoes remain infectious until death. This host–vector structure allows the transmission pathway between humans and mosquitoes to be represented explicitly while keeping the number of state variables manageable. Recent dengue models have increasingly incorporated nonlinear transmission, climate effects, control measures and optimal-control strategies, demonstrating the importance of parameter choice in determining long-term dynamics (Gu et al., 2023; Yoda et al., 2024). However, the present project focuses on a comparatively simple deterministic model in which seasonal transmission intensity is introduced through a periodic function, thereby retaining a structure that permits analytical equilibrium and stability analysis.

The research problem addressed in this study is the need for a mathematically manageable dengue model that can represent seasonal changes in transmission intensity without introducing an unnecessarily large number of compartments or intervention pathways. Accordingly, the study develops a deterministic SIR–SI model with seasonal transmission intensity, derives its disease-free and endemic equilibria, obtains the basic reproduction number using the next generation matrix method, and examines local stability through Jacobian analysis. Numerical simulations are then used to describe the temporal behaviour of the human and mosquito compartments and to examine how the baseline transmission rate, seasonal transmission intensity and mosquito natural death rate affect the infected human population. The study therefore links analytical threshold analysis with numerical investigation while maintaining the relatively simple model structure used in the original final-year project.

THE PROPOSED METHOD

Study Design and Data

The study uses a deterministic mathematical modelling approach supported by secondary dengue surveillance data. Weekly dengue case information was obtained from the Malaysia Open Data Portal as described in the final-year project, while biological and epidemiological parameter values were taken from published mathematical and epidemiological studies. The weekly data provide a basis for describing dengue incidence and its temporal variation, whereas the literature-derived parameters

provide the values required to formulate the host–vector transmission system. The project also describes parameter estimation using a least-squares approach to reduce the difference between reported dengue cases and model-simulated cases. MATLAB was used for numerical solution and simulation, while MAPLE was used during the mathematical analysis. The numerical experiments were designed to investigate both the general behaviour of the proposed system and the effect of selected parameters on the magnitude and timing of dengue outbreaks.

Model Formulation

Let $S_h(t)$, $I_h(t)$ and $R_h(t)$ denote the susceptible, infected and recovered human populations, respectively. Let $S_v(t)$ and $I_v(t)$ denote the susceptible and infected mosquito populations. The total human and mosquito populations are therefore represented by the sums of their corresponding compartments. New humans and mosquitoes enter the susceptible compartments at constant recruitment rates Λ_h and Π_v, respectively. Infected humans recover at rate α_h, while natural mortality occurs at rates μ_h for humans and μ_v for mosquitoes. Infected mosquitoes do not recover and remain infectious until natural death. The transmission from infected mosquitoes to susceptible humans is governed by β_h, while transmission from infected humans to susceptible mosquitoes is governed by β_v. Under these assumptions, the total populations are given by:

$$N_h(t) = S_h(t) + I_h(t) + R_h(t) \quad (1)$$

$$N_v(t) = S_v(t) + I_v(t) \quad (2)$$

The dengue transmission dynamics are represented by the following system of ordinary differential equations:

$$\frac{dS_h}{dt} = \Lambda_h - \beta_h S_h I_v - \mu_h S_h \quad (3)$$

$$\frac{dI_h}{dt} = \beta_h S_h I_v - (\alpha_h + \mu_h) I_h \quad (4)$$

$$\frac{dR_h}{dt} = \alpha_h I_h - \mu_h R_h \quad (5)$$

$$\frac{dS_v}{dt} = \Pi_v - \beta_v S_v I_h - \mu_v S_v \quad (6)$$

$$\frac{dI_v}{dt} = \beta_v S_v I_h - \mu_v I_v \quad (7)$$

To represent seasonal variation, the transmission coefficients are allowed to vary periodically with time. The seasonal transmission function used in the project is:

$$\beta_h(t) = \beta_v(t) = \frac{\beta_0}{1 + \alpha \sin\left(\frac{2\pi t}{T}\right)}, 0 < \alpha < 1, \quad (8)$$

Here, β_0 is the baseline transmission rate, α is the seasonal transmission intensity and T is the length of one seasonal cycle. For the numerical simulations, T is taken as 52 weeks to represent one annual cycle. The periodic function changes the effective transmission rate over time while retaining the five-compartment SIR–SI structure.

Table 1

Model Parameters and Initial Values

Symbol	Description	Value	Source
N_h	Total human population	56,000	Study dataset
$S_h(0)$	Initial susceptible humans	55,784	Study dataset
$I_h(0)$	Initial infected humans	216	Study dataset
$R_h(0)$	Initial recovered humans	0	Study setup
$S_v(0)$	Initial susceptible mosquitoes	168,800	Study setup
$I_v(0)$	Initial infected mosquitoes	0	Study setup
Λ_h	Human recruitment rate	15.10	Calculated in project
Π_v	Mosquito recruitment rate	16,800	Calculated in project
β_h	Mosquito-to-human transmission rate	0.75	Kong et al. (2018)
β_v	Human-to-mosquito transmission rate	0.375	Kong et al. (2018)
μ_h	Human natural death rate	0.0002967	DOSM (2024)
μ_v	Mosquito natural death rate	0.03	Kong et al. (2018)
α_h	Human recovery rate	0.3333	Hethcote (2000)
α	Seasonal transmission intensity	0.326	Naaly et al. (2024)
T	Seasonal period	52 weeks	One annual cycle

Equilibrium Analysis

An equilibrium point is a constant solution for which all derivatives in the model are zero. Two equilibrium states are considered. The disease-free equilibrium (DFE) represents the absence of dengue infection in both populations, while the endemic equilibrium (EE) represents persistence of infection in the human and mosquito populations. At the DFE, $I_h = 0$ and $I_v = 0$. Setting the derivatives to zero gives the equilibrium:

$$E_0 = \left(\frac{\Lambda_h}{\mu_h},\ 0,\ 0,\ \frac{\Pi_v}{\mu_v},\ 0\right) \tag{9}$$

The endemic equilibrium is obtained by setting all five derivatives to zero while imposing $I_h > 0$ and $I_v > 0$. The project expresses the positive equilibrium in terms of the state variables as $S_h = \Lambda_h/(\beta_h I_v + \mu_h)$, $I_h = \beta_h S_h I_v/(\alpha_h + \mu_h)$, $R_h = \alpha_h I_h/\mu_h$, $S_v = \Pi_v/(\beta_v I_h + \mu_v)$, and $I_v = \beta_v S_v I_h/\mu_v$. These relations describe the balance between recruitment, infection, recovery and natural mortality when dengue persists.

Basic Reproduction Number

The basic reproduction number R_0 is derived using the next generation matrix method and considers the infected compartments I_h and I_v. At the disease-free equilibrium, the new-infection matrix and transition matrix are constructed from the infected equations. The spectral radius of the resulting next generation matrix gives the threshold quantity:

$$R_0 = \sqrt{\frac{\Lambda_h \Pi_v \beta_h \beta_v}{(\alpha_h + \mu_h)\mu_h \mu_v^2}} \tag{10}$$

The threshold interpretation follows the standard epidemiological meaning: when $R_0 < 1$, each generation of infection produces fewer than one secondary infection on average and the disease-free

state is locally asymptotically stable; when $R_0 > 1$, the disease-free equilibrium is unstable and transmission can persist. This threshold provides the theoretical link between the model parameters and dengue persistence.

Stability Analysis

Local stability is examined by constructing the Jacobian matrix of the five-dimensional system and evaluating it at the relevant equilibrium. For the disease-free equilibrium, three eigenvalues are directly negative, while the remaining two are governed by the infection subsystem. The characteristic equation reduces to a quadratic whose constant term changes sign according to the value of R_0. Consequently, the disease-free equilibrium is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$. For the endemic equilibrium, the project evaluates the Jacobian at the positive equilibrium and uses the real parts of its eigenvalues to determine local stability. The endemic state is interpreted as stable when the relevant eigenvalues have negative real parts, whereas a positive real part indicates local instability.

Numerical Procedure

The model equations are solved numerically in MATLAB using the parameter values in Table 1. The main trajectory is examined over a 100-week simulation horizon so that the transient outbreak and subsequent approach towards a stable regime can be observed. One parameter is varied at a time in the sensitivity experiments while the remaining parameters are held constant. The baseline transmission rate β_0 is examined at 0.20, 0.36 and 0.50; seasonal transmission intensity α is examined at 0.10, 0.326 and 0.50; and mosquito natural death rate μ_v is examined at 1/14, 1/10 and 1/7. The numerical outputs are compared using the peak infected-human population and the approximate week at which that peak occurs. This procedure follows the structure of the original final-year project and focuses the analysis on the parameters that most directly influence dengue transmission intensity and mosquito survival.

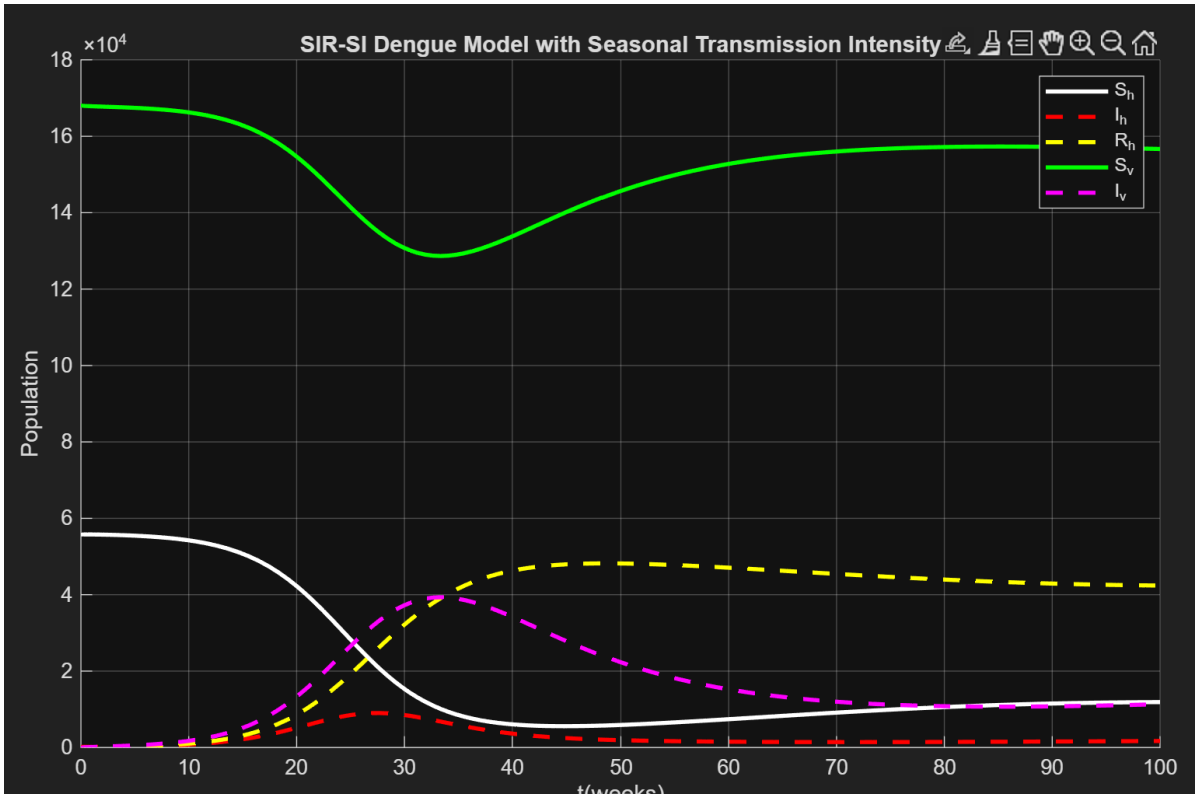
EVALUATION AND RESULTS

Numerical Dynamics of the Proposed Model

The numerical solution demonstrates a clear epidemic transition in both human and mosquito populations. At the beginning of the simulation, the susceptible human population decreases as susceptible individuals become infected through contact with infected mosquitoes. The infected human population rises rapidly and reaches an epidemic peak before declining as infected individuals recover and the susceptible pool is depleted. The recovered human population increases as infected individuals move into the recovered compartment. In the mosquito population, susceptible mosquitoes initially decrease as they acquire infection after feeding on infected humans, while the infected mosquito population increases and reaches its peak later than the infected human population. After the major outbreak phase, the five compartments move towards more stable values. The positive infected-mosquito component in the long-term trajectory indicates continued host–vector interaction under the parameter set used in the simulation.

Figure 1

Numerical solution of the proposed SIR–SI dengue model with seasonal transmission intensity



Human and Mosquito Population Dynamics

The human-population trajectory shows that S_h decreases from approximately 55,784 individuals and reaches its minimum around Week 40 before increasing towards a stable level. I_h rises rapidly and reaches its maximum at approximately Week 28, after which it decreases as recovery and depletion of susceptible individuals reduce transmission. R_h increases throughout the outbreak and approaches a positive equilibrium as recovered individuals accumulate. The mosquito trajectory shows a similar interaction but on a larger population scale. S_v begins at approximately 168,000 mosquitoes, falls to a minimum around Week 35 and then increases towards a stable value because recruitment continues while transmission pressure declines. I_v rises rapidly and peaks around Week 35 before decreasing towards an equilibrium. Together, these trajectories illustrate the two-way dependence of dengue transmission: infected mosquitoes drive human infection, while infected humans generate infection opportunities for susceptible mosquitoes.

Figure 2

Human population dynamics showing susceptible, infected and recovered compartments

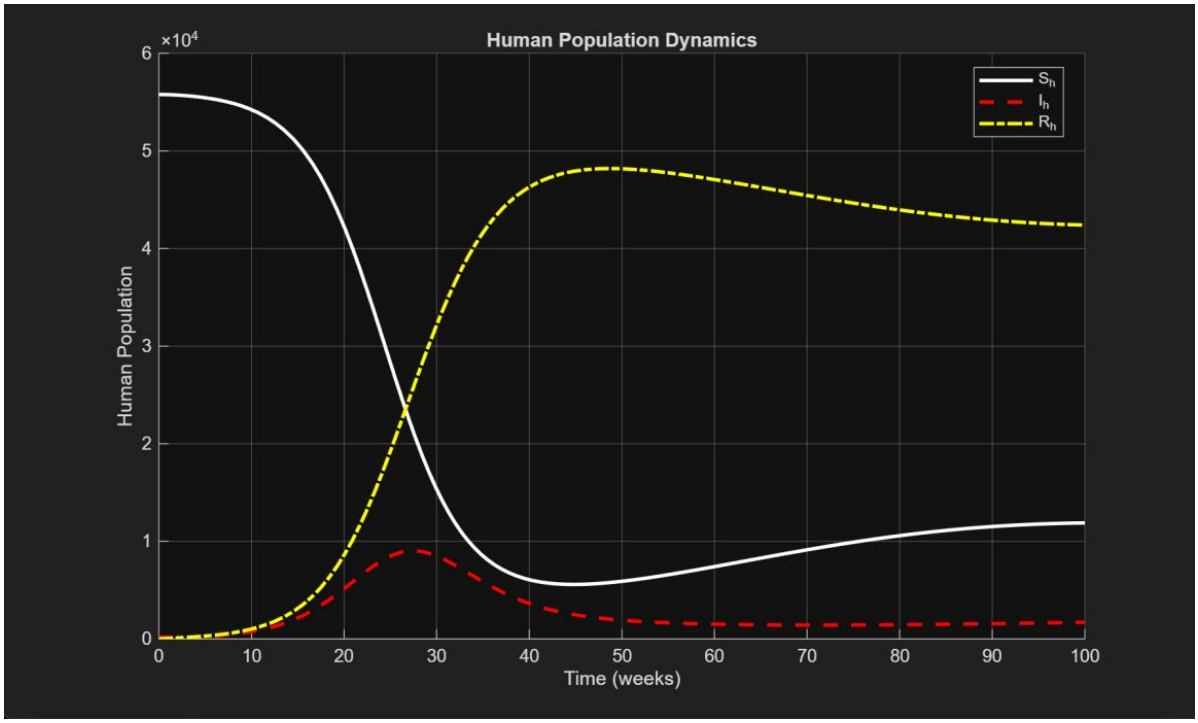
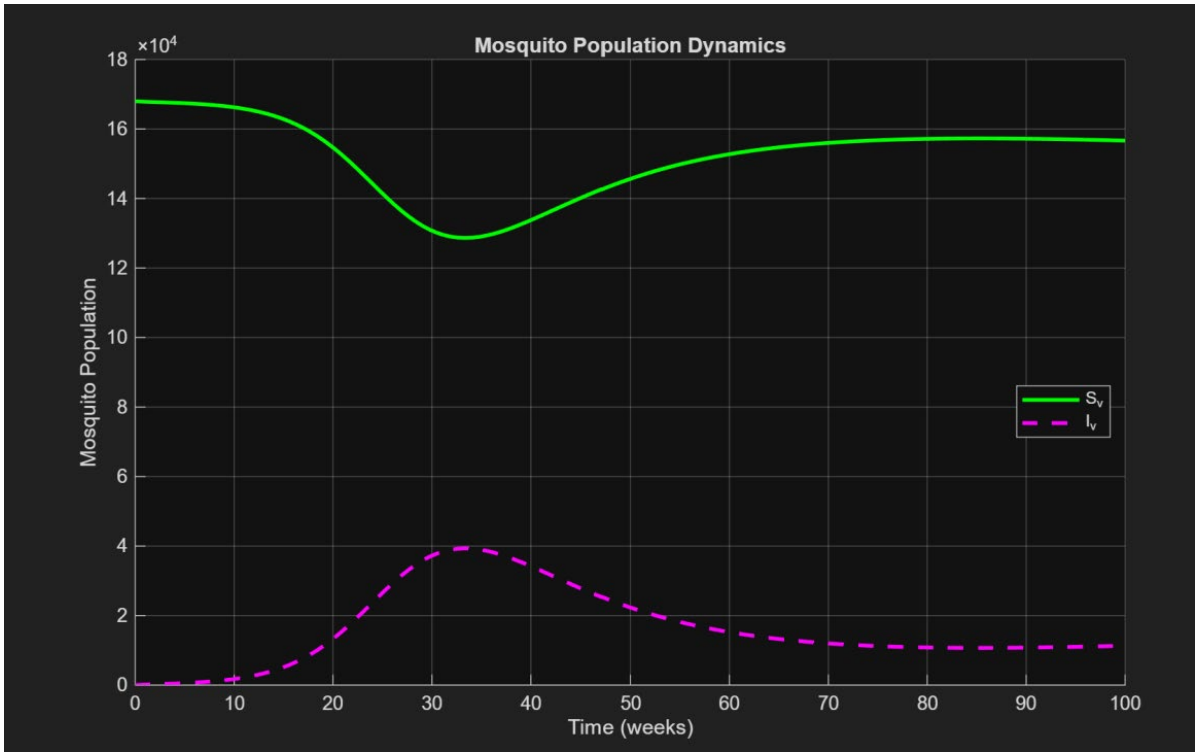


Figure 3

Mosquito population dynamics showing susceptible and infected compartments

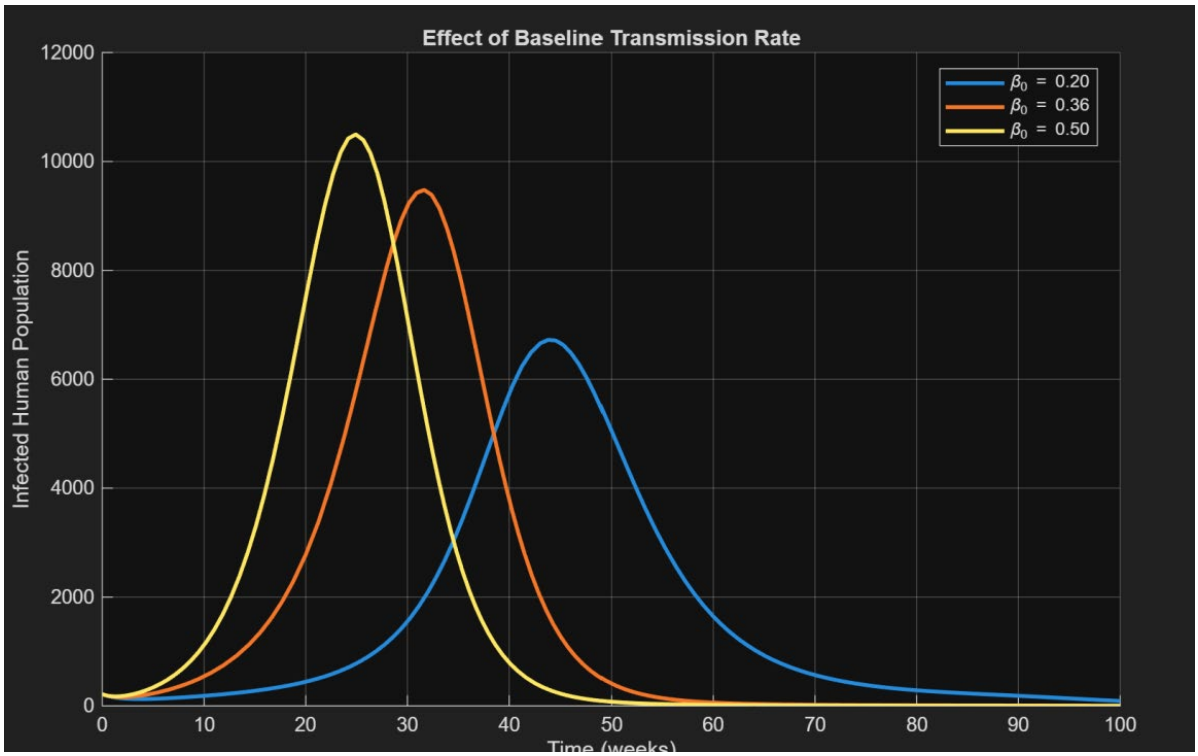


Effect of Baseline Transmission Rate

The baseline transmission rate has a strong effect on both the size and timing of the outbreak. When $\beta_0 = 0.20$, the infected human population reaches an approximate peak of 6,700 individuals around Week 44. For the intermediate value $\beta_0 = 0.36$, the peak increases to approximately 9,400 individuals around Week 32. When $\beta_0 = 0.50$, the peak rises further to approximately 10,500 individuals around Week 25. The direction of change is consistent across the simulations: increasing the baseline transmission rate produces a larger epidemic and causes the peak to occur earlier. This behaviour is expected because a larger transmission coefficient increases the rate at which susceptible humans acquire infection from infected mosquitoes. After the peak, the infected population declines as recovery and depletion of susceptible individuals reduce the number of effective transmission opportunities.

Figure 4

Effect of baseline transmission rate on the infected human population



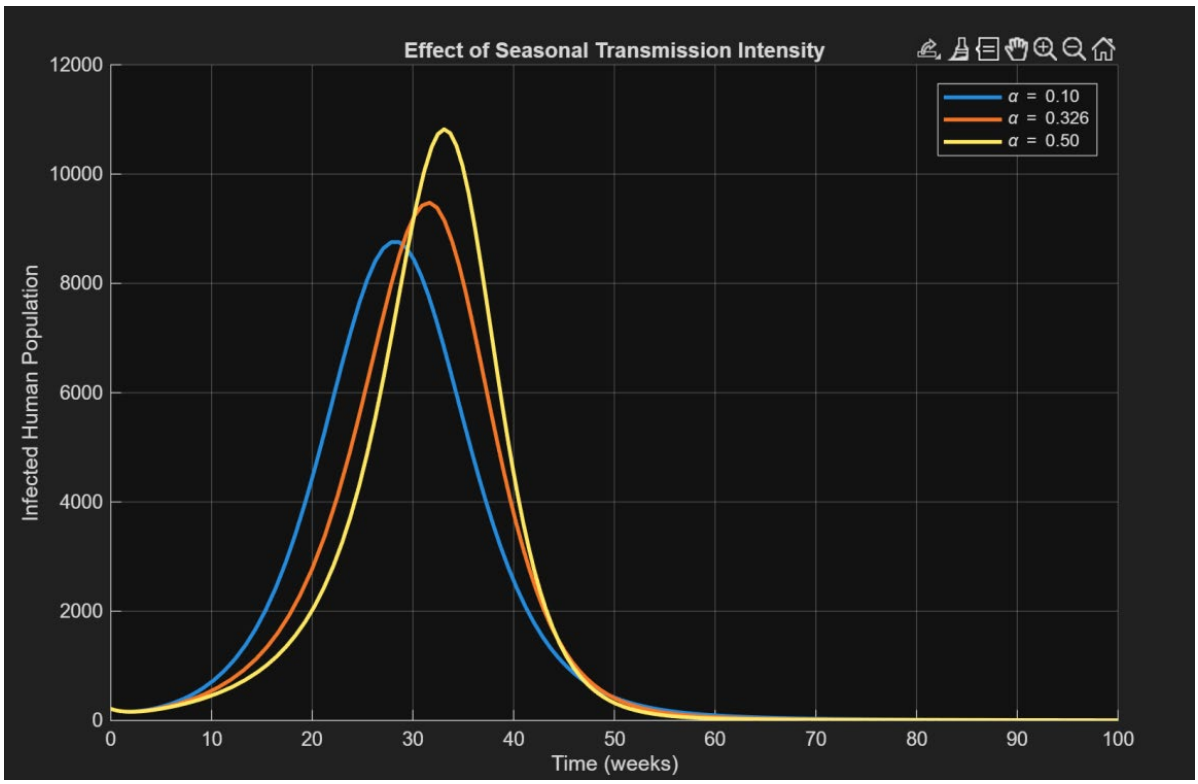
Effect of Seasonal Transmission Intensity

Seasonal transmission intensity also changes the magnitude of the simulated dengue outbreak. For $\alpha = 0.10$, the infected human population reaches an approximate peak of 8,700 individuals around Week 28. At $\alpha = 0.326$, the peak increases to approximately 9,400 individuals around Week 31. For $\alpha = 0.50$, the largest peak is approximately 10,800 individuals around Week 33. Thus, stronger seasonal forcing produces a larger outbreak, although the peak occurs slightly later in the scenarios reported by the project. The result indicates that periodic variation in transmission can materially change the severity of an outbreak even when the underlying compartmental structure remains unchanged. The decline after the peak occurs because infected individuals recover and the susceptible human population is reduced.

These results support the inclusion of a seasonal transmission term when the objective is to represent time-varying dengue transmission rather than a constant-rate epidemic.

Figure 5

Effect of seasonal transmission intensity on the infected human population



Effect of Mosquito Natural Death Rate

The mosquito natural death rate produces the opposite pattern. When $\mu_v = 1/14$, the infected human population reaches the highest reported peak of approximately 9,900 individuals around Week 30. At $\mu_v = 1/10$, the peak decreases to approximately 9,400 individuals around Week 32. For $\mu_v = 1/7$, the peak falls further to approximately 8,900 individuals around Week 34. Increasing mosquito mortality shortens the average lifetime of infected mosquitoes and therefore reduces the period during which they can transmit dengue to susceptible humans. The epidemic peak also occurs later as mosquito survival decreases. This sensitivity result provides a direct mathematical explanation for why interventions that reduce mosquito survival can weaken transmission. Within the assumptions of the model, the parameter therefore represents an important control-related mechanism because it affects both the magnitude and timing of the human epidemic.

Figure 6

Effect of mosquito natural death rate on the infected human population

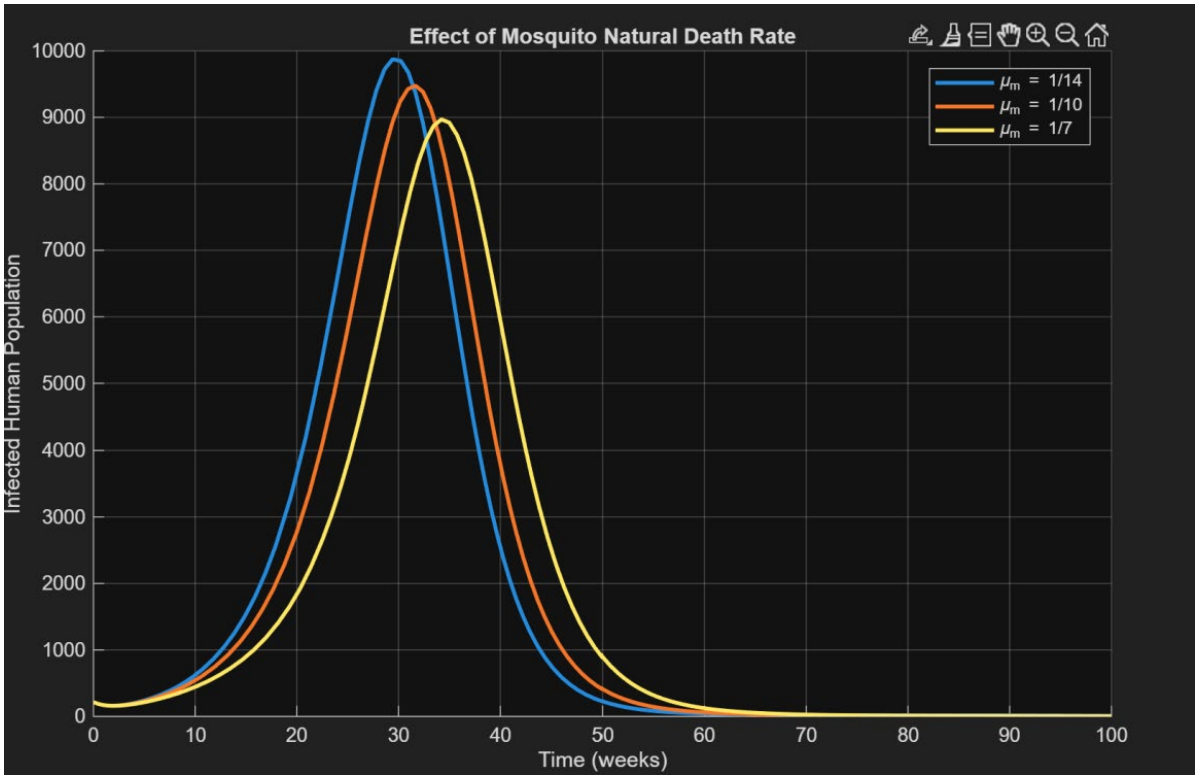


Table 2

Reported Peak Infected-Human Population Under Parameter Scenarios

Scenario	Approx. peak I_h	Peak week	Interpretation
$\beta_0 = 0.20$	6,700	44	Lowest transmission scenario
$\beta_0 = 0.36$	9,400	32	Moderate transmission scenario
$\beta_0 = 0.50$	10,500	25	Highest transmission scenario
$\alpha = 0.10$	8,700	28	Low seasonal intensity
$\alpha = 0.326$	9,400	31	Reference seasonal intensity
$\alpha = 0.50$	10,800	33	High seasonal intensity
$\mu_v = 1/14$	9,900	30	Lowest mosquito death rate
$\mu_v = 1/10$	9,400	32	Reference mosquito death rate
$\mu_v = 1/7$	8,900	34	Highest mosquito death rate

DISCUSSION

The numerical results show that the proposed deterministic SIR–SI structure captures the expected feedback between human and mosquito infection. An increase in baseline transmission produces a faster and larger outbreak, while stronger seasonal intensity increases the maximum infected-human population. These two parameters influence the force of infection directly through the time-varying transmission coefficient and therefore have a strong effect on epidemic severity. By contrast, increasing

mosquito natural mortality suppresses transmission because infected mosquitoes have less time to contribute to subsequent human infections. The direction of these effects is consistent with the broader mathematical-dengue literature, in which transmission parameters, climatic variation and vector dynamics are repeatedly identified as important determinants of disease persistence and outbreak intensity (Abidemi & Adekunle, 2022; Hamdan et al., 2020; Ogunlade et al., 2023). The model therefore provides a useful interpretable framework for examining how changes in transmission intensity and mosquito survival can alter dengue dynamics.

A key strength of the proposed approach is its balance between simplicity and seasonal realism. The model has only five epidemiological compartments, which keeps the equilibrium and stability analysis manageable, while the periodic transmission function allows transmission intensity to vary through time. This is useful because more detailed models can incorporate additional exposed classes, multiple intervention pathways or optimal-control variables, but those extensions also increase the number of parameters and mathematical relationships that must be estimated and interpreted (Gu et al., 2023; Yoda et al., 2024). The present results also agree qualitatively with the comparison discussed in the final-year project, where the susceptible human population declines during the outbreak, the infected human population rises to a peak and then declines, and the recovered population increases towards a steady state. Thus, the model retains the core epidemic behaviour expected from deterministic dengue systems while explicitly representing seasonal transmission intensity.

The results should nevertheless be interpreted within the model assumptions. Seasonality is represented by a mathematical periodic function rather than by directly modelling rainfall, temperature and humidity, so the model does not identify which environmental variable causes a particular change in transmission. The mosquito population is also represented by only susceptible and infected compartments, without an exposed stage, age structure or explicit incubation period. Consequently, the model is more suitable as an analytical framework for understanding transmission mechanisms than as a fully calibrated operational forecasting system. The parameter values are also partly literature-derived, and the final-year project identifies parameter estimation and sensitivity or uncertainty analysis as areas for future development. These limitations do not invalidate the qualitative sensitivity findings, but they restrict the extent to which the simulated trajectories should be interpreted as direct predictions of future Malaysian dengue cases.

CONCLUSION

This study presented a deterministic SIR–SI mathematical model with seasonal transmission intensity for describing dengue transmission between human and mosquito populations. The model divides humans into susceptible, infected and recovered compartments and mosquitoes into susceptible and infected compartments, with recruitment, infection, recovery and natural mortality represented through a system of ordinary differential equations. A periodic transmission function was incorporated to represent seasonal changes in transmission intensity while retaining an analytically tractable model structure. The disease-free equilibrium, endemic equilibrium and basic reproduction number were derived, and local stability was examined using the Jacobian framework. Numerical simulations further demonstrated the temporal interaction between human and mosquito infection and showed that the selected parameters can substantially alter the epidemic trajectory.

The sensitivity analysis produced three main conclusions. First, increasing the baseline transmission rate increased the epidemic peak and caused the peak to occur earlier. Second, increasing seasonal

transmission intensity increased the magnitude of the outbreak, confirming that seasonal variation can materially shape dengue dynamics. Third, increasing the mosquito natural death rate reduced and delayed the epidemic peak, highlighting mosquito survival as an important determinant of transmission. Overall, the proposed model provides a relatively simple mathematical framework for studying dengue transmission under seasonal conditions. Future work should extend the model by incorporating exposed compartments, climate variables such as rainfall and temperature, data-driven parameter estimation, and formal sensitivity and uncertainty analysis. Such extensions could improve the model's biological realism and its usefulness for dengue prediction and vector-control planning.

ACKNOWLEDGEMENT

The authors are very grateful for the support from the Faculty of Computer and Mathematical Sciences, Universiti Teknologi MARA Shah Alam, Selangor.

CONFLICT OF INTEREST

The author has no conflicts of interest to declare.

FUNDING

This research received no specific grant from any funding agency in the public, commercial or not-for-profit sectors.

REFERENCES

Abidemi, A., & Adekunle, A. I. (2022). Mathematical modelling and analysis of dengue fever transmission dynamics with seasonal variation. *Mathematical Biosciences and Engineering*, 19(6), 5908–5935.

Andraud, M., Hens, N., Marais, C., & Beutels, P. (2012). Dynamic epidemiological models for dengue transmission: A systematic review of structural approaches. *PLoS ONE*, 7(11), e49085.

Brauer, F., & Castillo-Chávez, C. (2012). Mathematical models in population biology and epidemiology (2nd ed.). *Springer.* https://doi.org/10.1007/978-1-4614-1686-9

Department of Statistics Malaysia. (2024). Abridged life tables Malaysia, 2024. Department of Statistics Malaysia.

Esteva, L., & Vargas, C. (1998). Analysis of a dengue disease transmission model. *Mathematical Biosciences*, 150(2), 131–151.

Gu, Y., Khan, M., Zarin, R., Khan, A., Yusuf, A., & Humphries, U. W. (2023). Mathematical analysis of a new nonlinear dengue epidemic model via deterministic and fractional approach. *Alexandria Engineering Journal*, 67, 1–21. https://doi.org/10.1016/j.aej.2022.10.057

Hamdan, N., Abdullah, F. A., & Mohd, M. H. (2020). Mathematical modelling of dengue transmission dynamics with seasonal variation. *Journal of Applied Mathematics*, 2020, 1–15.

Hethcote, H. W. (2000). The mathematics of infectious diseases. SIAM Review, 42(4), 599–653. https://doi.org/10.1137/S0036144500371907

Kafle, J., Bayalkoti, P., & Phaijoo, G. R. (2023). Mathematical study of effect of temperature on transmission dynamics of dengue disease. *Journal of Nepal Mathematical Society*, 6(1). https://doi.org/10.3126/jnms.v6i1.57476

Kong, L., Wang, J., Li, Z., Lai, S., Liu, Q., Wu, H., & Yang, W. (2018). Modeling the heterogeneity of dengue transmission in a city. *International Journal of Environmental Research and Public Health*, 15(6), 1128. https://doi.org/10.3390/ijerph15061128

Naaly, B. Z., Marijani, T., Isdory, A., & Ndendya, J. Z. (2024). Mathematical modeling of the effects of vector control, treatment and mass awareness on the transmission dynamics of dengue fever. *Computer Methods and Programs in Biomedicine Update*.

Ogunlade, S. T., Meehan, M. T., Adekunle, A. I., & McBryde, E. S. (2023). A systematic review of mathematical models of dengue transmission and vector control: 2010–2020. *Viruses*, 15(1), 254. https://doi.org/10.3390/v15010254

Yoda, Y., Ouedraogo, H., Ouedraogo, D., & Guiro, A. (2024). Mathematical analysis and optimal control of dengue fever epidemic model. *Advances in Continuous and Discrete Models*, 2024, 11. https://doi.org/10.1186/s13662-024-03805-8

This is an open access article under the CC BY-SA license (https://creativecommons.org/licenses/by-sa/4.0/).