

INVESTIGATION ON THE SPREAD OF DENGUE IN MALAYSIA BY USING SEIR MODEL

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Abstract

Dengue fever remains a major public health concern in Malaysia, driven by Aedes mosquitoes, climate change, urbanization, and population movement. This study uses the SEIR (Susceptible–Exposed–Infected–Recovered) model to understand dengue transmission, calculate the basic reproduction number (R_0), and analyze the stability of equilibrium points. Simulations over one, three, and six years reveal both short- and long-term transmission dynamics. Eigenvalue analysis shows that the disease-free equilibrium is unstable, indicating continued disease spread without effective intervention. Although the model includes births and deaths, it lacks key real-world factors such as vaccination, reinfection from waning immunity, and dengue-related deaths. The study highlights the urgent need for public health measures and suggests that incorporating these additional factors would enhance the model's predictive accuracy and usefulness for disease control strategies.

Keywords: Dengue transmission, SEIR model, Basic reproduction number (R_0), Epidemic modelling, Disease-free equilibrium

1. Introduction

This study aims to investigate the spread of dengue in Malaysia using the SEIR (Susceptible–Exposed–Infected–Recovered) model. The key objectives are to formulate the SEIR model, calculate the basic reproduction number, R_0 and analyze the stability of its equilibrium points. The model uses data from January 2019 to August 2024, sourced from Asia Dengue Voice and Action (ADVA). It focuses on dengue dynamics by considering transmission rate, disease rate, and recovery rates, tailored to Malaysia's specific environmental and socio-economic conditions. The scope is limited to Malaysia, enhancing the relevance of the findings. However, limitations such as inconsistent data and simplified model assumptions may affect precision. Despite this, the model offers valuable insight into dengue transmission and control.

2. Methodology

This study applies the SEIR (Susceptible–Exposed–Infected–Recovered) model to examine the dynamics of dengue transmission in Malaysia. The population is divided into four compartments, susceptible, exposed, infected, and recovered using a system of differential equations to describe disease progression over time (Ramírez-Soto et al., 2023). Key parameters include transmission rate (β), disease rate (ϵ), recovery rate (γ), and natural birth and death rate (μ), which influence the transitions between compartments (Mahto & Dey, 2018). The basic reproduction number R_0 is calculated using the Next Generation Matrix method. Python software is utilized to simulate model dynamics and compute eigenvalues from the Jacobian matrix, allowing for the analysis of disease-free and endemic equilibrium stability (Maulana & Ramdani, 2024).

3. Results / Findings

The results and findings of this study were obtained by simulating dengue transmission in Malaysia using the SEIR model, implemented in Python. Simulations were conducted for 1 year, 3 years, and 6-year periods using initial conditions and parameter values from sources such as Osman et al. (2017)

and S. & Noorani (2012). Across all timeframes, the simulations demonstrated typical epidemic behavior, the susceptible population declined sharply, exposed and infected groups peaked early, and the recovered group increased and stabilized over time. Most transmission occurred in the first 60 to 100 days.

The basic reproduction number, R_0 was consistently greater than 1, indicating an ongoing risk of transmission. Eigenvalue analysis of the Jacobian matrix (Maulana & Ramdani, 2024) confirmed instability in the disease-free equilibrium across all periods, suggesting endemic persistence of dengue in Malaysia and the need for continuous public health interventions.

4. Novelty of Research / Product / Project

The findings indicate that while dengue remains present in Malaysia and $R_0 > 1$, the basic SEIR model lacks the complexity to fully reflect real-world dynamics. Future studies should enhance the model by adding compartments for vaccinated individuals, temporary immunity, and dengue-related deaths. These additions are crucial, especially as Malaysia intensifies vector control and progresses in dengue vaccine development. Given the potential for reinfection with different virus serotypes, model flexibility is essential. Incorporating these elements will improve the model's realism, enable more accurate predictions, and support more effective strategies for dengue prevention and control.

5. Conclusion or Future Work

This study effectively used the SEIR model to analyze dengue spread in Malaysia, showing consistent outbreaks over 1 year, 3 years and 6-year periods. Results highlight that $R_0 > 1$, indicating endemic status. Continued mosquito control, public health strategies, and vaccination are essential to manage and reduce future dengue outbreaks.

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