

ANALYZING INFLUENZA A SPREAD USING THE SEIR EPIDEMIOLOGICAL MODEL

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Abstract

Influenza A remains a significant public health issue globally, with seasonal outbreaks causing widespread morbidity and mortality. In Malaysia, influenza A transmission patterns are influenced by various factors, including population density, urbanization, and climate. This study uses the SEIR (Susceptible–Exposed–Infected–Recovered) model to analyze the spread of Influenza A, calculate the basic reproduction number (R_0), and assess the stability of disease equilibrium points. Simulations over one, two, and three years reveal the disease's transmission dynamics, with eigenvalue analysis indicating that the disease-free equilibrium remains unstable, suggesting potential for continued spread without intervention. Although the model considers births and deaths, it does not account for vaccination, reinfection due to waning immunity, or mortality, which limits the model's real-world applicability. The study emphasizes the need for effective public health interventions and highlights areas for future research to improve model predictions.

Keywords: *Influenza A, SEIR model, Basic reproduction number (R_0), Disease transmission, Epidemic modeling*

1. Introduction

This study aims to investigate the spread of Influenza A 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 utilizes data from the Ministry of Health Malaysia (MOH) spanning from January 2022 to December 2024. The focus is on the transmission dynamics of Influenza A, incorporating transmission rates, disease progression, and recovery rates, while considering Malaysia's unique environmental, demographic, and socio-economic conditions. The scope of this study is confined to Malaysia, which enhances the relevance and applicability of the findings to local public health planning. However, the study is subject to limitations, such as potential data inconsistencies and simplified assumptions in the model. Despite these limitations, the study provides valuable insights into Influenza A transmission patterns and contributes to epidemic preparedness and response.

2. Methodology

This study applies the SEIR (Susceptible–Exposed–Infected–Recovered) model to examine the dynamics of Influenza A transmission in Malaysia. The population is divided into four compartments: susceptible (S), exposed (E), infected (I), and recovered (R). The transitions between compartments are described by a system of differential equations, with key parameters including the transmission rate (β), disease rate (σ), recovery rate (γ), and natural birth and death rate (μ) (Leonenko & Ivanov, 2016). The basic reproduction number (R_0) is calculated using the Next Generation Matrix method (Saito et al., 2013). Python software is used to simulate the model's dynamics and compute eigenvalues from the Jacobian matrix, allowing for the analysis of stability at both disease-free and endemic equilibrium points (Maulana & Ramdani, 2024).

3. Results / Findings

The results and findings of this study were obtained by simulating Influenza A transmission in Malaysia using the SEIR model, implemented in Python. Simulations were conducted for one-year, two-year, and three-year periods using initial conditions and parameter values sourced from the Ministry of Health Malaysia (MOH) and previous studies (Leonenko & Ivanov, 2016; Saito et al., 2013). Across all timeframes, the simulations displayed typical epidemic behavior: the susceptible population declined sharply, the exposed and infected groups peaked early, and the recovered group gradually increased and stabilized over time. Most transmission occurred within the first 60 to 100 days. The basic reproduction number, R_0 , was consistently less than 1, indicating a low risk of widespread transmission. Eigenvalue analysis of the Jacobian matrix (Maulana & Ramdani, 2024) confirmed instability in the disease-free equilibrium across all periods, suggesting the potential for endemic persistence of Influenza A in Malaysia and the need for ongoing public health interventions.

4. Novelty of Research / Product / Project

The findings indicate that while Influenza A remains a potential threat in Malaysia, with an R_0 consistently less than 1, the basic SEIR model still lacks the complexity to fully capture real-world dynamics. Future studies should enhance the model by adding compartments for vaccinated individuals, considering waning immunity, and including mortality due to influenza. These additions are crucial, especially as Malaysia continues its vaccination efforts and focuses on improving public health strategies. Given the possibility of reinfection and the emergence of new strains, model flexibility is essential. Incorporating these elements will improve the model's realism, enable more accurate predictions, and provide more effective strategies for Influenza A prevention and control.

5. Conclusion or Future Work

This study used the SEIR model to analyze Influenza A spread in Malaysia, showing low transmission risk ($R_0 < 1$). Future work should improve the model by incorporating vaccination, immunity, and mortality. Continued public health efforts are crucial to managing and reducing Influenza A outbreaks in the future.

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