



Faculty of Computer Science and Information Technology

**Individual-based Modelling on Vector Heterogeneity of Leptospirosis
Transmission in Sarawak**

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**Master of Science
2023**

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Individual-based Modelling on Vector Heterogeneity of Leptospirosis
Transmission in Sarawak

Chong Jia Wen

A thesis submitted

In fulfillment of the requirements for the degree of Master of Science

(Computational Modelling)

Faculty of Computer Science and Information Technology

UNIVERSITI MALAYSIA SARAWAK

2023

DECLARATION

I declare that the work in this thesis was carried out in accordance with the regulations of Universiti Malaysia Sarawak. Except where due acknowledgements have been made, the work is that of the author alone. The thesis has not been accepted for any degree and is not concurrently submitted in candidature of any other degree.



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ABSTRACT

Leptospirosis is a zoonotic disease prevalent in various places, particularly the tropical and subtropical regions. The infectious disease is endemic across Malaysia, especially in Sarawak. In recent years, the threats of leptospirosis continue to grow as the number of confirmed cases in Sarawak has risen since 2010. Compartmental models are popular in disease modelling. However, the models are not suitable if heterogeneity in the population is taken into account. For zoonotic or vector-borne diseases, the heterogeneity of the hosts or vectors can significantly influence disease transmission. Hence, this research proposes an individual-based model or IBM to model the leptospirosis spread as it has the ability to capture the heterogeneity of the population, such as vectors' active period and movement range. From the sensitivity analyses, the higher vector birth rate and higher transmission rate from susceptible to infected vectors generate more infected humans and vectors. The results also show that the active period durations of vectors do not influence leptospirosis transmission. However, a wider movement range of vectors causes more people and vectors to be infected. In the model validation with the actual prevalence data of leptospirosis in 2017, the coefficient of determination of more than 90% and normally distributed residuals for all three outbreaks indicate that IBM can model the leptospirosis spread in Sarawak. The actual prevalence data show three leptospirosis outbreaks occur within a year. By finding the correlation matrices, Pearson's correlations deduce that temperature rise and precipitation influence disease transmission. Additionally, other factors such as misdiagnosis of leptospirosis as well as occupational and recreational exposures affect the infection.

Keywords: Individual-based Model, leptospirosis, vector behaviour, active period, movement range

***Pemodelan Berasaskan Individu pada Kepelbagaian Vektor bagi Penularan
Leptospirosis di Sarawak***

ABSTRAK

Leptospirosis merupakan suatu penyakit zoonosis yang berleluasa khususnya di kawasan beriklim tropika dan sutropika. Penyakit berjangkit ini adalah endemik di Malaysia, terutamanya di Sarawak. Pada kebelakangan ini, ancaman leptospirosis didapati semakin meningkat dengan lonjakan kes di Sarawak sejak tahun 2010. Model kompartemen digunakan ramai dalam pemodelan penyakit. Tetapi, model kompartemen adalah tidak sesuai jika kepelbagaian populasi diambil kira. Bagi penyakit zoonotik atau penyakit bawaan vektor, kepelbagaian hos atau vektor dapat mempengaruhi wabak penyakit dengan ketara. Justeru, kajian ini menawarkan sebuah model berasaskan individu bagi penularan leptospirosis oleh sebab ia mempunyai kemampuan untuk mengambil kira kepelbagaian populasi seperti tempoh aktif vektor dan jarak pergerakan vektor. Melalui analisis sensitiviti, kadar kelahiran vektor dan kadar penularan daripada vektor yang mudah terdedah ke vektor yang berjangkit yang tinggi mengakibatkan lebih ramai orang dan banyak vektor dijangkiti leptospirosis. Dari segi sifat vektor, tempoh masa aktif vektor tidak mempengaruhi penyebaran leptospirosis. Walau bagaimanapun, jarak pergerakan vektor yang luas akan menyebabkan ramai individu dan banyak vektor dijangkiti penyakit. Dalam proses pengesahan model dengan perbandingan data pada tahun 2017, pekali penentu yang lebih 90% dan sisa yang bertaburan normal bagi ketiga-tiga wabak menunjukkan model berasaskan individu dapat meramalkan penularan wabak leptospirosis di Sarawak. Data tersebut juga menunjukkan terdapat tiga gelombang leptospirosis dalam tempoh setahun. Melalui matriks korelasi berserta kolerasi Pearson, peningkatan suhu dan taburan hujan merupakan antara faktor yang mempengaruhi penularan penyakit tersebut. Tambahan pula,

faktor lain seperti kesalahan diagnosis dan pendedahan dari segi pekerjaan serta aktiviti rekreasi juga menjejaskan penularan wabak.

Kata kunci: *Model berasaskan individu, leptospirosis, sifat vektor, tempoh aktif, jarak pergerakan*

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LIST OF ABBREVIATIONS

ABM	Agent-based Model
COVID-19	Coronavirus Disease 2019
CSV	Comma Separated Values
DOSM	Department of Statistics of Malaysia
IBM	Individual-based Model
MAE	Mean Absolute Error
MAPE	Mean Absolute Percentage Error
MCO	Movement Control Order
MOH	Ministry of Health
MLE	Maximum Likelihood Estimate
MSE	Mean Squared Error
MSEIR	Maternally Derived Immunity - Susceptible - Exposed - Infected – Recovered
MSEIRS	Maternally Derived Immunity - Susceptible - Exposed - Infected - Recovered – Susceptible
OLS	Ordinary Least Squares
RMSE	Root Mean Squared Error
SEI	Susceptible - Exposed - Infected
SEIR	Susceptible - Exposed - Infected - Recovered
SEIRS	Susceptible - Exposed - Infected - Recovered - Susceptible
SEIS	Susceptible - Exposed - Infected - Susceptible
SI	Susceptible - Infected
SIR	Susceptible - Infected - Recovered

SIRS	Susceptible - Infected - Recovered - Susceptible
SIRS-SI	Susceptible - Infected - Recovered - Susceptible - Susceptible - Infected
SIS	Susceptible - Infected - Susceptible
SMAPE	Symmetric Mean Absolute Percentage Error
UI	User Interface
WHO	World Health Organisation

CHAPTER 1

INTRODUCTION

1.1 Research Background

Malaysia is a country blessed with amusing diversity of natures and cultures. In East Malaysia, Sarawak or the ‘land of hornbill’, is a place steeped in rich natures and indigenous cultures. Although the tropical climate contributes to biodiversity in Sarawak, the weather conditions also cause some negative consequences simultaneously. For instance, the spreading of infectious disease by pathogenic microorganisms or pathogens. From a medical perspective, there are many ways for diseases spreading such as contact transmission (direct contact or indirect contact), droplet transmission (via coughing or sneezing), and airborne transmission (via inhalation of the air) (Stilianakis & Drossinos, 2010). As Sarawak is large in geographical area, it requires extra caution when monitoring the conditions of diseases spreading in the region.

Infectious diseases bring numerous devastating impacts to public health and economic growth across various countries. In 2013, China experienced an outbreak of H7N9 avian influenza that caused more than 680 confirmed cases including 275 deaths (Qiu et al., 2018). At the same time, the poultry industry of China underwent more than RMB 40 million in economic loss (Qiu et al., 2018). In the context of Malaysia, from September 1998 to July 1999, the Nipah virus outbreak occurred throughout the country. The disease had caused acute encephalitis with more than 260 notified cases and nearly 110 deaths (Looi & Chua, 2007). The infection brought deep impacts on the hog-raising industry and resulted in more than RM 500 million in economic loss to Malaysia (Hosono et al., 2006).

Apart from the Nipah virus outbreak, Malaysia also suffered from Coronavirus Disease 2019 or COVID-19. Compared to the Nipah virus, the impacts of COVID-19 were destructive to the economy and societies of the country. Malaysia lost RM2.4 billion a day during the Movement Control Order (MCO) period (Hashim et al., 2021). MCO was an enforced strategy of the government to control the COVID-19 outbreaks in the country and close most of the economic sectors same time (Hashim et al., 2021). Besides impacting the economy, COVID-19 caused many issues in societies. For example, the increase of negative emotions such as stress and anxiety among people, and job or domestic violence including suicide (Yong & Sia, 2021).

Disease control and prevention are essential as infectious diseases bring devastating and chaotic impacts to societies. One of the measures is through modelling as it is a technique of transforming a situation into a model for problem-solving and future prediction. The implementation of modelling in infectious disease studies allows the researchers to understand the epidemiology of the infections. Furthermore, the obtained results can predict the possible outcomes of disease transmission. As a result, modelling possesses a significant role in public health and epidemiology as model formulation covers the planning and implementation of the public health response to overcome the crisis brought by infectious disease (Lessler & Cummings, 2016).

In Sarawak, the local authorities and the public are aware of the disease outbreaks in recent years such as leptospirosis outbreaks. Leptospirosis is a widespread zoonosis caused by the pathogenic *Leptospira* (Levett, 2001). This infectious disease is endemic in tropics such as East Sub-Saharan Africa, Southeast Asia, the Caribbean and Oceania (Rajapakse, 2022). Leptospirosis is curable; however, it is also an underreported and underdiagnosed

disease (Sembiring, 2018). The disease is hard to diagnose as the infected people will show symptoms identical to other diseases such as dengue fever and influenza (Biscornet et al., 2020). Therefore, leptospirosis is hard to be detected unless the individual has gone through clinical laboratory examinations. The following Chapter 2 will discuss the historical aspect, transmission route, clinical features and threats of leptospirosis in Sarawak in more detail.

1.2 Research Motivation

Leptospirosis endangers people throughout Malaysia. The most critical situation was 1,976 cases in 2011 skyrocketed to 8,291 cases in 2015 (Malaysia Ministry of Health [MOH], 2018). A similar occasion also occurred in Sarawak where 157 cases were reported in 2011 and increased to 844 cases in 2016 (Malaysia MOH, 2018). In the preliminary work of Chong et al. (2022), the Susceptible-Infected-Recovered-Susceptible-Infected (SIRS-SI) model is not suitable to model the spread of the disease in Sarawak as the result of the second wave of the outbreak does not fit well with the real prevalence data. The details will be further explained in Section 2.9. Therefore, the considerations of the other models such as the individual-based model (IBM) and other factors that might affect the disease transmission to increase the validity between the simulated results and real prevalence data become another motivation for this research.

1.3 Problem Statement

The compartmental models such as SIR, SIRS, SI and SIRS-SI (Chong et al., 2022) assume homogeneity exists in a population whereby each individual shares the same characteristics and behaviours. However, the compartmental models are not adequate for the system or model that considers the individuals who possess significant differences (Black & McKane, 2012). Each individual possesses unique attributes that change with time such as