PREDICTING DENGUE FEVER IN PENINSULAR MALAYSIA USING GEOGRAPHIC INFORMATION SYSTEM AND ATTENTION-BASED LONG SHORT-TERM MEMORY

By

DALLOO MOKHALAD AZZAT MAJEED

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the Requirements for the Degree of Doctor of Philosophy

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DEDICATION

My family and all of my close friends are the recipients of my dissertation effort. I would want to express my deepest thanks to my lovely parents, Associate Professor Azzat Majeed and Mom, whose words of support and encouragement to be persistent continue to reverberate in my ears. My brothers and sisters are incredibly significant to me since they have never left my side of the bed.

At the same time, I would want to dedicate my dissertation to all of my friends who have been there for me during the whole process. I am going to be eternally grateful to them for all they have done, my colleagues who have assisted me in developing my technological abilities, and Associate Professor Dr. Helmi Shafri for the several hours that she has spent supervising me on this project. Additionally, I would like to express my gratitude to the two members of my supervising committee, Associate Professor Dr. Aimrun Wayayok and Associate Professor Dr. Zed Zulkafli, for their assistance in enhancing the overall quality of my thesis.

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Chairman : Associate Professor Helmi Zulhaidi bin Mohd Shafri, PhD
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Dengue fever is a rapidly growing public health concern, particularly in tropical and subtropical regions such as Malaysia. This thesis proposes the use of recurrent neural networks (RNNs) with integrated spatial-temporal attention for dengue fever prediction. The research empirically uses the weekly numbers of dengue cases from five Malaysian states and a set of covariates which are the climate, land use, vegetation and GIS factors. The envisaged method is based on the long short-term memory (LSTM) models, and many attention mechanisms are considered to improve the efficiency of the system. The model efficiency is assessed by the root mean squared error (RMSE) parameter. The designed approach was contrasted to five reference models which are the Random Forest, Decision Tree, Support Vector Machine (SVM), Shallow Artificial Neural Network (ANN), and Deep ANN. In the first test, LSTM models with temporal attention were better than the benchmark ones. The A-LSTM model, which is the Attention LSTM, had the best performance, with the average RMSE of 3. 663. The Stacked Attention LSTM (SA-LSTM) was second in the

ranking and it had a RMSE of 3. 674. Also, both LSTM and Stacked LSTM (S-LSTM) models did almost the same, as their RMSEs were 4. 154 and 4. 133, respectively. The presented LSTM models with attention were the best among the models, hence, they outdid the benchmark models. The second experiment brought spatial attention into the picture and the model that was built using the Stacked LSTM with spatial attention (SSA-LSTM) was the one that showed the best results. It got an average RMSE 3.17, across all the lookback periods. The SSA-LSTM model in comparison with three benchmark models (SVM, DT, and ANN), the SSA-LSTM model shows a significantly lower average RMSE. Besides, the SSA-LSTM model was also tested in different states in Malaysia, and the RMSE values ranged from 2. 91 to 4. 55. The spatial attention models usually than the temporal attention ones beat the predictions of the cases of dengue. A third experiment showed that the spatial-temporal attention stacked LSTM (ST-SLSTM) model had the best performance out of all the models. It had the lowest average RMSE (2. 66), which shows that it was the most accurate in terms of the predictions. The ST-SLSTM model proved to be stable and had the capacity to be applied in different states and at different forecast horizons. Nevertheless, its complexity and computational demands were the main prohibitive factors. These research results give necessary information for the public health authorities in Malaysia and other countries that also have dengue fever issues. The LSTM models with the attention mechanisms are the basis of the proposed models that are more accurate and thus, the disease prevention and control strategies are developed.

Keywords: Dengue; LSTM; attention, deep learning; Malaysia

SDG: GOAL 3: Good Health and Well-Being, GOAL 15: life on Land

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

MERAMALKAN DEMAM DENGGI DI SEMENANJUNG MALAYSIA MENGGUNAKAN RANGKAIAN SARAF BERULANG DENGAN MEKANISME PERHATIAN

Oleh

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Kebimbangan kesihatan awam yang berkembang pesat adalah demam denggi, terutama di kawasan tropika dan subtropika seperti Malaysia. Tesis ini mencadangkan menggunakan rangkaian saraf berulang (RNN) dengan perhatian ruang-waktu bersatu untuk meramal demam denggi. Kajian ini menggunakan kes denggi Mingguan dari lima negeri Malaysia dan pelbagai kovariat termasuk iklim, penggunaan tanah, tumbuh-tumbuhan, dan faktor Sistem Maklumat geografi (GIS).

Dicadangkan untuk menggunakan model memori jangka pendek Panjang (LSTM) dan meneroka pelbagai mekanisme perhatian bagi meningkatkan prestasi. Model prestasi dinilai dengan menggunakan metrik ralat kuadrat minima purata (RMSE). Pendekatan yang dicadangkan dibandingkan dengan lima model penanda aras termasuk hutan rawak, Pokok Keputusan, mesin vektor sokongan (SVM), rangkaian saraf buatan cetek (ANN), dan Deep ANN.Dalam eksperimen pertama, model LSTM dengan perhatian temporal mengatasi model penanda aras. Model Attention LSTM (A-

LSTM) mencapai prestasi terbaik, dengan purata RMSE 3.663. LSTM perhatian yang disusun (SA-LSTM) berada di tempat kedua dengan RMSE 3.674. Kedua-dua model LSTM dan Stacked LSTM (S-LSTM) berprestasi hampir sama, dengan RMSEs masing-masing 4.154 dan 4.133. Model LSTM yang dicadangkan dengan perhatian mengatasi model penanda aras, mempamerkan keunggulan mereka.Eksperimen kedua memperkenalkan perhatian ruang, dan model LSTM yang disusun dengan perhatian ruang (SSA-LSTM) melakukan yang terbaik. Ia mencapai RMSE purata 3.17 di semua tempoh lookback. Apabila dibandingkan dengan tiga model penanda aras (SVM, DT, ANN), model SSA-LSTM menunjukkan RMSE purata yang jauh lebih rendah. Selain itu, model SSA-LSTM menunjukkan prestasi yang baik di negeri-negeri yang berbeza di Malaysia, dengan nilai RMSE antara 2.91 hingga 4.55. Model perhatian spasial umumnya mengatasi model perhatian temporal dalam meramalkan kes denggi.Dalam eksperimen ketiga, model LSTM (ST-SLSTM) bertindan perhatian spatial-temporal menunjukkan prestasi terbaik antara semua model. Ia mempunyai purata RMSE terendah (2.66), menunjukkan ramalan yang lebih tepat. Model ST-SLSTM menunjukkan ketahanan dan generalisasi, berprestasi baik dalam keadaan yang berbeza dan pada cakrawala ramalan yang berbeza. Walau bagaimanapun, kerumitan dan keperluan pengiraan adalah batasan yang berpotensi.Penemuan ini memberikan pandangan yang berharga kepada pihak berkuasa kesihatan awam di Malaysia dan negara-negara lain yang menghadapi demam denggi. Model LSTM yang dicadangkan dengan mekanisme perhatian menawarkan model ramalan yang lebih tepat, membantu dalam pembangunan strategi yang berkesan untuk pencegahan dan Kawalan Penyakit.

Kata Kunci: Denggi; LSTM; Perhatian, Pembelajaran Mendalam; Malaysia

SDG: MATLAMAT 3: Kesihatan dan Kesejahteraan yang Baik, MATLAMAT 15: Kehidupan di atas Darat

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First and foremost, I would want to convey my profound appreciation to my parents for the unending love and encouragement they have provided throughout my life. I will be obliged to them for the rest of my life.

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LIST OF ABBREVIATIONS

AHP	Analytic Hierarchy Process
ANN	Artificial Neural Network
ARIMA	Autoregressive Integrated Moving Average
ASEAN	Association of Southeast Asian Nations
BigML	BigML.com
CGIAR	Consultative Group on International Agricultural Research
CMORPH	Climate Modeling Gridded Product
CNNs	Convolutional Neural Networks
ConvLSTM	Convolutional Long Short-Term Memory
DHF	Dengue Hemorrhagic Fever
DT	Decision Tree
DW	Dynamic Wavelet
EA	Evolutionary Algorithm
FE	Feature Engineering
FUTURE	Forecasting Using Time Series and Regression
GA	Genetic Algorithm
GIS	Geographic Information System
GLC2000	Global Land Cover 2000
GPU	Graphics Processing Unit
GWO	Grey Wolf Optimization
LASSO	Least Absolute Shrinkage and Selection Operator
LR	Logistic Regression
LSSVM	Least Squares Support Vector Machine
LSTM	Long Short-Term Memory
LSVM	Linear Support Vector Machine

LULC	Land Use Land Cover
MAE	Mean Absolute Error
MFO	Multi-objective Fuzzy Optimization
MODIS	Moderate Resolution Imaging Spectroradiometer
MSE	Mean Squared Error
NEM	Network Enabling Model
NNAR	Neural Network Autoregressive Model
NPV	Negative Predictive Value
PA	Probabilistic Atlas
PPV	Positive Predictive Value
QGIS	Quantum GIS
RBF	Radial Basis Function
RBFSVM	Radial Basis Function Support Vector Machine
ReLU	Rectified Linear Unit
RF	Random Forest
RH	Relative Humidity
RMSE	Root Mean Squared Error
RNN	Recurrent Neural Network
SARIMA	Seasonal Autoregressive Integrated Moving Average
SVM	Support Vector Machine
SVR	Support Vector Regression
TA	Transfer Learning
USA	United States of America
WHO	World Health Organization
ZIGAM	Zero-Inflated Generalized Additive Model

CHAPTER 1

INTRODUCTION

This chapter provides the research study's introduction and includes background information that is crucial, a problem statement that is clear, goals and objectives for the research, a description of the study area, novelty and contributions of the research, and an explanation of how the thesis will be organized.

1.1 Background of Study

Public health concerns about dengue fever are fast expanding, particularly in tropical and subtropical areas like Malaysia. This disease, which is brought on by the Aedes mosquito and spread by the dengue virus, can cause serious health issues and even death. Over the past few years, there has been a notable rise in the occurrence of dengue fever in Malaysia, highlighting the urgent need for effective prediction and control measures. Dengue datasets have a mix of linear and nonlinear patterns, thus, the modelling of their complex autocorrelation structures is time-consuming and difficult. Thus, now we will come up with the designs and developed the models which will show these patterns and will give the exact predictions. Besides, the relationship between epidemiological and environmental variables is very complex therefore, the prognosis of dengue cases is a challenge. The complex chain of causal circumstances is portrayed by the different incidence patterns that are seen in different geographic areas. Besides, the studying of statistical analysis is hampered by the shortage of long-term historical records of the disease occurrences and the environmental factors that determine the risk. The correct prediction and classification of time series data are the keys to the accurate dengue fever forecasting. Nevertheless, the time series prediction models for dengue prediction, which are already in place, are usually not able to deal with long sequences. These models do not manage to obtain the important data that is contained in long length time-series data. The models of deep learning, for example, the RNNs and Convolutional Neural Networks (CNNs), have proven to be the best in dealing with time series data and image data, respectively. Still, the standard deep learning models with their regular architectures also have the problem of forgetting things in the long time-series data. The latest research has shown the attention mechanisms as a possible solution to the problem of the phones being a distraction. Attention mechanisms choose the significant variables among different feature time series data and through them, the predictions are more accurate. Dengue fever is a major public health problem worldwide, and the effect of climate change on it is going to be very harmful. The creation of a dengue fever early-warning system has been recognized as one of the main health adaptation measures in many countries. The forecasting of dengue using machine learning and deep learning models, on the other hand, has been utilizing environmental and meteorological factors to predict the dengue fever cases in the specific areas. The models for deep learning, for instance LSTM and CNN, have also proved to be successful in dengue prediction. Nevertheless, the LSTM model's capacity to cope with long sequences and to comprehend the temporal dependencies is especially important for the dengue prediction. The latest research shows that LSTM models are useful in predicting accurately the dengue infection and deaths in India and China. The use of LSTM models for dengue prediction has brought the accuracy of the prediction systems to a higher level than the other previously used models. Nevertheless, the LSTM models still have problems in the accurate retention of information in long time series data.

The attention mechanism is the solution to the problem and it has been successfully used in other areas like computer vision and time-series data analysis.

1.2 The Problem Statement

To be more specific, in tropical and subtropical areas such as Malaysia, dengue fever is a grave public health issue. In Malaysia, the incidence of the dengue fever is on the increase, and the number of the cases in the recent years is also increasing. Timely prediction of dengue fever cases is of great importance to the public health authorities so that they can take the necessary actions for prevention and control. Although many machine learning as well as statistical models have been designed for dengue prediction, there are still a lot of the problems which have to be solved. Dengue datasets have complicated autocorrelation patterns - both linear and non-linear - which require the design of forecasting models that are able to precisely capture these complexities. Furthermore, the complicated interaction between environmental and epidemiological variables makes it hard to predict dengue cases, and the incidence patterns of this disease are different in many geographical areas. Besides, the complexity of statistical analysis is also affected by the absence of long-term records of disease incidence and the relationship of environmental factors on risk. The existing time series models for the prediction of the dengue cases are usually shallow and do not process long sequences and remember important information in the data. The LSTM and CNN models, which are the deep learning models, have been the ones that have been used to handle the time series and image data, respectively. Nonetheless, the conventional deep learning models also have difficulties with storing long-term information in time-series data. New studies have demonstrated the possible of attention mechanisms in the models of deep learning to record long dependencies in time series data. Nevertheless, the use of LSTM attention mechanisms in dengue prediction is still a new thing, hence, a significant research gap in this field is still open.

1.3 Research Goal and Objectives

This research aims to design, develop, as well as validate a dengue prediction model based on RNN with a novel attention mechanism. Most of the time series models suffer from the incapability of the system to remember longer sequences. The attention mechanism is a way to resolve this problem. The specific objectives are:

1. Develop a prediction model based on LSTM with temporal attention for the prediction of monthly dengue cases,
2. Develop a spatial attention mechanism for the LSTM model that could effectively incorporate the spatial relationships between the dengue cases and relevant GIS and climate variables, and
3. Develop an integrated spatial-temporal attention for the LSTM models to improve the performance of the dengue prediction.

1.4 Description of Study Area

The research region of Malaysia, a Southeast Asian nation that is situated between 1° and 7° North and 99° to 105° East, is the primary subject of this thesis investigation. Mainland Malaysia is comprised of two distinct regions: Peninsular Malaysia and East Malaysia. The South China Sea serves as the dividing line between both area. Peninsular Malaysia is the most populous part of the nation, whereas East Malaysia is comprised of the states of Sabah, Sarawak, and Labuan, which are together referred to as Malaysian Borneo. A graphical depiction of the research region is shown in Figure 1.1.

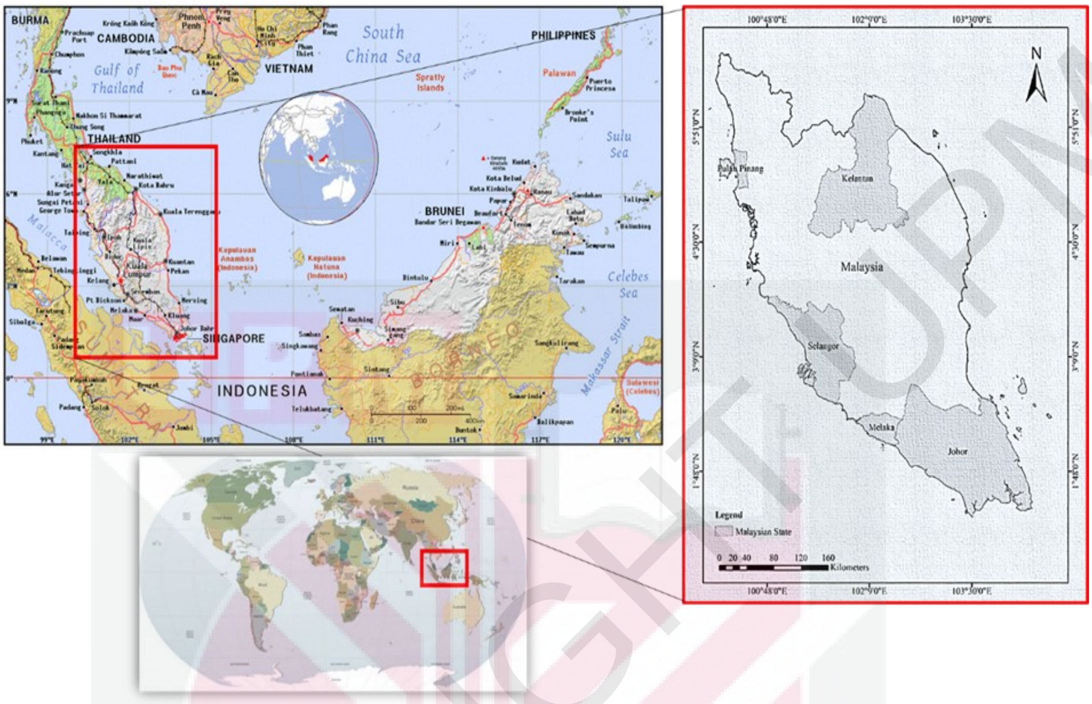


Figure 1.1 : Study Area Map

The first case of dengue fever, a serious public health issue, was discovered in Malaysia in 1902 (Teng and Singh, 2001). However, it gained greater attention in the 1970s when the first major outbreak occurred. Since then, there has been a consistent rise in dengue cases. According to recent figures, there were 361 cases per 100,000 persons in 2014 compared to 32 cases per 100,000 people in 2000. Most dengue patients are between the ages of 15 and 49, with urban regions accounting for about 80% of cases. Malaysia's geographical location as well as environmental characteristics make it susceptible to dengue fever. The country features a diverse landscape, including floodplains, hills, and coastline zones. It has a tropical climate that is humid, with temperatures between 21°C to 32°C. Malaysia experiences two distinct rainy seasons: the Northeast Monsoon (NEM) from October-March as well as the Southwest Monsoon (SWM) from May-September, with the transitional month of April also receiving significant rainfall. Certain Malaysian states, such as Selangor, Kelantan, Pulau Pinang, Johor, and Melaka, have a higher incidence of dengue fever compared to other states. In general, Selangor alone is the one that consumes 90% of the national dengue cases. These states together have a sum of the population of 15. 97 million in 2023. Consequently, these states become the centers for dengue fever studies and predictions in Malaysia. The knowledge of the dengue fever in Malaysia is very important for the health authorities in the public sector to take the appropriate preventive and control actions. Through the analysis of the facts and the variables that are behind the spread of dengue in this specific research area, the real-life wisdom can be found which will be helpful to create the strategies for the problems that are related to the spread of dengue in Malaysia.

1.5 Thesis Organization

The thesis is arranged into five chapters, each of which is designed for a different purpose in the study and the analysis of dengue fever prediction by using RNN with the attention mechanisms.

Chapter 1: Introduction

The first chapter starts the research and also reveals the problem statement. It explains the main reasons of dengue fever as a public health issue, especially in the tropical and subtropical areas like Malaysia. The chapter also emphasises the importance of the correct forecasting of the dengue fever cases and introduces the suggested method of using RNNs with integrated spatial-temporal attention. The research objectives, research gaps, research novelty, and research contributions are discussed, which thereby generates the base for the other chapters.

Chapter 2: Literature Review

The second chapter brings together all the research that has already been done on the machine learning methods that are used in this case and also, predicting the dengue fever. The paper reviews the different machine learning models that are employed for the dengue prediction, such as, decision trees, support vector machines, random forests and neural networks. Moreover, it looks into the latest developments in deep learning models especially LSTM and CNN and their uses in the prediction of dengue fever. The chapter, on the other hand, points out the strengths and weaknesses of these models and highlights the research areas that the present study is supposed to fill.

Chapter 3: Methods and Materials

The third chapter describes the research methodology and materials used in the study. It gives a detailed overview of the dataset that is used, which comprises of the weekly dengue cases from five Malaysian states and the various covariates such as climate, land use, vegetation, and GIS factors. The chapter describes the way of using the RNNs with the spatial-temporal attention put together with the LSTM models. The paper also talks about the investigation and rendering of spatial attention, temporal attention, and combined spatial-temporal attention mechanisms to improve the efficiency of the LSTM. The evaluation metrics, which are talked about in depth, include the RMSE.

Chapter 4: Results and Discussion

The fourth chapter tells the reader about the results of the experiments which were carried out using the approach that was put forward. It talks about the LSTM models with attention mechanism's performance in predicting the dengue fever cases in Malaysia. The chapter firstly, presents the results which are then compared with the benchmark models including RF, DT, SVM, S-ANN and D-ANN. This comparison is designed to highlight the fact that the suggested method works. The discovered results are scrutinized, and the implications of the findings are discussed in connection with the research objectives and research gaps identified in the literature review.

Chapter 5: Conclusion and Recommendations

The last chapter provides a summarizing of the research facts and their results. It rephrases the research objectives and emphasizes the ideas which was the research. The chapter also elaborates on the research's limitations and underlines the fields for the future studies. After analyzing the results and the insights, conclusions are made about the applicability of the suggested LSTM models with attention mechanisms for the prediction of dengue fever in Malaysia. Moreover, the study concludes with the proposing of the practical recommendations for the public health authorities and the policymakers to design the effective strategies for the prevention and the control of the dengue fever spread.

CHAPTER 2

LITERATURE REVIEW

The current chapter is a chapter in which the writer has carried out an extensive literature review on the prediction of dengue fever. It gives a definite description of the research that has been done in this field till now. The literature review is meant to give a general idea about the current state of the field, find out the areas of research that are not covered yet, and also to set the stage for the following chapters of this thesis.

2.1 Introduction

Dengue fever is brought on by the dengue virus, which is spread by mosquitoes. The virus is carried by different species of mosquito, specifically Ae. Aegypti. Dengue is a common disease that is widespread in the tropics. It is greatly affected by the amount of rainfall, the temperature, the relative humidity, and the rate of urbanization. The virus also causes a wide spectrum of diseases that can range from severe flu symptoms to those infected. Over the years, the number of those infected by the virus has grown significantly around the world; moreover, a vast majority of the cases are unreported, and hence there is under-representation in the number of cases reported. Its outbreak is among the top ten death-causing diseases all over the world. From the WHO data, dengue infections have increased globally, and 50-100 million new infections every year in more than 70 countries. Malaysia, for example, between 2014 and 2016, had an extraordinary dengue disease outbreak. The outbreak resulted in an increase in the number of cases reported in hospitals as well as an increase in mortality number as in comparison to earlier years (Suppiah et al., 2018). The case of the outbreak can be multifactorial as their significant factors leading to the outbreak. One avenue that many researchers are working on is integrating computer science in developing statistical data that can predict the potential outbreak of the disease. Dengue incidence in Malaysia has increased from 1973 to 2014, with more than 60% of cases in the Klang Valley region, and case fatality rates increasing from 0.16% to 0.62% between 2000 and 2013 (Kadir et al., 2015). Dengue deaths in Malaysia primarily occur in adults, with dengue shock syndrome being the leading cause of death, emphasizing the need for early recognition and aggressive intervention (Woon et al., 2016). Dengue vector control activities in Malaysia cost US$73.5 million in 2010, 72% above the annual cost of dengue illness, increasing the estimated total cost to US$175.7 million (Packierisamy et al., 2015). Earlier research has incorporated the use of machine learning as well as statistical models which have shown varying performances for time series prediction (Makridakis et al., 2018). The model is essential in tracking dengue dynamics which utilizes specific functions in predicting the dependent variable (dengue cases) from several predictors (covariates) including geographical and environmental factors. Machine learning has significant potential for developing algorithms that can carve high dimensional data space and hence it is essential in multicollinearity situations. Machine learning algorithms have proven to be essential in making accurate predictions, the system assumes giving outcomes quicker by different algorithms. Such computations are intriguing because they can only be deployed using individual portable gadgets. Assuming that there was no significant increase in dengue outbreak during the time, the model can be useful in predicting the outbreak. However, it is essential to include various geographical factors and factors related to the environment such as relative humidity and other variables as predictor variables in the model. As a control for the long-term trend in seasonality, weekly or annually observations can also be included in the model. To affirm the observation, performance of the model can be evaluated using dengue surveillance data from other regions or at different times.

Previous studies have been using Remote sensing, spatial statistics, and GIS to identify dengue cases in a country and assess the connection between dengue occurrence and other factors such as environmental, demographic or climate factors. Remote sensing gives near real-time utility of climatic data. Together with previous dengue incidences, GIS enables the forecasting of dengue outbreaks. These tools help in planning, monitoring, and enforcing vector control interventions in high-risk areas. The skill to examine the movements of dengue transmission and its growth trend with respect to spatial statistics, statistical analysis and machine learning will be in a position to be provided. Public health interventions should be planned in the preparedness programs by using the predictions of the number of deaths due to dengue. There are the regression approaches, the spatial-temporal modeling, the time-series methods, and the most recently the deep learning methods which are statistical tools employed for the analysis and the forecasting of various scenarios. Many cycle research studies used time series techniques because of the increasing number of instances over time (Chakraborty et al., 2019; Mussumeci and Coelho, 2020).

2.2 Modelling Data and Materials

This part is the one that speaks about the data and the factors that are used for the forecasting of dengue cases. It provides the information on the data sources of the data that is needed for the spatial and statistical data of the dengue cases in order to forecast the dengue cases. Besides, it teaches us the reasons and the ways in which these factors and the methods of choosing them in the modelling of the prediction of dengue fever are considered.

2.2.1 Data Sources

The several data sources from the different databases are the sources that can be used for dengue prediction. The data sources are the Ministry of Health for a country, the Department of Meteorology, some hospitals, the scholars' studies in the field published by other authors, social media, and the World Health Organization (WHO) (Siriyasatien et al., 2018). Figure 2.1 presents different data sources from which dengue forecasting systems can be developed. The information obtained can be further enhanced by the other sources that this country supplies. For instance, the data regarding the number of dengue cases in Malaysia can be fetched from Malaysia Open Data. Besides, the website also has demographic databases of various periods. Data on other things like environment and climate can be got from the internet resources for example MODIS. Besides, there are different sources that offer free spatial data such as Diva GIS which may be useful for dengue prediction systems.

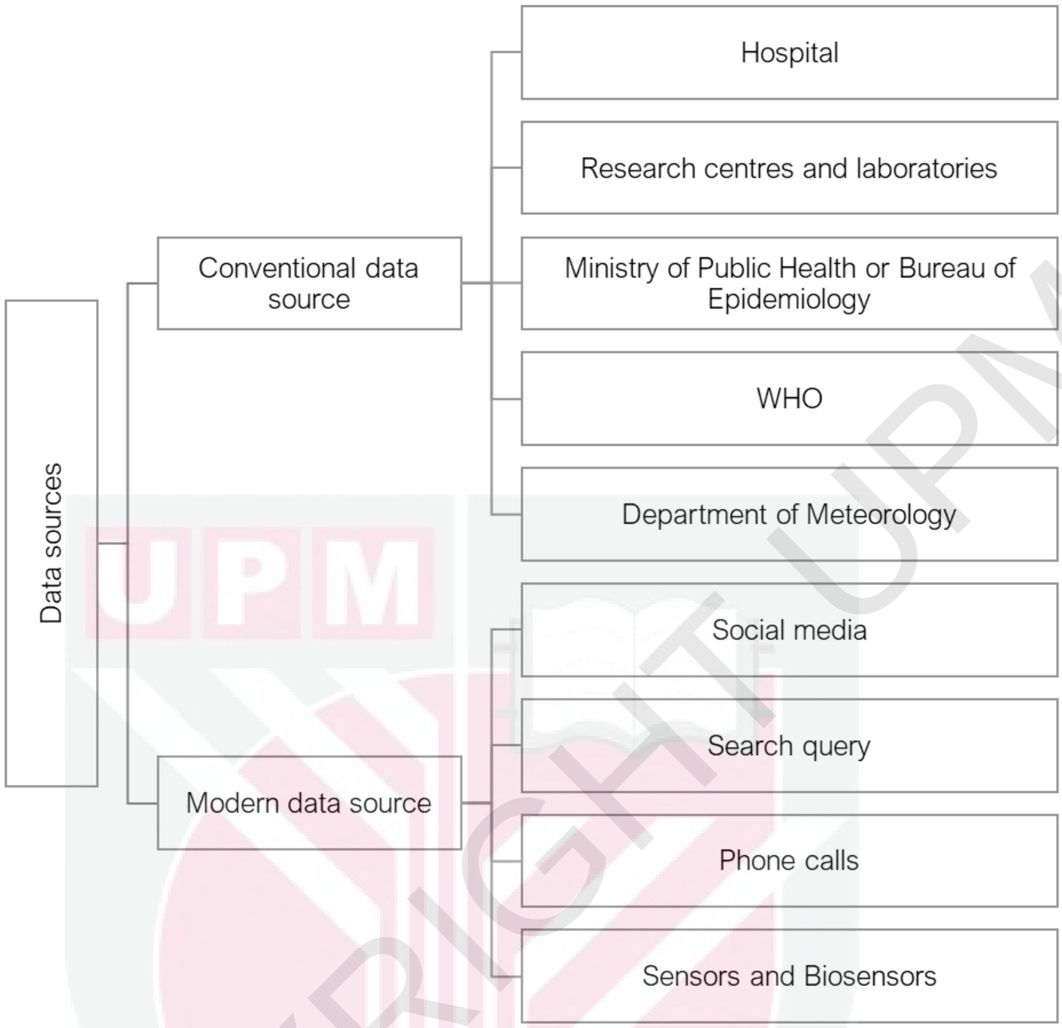


Figure 2.1 : Traditional and Modern Data Sources for Dengue Prediction System (Suggala et al. 2019)

2.2.2 Dengue Data

Dengue cases are recorded with information about the location of the incidence and many other relevant variables including demography, geography, environmental and climate data, useful for modelling. Dengue cases are often recorded daily and for modelling aggregated data are used. For example, daily, weekly, quarterly, or annual observations are used to generate predictions, depending on modelling settings. Modelling can be performed for long periods and short periods as well. According to a review by Aswi et al. (2019), the average study duration was 7 years, and the median study duration was 4 years. The longest study duration was 384 months (32 years), and the smallest study duration was 3 months (91 days). The dengue data can also be aggregated spatially. For example, modelling can be performed at state level or country level or any other spatial scales.

2.2.3 Covariate Data

As indicated in several previous studies, there are both indirect and direct and influences of climate in the transmission of dengue disease, vector breeding and establishment, and distribution (Gubler et al. 2001). According to studies (McMichael et al. 2006), climate change both influences and contributes to the global spread of arboviral infections. Temperature affects the vector's ovarian development and survival at various periods of its life cycle. The relationship between temperature and precipitation effects the dynamics of the vector, and as a result, temperature indirectly affects precipitation through controlling evaporation. These then affect the availability of aquatic environments for the breeding of Aedes vectors. Studies done in the past have demonstrated the connection between rainfall and dengue outbreaks (Kolivras 2010). Rainfall helps to establish and sustain vector breeding habitats. Studies used many other factors as predictors in dengue prediction systems, summarized in Table 2.1. The factors are categorized into five main factor categories including climatology, demography, socio-economic, entomology, and geography. There are several subfactors in each category. The number of factors used in a study depends on the data availability and research aims. The type of models used also controls the selection of factors. For example, some models can only deal with small number of factors due to multicollinearity problem while other models can deal with more factors.

Table 2.1 : Covariate Factors Used for Dengue Prediction in Previous Studies

Covariate category	Included factors
Climatology	El Niño Southern Oscillation Index Precipitation Oceanic Niño Index Temperature
Demography	Age structure Household density Density of population Human daily mobility Percentage of urban population Ratio of male and female percentage of foreign visitors The mean age of population
Socio-economic	Index of Human Development for the District Garbage collection Income Literacy Living condition (slums) average number of residents per household Occupation Sewage disposal Black people Percentage Water supply
Entomology	Breteau index Housing Health Index Indoor residual spraying (IRS) Larva -Free Home Index Mosquito density
Geography	Non -linear temporal trend Year Temporal Covariate -specific distributed lags The location of important breeding sites for Aedes aegypti percent of land that is covered by mountains. Latitude Longitude Census tracts and distance to public emergency health unit Elevation range (m) Mean elevation (m) Mean vegetation index Altitude

2.2.4 Covariates in Dengue Studies

According to the literature review on covariates used in dengue studies are land surface temperature, precipitation, density of population, and level of education. The climatic variables land surface temperature and precipitation were extensively studied by researchers and their impacts on dengue are well understood. According to Jetten and Focks (1997), they have an impact on dengue by accelerating mosquito development, population increase, virus replication, and mosquito-human interactions. Temperature affects the mosquito vector's ability to reproduce and bite as well as the extrinsic incubation of the dengue virus (Gratz, 1999). The right breeding grounds for Ae. aegypti are provided by precipitation, which can increase the number of female mosquitoes and cause epidemics (Lindsay and Mackenzie, 1997). wind speed and humidity are additional meteorological factors that are employed in dengue forecasting. According to Hasles et al. (2002) and Mellor and Leake (2000), humidity frequently affects the virus's ability to replicate quickly in the vector and how long it may survive. It has been demonstrated that wind speed reduces mosquito flight, which has an impact on their oviposition and density (Depradine and Lovell, 2004). Urbanization and population density are significant risk factors for the recurrence of dengue. As a highly domesticated urban mosquito called Aedes aegypti, which loves to coexist with humans, feeds preferentially on humans, and lays eggs in human-made artificial containers, population expansion and urbanization present ideal conditions for breeding and dissemination (Struchiner et al. 2015). Adult literacy rate (the percentage of adults over 15 who can write and read) is taken into account when predicting the prevalence of dengue because it is linked to a lower incidence of the disease (Ferreira and Schmidt, 2006). Several studies have focused on a single category of dengue covariates. For example, studies have explored the relationship between the climatic covariates and dengue cases (Nan et al. 2018). The ultimate purpose of these studies was to find out the impacts of the climatic variables on the dengue cases instead of developing highly accurate and complex dengue prediction models which are based on many covariates. Stolerman et al. (2019) conducted a research on the climate conditions for dengue fever forecasting in Brazil. The aim of their research was to find out the climate variables and their relationships to dengue epidemics that are, in turn, used to create the model predictions which will have a more accurate and, thus, will assist in the early warning systems. The geographical places of the research sites are crucial to the identification of the variables that should be taken into account in the dengue prediction models. To illustrate, for example, populated and urban states of Malaysia, Selangor, has observed several major dengue outbreaks because of some universal variables. Salim et al. (2021) used the climate data, which include humidity, rainfall, temperature and wind speed, with different machine learning models to predict the dengue outbreaks in Selangor, Malaysia. They demonstrated that although some models chose maximum temperature as the most crucial indicator of dengue outbreaks, maximum temperature wasn't consistently associated with the highest number of outbreaks of dengue in the data. Zainudin and Shamsuddin (2016) presented prediction models for dengue cases highlighting the importance of residential areas to prevent dengue spread. Climate variables such as humidity, rainfall, temperature was successfully used for dengue prediction in the Philippines (Zafra 2020). In China, Xu et al. (2020) predicted dengue fever cases in 20 cities (i.e., Guangzhou, Foshan, Sinsong Panna, Dehong, Chaozhou, Zhongshan, Hangzhou, Zhanjiang, Fuzhou, Jiangmen, Shenzhen, Nanning, Zhuhai, Lincang, Shantou, Dongguan, Yangjiang, Putian, Qingyuan, and Zhaoqing) with climate variables. However, in some cities they did not obtain high accuracy. They suggested that the reason is behind the not considering other relevant potential socio-economic factors. Chen et al. (2020) established a dengue prediction model with climate variables. Due to urban development, dengue diseases are no longer only found in urban areas, as Bal and Sodoudi (2020) demonstrated by a surge in dengue infections in suburban districts (Kolkata, India). In the dry season, people in Africa store water in containers, which can provide favorable breeding grounds for Ae. aegypti (Ebi and Nealon 2016). According to a study by Liu-Helmersson et al. (2016), if greenhouse gas emissions continue at their current rate, a dengue pandemic for Aedes aegypti could break out in 10 European cities by the end of the century (Madeira, Malaga, Athens, Rome, Nice, Paris, London, Amsterdam, Berlin, and Stockholm). Altassan (2020) and Abualamah et al. (2020) evaluated the impact of several environmental and societal factors on the emergence and spread of dengue in Saudi Arabia. The distribution of dengue risk linked to socio-environmental factors was examined by Costa et al. (2013). And in Colombia, Ye and Moreno-Madrián (2020) discovered that among the contributing variables to identifying prospective dengue outbreak sites were population density, elevation, daytime, and nighttime land surface temperatures; precipitation and vegetation variables, however, were not significant. It can be seen from the above studies that the selection of variables in dengue prediction models is based on geographic locations. The effect of a specific variable can have different correlations with the dengue cases depending on the geographic location of the analysis. As a result, the geographic location determines the important variables that need to be included in dengue prediction models. Stagnant water is artificial or natural standing water usually experiencing low flow or usage. It is the main source of breeding for Aedes mosquitoes (Rozilawati et al. 2007). The latter usually breed in clean stagnant water in a wide variety of sites including manmade containers in the domestic and peridomestic urban environment (Kumarasamy 2006).

There are several ways to represent stagnant water affects in dengue fever prediction model, as explained by the following points:

1 Land use and land cover (LULC) data contains the class of water bodies, waterways, and man-made features (buildings, infrastructures, etc.). Stagnant water thus can be represented by including those features into the prediction model. For example, water bodies can be represented as a binary raster map (0 for non-water areas, 1 for water areas). Similarly, waterways can be represented by taking the distance from the nearest waterway feature to the selected pixel in the raster dataset. In Selangor, Malaysia, Cheong et al. (2014) found links between dengue cases and human settlements, water bodies, mixed horticulture, open space, and neglected grassland. In addition, other man-made and infrastructure features can be used to indicate the development status of an area. For example, the poor infrastructure development in rural areas such as poor drainage systems and sewage systems may increase the potentials of mosquito breeding (Sabir et al. 2018). This research uses detailed LULC data including water bodies, waterways, and several other water-related features for the prediction of dengue fever. The data will be used to establish several covariates to include into the prediction model such as distance from water bodies, distance from waterways, water features density, etc.

2 As Aedes mosquitoes mostly breed in clean stagnant water rather than just a standing water (Kumarasamy 2006). This can be represented in the dengue fever prediction model through including water quality indices or some other indices that indirectly represents the cleanness of the water such as vegetation indices and land surface temperature (Dom et al. 2016, Pham et al. 2018). This research uses both vegetation indices and land surface temperature data to represent the effect of stagnant water in the prediction model.

2.2.5 Selection of Covariates in Dengue Studies

Aswi et al. (2019) presented a review paper in which they divided covariates into six categories based on 31 dengue studies, namely climatic, geographic, demographic, entomological, socioeconomic, and temporal covariates. In the majority of research, only a few covariates from two or three categories were employed. The most used category is climatic (65%). Among the climatic covariates, temperature and precipitation are the most used. Land surface temperature extracted from remote sensing sources are commonly used to represent temperature (Wijayanti et al. 2016, Martínez-Bello et al. 2017, Martínez-Bello et al. 2018). Demographic variables such as age structure, age of population and household density are the used variables in this category (42% of the studies). However, the most common being population density. Almost 23% of the research made use of various socioeconomic factors. The most typical one is the level of education. As a result of the difficulty in obtaining the data, only 19% of the research included entomological variables in their models. Nearly 29% of the students made use of geographic factors. Vegetation was taken into account as the explanatory variable in three articles (Martinez-Bello et al. 2017, Martinez-Bello et al. 2018, and Wijayanti et al. 2016). In one study, elevation was used as the explanatory variable (Kikuti et al. 2015). Temporal lag factors were included in over 32% of the studies. The climate data used in these investigations typically had a temporal lag. To assess the dynamics of dengue cases, Restrepo et al. (2014) added time in years as a categorical variable. Expert opinion can be used as a method for selecting covariates in dengue fever prediction studies. A list of covariates can be prepared to provide to several experts in areas related to the subject and ask them to rank the covariates according to their importance for the aim of study. Then, a decision-making technique like AHP can be utilized to find the most important covariates according to the experts. The research then can use a subset of the highly important covariates. However, this is not a common procedure in dengue fever prediction studies. Reasons include the very large number of interrelated and complex covariates which can lead to bias and confliction among the experts. In addition, the selection of the decision-making method to rank the covariates and the subset percentage of the most important covariates also can be highly subjective and subsequently lead to a biased selection of the covariates. Moreover, the recent sophisticated deep learning models are capable of learning spatial-temporal features automatically. The models by their internal structures suppress the less useful features. As a result, these modern predictive models do not require selection of relevant features rather they automatically learning important features and use them for the prediction task. Deep learning identifies patterns in feature distributions in scenarios involving huge amounts of data, and it then takes advantage of these patterns to improve the accuracy of the task (Appice et al. 2020).

2.3 Data Preparation and Processing

Raw data that is collected from the field or from online sources are not ready for data analysis and modelling. Therefore, data needs to be prepared by applying some pre-processing techniques which can include data cleaning, transformation, normalization, and any other steps before training a model. Raw data also can be used as a source data which means additional data can be extracted by remote sensing techniques such as image processing and feature extraction. In the process of data preparing for developing a forecasting model, data must be cleansed and transformed into the appropriate format, which can create a forecasting model (Siriyasatien et al., 2018). Important factors that must be available related to dengue infection include temperature, RH, as well as population density. The flowchart presented in Figure 2.2 shows the data sources, data types that can be used in a dengue prediction system. Spatial scale and temporal resolution of the data can vary from study to another depending on the needs and data availability. Table 2.2 shows the details of spatial scales and temporal resolutions used in previous studies. Data preparation can be performed using free and open-source GIS software or programming languages such as Python. For GIS analysis and mapping, QGIS software (https://qgis.org) can be used. For model construction, training and validation, Python-based tools can be used such as Scikit Learn (https://scikit-learn.org) and Keras (https://keras.io). Depending on the data volume and spatial scale of the study, personal computers can be used to perform data analysis and modelling. However, whenever faster hardware is needed, Google Collab (https://colab.research.google.com) can be used which has free GPU to use for research purposes.

Table 2.2 : Setting and Parameters Used in Predictive Dengue Model Creation

Spatial scale	Collection time frame
Multi- country	
Country	Bi-annually
City	Annually
Province	Bi-monthly
Municipality	Monthly
District	Weekly
Parish	Daily
Community	

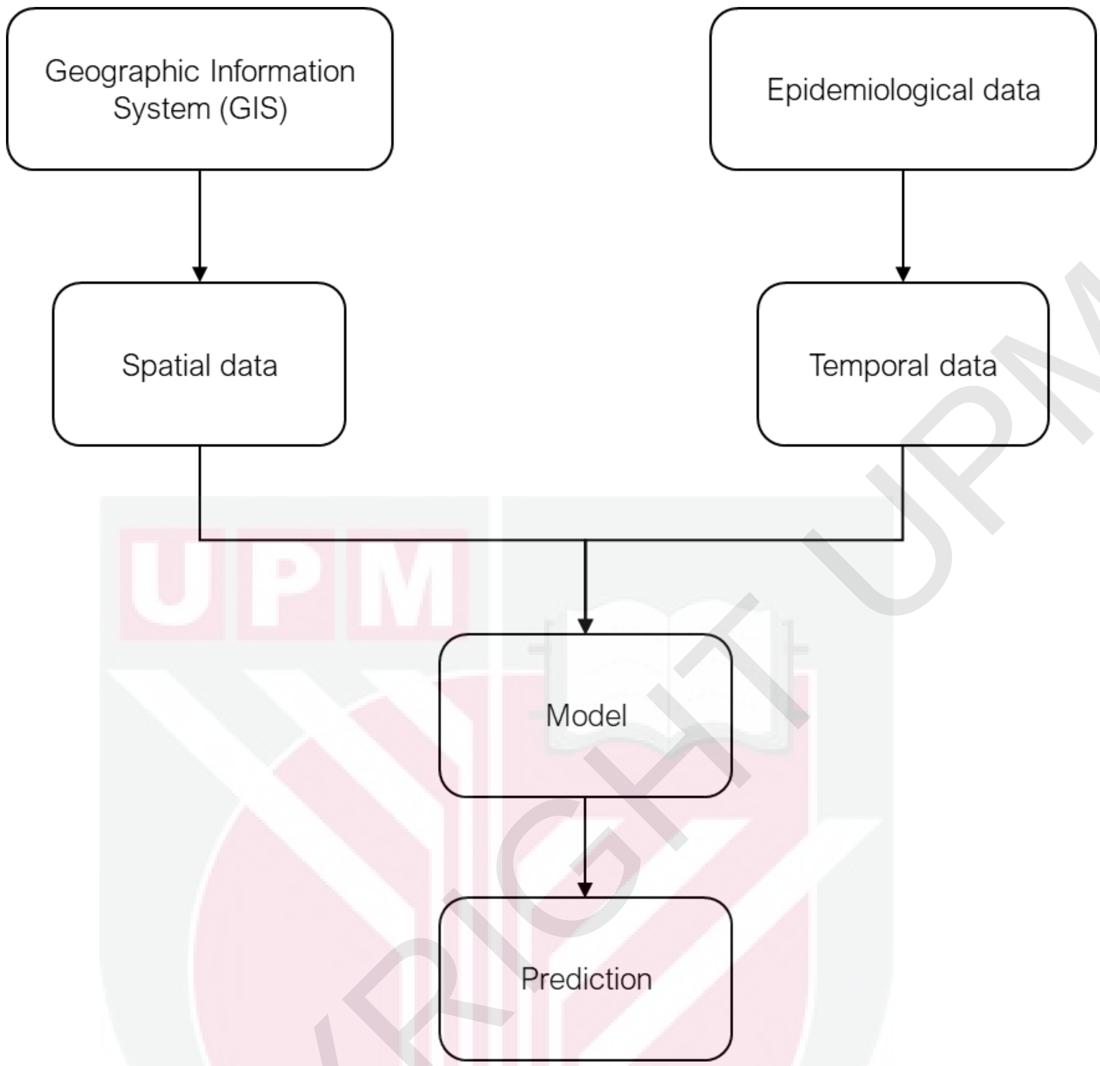


Figure 2.2 : Flowchart Shows the Data Sources and Data Types Used for Dengue Prediction

2.4 Dengue Forecasting Models

Data predictions are based on past data. However, to create correlations between variables, data mining techniques are used. The two categories of data mining approaches are supervised learning and unsupervised learning. Several techniques have been developed and examined for the prediction of dengue fever around the world based on statistical, machine learning, and more recently deep learning techniques. This section reviews and discusses studies used those techniques for dengue fever prediction. Table 2.3 presents the common models for dengue prediction in previous studies.

2.4.1 Statistical Models

In order predict dengue fever epidemics, statistical models such as linear regression and Autoregressive Integrated Moving Average (ARIMA) are frequently used. Linear regression is mostly used in dengue fever prediction due to its simplicity and the interpretability features. Sirisena et al. (2017) through a regression model were able to find out the relations between dengue incidence and population and meteorological indicators in Sri Lanka using the data of the years 2009 to 2014. To name a few, there was a slightly positive connection between dengue cases and rainfall, while there was a big negative link between dengue cases and temperature. Moreover, using abound dengue fever incidence and the humidity that increased than or equal to the average one month previously to the study also found to be correlated. Furthermore, Thiruchelvam et al. (2017) also presents the dengue forecasting model using linear regression process, and they tested the model in Petaling, Malaysia. They included four meteorological data such as the average temperature, the average relative humidity, the total accumulated precipitation, and the number of cases of dengue. Information gathered indicated that the one-step-ahead model was simple and accurate to predict the number of dengue fever and other infections. In his summation, Cousien et al. (2019) have used the linear regression model to predict the dengue outbreak's maximum development size in Cambodia. The outcome before the outbreak was implemented with an accuracy of 90 percent. The model was also used to estimate dengue epidemics' peak size. In 2016, Ramadona and his colleagues in Yogyakarta, Indonesia, developed the generalized linear regression models for the prediction of dengue epidemics. These models were widely used and were built using data from 2001 to 2010. They demonstrated that the best tools for the prediction of the dengue occurrence and incidence in the region were the combination of surveillance and meteorological data with the lag patterns that go back to years ago. Besides, some of the scholars emphasized the data transformation techniques on the application of the specific data transformation methods before the linear regression models construction. To illustrate, Anggraeni et al. (2017) suggested a regression method with the Least Square and Natural Logarithmic transformation for the determination of dengue incidences in Malang Regency, Indonesia. They proved that the logarithmic natural transformation of the model increased the accuracy of the predictions of the model when compared to the other model which did not have transformation. Scientists also took the approach of using models based on Fixed Effects (FE) and Random Effects (RE) to foresee the dengue fever outbreaks. Qureshi et al. (2017) applied these models in Pakistan and demonstrated that both models had a low performance and they implied that the models' predictive ability could be improved by including the socioeconomic and demographic variables. Besides, the scholars have always been working on and testing the models based on various types of regression models including linear regression models. Through the use of a Negative Binomial regression, Pushpakanthi and Perera (2018) made the prediction of dengue cases in Colombo, Sri Lanka with the rainfall and temperature data. The results showed that the average rainfall and the average maximum temperature before 10 weeks are the factors that determined the number of dengue cases in a week in the area, and the number of dengue cases each week in the area followed a negative binomial distribution. Li et al. (2017) conducted similar research to analyze the effect of climate change on the development of dengue fever. The research crew engaged long-term time series data from 1998 to 2014 and the Poisson analysis, the generalized additive model. These models showed that dengue fever rate can be reduced by controlling seasonal diseases and by mitigating emissions of greenhouse gases. Additionally, Yuan et al., in 2019, conducted a study on how extreme weather conditions affect the number of annual cases of dengue fever in Taiwan. Their models were Poisson regression to predict the number of dengue cases per year and the leave-one-out approach for validation. It was established that there is a significantly positive association between early summer low temperature and the early phase of dengue transmission for the forecasters. Conversely, the early epidemic phase of the dengue outbreaks has a negative correlation with the maximum 24-hour rainfall predictors. Besides, Chuang et al. (2017) examined the dengue cases from 1998 to 2015 in the southern Taiwan. They employed the rather complicated distributed lag non-linear modeling and the local climatic predictions. The results proved the delay and non-linear effect of the minimum temperature and precipitation. The results reveal that the transmission of dengue in southern Taiwan might be influenced by regional and local climate changes. Zhu et al. (2019) suggested a prediction model with the mutually dependent effects of the climatic characteristics in the Guangdong, China, based on the weekly dengue fever cases in this region from 2008 to 2016. The weekly predictive model for the probit regression was 0. 72. A goodness of fit score of 0 indicates a disaccord between the individual and his environment. 60, was the stomping of the dengue cases for the 1st 41 weeks of 2017. There are various other statistical tools which are used to predict the dengue fever outbreaks. A typical method that can be used is ARIMA. This system is used and tested in many countries all around the world. Siregar and Makmur (2019) created the ARIMA model for the assessment of dengue fever by the climate data which was taken from Medan, North Sumatra, Indonesia.

They proved by the monthly data for the period of 2012-2016, the proposed models were the most suitable for predicting the dengue incidences in the area. The researchers, Nayak and Narayan (2019), came up with a new ARIMA model that is seasonal to forecast the dengue cases in the Kerala state, India. The models were trained on the data for a month for the period of thirteen years from 2006 to 2018. In the research of Jayaraj et al. (2019), the Poisson regression model, the Seasonal SARIMA model, and the SARIMA with external regressors were compared for the dengue prediction in Tawau, Malaysia. They made use of the monthly dengue dataset that spanned 12 years, from 2006 to 2017. The researchers have the climate-related variables as the predictors which were the maximum temperature, minimum temperature, mean temperature, mean rainfall and mean relative humidity. The proposed model proved the possibility of foreseeing the potential dengue attacks 1 to 4 months ahead. Besides, the other scholars have applied different statistical models to anticipate dengue fever outbreaks. Adde and his collaborators (2016) created the dengue fever prediction model which uses climate indicators and logistic regression in French Guiana. The model was used to analyze the data from the period of 1991-2013, and only 15% of the years when an outbreak did not happen, were mistakenly predicted by the model, which could accurately predict 80% of the outbreaks. Abas and his colleagues (2018) studied two models the Double Exponential Smoothing and Holt-Winters and they applied them to the prediction of the weekly dengue cases in Malaysia. The models were modified to the dengue data (2011-2016) and the outcomes showed that the Holt-Winters method was the most suitable. Sánchez-González et al. (2018) created a mathematical model of dengue transmission that took into account both the human behavior and the impact of the environment on the spread of the disease. This model rightly showed the truth that the really rapid spread of dengue in the past years in four states in Mexico was correctly shown after the historical data on human population density, temperature, and rainfall, were added.

2.4.2 Machine Learning Models

Machine learning is the most popular method for many prediction problems, including dengue fever prediction. Numerous models designed on the machine learning techniques have been the foundation for the dengue fever outbreaks prediction. To investigate climate data (the frequency of rainfall and the average temperature) and how they related to dengue cases in seven Brazilian state capitals, Stolerman et al. (2019) developed machine-learning algorithms. The findings showed that the climate data goes in tandem with the total number of human dengue-cases. A system, which was developed by Jain et al. (2019), was used to forecast the spread of dengue in fifty Thai districts. The machine learning-based models that have been suggested which include the generalized additive models and the indicators that are formed using meteorological, clinical, clinical lag, socioeconomic, and lag factors of disease surveillance data. The researchers did demonstrate capabilities of the models built to predict the disease occurrence one month ahead and explain the forecasting variable's statistical importance. For example, Agarwal et al. (2018) used the Nave Bayes algorithm to model the relationship between multiple meteorological factors and the number of illness cases. They developed the spherical k-means clustering approach to identify zones with conditions analogical to the current field being studied. Zhao et al. (2020) examined strategies based on random forests to forecast the weekly dengue monitor data in Colombia twelve weeks ahead. The models used a variety of factors that included past relevant dengue cases, air temperature, vegetation, rainfall, counts of residence, level of commitment disparity level, and English learning. In judging the results, the researchers found that the random forests models were more accurate than artificial neural networks. Therefore, the model shows that socio-demographic characteristics are the first to be applied for the prediction for a long period of time, while environmental and meteorological factors usually appear to be the most indicators for the forecast for the short term. The very idea of dengue illness prediction was repeated by authors under the names of Nan et al. in 2018. The model is based on the XGBoost algorithm and the climate factors influence. The test of the prototype was done in Guangzhou, China. Based on the findings, the model are very precise tool that can reliably predict the actual number of cases of dengue fever for the region. Consequently, Ughelli et al. (2017) confirmed climate data usage for Dengue case forecasting in Paraguay by neural networks analysis. The outcome of the model's forecast for the period of four weeks was impossible to predict. The classification study of the dengue fever prediction models. The models were obtained from artificial neural networks and tested in San Juan, the Puerto Rico (United States of America), coastal town of the state of Parana, Mexico, and in San Juan, Puerto Rico were offered by Laureano-Rosario et al. 2018.In order to train the models, the researchers have collected information about the dengue disease during 19 years. As a dataset for the forecasting process has been used climatic and demographic information: air temperature, surface sea temperature, humidity, population, precipitation, and the number of dengue cases that has happened in the past. The models that have been built for the final research have been able to pass through the real occurrences of the epidemics of dengue fever that has taken place in the areas examined. For example, by the Elman-Levenberg-Marquardt neural network approach, Saptarini et al. (2018) developed a model that can predict the number of dengue cases in Kupang, Indonesia. In their study, the authors formulated this model. The independent variables used in the model include normal temperature, average precipitation, average relative humidity and mean sea level. The article dwells primarily on the application of these factors by researchers. The authors presented proofs that pointed out how well their model could forecast dengue cases in a given locality. Mathulamuthu et al. (2017), manifold learning based approach was developed for forecasting dengue disease. This method was later adopted in Malaysia. After the annual climatic variables were gathered, the model was trained using the data from them. After the reduction of the dimension and the cluster-based regression, the results were that the proposed method has the potential to be more successful in the prediction of the future. Fuzzy logic was used by the researchers Idris et al. (2018) in order to predict the number of dengue cases in the state of Selangor, Malaysia. A model that was trained on the data set that covered the years 2010 to 2013 and that used the total rainfall and the total number of wet days as predictors was created. The studies show that the approach that was created can be used for predicting dengue.

2.4.3 Deep Learning Models

Neural networks which are the foundation of the deep learning model are what make deep learning, a machine learning model, possible. The awaited dengue fever attacks have been realized by many researchers through the application of the various deep learning models of the dengue fever outbreak. The most important model is Long Short-Term Memory or LSTM which is a type of recurrent neural network. The synthetic data was made by Bogado et al. (2020) from the models' predictions and after that, it was used in the deep learning models for the prediction of the dengue cases. The results showed that the LSTM models could be applied to the forecasting of dengue cases. Nonetheless, they stated that the other factors such as demographic, geographic, and environmental can be taken into account and that the epidemic behavior in different regions could be described. The scientists of Xu and his group created a model for the prediction of dengue fever using the LSTM method which considered the monthly dengue cases and the climate data. According to the research findings, it has been demonstrated that how the data contradict the published prediction models and that LSTM was the best in predicting the dengue cases. In the studies that the researchers conducted, the results shown that the LSTM outperformed the other techniques during a series of experiments on different geographical areas. For example, Mussumeci and Coelho assert the following: "The LSTM also outperformed the following ML methods in predicting weekly dengue incidence in 790 Brazilian cities: LASSO and random forest". Thus, it could be concluded that LSTM is the best among the three. Xu et al. (2020) made the density frenzy prediction model for the LSTM by using the local weather data and the dengue cases from 2005 to 2018 in the top 20 Chinese cities. In contrast to the ZIGAM and the SIR models, the results were showing that the LSTM model which was made by only local data had lower performance. If the monthly dengue cases prediction made by the LSTM model will be based on the transfer learning, it will be a good tool. Furthermore, predicting the dengue fever outbreak has been harbored by various deep learning models, particularly CNN. In a study carried out by Andersson et al. (2018) the CNN model and the street-level images were used to predict DHF and DF in the city of Rio de Janeiro in Brazil. Their results indicated that street-level images have the potential to predict DF in urban settings.

2.4.4 Hybrid Models

As the improvement of the forecasters' ability to predict the dengue fever outbreak was continuing, another group of filers came up with hybrid models, which are a combination of two or more methodologies that are known as ensemble models. Buczak and his colleagues argue that the ensemble method for dengue sickness forecast was developed. There are three distinct component models which were used in order to develop the final model:

To differentiate between the prediction accuracy of a single model ensemble of the combinations of two models the following models were tried to comprehend the total number of dengue cases reported during the transmission season and the peak height in Iquitos, Peru; the models: two additive Holt-Winters models, with and without wavelet smoothing; two-dimensional Method of Analogues models combining the dengue and climatic data model; basic historical models. The new model blended from the models and ARIMA and neural network autoregressive was created by Chakraborty et al. (2019) to comprehend the number of dengue cases that would happen in San Juan, Iquitos, and the Philippines. What the experiment established was that the scientists had constructed a new model by which they could be able to give an accurate prediction about the number of dengue cases that took place in those areas on study. In their 2018 study, Pham and his colleagues concentrated on using machine learning as well as deep learning models to predict dengue disease in Kuala Lumpur, Malaysia. The independent variables were daily mean temperature, wind speed, daily rainfall, humidity and enhanced vegetation index from 2002 to 2012. It worked out between 2002 and 2012 according to a university conducted research. The researchers then used four different models, which included the Decision Tree, the Linear

Regression, the Genetic Algorithm, and the enhanced Recurrent Neural Network. They established that GA-RNN was the best of the best among the judged alternatives. The Flower Pollination Algorithm was also used to determine the LSSVM parameters, as in Mustaffa et al. (2018) model, and they were used in the prediction of the dengue disease in Yogyakarta, Indonesia. The main focus of the PA model in this case is to find out the best demonstrated with the regularization parameter and kernel parameters. The accuracy of their models was verified by the researchers on the basis of data obtained from illness monitoring and climate. They reached a conclusion that the proposed method was superior to the existing models in the error rate reduction ability. According to Mustaffa et al. (2019) the Least Squares Support Vector Machines was enhanced through the employment of swarm intelligence techniques, such as the ABC algorithm, GWO, MFO, and FA, which were employed in the prediction of dengue disease in Indonesia. The researchers eventually managed to form an idea that the hybrid algorithms discovered had the potential of producing a winning one. More specifically, the ABC technique would perform just a little bit better than the rest.

Table 2.3 : Dengue Prediction Models Applied Around the World

Country	Main Season	Model	Reference
Cambodia	May–October	Linear Regression	Cousien et al. (2019)
Sri Lanka	October to December and May to July	Negative Binomial Regression	Pushpakanthi and Perera (2018)
Colombia	May to November	Random Forest	Zhao et al. (2020)
Brazil	January to May	LSTM	Mussumeci and Coelho (2020)
India	April to November	Naïve Bayes	Agarwal et al. (2018)
		Seasonal ARIMA	Nayak and Narayan (2019)
Malaysia	East Peninsular Malaysia, Sarawak, and Sabah from October to February; West Peninsular Malaysia from July to August	Holt-Winters	Abas et al. (2018)
		Fuzzy Logic	Idris et al. (2018)
		SARIMA	Jayaraj et al. (2019)
		Manifold Learning	Mathulamuthu et al. (2017)
		Genetic Algorithm enhanced Recurrent Neural Network	Pham et al. (2018)
China	June to November	LSTM	Xu et al. (2019)
		Poisson analysis with the Generalized Additive Model	Li et al. (2017)
Paraguay	October to April	Neural Network	Ughelli et al. (2017)
Indonesia	November to April	Generalized Linear Regression	Ramadona et al. (2016)
		Regression with Least Square and Natural Logarithmic transformation	Anggraeni et al. (2017)
		Least Squares Support Vector Machines and Flower Pollination Algorithm (PA)	Mustaffa et al. (2018)
		XGBoost	Nan et al. (2018)
Taiwan	June to December	Poisson Regression	Yuan et al. (2019)
Thailand	April to December	Generalized Additive Models	Jain et al. (2019)

2.5 Current States of Dengue Prediction

2.5.1 Dengue Prediction with Statistical and Machine Learning Methods

Previous research has included the use of machine learning as well as statistical models, with varying results for prediction of time series. The model is critical in tracking dengue dynamics because it employs specific functions in predicting the dependent variable (dengue cases) from a variety of predictors (covariates) such as geographical and environmental factors. Climate has both direct and indirect effects on dengue disease transmission, distribution, vector breeding, as well as establishment (McMichael et al. 2006, Gubler et al. 2001). Rainfall as well as temperature are interdependent; since temperature controls evaporation, which in turn affects the dynamics of the vector, temperature indirectly affects rainfall. These then affect the availability of aquatic environments for the breeding of Aedes vectors. Studies conducted in the past have demonstrated a link between rainfall and dengue epidemics (Kolivras 2010, Polwiang 2020). Many factors, like climatology, socioeconomics, entomology, demography, as well as geography, have been studied as predictors in dengue prediction systems. Each category contains several subfactors. The number of factors used in a study is determined by the objectives of the research and data availability. The choice of the factors that are to be selected is also influenced by the models themselves. For "an instance, because of the multicollinearity issue, some models end up handling just a few factors, while others can accommodate many factors". In fact, for this reason to date, a large number of techniques have been designed and developed based on statistical analysis and machine learning to predict the vanguard of dengue fever. In the field of dengue fever forecasting, the statistical models LR and ARIMA are the most commonly used. It is the LR technique, the most straightforward to understand; as a result, it is used most frequently for dengue illness forecast. Research conducted by Sirisena et al. (2017) further demonstrated that using the regression model; the connections between the number of dengue fever cases and the population fluctuation and the certain of the climatic variables in Sri Lanka from 2009 to 2014 could be evaluated. Most importantly, it was discovered that, in this case, rainfall was the most crucial factor having a strong and positive correlation with dengue cases as well as temperature factor was the most important having a strong and negative relationship to it. It can be thus stated that both relationships were of great importance. Finally, the LR-based dengue forecasting model was also developed by Thiruchelvam and co-worker 2017. The model was also applied in Petaling, Malaysia, for testing purposes, with the usage of the following meteorological factors: the mean temperature of dengue cases, cumulative rainfall, and relative humidity. The results of the study demonstrate that a one-step-ahead prediction of the pattern of dengue cases was made successfully. Using the model, Ousabgali et al. 2019 first created LR and then used it to predict the peak size of dengue epidemic in Cambodia. Their correctness was 90%. Hence, they had LR models developed through sampling data in the range of 2001-2010 in Yogyakarta, Indonesia, and their aim was to predict dengue outbreaks. The differences are validated by closing the opportunity gap, as researchers uncover. Among the features analyzed, the two was more closely related to the incidence of dengue in the area explored. What was interesting is that the researchers who implemented the LR models differed in character from those who dealt with unconventional data transformation methods. The work of Anggraeni and colleagues (2017) for instance used a regression method that combines the techniques of Least Squares and Natural log transformation for the prediction of dengue incidences in Malang Regency, Indonesia. Researcher’s data revealed that a logarithmic natural conversion, in any case, is better than the prediction assessments that use no transformation. Researchers also took the linear regression model and all the nonlinear regression models into account. The Hotspot of dengue prediction cases in Colombo, Sri Lanka, was analyzed by Pushpakanthi and Perera (2018), using negative binomial regression with the data in rainfall and temperature. Yuan et al. (2019) carried out a study on the association between extreme weather and the annual number of cases of dengue fever in Taiwan by involving the Poisson regression model for the prediction of annual dengue cases. It said that at the current stage of dengue outbreaks there is a negative correlation with all the 24-hour rainfall forecasters and there is the positive correlation with early summer minimum temperature forecasters. Over this period of 1998 to 2015, Chuang, et al. conducted their study on dengue cases in south Taiwan. Our trend analysis is based on distributed lag non-linear modeling, and we project weather based on local climate predictors. It turned out that both lags and nonlinearity of the least temperature and precipitation were shown to be of big importance. The findings suggest that the heterogenous distribution of dengue in southern Taiwan is mostly attributed to the locally and regionally influenced climates. model of the consequences of climatic elements connected through the network was presented by Zhu et al. (2019) of Guangdong from 2008 to 2016 election based on the weekly frequency of dengue fever cases. A coefficient of 0. 72 was weekly predictability value of a regression model got. Zero goodness of fit corresponds to the made fit and a good indicator of fit. For the first 41 weeks of 2017, there contained 60 cases of dengue. The climate data from Medan, North Sumatra, Indonesia, were used and then the ARIMA model was built by Siregar and Makmur (2019) in order to forecast dengue fever realistically. They verified that the forecasted models possess the ability to precisely predict the percentage of dengue cases in the area with a monthly data of range from 2012-2016 as evidence. Nayak and Narayan (2019) have designed a seasonal ARIMA model for predicting dengue in Kerala state. Using the data of the monthly statistics from the year of 2006 until the end of 2018 as a whole, we trained our models for thirteen years in total. In t twentieth century's Tawau, Malaysia, for dengue forecasting, Jayaraj et al. (2019) looked at using Poisson regression model, the Seasonal SARIMA model and SARIMA with external regressors and compared these models. They gathered the data of monthly dengue from 2006 to 2017. We used a set of variables related to climate such as minimum temperature, mean temperature, maximum temperature, mean relative humidity, and mean rainfall as predictors. The model, as the case study proved, was the one that could predict the dengue outbreaks 1 to 4 months in advance. Another model that is usually applied in dengue fever prediction, is machine learning. By employing machine-learning models, Stolerman et al. (2019) analyzed the connection between the climate data and dengue cases in the seven state capitals of Brazil. The results demonstrated that climate data relate to the general number of dengue cases. Jain et al. (2019) created the generalized additive models that were capable of predicting the number of cases of dengue fever in fifty Thai districts. They proved that the made models could tell us about the one-month forecasts and the statistical significance of the variables that were used to explain the forecast. The Agarwal et al. (2018) researchers constructed the relationship between the number of dengue cases and the weather conditions by using Naive Bayes. The researchers Nan et al. (2018) proved that XGBoost is a good tool to predict the dengue cases in Guangzhou, China. Besides, Zhao et al. (2020) employed the random forests technique to predict weekly dengue cases in Colombia for the next 12 weeks. The models employed different predictors, that is, historical dengue cases, , population, income inequality, vegetation, rainfall, air temperature as well as education. The outcome of the research revealed that the models that were built on the basis of the random forests were better than the artificial neural networks. The former ones, on the opposite, were the ones to develop models that were far better in the prediction of the number of dengue infection cases. As revealed by Ughelli et al. (2017) the neural networks could predict the dengue cases by up to four weeks. Likewise, in 2018, PJ-Laureano-Rosario and his colleagues provided the models for the prediction of dengue fever based on the neural networks. The ecological models were produced in San Juan, Puerto Rico and the coastal locations of Yucatan towns of Mexico, US. Several different climatic and demographic factors were assessed and used for modellers' projections. The components of the soundings are the temperature of the surface of the sea and the surface air temperature as well as the humidity, the precipitation, the number of inhabitants living in the area, and the number of dengue cases registered before. One might duplicate the facts displayed in the simulation of the dengue fever epidemic with the help of the mathematical model developed for such an event. Saptarini et al. (2018) also recommended ELDN model as model for the forecast of number of dengue suspected patients that may appear in Kupang, Indonesia. They considered the statistics as the forecast, which include average temperature, the average rainfall, the average humidity, as well as average sea level. The model that they come to use turned out to meet even the dengue cases that happened in that region. Not only does the chosen learning model do dengue predictions but so did other learning models as well(Mathulamuthu et al. 2017). I add this remark also with reference to the old postulation. Concerning the Lakelands Carnivore Preservation Accord (2017) and fuzzy logic models (Idris et al. 2018), during which review, four model have been proved to be excellent throughout the whole of the competition.

2.5.2 Dengue Prediction with Deep Learning

Dengue fever not only affects even a small part of the world but also presented in the form of a major health problem and expected which is becoming more and more aggravated by the rapid change of climate. Generally, the county wide, the early dengue warning system ranks as one of the leading health adaptation practises. A plethora of machine learning techniques have been explored by many studies focused on dengue outbreak predictability, these are some the algorithms. There are a lot of statistical and machine-learning models available for the purpose of forecasting dengue incidence and they can be tailored to the data for this task. The models depend on the meteorological data that are very numerous, for example ranging from temperature, rainfall, and humidity. Furthermore, land use index, population density and breeding habitats of Aedes mosquito can also be considered in the projected models. Machine learning has continued developing since the year 2019 as elaborated by the study of Hossain et al. in 2019 that analyzed the variety of machine learning techniques used for detecting dengue. A set of techniques such as decision trees, support vector machines, artificial neural networks, and random forests is used for that purpose. In addition, authors provide a coherent exposition of the methods' pros and cons, giving practical information on what makes each approach more suitable and what aspects should be taken into consideration for better results. Hence, this assessment is very helpful in terms of seeing how each method could be used in the observation of dengue and also for finding out the area that may be needing new method of study. The two main ones all the time are the SVM (Lopez et al. , 2017; Gao et al.). 2016, Lopez et al. 2018, Gao et al. 2017, Gao et al. Of these advanced techniques (Rahman et al. , 2018), decision tree (Lakshmi and Kavitha, 2018), random forests (Wang et al. , 2016, Wang et al. , 2017), and neural networks (Shrestha and

Gautam, 2019) are the most prominently used in worldwide MSR applications studies have compared those machine learning models for dengue prediction in different contexts (Ahmed et al. 2017, Zare et al. 2018, Nguyen and Tran 2016, Aman et al. 2018, Balaji and Kavitha 2018, Pradhan and Singh 2017, Ali and Rehman 2019, Chauhan and Kaur 2019, Tariq and Chaudhary 2019, Abbasi and Abbasi 2018, Das and Roy 2018, Yadav and Bhatia 2015, Ahmed and Hossain 2018, Deshmukh and Deshmukh 2017, Hossain and Ahmed 2017, Jawaid and Raza 2018, Kumar and Kaur 2018, Mohd and Mahmod 2018, Mondal and Kundu 2018, Nguyen and Pham 2020, Ooi and Wong 2018, Pan and Chen 2019, Perera and Ellepola 2020, Ramírez and Díaz 2020, Wang and Zhang 2020). Lately, models of deep learning like LSTM and CNN have been created for dengue prediction. The LSTM model was utilized by Doni and Sasipraba (2020) in order to predict the consequences of dengue cases in India. They concluded that the model had an 89% accuracy in predicting the dengue infection and 81% in predicting deaths. Besides, they also found out that the Root Mean Squared Error (RMSE) lowered as the number of iterations increased. The technology used by Xu et al. (2020) to develop their research is effective because it allows providing a timely and correctly measured forecast of the number of dengue fever cases in China. The researchers used the analysis of the performance of LSTM models to predict dengue fever and the data on forecasting one month before the outbreak. This performance was compared to other published preexisting models. As a result, the authors prove that "the LSTM model is better than other models in the dengue fever prediction process". Indeed, as evidenced by the result that on average the RMSE of the predictions was lowered from 12. 99% to 24. 9% of the other candidate models, and during the outbreak periods, the LSTM model was more successful in predicting the cases of dengue fever than all the other models, with the RMSE ranging from 15.

09% to 26 Overall, the LSTM long short term memory time series forecasting of the dengue illness incidences in Malaysia has an accuracy value accompanied by 82%. In different researches, Saleh and Baiwei in (2021) presented their research regarding the LSTM to predict the number of dengue cases for Malaysia. They conducted the research independently from the research in opening. Having evaluated the results of two models, they highlighted that the Long Short-Term Memory model predicted dengue cases better than the SVR model. In addition, the scientists found out that when the environmental factors were included in the LSTM model, it worked more efficiently. Precisely, the variable were the temperature and the humidity. The project was based on the research by Saleh and Baiwei in 2021 in which the LSTM is employed to predict when dengue fever will occur in Malaysia. The experts gathered their dengue dataset, which is a combination of meteorological and climate datasets, then built the LSTM model. Finally, they contrasted the LSTM with the SVR model. The research findings support the zero R2 scores baseline by indicating that roads with no spectators occupied were more effective than those with spectators. Moreover, the LSTM model was the most successful model out of the SVR, RF and the Random Forest models. The estimated value and the MAE score are 75 and 8 respectively. The Random Forest model was the least successful of all the models. The LSTM model may be used to predict dengue without the expected weather data. The model can identify both long-term patterns as well as the connections between the rise and fall of the number of dengue instances Each additional research that performed the dengue forecast Models using the deep learning methodology are shown in Fig.. Furthermore, this research was also confirmed by the various research that has also done dengue forecast model that was using the deep learning technology at the same time. For example, Zare et al. (2020) developed a hybrid model that would predict DF cases in

Iran. The model if a fusion between CNN and Long-Short Term Memory neural networks. The model was trained to predict the disease frequency during its training session using the meteorological parameters and the disease data from 2011 to 2016, after it trained it was able to predict the disease for the test data set in 2017 to 2018 dataset at high accuracies. Similarly, Maia and co-woker (2019) developed a model to predict dengue fever in Brazil using Long-Short Term Memory neural networks combined with CNN. The dengue incidence data from 2002-2014 was used to perform the training of the model, which allowed the prediction of the test dataset, consisting of cases of dengue from 2015 until 2016. Output was derived from these studies and according to them, the models that incorporate CNN and LSTM hybrid arrangement performed well in dengue forecasting in different regions. LSTM model was also examined by the study of Mussumeci and Coelho; they paid much heed towards the comparison between the LSTM and random forest regression only to predict cases of dengue fever in Brazil. Highpoints. They found out that Linear Support Vector Machine over performed their goal than Random Forest Regression. As key findings in the study, they found that of all expected sizes of city, in the LSTM model the disease spread forecasting likelihood was the highest. Nadda et al. (2020) affirmed that a neural network for a LSTM modelling which is thoroughly connected turned out to be at the highest accuracy in comparison to cross-entropy loss function when going through dengue fever from text symptoms. According to the investigators, the reality was such. Moreover, the comparison of the models' results (SARIMA and LSTM model) for Jambi, Indonesia was also done by Mix and her colleagues (2020). They had proof that both models were handy in plotting the number of the dengue cases. Hence, in both the instances, model's purposeness of predicting total dengue cases was achieved. LSTM technique was far more superior as compared to aforementioned machine learning approaches such as decision trees, artificial neural networks and support vector machines which was used to forecast the dengue cases in China. While LSTMs was examined, which had the performance comparison by Liu and Guo (2021), other algorithms were also considered. They have taken all the models and compared them, held against the bar of other models with a high level of accuracy when compared with the others.

It further becomes unequivocal that LSTM models can serve this purpose given the rigorous researches it has been consistently subjected to. From within LSTM which is a RNN (recurrent neural network) specialized type that successfully handles time series data and discovering long-term dependencies within the data. These characteristics although or even, more eminently make LSTM models specifically appropriate for dengue fever forecasting. Besides, several researches have been done which showed that learning methods like combining with or transfer learning by using additional inputs data, e. g. climate conditions and demography statistics, usually gives better results than the basic one. Different evaluation metrics were used by researchers to evaluate the models performance; Mean Absolute Error (MAE), Root Mean Square Error (RMSE) and Geometric Mean (G-mean) are means of this evaluation. Owing to the fact that different measures were used in various studies, it has become very difficult to compare one study against the other. It is as well necessary to keep in mind that the performance of the LSTMs models depends on the fact of the data being precise and representative for training. It is, however, noteworthy that the strength is depending on the quality and setting of the data as the input. Consequently, it is critical to make sure that the methodology of data selection and processing is solid so that the results from the use of LSTM for dengue fever predictions can become steady and trustworthy. Besides, Nadda et al. (2012), discovered that LSTM is capable of predicting future values with better accuracy than other models at long term relationship in time series. And it is also very effective bloodless technique in handling cases of dengue. What gets compared is the LSTM models. In terms of their performance the models are turned into the best ones after combining them with different machine learning methods having for example the feature selection algorithms or the fully connected neural networks. Moreover, transfer learning allows adjusting one's already existing model to a new dataset, thus it could be used as a tool for improving the learning capabilities of dengue-ridden areas, which have a few dengue cases. However, many studies have proved that the attention processes could be the solution to the problem of improving the LSTM models for the prediction of dengue. LSTM models are put into the attention processes to give a different weight to each input variable, which is decided by the importance of the variable for the prediction. Since the fact that different climate and epidemiological conditions might have different impacts on the transmission of dengue, this is of great importance in the field of dengue prediction. Transformer, LSTM, CNN, as well as Attention-enhanced LSTM (LSTM-ATT) are some of the deep learning models that were used in the development of the model of dengue sickness in Vietnam that was carried out by Nguyen et al. in the year 2022. These models were created using of the data that was ahead of dengue disease occurrences and meteorological variables including rainfall, temperature, sunlight hours, humidity, and evaporation, from twenty provinces in Vietnam between the years 1997 and 2013. It was finally decided that the RMSE and MAE of the models could be calculated by using the data from 2014 to 2016. It is a grade of one on average. A RMSE-based rating of 60 was given to the group, and the rest of the class got a score of one. The research findings show that the LSTM-ATT had the best performance, with a score of 95 for the MAE-based ranking.

Moreover, it was able to predict precisely the occurrence as well as outbreak of dengue fever as well as danger within a period of up to three months. Contrarily, its short-term estimates were less accurate. As a result, the importance of attention processes in LSTM models for dengue prediction. Also, the attention process makes it possible for LSTM to identify those most important variables that are critical in predicting as well as assigning weights to them thereby enhancing better performance. These studies have a significant shortcoming in that they do not provide an all-inclusive view about how good these models are at making long term projections. The majority of studies were based on information gathered over a long time span; hence such data was utilized by the models during training and validation meaning that there are uncertainties with regard to their future performances when it comes to long-range forecasts. Moreover, studies employed information from one specific period and area that may limit the generalization of the results to other places or times; this is a very important consideration. The results need further research to determine if they are applicable and evaluate how models perform under long-term prediction scenarios. In conclusion, these experiments presented that LSTM could a good deep learning model for dengue prediction which gets better when an attention mechanism is added. Besides, further researches have to be done by the researchers to find out the most effective method of applying LSTM and attention processes for the purpose of dengue prediction, and to see if these results can be used in other areas as well.

2.5.3 Spatiotemporal Modelling of Dengue

The Aedes aegypti mosquito, which is the most common vector of the mosquito that carries the dengue virus, bites people and thus spreads the disease. This disease passes through a complex spatiotemporal process which involves the hidden interactions between hosts, vectors, viruses, and the environment among the hosts, viruses and the environment as well as the hosts, viruses and the environment. Besides, the individuals who are infected with the virus can also be a source of transmission of the infection to mosquitoes. These people can be either the ones who are already having the symptoms of a dengue infection, the ones who still have not shown the symptoms yet, and those who are asymptomatic. A pregnant lady might even transfer the infection to her unborn child. The way the dengue virus spreads mainly through epidemic and hyperendemic dengue. The former is when a single viral strain of dengue virus is launched in an isolated incident in a territory. The latter is the characteristic of the continuous and many-serotypes of the virus in a region where the large number of susceptible hosts and the effective vector (with or without the seasonal variation) are constantly present. The building of predictive models is the most complicated task because of the dynamics of dengue. Nevertheless, the development of better predictive models, their becoming easy-to-use, the increase of the processing power, and the inclusion of additional significant predictors have made the tools required to solve this problem available. Many socioeconomic, environmental, and climatic factors have been discovered to be the causes of the dengue spatiotemporal transmission by either the increase of viral multiplication or replacement or the favoring of the vector survival, as per the research done before (Zhu et al. 2018). The Dengue viruses can apparently be transferred to areas which were earlier low-transmission or dengue-free areas because of the human migration, which is the established spatiotemporal causation of the transmission dynamics (Zhu et al. 2018). The usual prediction models, which do not consider the temporal correlation between the increased incidences of disease caused by the short- and long-term memory, presumably correlate the incidence data between regions instantly. On the other hand, there is a temporal order to epidemics (if one region is in the front or the other is behind) (Ferdousi et al. 2021). In near contact with each other, the epidemics can occur after a long period of time with no cases between them. Moreover, it is hard to forecast the fluctuating outbreaks which vary in time and space by the usual methods which involve the identification and the assessment of the occurrence of dengue fever with the reference to the climate variables on a large space-time scale. Therefore, modelling of the temporal dynamics of the disease environment can be the key factor to the incidence predictions especially when the model has the ability to remember the long dependencies in the data. The phase relations of such data are detected using the time-lagged cross-correlation (Schoenherr et al. 2019). The phase data may be utilized to measure the similarities of the epidemics in the near-by areas. The reason for the outbreak of one epidemic being so near to another is that the locations of the two outbreaks are close enough to one another and that the size of outbreak is that it is plausible, studies have theorized that the time dynamics of one epidemic is what makes the dynamics of another epidemic. The finding may be biased as it uses a single computational run of correlation coefficients for the whole period of time under analysis or even for different subsets. Now, the time series of this phase can be divided into several windows and the sequences in each window can be compared by calculating the correlation and phase and then we can get more details about the seasonal pattern of the dengue outbreak. LSTM (the model developed by Hochreiter and Schmidhuber in 1997) is the one that mostly implemented as a time series prediction model because it can modulate long term dependencies. LSTM and its variants have proven highly effective in predicting sequential data （Laptev et al. 2017, Hua e at al. 2019）. They were outperformed by the most other traditional methods as well as by the machine learning schemes in 2019, for the most part. (Zhu et al. 2017). The LSTM-based model may be capable to find notice possible-periodicity patterns which steps are not lineal over multiple times (Xu et al. 2020). In addition, Anno and et al. (2019) produced a climate model-based forecast of dengue epidemics, but alongside a memory module the LSTM Convulutional could be used to forecast proper time and space distribution of the epidemics which should be employed for the further enhancement. Nevertheless, Xu et al. Dengue viral molecular epidemiology (2019) observed that the LSTM representation ceases to represent the features of viral spreading in low engagement areas in dengue cases of occurrence. LSTM merging would however bring in an age where transfer learning higher the accuracy (Xu et al. 2020).

2.6 Model Assessment Methods

The following metrics will be used to assess the model's effectiveness and forecast precision based on the inverse logarithm of the model outputs: RMSE, R2, NPV, specificity, and PPV are the most common metrics which are efficient for measuring the performances of different machine learning techniques. The multi-step tracking was used by applying different percentages of actual from the expected values as diagnostic metrics to evaluate the continuous variable (Hyndman and Koehler, 2006).

2.7 Summary

Datasets of dengue are neither strictly linear nor nonlinear. By majority of the cases, they consist of both nonlinear and linear patterns. A good predictive model should be created in order to correctly model such complicated autocorrelation systems. The complicated relationships between the epidemiological and environmental variables constrain the anticipation of dengue cases. The different geographical locations, in which the incidence patterns are not the same, is the sign of the complex situation of the causes of these patterns of variation. The statistical analysis of the prevalence of diseases is even more difficult because there is a lack of long-term historical data of disease incidence and the environment which affects the risk is an additional factor. Dengue fever forecasting demands the necessity of precise prediction and the classification of the time series data. The present models used for time series forecasting of dengue prediction are still in the elementary stage. The models with the aspects of interpretability, limited data, ease of use, and training cost are in a contrast with the ability to process long sequences which they lack. The prototypes are unable to recall the important facts in the time-series data that are quite long. Though there is no one solution that can solve all these problems, recently, the deep learning models have proved to be successful for computer vision and time-series data tasks (CNN) and (RNN) respectively. Nevertheless, in most cases, deep learning models which have the regular architectures also cannot recall information in the long-time-series data. The research proves that deep learning with attention could be a good reason to talk about. Choosing the variables that are really helpful in predicting can be achieved by using the attention mechanism. The main goal of attention is to pick the right data from the bunch of feature time series data for predicting the target time series.

CHAPTER 3

METHODOLOGY

This chapter presents the description of the study area, datasets, pre-processing, and proposed models for dengue prediction including LSTM with attention mechanism (temporal, spatial) and benchmark models. Finally, it presents the evaluation methods used to measure the performance of the proposed models.

3.1 Study Area

According to Wang et al. (2009), Malaysia is a country situated in Southeast Asia, extending across latitudes from 1° to 7° North and longitudes from 99° to 105° East (see Figure 3.1). The nation is divided into two primary regions: East Malaysia as well as Peninsular Malaysia, the latter comprising the states of Sarawak, Sabah, as well as the Federal Territory of Labuan, collectively referred to as Malaysian Borneo. These two territories are separated by the South China Sea. Peninsular Malaysia covers a land area of 131,587 square kilometers.

Figure 3.1 illustrates the map of the region under study. Malaysia's geographical location as well as climatic conditions make it particularly vulnerable to the spread of infectious diseases like dengue fever. The country features diverse topographical elements, including floodplains, hills, and coastal areas, and experiences a humid tropical climate with temperatures typically ranging from 21 to 32 degrees Celsius. Malaysia experiences two main monsoon seasons: the Northeast Monsoon, which lasts from October to March, as well as the Southwest Monsoon, occurring from May to September (Diong et al., 2015; Moten et al., 2014). These weather circumstances are key to the local environmental factors that promote the spreading of vector-borne diseases like dengue, hence making this a pressing public health issue in the area. These monsoons are found particularly in the country of Malaysia. About a third of the year's total precipitation falls on this transitional month (Wang et al. , 2009). While dengue incidences are not common in all districts of Malaysia, some states are especially challenged by this disease - Selangor, Kelantan, Johor, Pulau Pinang, and Melaka. Notably, Selangor stands out as the most severely affected state, accounting for a staggering 90% of the total dengue cases reported nationwide in Malaysia (Ministry of Health Malaysia, https://www. moh. gov. my/). It can be explained by a set of factors such as a high number of residents of Selangor, the urbanization process, and conditions that are suitable for the breeding of Aedes mosquitoes – the major carrier of dengue virus. The urban landscapes and the abundance of person in highly populated areas creates a lot of sites where mosquitoes can breed thereby enhancing the spread of the virus. Additionally, even other states such as Kelantan, Pulau Pinang, Johor, and Melaka have to contend with similar difficulties as well when it comes to preventing the transmission of dengue. These regions acquire high transmission rates because of factors such as climate conditions, building of new settlements and concentrated populations that give mosquitoes a suitable environment for breeding and the spread of diseases.Dengue outbreaks in these regions prove that a vigilant public health intervention comprising a community driven approach is crucial for the effective prevention of this mosquito-borne disease. The history of dengue infections in Malaysia started in the year 1902 when two cases under official documentation were identified. Nevertheless, Dengue did not really emerge as a big public health concern in the country until the late seventies. The incidence of dengue fever was first observed in a big scale in 1973, according to Shepard et al. (2013) and Mohd-Zaki et al. (2014). In the course of the in the past few decades, the trend of the dengue cases reported in Malaysia has been on the raise. Based on the latest statistics, the incidence has soared from 32 per 100,000 persons in 2000, to about 361 in 2014.According to the Ministry of Health in Malaysia, the majority of dengue patients in Malaysia are between the ages of 15 and 49, as well as according to the Ministry, roughly 80 percent of cases occur in metropolitan areas. Dengue fever normally reaches its peak four to six weeks following an epidemic in Malaysia and then begins to decline after that.

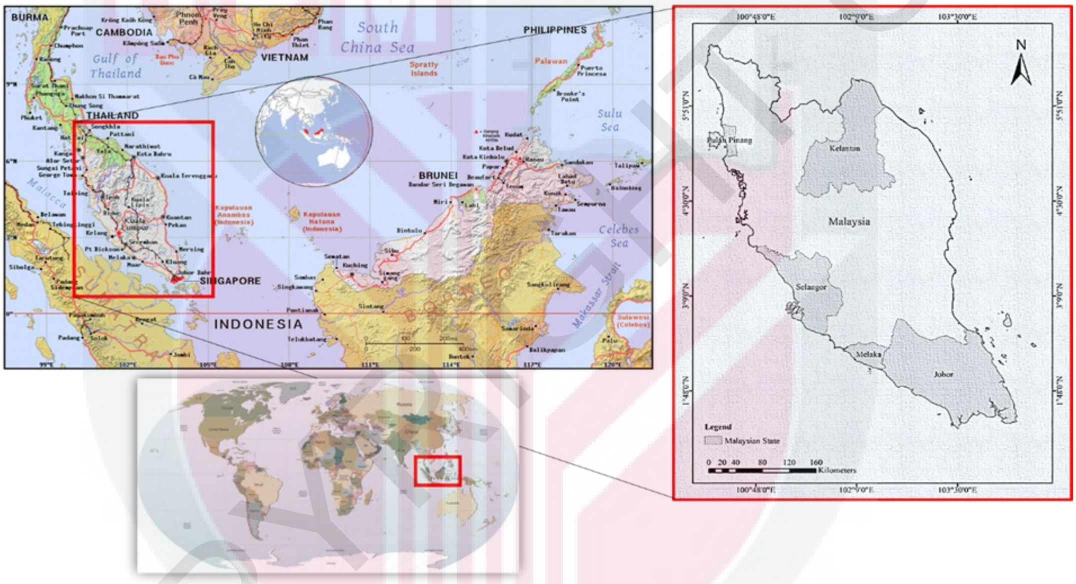


Figure 3.1 : Map of the Peninsular Malaysia Showing the Five States Studied in this Work

3.2 Data Used

For this research, the information was obtained from an open data repository available at the Malaysia Open Data website, which presented a weekly dengue incidence at the state level across Malaysia from 2011 to 2016. The dataset which have been the Ministry of Health data deals with the Selangor, Kelantan, Pulau Pinang, Johor and Melaka state. This report presents death cases of Dengue from all states in a week and summed this up monthly for the purpose of analysis. The data array gives the detailed summary about dengue fever occurrence in the country on a span of seven years, which makes it a great tool for trends and pattern identification of this infectious disease. Through studying this wealth of data, researchers can catch a clear picture of the spatiotemporal nature of dengue epidemics. Such information is of great importance, giving a chance to develop sophisticated prevention and control strategies. Table 3. 1 in this research is the detailed information on the datasets used in the analysis and how the obtained data are classified. This facilitates an in-depth analysis of dengue spread's factors, thus, helps in realization of the general health status of the affected states in terms of dengue fever consequences. Among the main aims of this analysis is to provide support in scientific evidence for better-informed public health policies and interventions.

Table 3.1 : Data Sources and Details That Used to Extract Attributes Used in Dengue Prediction Models

Variable	Data	Period	Temporal Resolution	Spatial Resolution	Source
Dependent	Dengue cases	2011-2016	Monthly	State-level	Malaysia Open Data
Climate	Rainfall	2011-2016	Daily	0.25 degree	CMORPH precipitation
	Land surface temperature	2011-2016	Monthly	0.05 degree	MODIS
Geographic	Vegetation index	2011-2016	16-days	0.05 degree	MODIS
	Digital elevation model	nan	nan	30 arc-seconds	Diva GIS (CGIAR SRTM)
	Land cover	nan	nan	30 arc-seconds	Diva GIS (GLC2000)
	Road networks	nan	nan	nan	Diva GIS (Digital Chart of the World)
	Water bodies	nan	nan	nan	Diva GIS (Digital Chart of the World)
Demographic	Population	2011-2016	Yearly	State-level	Malaysia Open Data

In Malaysia, there are five states of particular interest: Ji Jor, Kelanten, Pulau Pinang, Melaka Kurnal, together with Selangor. Figure 3. 2 describes the number of monthly dengue cases from October 2011 to October 2016 in details. The table, being in digressive order, has columns for each month and year, where the states' number of cases are shown in the respective columns.

The data showing the month-wise variations and the disparity across states is very interesting. Moreover, selangor has seen more dengue cases than other states over the time period considered. This variation is vividly manifested through months with a high incidence of dengue and during other months with much lower reported numbers. The dataset showed that some states didn't reported even one case of dgengue that means there were such periods when transmission rate was low. The dataset is led by January 2011 since it lists the highest number of dengue cases in one month, when Selangor recorded 480 cases. This surge demonstrates the dynamic character of dengue outbreaks and the requirements for continuous monitoring and targeted public health measures instituted for the purpose of managing the disease outbreak within the context of its control. Altogether, the data from these five states give a complete idea of the dengue trends for the 6-year-duration period by signposting problem areas/regions that require interventions for dengue eradication and control. And the standard deviation of 37. 3. there was an average of 22 cases of dengue disease every month in Johor. 8. The calculate average and standard deviation for Kelantan were similarly obtained. 5 and 10. 6 respectively. Both Melaka and Pulau Pinang showed 2. 9 medio de actuación del 15. 27. 23 and 2 units of standard deviation. 8. Melaka's average was 14. The mean of the unemployment rate between 2017 and 2019 for S'pore was 2, while the standard deviation for Pulau Pinang was 16. 4. Finally, Selangor has a standardized mean of 177. 9 and standard deviation was 116. 3 on the scale.

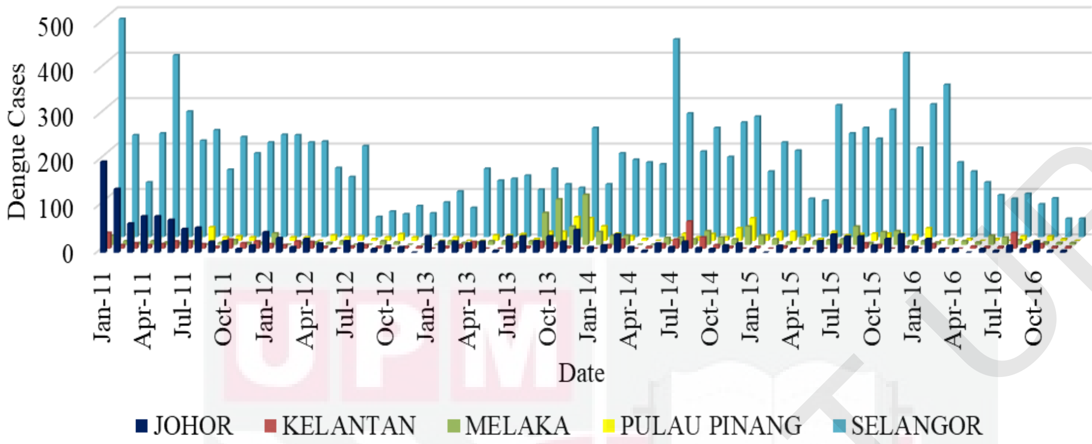


Figure 3.2 : Monthly Dengue Fever Incident Cases for Five Different States in Malaysia from 2011 to 2016

The number of dengue cases that occurred each month in the other states was significantly varied from one another, which is another point that should be brought up. While the range for Johor was 180 instances (200 in January 2011 to 20 in March 2011), the range for Selangor was 455 cases (480 in January 2011 to 25 in October 2011). For example, the range for Johor was 180 cases. This demonstrates that the distribution of dengue cases was more unequal in some areas in comparison to other states throughout the country. Due to the fact that the transmission of the illness is impacted by a variety of variables at both the state and local levels, the data demonstrates that dengue is a complex as well as multi-layered issue in Malaysia. Using a multi-pronged strategy that takes into consideration all of these different elements and seeks to uncover the origins of the condition is probably going to be required in order to find a solution to the problem. Furthermore, the present research is based on a dataset that covers all of the parameters that are connected to dengue fever incidences in Malaysia from 2011 to 2016. One of the critical things that affect the distribution of goods and services is climate, geography, and demography. The variance of dengue cases manifested at the state level with a monthly measurement is the dependent variable that our dataset is formed of as regards the information. Establishment of the platform, which is known as Malaysia Open Data paly the role of being the background on which this dataset is accessible. It includes in the forecast the temperature of soil as well as the rate of precipitation. These air materials are given with a spatial preciseness of 0. 25 degrees in the case of resolution that only goes down to daily interval in the case of satellite and to monthly in the case of the weather balloon. The rainfall data is obtained from the CMORPH data product, whereas the land surface temperature data is extracted from the MODIS dataset. Besides climatic data, as well as the dataset brings in those geographic factors. They might contain different factors such as the vegetation index, digital elevation model, land cover, the road network, and the water bodies. The spatial resolution depends on the imaging product type and varies from 0 for vegetation index to 10 km for land surface temperature. 005 degrees and up to 30 arc-seconds. At the same time, the digital elevation model, land cover, road network, and water body are imported respectively with resolutions of 30 arcseconds. The vegetation index integrates the MODIS dataset and the Diva GIS platform that extracts data from the Digital Chart of the World and CGIAR SRTM, respectively. Spatially, the data will be generated over a consistent transect, which will allow a detailed analysis of the varying agricultural practices. MODIS is the big fish in the academic pond as far as the provision of this data is concerned. Moreover, the dataset contains a set of demographic variables, each unique, such as, census count (a single-year temporal resolution). In short, the dataset is comprised of diverse climatic, geographic and demographic traits, and as a result it has proven to be a robust platform of analysis and appreciation of the factors behind the distribution of dengue fever in Malaysia.

3.3 Methodology

3.3.1 Data Pre-Processing and Preparation

In order to analyze the aforementioned dengue data set, there were a few preparatory steps that had to be put in place so that it remained reliable and useable for the study. This data management activities focused on the capture of data records and their cleaning and filtering processes ensuring thoroughly acceptable standards. Data translation covers the general task of moving data from one format to another and synchronization of datasets, either by time and location. Data preparation, the fundamental data engineering process, generally required for correct datasets consistency and accurate analysis is critical during integration and usage. Therefore, this highlights the importance of careful data preparation needed in the main analysis in order to ensure the validity and dependability of the analyses. As it came to the appropriate dengue data processing, the leading roles of lag variables were impossible to underestimate. The argues that these is the ones that determine what a particular variable takes in a past date. Specifically, lags variables were inserted in the model for the time periods of 1 to 6 months lagged. Thus, the relationships between factors are analyzed over the time; hence they provide trends and patterns, otherwise, we may spend a lot of time looking at the data without noticing anything. Anyway, those preprocessing procedures where the reason why that dataset could be a good choice for the analysis that , of course, gave me confidence because the results were accurate and reliable.

3.3.2 LSTM

The feed-forward neural networks are known to be good at the feature learning from the data, however, they are not the ideal model for the sequential data. RNNs are the solution to this problem because they are created to include the feedback connections that help the model to directly capture the sequential data and its temporal dynamics. In contrast to feed-forward networks, RNNs are more biologically plausible because they contain a memory of the previous activations which makes them learn the underlying temporal structure of the data. Nevertheless, RNNs are usually not good enough as the vanishing or exploding gradients can, in fact, be a serious problem that will affect the performance of the RNNs.

The fundamental obstacles encountered by LSTM networks are related to the mitigation measures for the overfitting problem and gradients vanishing, which were first pointed out and solved by researchers Hochreiter and Schmidhuber in 1997 when a new concept for the Long Short-term Memory networks was introduced. Unlike conventional RNNs, LSTM networks are designed as an extension, incorporating memory blocks composed of self-linked memory cells as well as three multiplicative units: don't worry them too much with gates, inputs, and outputs. Their main task is basically controlling information incoming in the memory domain and making it possible to perform efficient operations. Through such effective regulation, LSTM networks have been shown to be able to grasp and keep in mind long-term relationships of sequential data and this enhances the accuracy of representation of the complex temporal processes. To sum up, during training, LSTM networks with expanded memory blocks and multiplication units acquire unmatched capability to distinguish and comprehend complex temporal sequences. Hence, the LSTMs are ultimately more capable of analyzing sequential data when they are equipped with the additional multiplicative units and memory blocks during training. Such advanced architecture resolves the common weaknesses of the traditional RNNs and caps the way for engergy-efficient and more accurate performance in many applications like those of natural language processing and time series forecasting. In the following manner, the mathematical formulation of an LSTM unit may be stated (see to Figure 3. 3):In the following manner, the mathematical formulation of an LSTM unit may be stated (see to Figure 3. 3):

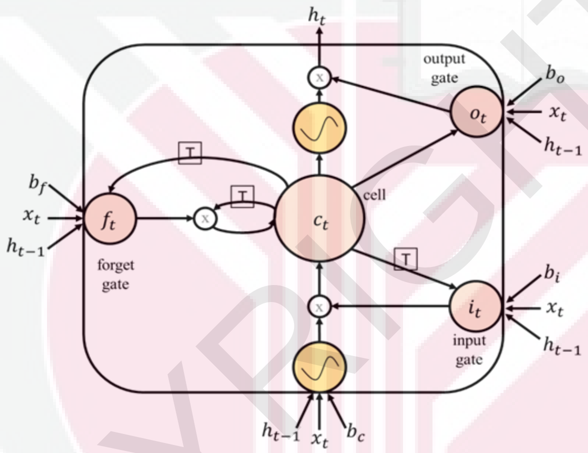


Figure 3.3 : A Basic Single-Cell LSTM (Hochreiter and Schmidhuber, 1997)

The input gate, i, controls whether to allow new information to enter the memory block. It is defined as:

$$i = sigmoid(W_{ii} * x + W_{hi} * h + b_i) \tag{3.1}$$

where x is the input to the LSTM unit, h is the previous hidden state, W_{ii} and W_{hi} are the weights connecting the input and previous hidden state to the input gate, and b_i is the bias term for the gate of input.

The forget gate, f, controls whether to erase the previous information stored in the memory block. It is defined as:

$$f = sigmoid(W_{if} * x + W_{hf} * h + b_f) \quad (3.2)$$

where W_{if} and W_{hf} are the weights connecting the input and previous hidden state to the forget gate, and b_f is the bias term for the forget gate.

The output gate, o, controls whether to output the information stored in the memory block. It is defined as:

$$o = sigmoid(W_{io} * x + W_{ho} * h + b_o) \quad (3.3)$$

where W_{io} and W_{ho} are the weights connecting the previous hidden state and input to the output gate, and b_o is the bias term for the output gate.

The memory cell, c, stores the information in the memory block. It is updated using the input and forget gates as follows:

$$c' = f * c + i * tanh(W_{ic} * x + W_{hc} * h + b_c) \quad (3.4)$$

where W_{ic} and W_{hc} are the weights connecting the previous hidden state and input to the memory cell, and b_c is the bias term for the memory cell.

The hidden state, h, is updated using the output gate and memory cell as follows:

$$h = o * tanh(c') \quad (3.5)$$

This is the kernel of the LSTM unit that includes the computation of the four basic functions which are transient at the center of the machine's operations. Through the stacking together of numerous LSTM units one upon another, it can therefore be possible to build a luminescent LSTM network that is a versatile framework where a variety of tasks can accommodate extremely well for example, dengue prediction. The neural networks are proficient at handling the nature of time series data by modeling and learning about the complex temporal dynamics, thus making it possible to have accurate predictions and insights into the progression of disease outbreaks such and as osteomyelitis.

3.3.3 Temporal Attention Mechanism

The contemporary trend to make the models more reliable and attain a better deep learning is the development of attention mechanisms. As Raffel and Ellis (2015) emphasize, preference mechanisms ensure that the input is matched output at a given point to a specific time. Figure 3. Considering the loop as a notion, the research is conducted in the next paragraph.

Let us assume that a model generates a hidden state h_t at each time step, Attention models construct a "context" vector c_t as the weighted mean of the state sequence h by:

$$c_t = \sum_{j=1}^{T} \alpha_{tj} h_j \tag{3.6}$$

where T is the time steps total number in the input sequence and α_{tj} is a weight computed for each state h_j at each time step t. These context vectors used to compute a new state sequence s, where s_t depends on s_{t-1}, c_t and the model's output at $t-1$. The weightings α_{tj} computed by:

$$e_{tj} = a(s_{t-1}, h_j), \alpha_{tj} = \frac{exp\,(e_{tj})}{\sum_{k=1}^{T} exp\,(e_{tk})} \quad (3.7)$$

For this formulation, the letter 'a' represents a learned function that looks at the "importance" value of 'hj' but when the function is already looking at 'hj', the previous state value is already available at 'st-1'. This kind of mechanism provides singes of the better parts of the state space for the purpose of executing transition from one state sequence to the other 'h'. Many kinds of time transductioning works, such as predicting diseases (Men et al. , 2021), forecasting floods (Ding et al. , 2020), solving traffic problems (Zheng et al. , 2020), and predicting time series (Li et al. , 2019), have already proven the efficiency of attention-based RNNs. Here the jobs illustrate how attention mechanisms not only enhance repetitiveness but also contribute to intricate features and therefore lead to predictive networks.

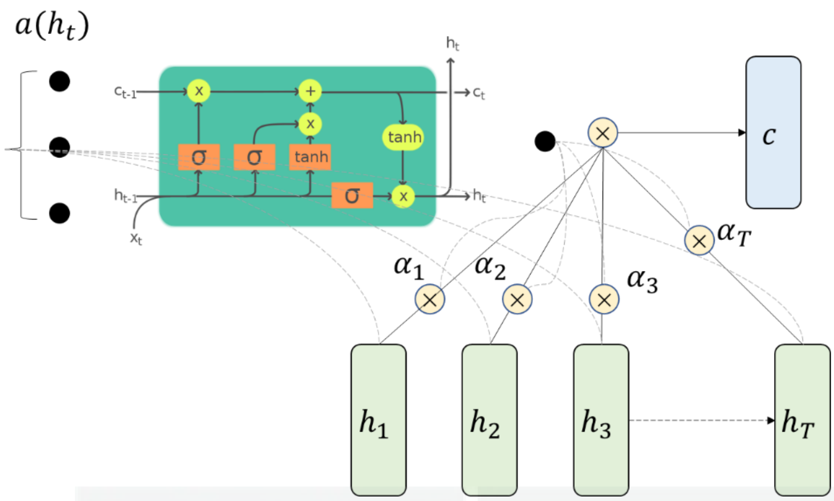


Figure 3.4 : The Basic Concept of Working of the Proposed Temporal Attention (Song et al. 2016)

3.3.4 Spatial Attention Mechanism

Spatial attention is an LSTM technique to scan input data at different times in a different way rather than processing the entire input in a similar manner. This is helpful for dengue prediction tasks since it enables the model to identify the most significant data information on which it should pay attention. Therefore, it will not be overwhelmed via noise or irrelevant information. A spatial attention module is typically, located between input layer and LSTM layers of an LSTM network. It is its customary place. By using weights obtained during training process, spatial attention module sums up all inputs during training phase. These weights depict how important each attribute of the input was when considering the particular task being performed by this model. The next is a description of the mathematical formulation of the spatial attention module at a mathematical level: The following represents the mathematical description of the spatial attention module: Normally, this gets its input into a matrix with dimensions N x D where N is the number of time steps as well as D is the number of input features. In combination with W and b which are learnt parameters, input data are used by spatial attention module to determine weights for each input feature. We calculate the weights as follows; Using both input data and learnt parameters (W, b), weight (a) can be computed for each individual element in an entire range. These weights come from what value we receive after entering the corresponding elements into our equation.

$$a = softmax(XW + b) \tag{3.8}$$

The softmax function is a function that transforms the input values to a probability distribution of the input features.

The weighted is then calculated as:

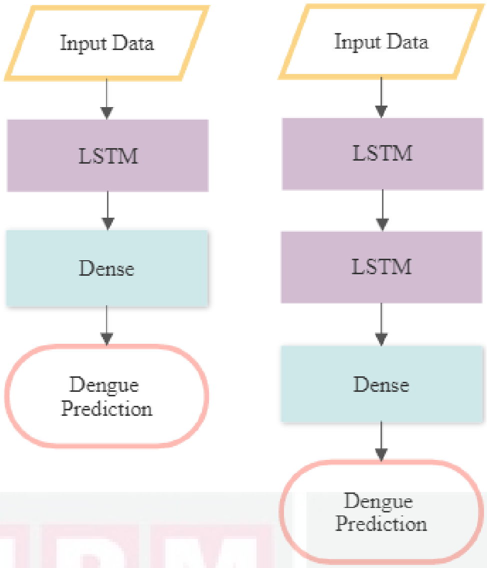
$$X' = Xa \tag{3.9}$$

The output is a weighted sum that furthermore is a concise description of the data, where the strengths most important for the model are emphasized. Shortly after this, the inputs go through the quality control procedure to produce the output that will be relayed to the LSTM layer the same way as any other input. In addition to that, the hidden state undergoes yet another update in accordance with the previously described rules. This last step employs the LSTM layer bottom-up out to predict the number of dengue cases occurrenctly in next time step. By employing the spatial attention module, the integration of it increases the selectivity power in LSTM network about the input features of highest interest in dengue predictions. This critical approach of core input attributes may hold promise towards high fidelity as well as dependable outcomes, resulting in an enhanced model with more accurate and reliable predictions.

3.3.5 The Proposed LSTM

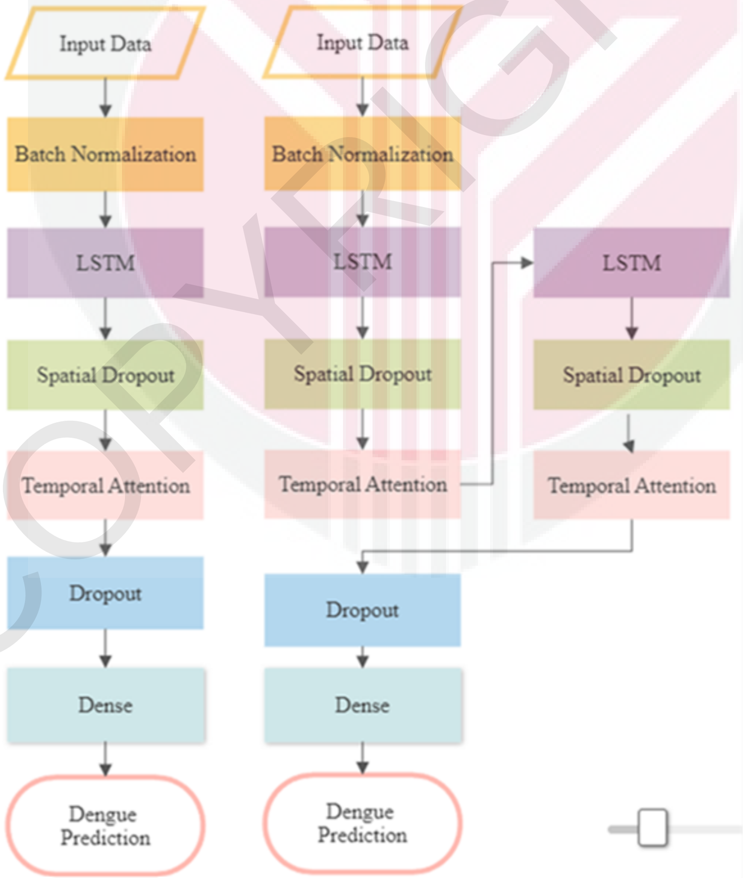
3.3.5.1 LSTM Architecture

Many models can be implemented in Malaysia for a prediction of dengue fever, these are composed of different frameworks that specifically address this one task. This model names comprise of Long Short-Term Memory (LSTM), Stacked LSTM (S-LSTM), Stacked LSTM with temporal attention (TA-LSTM), LSTM augmented with temporal attention (TA-LSTM), LSTM enhanced with spatial attention (SA-LSTM), and the Stacked LSTM with spatial attention (SSA-LSTM). The LSTM design is called for; this calls for a single-layer LSTM to serve as the first layer; the last layer should be dense. The LSTM layer has four units and input is provided in form a three-dimensional tensor which is (batch size, look_back, n_features). The parameter 'look_back', as the previous step, refers to the count of preceding time steps, whereas 'n_features' describes the number of features present in the input data. The proposed 'Spatiotemporal' structure provides the basis for the model to dynamically adjust parameters and handle important temporal correlations and features capable of capturing the temporal propagation process inherent in dengue fever.In Figure 3.5, the dense layer is comprised of a single unit that ultimately results in a two-dimensional tensor with the form (batch_size, 1). Due to the fact that the S-LSTM design is composed of two LSTM layers stacked on top of each other, it is able to distinguish more intricate patterns within the data (refer to Figure 3. 5). At every time step, the temporal attention mechanism is applied to the input sequence by TA-LSTM in order to make a prediction. With this information, the model is able to hone down on the most significant aspects of the input. Figure 3.6 illustrates how attention processes may be effective in situations when the input sequence is lengthy as well as may include a great deal of noise or information that is not relevant to the task at hand. In terms of its structure, STA-LSTM is comparable to TA-LSTM; however, it is distinguished by the presence of two LSTM layers that are stacked on top of each other, as seen in Figure 3. 6. The SA-LSTM algorithm is similar to the TA-LSTM algorithm; however, rather than paying attention to the sequence of inputs throughout the course of time, it focuses on distinct components of the input at each time step (Figure 3. 7). There are situations in where the input is a two-dimensional spatial map, and the model has to concentrate on various portions of the map at different times. This may be beneficial in such situations. As seen in the image (image 3. 7), the SSA-LSTM is a variant of the LSTM that is composed of the S-LSTM and the spatial attention processes. Other layers were incorporated in the design of all of the models, with the exception of the LSTM model. (1) A Batch Normalization layer that accepts a three-dimensional tensor of shape (batch_size, look_back, and n_features) as its input. Through the use of this layer, the input data is normalized across the batch dimension, which enhances the model's capacity to learn. In order to facilitate the model's ability to generalize to new data, a Spatial Dropout as well as Dropout layer with a dropout rate of 0.2 is used. This layer randomly assigns a portion of the input units to 0 while the model is being trained. The models were built using the'mean_squared_error' loss function and the 'nadam' optimizer working together. The run_eagerly option was set to True throughout the compilation process. The'mean_squared_error' loss function is a popular option for regression tasks, as well as the 'adam' optimizer is often quick as well as memory economical. Both of these functions are described here.



(a) LSTM (b) S-LSTM

Figure 3.5 : Architecture of (a) LSTM and (b) S-LSTM



(a) TA-LSTM (b) STA-LSTM

Figure 3.6 : Architecture of (a) TA-LSTM and (b) STA-LSTM

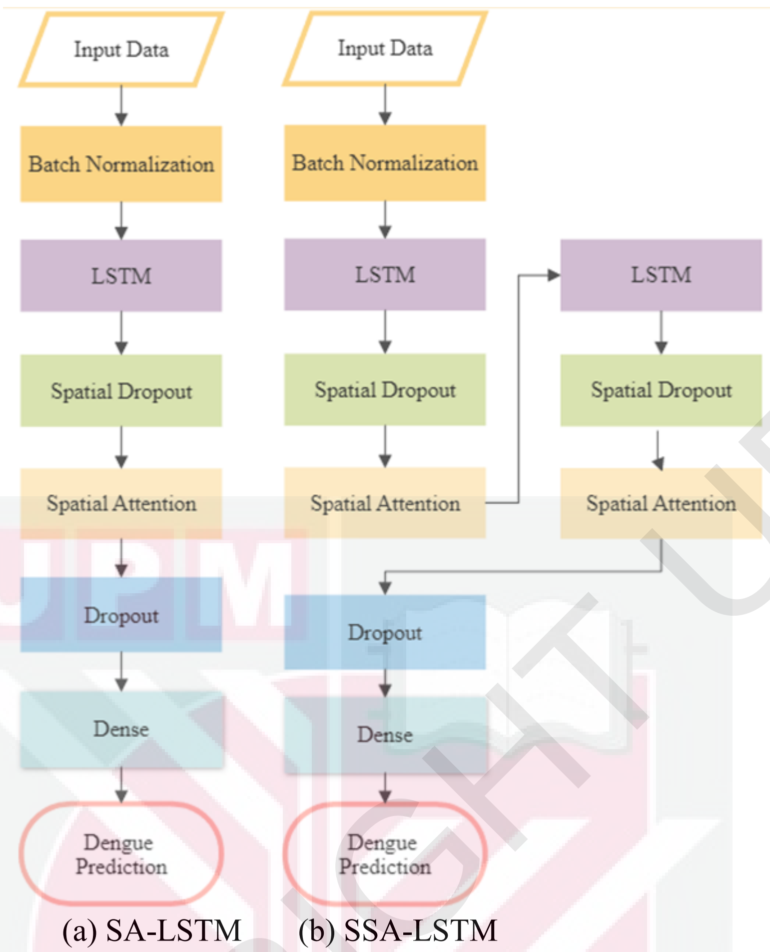


Figure 3.7 : Architecture of (a) SA-LSTM and (b) SSA-LSTM

Moreover, the LSTM with integrated temporal as well as spatial attention models, specifically the ST-LSTM and ST-SLSTM, were developed for dengue fever prediction (Figure 3.8). These models leverage the strengths of LSTM, temporal attention, and spatial attention to capture long-term dependencies, focus on relevant time steps, and consider spatial factors in the prediction process. The ST-LSTM model (Figure 3.8) consists of multiple layers, including batch normalization for improved training stability, an LSTM block (Figure 3.8) for capturing long-term dependencies, dropout for preventing overfitting, dense layers for mapping LSTM outputs, and an output layer for predicting dengue cases. The ST-SLSTM model (Figure 3.8) shares the same architecture as ST-LSTM, however, with the inclusion of two LSTM blocks instead of one. This extra complexity enables the model to acquire the more complicated temporal dependencies, thus, it was able to improve its prediction capacity.

Dengue fever is dependent on the varying time-varying factors such as climate variables, population dynamics, and human behavior. Temporal attention gives the LSTM model the chance to concentrate on the particular time steps and to give the importance to the different time periods when it makes the predictions. The model, in turn, will be able to deal with the crucial temporal patterns and the long-term dependencies of the dengue transmission dynamics and will, therefore, be able to come up with accurate predictions. Besides, dengue is not a homogenous process, so the transmission of the disease can be different in different areas of the world. Spatial attention is the tool that lets the LSTM model to concentrate on the specific spatial features, like local climate conditions, land cover, and population density, while predicting the dengue cases. Through the inclusion of the spatial data, the model is able to get the spatial patterns of dengue transmission and thus, the predictions are given based on the location. Besides, dengue cases are usually found in a specific place or hotspot because of the local factors such as stagnant water sources, urbanization and socioeconomic conditions of the place. The LSTM model, through the use of spatial attention, is able to recognize and to be aware of the high-risk areas and thus assigns the higher weights to the spatial features that are relevant to these areas. This allows for the focused interventions and allocation of resources to the areas that are more affected by dengue hence control of the disease becomes more effective.

In a nutshell, the combination of both the temporal and spatial attention in LSTM models, on the one hand, enables a fuller grasp of the intrinsic dynamics of dengue transmission. The study of the temporal and spatial dimensions will allow the model to discover the complex relationships and interactions between different factors which influence dengue and consequently it will increase the accuracy of the prediction. Thus, this can be a helping hand to public health authorities in making the decisions in a proactive manner, on the allocation of resources and the implementation of preventive measures.

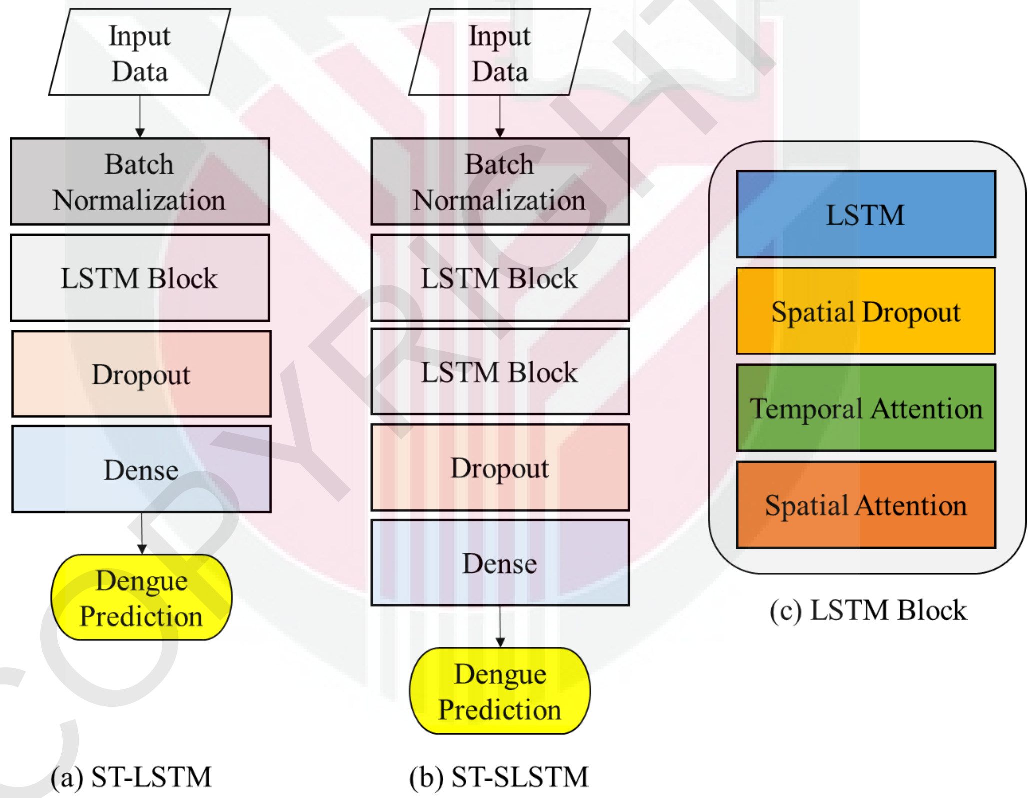


Figure 3.8 : Architecture of the LSTM Models (ST-LSTM, ST-SLSTM)

3.3.5.2 Training Process

The LSTM model training process for dengue prediction consists of the successive tuning of the parameters model in order to decrease the variance of the model obtained from the actual and the predicted dengue cases. The procedure of the optimization algorithm which adjusts the parameters of the model is a significant element that can determine the performance and the convergence speed of the model. The most of the time, the Adam algorithm is the one that is used for the LSTM models optimization. Adam is a stochastic gradient descent optimization algorithm that combines the benefits of two other prominent optimization algorithms: RMSprop and AdaGrad are the pairs of models whose descriptions will be given below. A technique was developed to obtain the learning rate based on the exponential decay of the average of squared gradients from the distant past. Thus, the learning is adapted in such a way as to make a gradual reduction to the magnitude of a gradient is proportional to the average magnitude of the gradients that precede it. This shall be carried out for the purpose of realizing that the learning shortcuts are appropriate. This is why Adam can gradually reduce the learning rate during the training process for each parameter while taking into account its historical gradients.This, in turn, helps the model to converge more quickly, which in turn helps to avoid the issue of becoming trapped in local minima altogether. The increment size of the optimization process is determined by the learning rate, which is a hyperparameter. A slower learning rate may help the model converge more gradually as well as with stability, but it can also create a delay in the training process. When the learning rate is slower, the model is more likely to converge with stability. Furthermore, the growth rate causes the model to fluctuate or diverge, despite the fact that it speeds up the training process. We utilized a learning rate of 0.001 in our dengue model of prediction since it is the default value that is most widely used and has shown to be the most successful in a variety of action situations. The loss function is the difference between the number of lung disease cases that were anticipated and the number of actual lung disease cases. This instrument is used to evaluate the performance of the model throughout the training phase, and as a result, it serves as a second assistant for the optimization process. Both the nature of the job and the qualities of the data are taken into consideration when determining the appropriate setting for the loss function. When it comes to assignments involving dengue prediction, the MSE loss function would be the most suitable option since it calculates the average of squared differences between the dengue cases that were predicted and those that actually occurred. The MSE is a loss that is sensitive to outliers and has the ability to make big mistakes more penalized than the little errors; as a result, it is an excellent option for the tasks that contain continuous variables. The following steps were applied:

1. The data for the training is prepared by preprocessing and formatting it thus, the model can take it as an input. This would be the method of reducing the data to the same scale, the handling of the missing values, and the generation of the lag variables for the series.

2. Following this, you will begin the process of initializing the parameters of the model, as well as the optimization method, the learning rate, and the loss function.

3. The information is divided into smaller batches and then iterated over each of those portions. Apply the input data to the LSTM model for each mini batch, and then use the projected dengue cases to calculate the loss using the loss function that you have chosen.

4. The fourth step is to apply the Adam optimization algorithm to the parameters of the model in such a way that it is updated in line with the calculated loss and the learning rate.

5. Repeat steps 3 and 4 for a predetermined number of epochs or until the loss has reached a level that is acceptable or until it has ceased improving.

6 In order to maintain control over the training process, it is necessary to assess the performance of the model on a validation set. This validation set is a

portion of the training data that is used to test the model's capacity to generalize. In this manner, it is possible to prevent the model from being overfit, and it will not acquire knowledge from the noise that is present in the training data.

7. Saving the trained model and its parameters for later use is a necessity.
8. To verify if the model learnt anything, try running it with a different test set or part of data that was never trained nor validated. Consequently, we can examine how effective the model is in real life for data that it had no exposure to before.

3.3.6 Benchmark Models

The suggested model was built to enable comparison with the best performing benchmark models, and understand its performance in comparison with other alternatives it had. This comparison considered three models; Artificial Neural Network (ANN), Decision Tree Support (DT) and Vector Machine (SVM). These sources however make up some of the best references for scientific papers on dengue prediction that can be used when working on new models. The non-linear support vector machine (SVM) which uses radial basis function kernel to solve complicated as well as nonlinear problems is an SVM model. It is a powerful and accurate model which can handle difficult data sets but has a very high computational cost for training, and requires careful selection of parameters. To find the best hyperparameters C and gamma that regulate respectively a regularization term and a radial basis function kernel, we trained an SVM model with grid search over these two parameters. DT model was an easy yet powerful model using tree structure for making predictions matching input features. It's also popular in designing quick and simple methods for handling difficult large-scale datasets such as Decision Trees. Nevertheless, if the tree is too deep, it may be seen as overfitting. In order to obtain optimal values, a grid search was made on the DT model for changing hyperparameters associated with best split, splitter, maximum tree depth. On the other hand, neural network (ANN) is an artificial network that has several layers whereas this allows for representing complex associations and regularities in it. BERT model is a reliable and maintainable one which is just right for projects involving huge datasets with sophisticated natures. However, it might need more training data compared to simpler models so that training will be expensive as well. The BERT model fits well into tasks that come with such challenges. To select hyperparameters that are most appropriate, the grid search considered hidden layer sizes, learning rate, optimizer, activation function and number of epochs. The SVM model's hyperparameter C is set at 1. A higher value for C suggests that there is a greater degree of regularization since C determines the amount thereof. The only single element in artificial neural network (ANN) is the hidden_layer_sizes tuple with the value 100. Consequently, this implies that the model has only one single hidden layer with a hundred neurons on it. The solver is "adam", the activation function is "relu" as well as the alpha regularization term equals to 0.0001; it means that 'adam' is also a solver

The batch_size parameter is configured to utilize the 'auto' setting, while the learning_rate parameter is assigned the 'adaptive' setting, and a specific value of 0.001 is designated to facilitate the model's operation over a duration of 200 seconds. Activating the Early_stopping flag enables the model to leverage the early stopping functionality, which intervenes in the training process if the validation score fails to exhibit improvement. For our DT model, the mse criterion is adopted, which is defined as "mse", and the splitter defined is "best". " As for a more detailed setting, the max_depth parameter is set to 4, while the max_features parameter is configured to 'auto' ". These collectively settings prepare the decision tree model perfectly for learning and prediction, so that the model will be rich enough to contain complex relationships in the data and also ideal for performing the given task. There will be a variety of combinations to use if the experiment is to produce results as desired. The splitter component is the one that determines the split at every node, max_depth is the component that controls the depth of the tree, and max_features is the one that is related to the number of features to be considered while either searching or looking for the optimal split. The features influencing the function are depicted by the separated evaluate function hypermnesis. In table 3, four model's boundaries which serve as reference points has been presented. 2.

Table 3.2 : The Configuration of Benchmark Models' Hyperparameters

Model	Hyperparameter	Optimal Value (by grid search)
LSVM	C	10
RBFSVM	C	10
	Gamma	scale
DT	Best split criterion	Mean Square Error (MSE)
	Splitter	best
	Maximum tree depth	4
Shallow ANN	Hidden layer sizes	(128,)
	Activation function	ReLU
	Optimizer	Adam
	Learning rate	0.001
	Epochs	200
Deep ANN	Hidden layer sizes	(128, 64, 32)
	Activation function	ReLU
	Optimizer	Adam
	Learning rate	0.001
	Epochs	200

3.3.7 Validation

The root mean square error (RMSE) is an approach used to assess the accuracy of model predicted values and check how they conform to real values. To compute the root mean square error (RMSE), you must square the difference between predicted as well as observed values, sum all squared differences, divide by the total number of pairs of data, and calculate a square root for mean square error (MSE), which is defined as an average of squared differences between predicted and actual values. Because it provides a precise summary that details mistakes made by the model, RMSE is often employed as a benchmark for various model's performance. The initial stage involves the model generating predictive values associated with a given input data group. These are compared with actual instances contained in the data as further inputs into RMSE computation based on differences between both sets of variables. The RMSE goes down as the model gets more accurate in predicting dengue cases. There is one advantage of root mean square error (RMSE) for evaluating prediction models for dengue. Initially, it is the most used, familiar and easiest measure to understand and verify. Also, this is not affected by any outliers within the data set. Moreover, aside from other uses, the root mean square error (RMSE) is a way of quantifying the difference between the mean and a certain data point that changes with size of data. This becomes very important where datasets have various different values. In summary, RMSE or Root Mean Squared Error helps access how well the dengue prediction models perform while indicating which models are most accurate and effective regarding predictions made using them.

$$RMSE = \sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(Y_t - \underline{Y_t}\right)^2} \tag{3.10}$$

In this formula, yt is the number of dengue cases forecasted by the model, and yt is the number of dengue cases that were observed during time-based observation. The lowe rRMSE value demonstrates that the model's prediction ability has improved, meaning that differences between predicted values as well as actual values are also lowered down.

CHAPTER 4

RESULTS AND DISCUSSIONS

In the section "Results," we can see a detailed scrutiny and appraisal of LSTM models furnished with spatial-temporal attention, that were developed for predicting dengue occurrence in Malaysia. The chapter gives a comprehensive account of how the experiments were done, data collected, model trained and evaluation indices used. Also, it contains major findings and comparison between LSTM models and benchmark models indicating that LSMs are preeminent at forecasting overall number of dengue fever cases.

4.1 Results of First Experiment (LSTM with Temporal Attention)

4.1.1 Performance of LSTM Models

In the exploration of monthly dengue case prediction across five Malaysian states, four distinct variants of LSTM models were employed. The summarized performance metrics of these models are presented in Table 4.1. Throughout the experimentation process, the entire dataset encompassing samples from all five states was utilized for training and testing. The outcomes are depicted across various lookback values spanning from one month to six months. An analysis of the results reveals that A-LSTM emerged as the top-performing model, boasting the lowest average Root Mean Square Error (RMSE) at 3.663. Following closely behind, SA-LSTM secured the second position with an RMSE of 3.674. Meanwhile, LSTM and S-LSTM exhibited nearly identical performances, with respective RMSE values of 4.154 and 4.133. These findings underscore the efficacy of integrating attention mechanisms into LSTM models, as evidenced by the enhanced predictive accuracy achieved in the study area.nNotably, both LSTM and S-LSTM models demonstrated improved accuracy attributed to the incorporation of attention mechanisms. This indicates that the attention mechanism plays a pivotal role in capturing and leveraging crucial information within the data, leading to more precise predictions of dengue cases across the Malaysian states under investigation.

Table 4.1 : Summary Results of LSTM Models' Performance with Different Lookback Values Based on Test Samples

Lookback	Performance (RMSE)			
	LSTM	S-LSTM	SA-LSTM	A-LSTM
1	3.75	3.72	3.26	3.27
2	3.57	3.62	3.12	3.10
3	5.06	5.11	4.55	4.58
4	3.74	3.85	3.42	3.23
5	3.99	3.85	3.36	3.42
6	4.78	4.62	4.31	4.34
Min	3.57	3.62	3.12	**3.10**
Max	5.06	5.11	**4.55**	4.58
Average	4.15	4.13	3.67	**3.66**
Std.	0.61	**0.59**	0.60	0.63

4.1.2 Impacts of Temporal Attention

In LSTM models, attention enhances the model's memory for long dependencies. However, the effects of attention in these models have yet to be tested for dengue case prediction. As a result, this study examines the effects of temporal attention on LSTM and S-LSTM models. According to the results of this research, attention improves the effectiveness of both LSTM and S-LSTM in terms of producing accurate predictions. The results, on the other hand, indicate that the LSTM model reaps more benefits from the attention than the S-LSTM model does. LSTM models have the capability to modeling complicated dengue data; however, this capability is generally coupled by the issue of overfitting, which is caused by the increased number of model parameters.

Nevertheless, the discoveries of this research prove that this can be solved using the attention mechanism by allowing the model to concentrate on the important sequences of the input data while training and making predictions. Nevertheless, the results of this project show that the model can be trained and predict by focusing on the critical sequences of the input data when there is a problem of the model by using the attention mechanism.

4.1.3 Comparison of LSTM and Benchmark Methods

To assess the justified LSTM models, five benchmark models were utilized for predicting dengue cases. Table 4. 2 states the mean performance of various models on the five Malaysian states. With an average RMSE of 4.597, the model RBFSVM performed the best. With an average RMSE of 4.910, the LSVM performed worse than the RBFSVM. The fact that the RBFSVM outperformed the LSVM suggests that the dengue data is nonlinear. The D-ANN, on the other hand, outperformed the S-ANN and the DT. It had an RMSE of 4.636 on average. The S-high ANN's error rate (5.354 RMSE) demonstrates that dengue data is nonlinear and difficult to model. With an average RMSE of 5.354, the DT model performed the worst. Figure 4.1 shows the comparison among LSTM models and benchmark models.

Table 4.2 : Summary Results of Benchmark Models' Performance with Different Lookback Values

Lookback (months)	Performance (RMSE)				
	LSVM	**RBFSVM**	**S-ANN**	**DT**	**D-ANN**
1	4.98	4.44	5.47	4.82	4.66
2	4.91	4.37	5.32	5.58	4.42
3	5.04	4.76	5.43	5.60	4.53
4	4.64	4.44	5.13	5.93	4.42
5	4.76	4.67	5.17	5.69	4.76
6	5.11	4.86	5.58	4.96	5.00
Min	4.64	**4.37**	5.13	4.82	4.42
Max	5.11	**4.86**	5.58	5.93	5.00
Average	4.91	**4.59**	5.35	5.43	4.63
Std.	0.17	0.20	**0.17**	0.43	0.22

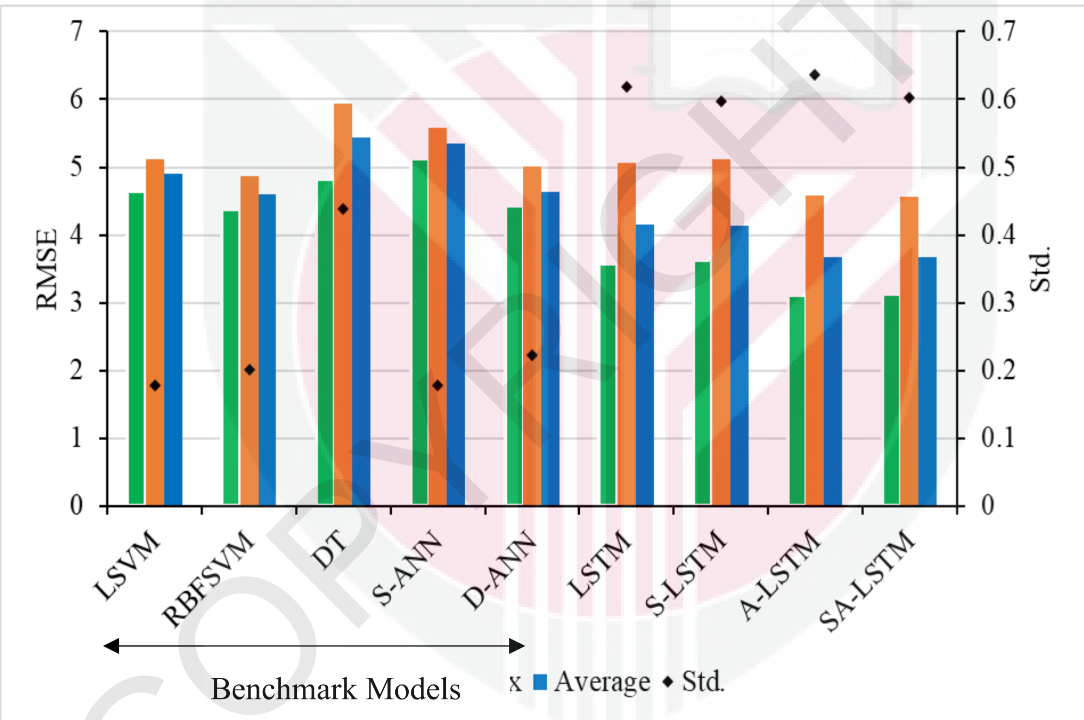


Figure 4.1 : Comparison of LSTM Models and Benchmark Models

4.1.4 Impacts of Attribute Selection

4.1.4.1 Impacts of Attribute Selection on LSTM

In this research, three different kinds of attributes—climatic, geographic, and temporal—were investigated specifically for the purpose of predicting dengue cases.

The climatic category included both the temperature of the land's surface and the amount of rainfall. All of the elements that comprised the geographic group were the vegetation index, elevation, land cover, road networks, and bodies of water included. Additionally, a demographic characteristic, such as population, was included into this specific group. It was decided to incorporate the lag time of the properties that were specified in the temporal group. A comparison is shown in Table 4.3 between the performance of various LSTM models on different groups of characteristics and the performance of all the groups. By using the LSTM models that were provided, the primary objective of this study was to investigate the ways in which each attribute group influenced the accuracy of dengue case prediction. The findings show that almost all the models performed better across all attribute groups (climatic, geographic, temporal). All the 1–6-month lookbacks that were evaluated yielded similar results. The findings indicate that the models perform better with more extra parameters in addition to the climatic ones. Furthermore, the findings reveal that for the prediction of dengue cases, geographic variables are more important than temporal attributes.

Table 4.3 : Summary Results of LSTM Models' Performance with Different Attribute Selection and Lookback Values

Lookback	State	Performance (RMSE)			
		LSTM	S-LSTM	SA-LSTM	A-LSTM
1	Climatic	5.478	5.721	6.766	5.589
	Climatic + Temporal	3.849	3.919	4.970	3.950
	Climatic + Geographic	3.841	3.769	3.993	6.000
	Climatic + Temporal + Geographic	**3.759**	**3.729**	**3.266**	**3.278**
2	Climatic	4.504	4.023	3.593	4.129
	Climatic + Temporal	5.010	4.580	4.001	4.443
	Climatic + Geographic	4.176	4.364	3.478	4.047
	Climatic + Temporal + Geographic	**3.575**	**3.620**	**3.124**	**3.100**
3	Climatic	5.238	5.914	5.987	5.322
	Climatic + Temporal	5.361	6.311	6.031	5.584
	Climatic + Geographic	5.304	6.051	5.040	4.975
	Climatic + Temporal + Geographic	**5.061**	**5.113**	**4.557**	**4.589**
4	Climatic	4.237	4.280	**3.008**	3.474
	Climatic + Temporal	4.546	4.878	3.736	3.857
	Climatic + Geographic	4.328	4.574	3.495	3.414
	Climatic + Temporal + Geographic	**3.748**	**3.856**	3.421	**3.237**
5	Climatic	6.684	5.646	5.971	5.385
	Climatic + Temporal	5.895	5.357	4.743	4.527
	Climatic + Geographic	4.942	4.835	4.354	4.277
	Climatic + Temporal + Geographic	**3.991**	**3.853**	**3.364**	**3.423**
6	Climatic	6.981	7.435	6.986	6.354
	Climatic + Temporal	5.879	5.598	6.207	5.141
	Climatic + Geographic	5.044	5.016	5.251	4.437
	Climatic + Temporal + Geographic	**4.789**	**4.629**	**4.313**	**4.349**

4.1.4.2 Impacts of Attribute Selection on Benchmark Models

A number of attribute groups were evaluated using benchmark models in order to determine the significance of their role in the prediction of dengue cases (Table 4.4). Both the linear and the RBF SVM models worked well when the meteorological and geographic data were combined. When all of the characteristics were considered together, the other models, DT, S-ANN, and D-ANN, presented the best performance.

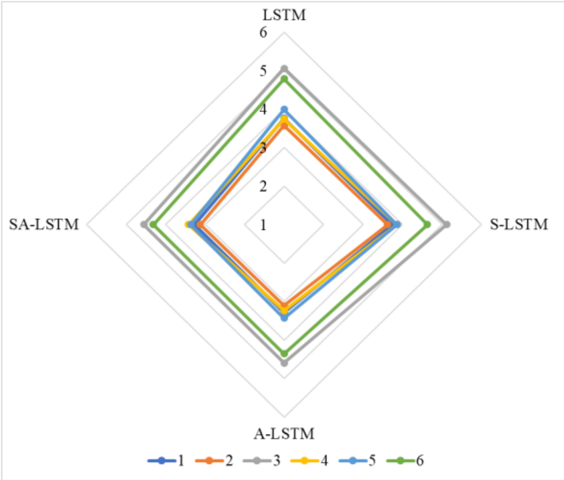
When all of the qualities were matched with certain lookback values, LSVM performed at its highest level. The results suggest that the RBFSVM could better model the data's complex nonlinear interactions. The LSVM, on the other hand, requires the additional temporal variables to achieve the best results.

Table 4.4 : Summary Results of Benchmark Models' Performance with Different Attribute Selection and Lookback Values

Lookback	State	Performance (RMSE)				
		LSVM	RBFSVM	D-ANN	DT	S-ANN
1	Climatic	5.057	4.544	4.933	5.297	5.901
	Climatic + Geographic	**4.979**	**4.359**	4.766	5.294	5.593
	Climatic + Temporal	5.431	4.708	4.900	4.854	5.801
	Climatic + Temporal + Geographic	4.984	4.448	**4.661**	**4.824**	**5.474**
2	Climatic	5.655	4.427	4.704	6.294	6.070
	Climatic + Geographic	4.949	**4.292**	4.530	6.291	5.416
	Climatic + Temporal	5.625	4.697	4.649	5.601	5.910
	Climatic + Temporal + Geographic	**4.911**	4.375	**4.427**	**5.581**	**5.324**
3	Climatic	5.938	4.855	4.902	5.910	6.569
	Climatic + Geographic	5.049	**4.657**	4.741	5.883	5.599
	Climatic + Temporal	5.928	5.113	4.801	5.623	6.405
	Climatic + Temporal + Geographic	**5.041**	4.767	**4.536**	**5.603**	**5.432**
4	Climatic	5.644	4.508	4.638	5.965	6.256
	Climatic + Geographic	4.648	**4.349**	4.508	5.944	5.197
	Climatic + Temporal	5.579	4.739	4.488	5.964	5.931
	Climatic + Temporal + Geographic	**4.643**	4.449	**4.429**	**5.934**	**5.131**
5	Climatic	5.538	4.715	4.946	5.712	6.248
	Climatic + Geographic	**4.755**	**4.612**	4.798	**5.699**	5.199
	Climatic + Temporal	5.492	4.946	**4.747**	5.709	6.059
	Climatic + Temporal + Geographic	4.763	4.674	4.762	**5.699**	**5.177**
6	Climatic	5.943	4.940	5.287	4.971	6.538
	Climatic + Geographic	5.134	**4.837**	5.126	**4.963**	5.599
	Climatic + Temporal	5.929	5.205	5.122	**4.963**	6.402
	Climatic + Temporal + Geographic	**5.119**	4.869	**5.003**	**4.963**	**5.587**

4.1.5 Impacts of Lookback Steps on Modelling Outcomes

The performance of the proposed LSTM and benchmark models for forecasting dengue cases with a variety of lookback parameters is shown by the graphs in Figure 4.2. With lookback values ranging from one to two months and four months, the LSTM models fared the best when it came to predicting dengue cases. Their performance was the poorest when looking back at data from six and three months ago. Different results were obtained by each of them in the benchmark models. DT fared the best while looking back at the data from one month, whereas the other models performed the best when looking back at the data from four months. With four months of lookback, DT did not perform well. With a six-month lookback, the other models performed the worst. The detailed results of this experiment are summarized in Tables 4.5 and 4.6.



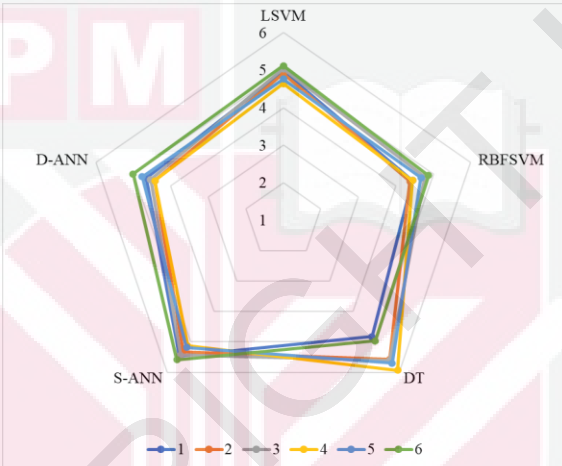


Figure 4.2 : Radar Charts of Prediction Performance of the Proposed and Benchmark Models with Different Lookback Values

Table 4.5 : Summary Results of LSTM Models' Performance in Different Malaysian States and Different Lookback Values

Lookback	**State**	**Performance (RMSE)**			
		LSTM	**S-LSTM**	**SA-LSTM**	**A-LSTM**
1	Selangor	8.77	8.772	0.671	8.363
	Johor	4.498	4.493	1.786	4.007
	Pulau Pinang	2.241	2.234	1.463	1.841
	Kelantan	1.269	1.208	4.111	0.762
	Melaka	2.019	1.937	7.452	1.418
2	Selangor	7.905	7.863	0.971	7.355
	Kelantan	1.463	1.386	4.219	0.958
	Melaka	2.018	2.099	9.529	1.699
	Johor	4.682	4.919	1.285	4.212
	Pulau Pinang	1.807	1.831	1.694	1.275
3	Selangor	10.076	10.342	0.87	9.794
	Kelantan	1.437	1.413	5.839	0.881
	Johor	6.275	6.288	2.209	5.815

Table 4.5 : Continued

	Pulau Pinang	2.639	2.67	4.336	2.111
	Melaka	4.878	4.85	6.021	4.342
4	Selangor	6.223	6.515	2.264	5.674
	Kelantan	2.725	2.756	5.15	2.236
	Melaka	2.244	2.44	7.514	1.664
	Johor	5.27	5.293	1.862	4.774
	Pulau Pinang	2.276	2.278	1.808	1.839
5	Selangor	8.374	7.765	0.64	7.417
	Kelantan	1.336	1.198	5.222	0.875
	Melaka	2.391	2.247	8.905	1.805
	Johor	5.628	5.76	1.916	5.243
	Pulau Pinang	2.225	2.294	1.528	1.775
6	Selangor	9.653	8.814	2.088	8.952
	Kelantan	2.738	2.495	5.719	2.066
	Johor	5.92	6.096	1.599	5.808
	Pulau Pinang	1.782	1.923	3.252	1.599
	Melaka	3.851	3.817	8.301	3.319

Table 4.6 : Summary Results of Benchmark Models' Performance in Different Malaysian States and Different Lookback Values

Lookback	State	Performance (RMSE)				
		LSVM	RBFSVM	D-ANN	DT	S-ANN
1	Selangor	10.292	7.471	8.300	7.569	12.623
	Kelantan	2.504	2.615	2.629	3.128	2.536
	Melaka	5.210	5.252	5.017	5.230	5.123
	Johor	4.370	4.280	4.587	4.010	4.535
	Pulau Pinang	2.544	2.623	2.771	4.181	2.552
2	Selangor	10.358	7.529	8.422	8.973	12.863
	Kelantan	2.571	2.567	2.419	2.993	2.387
	Johor	4.828	4.946	4.497	5.410	4.752
	Pulau Pinang	3.490	3.631	3.404	4.911	3.416
	Melaka	3.310	3.201	3.394	5.616	3.200
3	Selangor	12.458	10.838	9.895	11.108	14.615
	Kelantan	2.476	2.398	2.484	2.479	2.441
	Melaka	3.137	3.261	3.194	5.639	3.039
	Johor	4.722	4.706	4.436	4.689	4.599
	Pulau Pinang	2.413	2.632	2.670	4.101	2.465
4	Selangor	9.566	8.453	8.649	11.893	12.314
	Kelantan	2.719	2.524	2.393	3.160	2.415
	Johor	4.148	4.174	4.110	4.740	4.135
	Pulau Pinang	2.544	2.888	2.826	4.106	2.657
	Melaka	4.237	4.205	4.167	5.771	4.132
5	Selangor	9.410	8.853	9.202	11.231	11.842
	Kelantan	2.622	2.591	2.732	2.813	2.436
	Melaka	5.096	5.134	4.950	5.151	4.957
	Johor	3.960	3.948	3.984	4.682	3.954
	Pulau Pinang	2.729	2.844	2.944	4.618	2.697

Table 4.6 : Continued

6	Melaka	5.473	5.511	5.380	5.262	5.372
	Kelantan	2.188	2.349	3.167	2.802	2.332
	Johor	4.251	4.218	4.057	4.203	4.114
	Selangor	9.457	8.039	8.400	8.454	11.996
	Pulau Pinang	4.225	4.227	4.011	4.095	4.123

4.1.6 Modelling Performance in Different Malaysian States

This study's dengue prediction has been tested in five Malaysian states: Selangor, Kelantan, Johor, Pulau Pinang, and Melaka. In terms of complexity and quantity, the data from different states differ. Though, for practical reasons, a comparison of the proposed models in these states is useful. In Kelantan and Pulau Pinang, the models performed best. In Selangor, they scored the worst. The models performed moderately in the other two states, namely Johor and Melaka, as compared to the other states. Figures 4.3 and 4.4 show the results of the comparison.

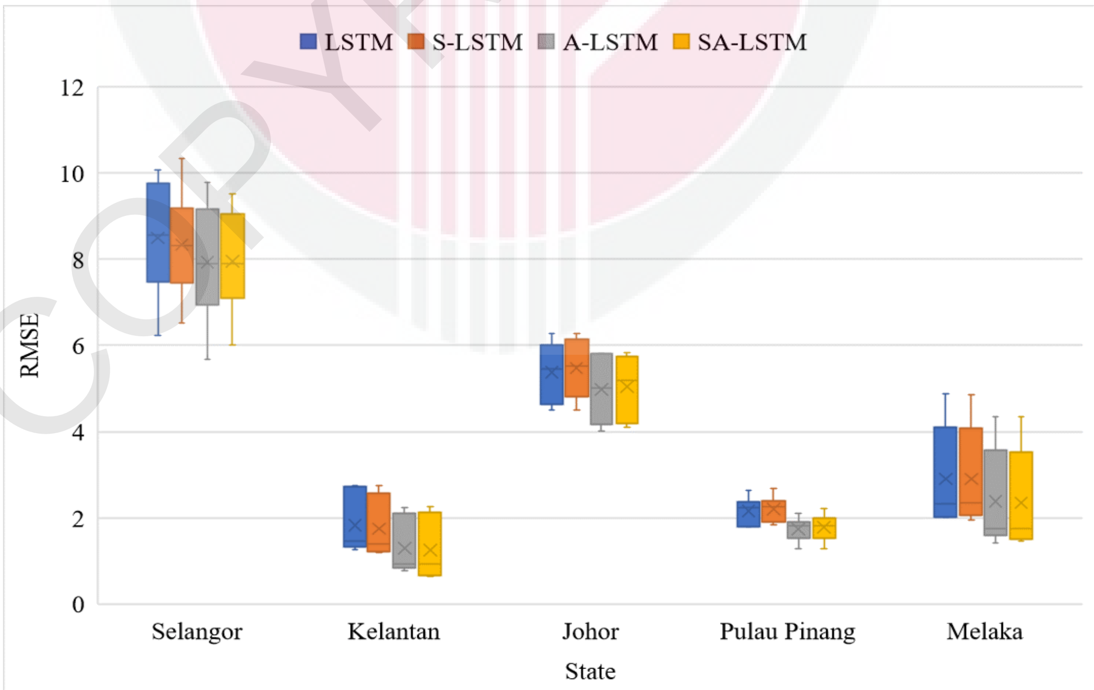


Figure 4.3 : Comparison of LSTM Models' Performance in Different Malaysian States

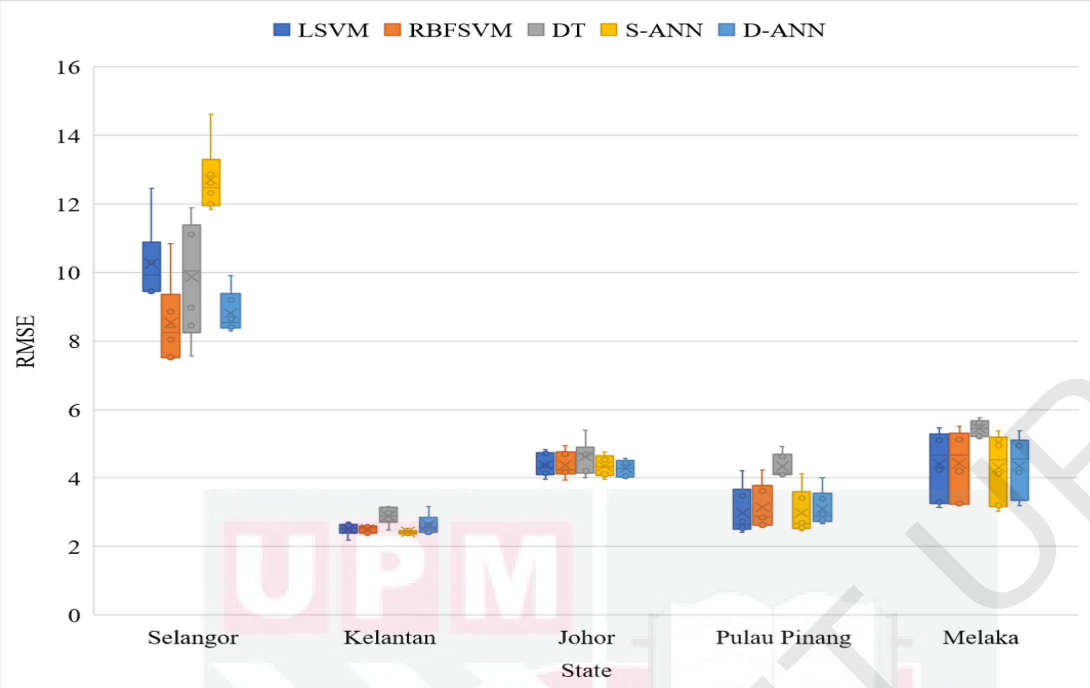


Figure 4.4 : Comparison of Benchmark Models' Performance in Different Malaysian States (Each Box Represents the Various Lookback Experiments)

4.2 Results of Second Experiment (LSTM with Spatial/Integrated Attention)

4.2.1 LSTM Model Evaluation

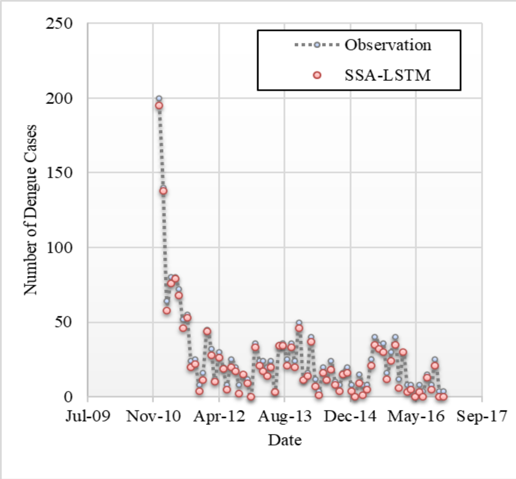
Table 4.7 provides a comprehensive comparison of several distinct models, including LSTM, S-LSTM, SA-LSTM, STA-LSTM, TA-LSTM, as well as SSA-LSTM. The primary distinguishing factor among these models lies in the type of attention mechanism employed. While some models incorporate temporal attention (STA-LSTM, TA-LSTM), others integrate spatial attention (SSA-LSTM, SA-LSTM). Notably, both LSTM as well as S-LSTM models operate without any attention mechanism.

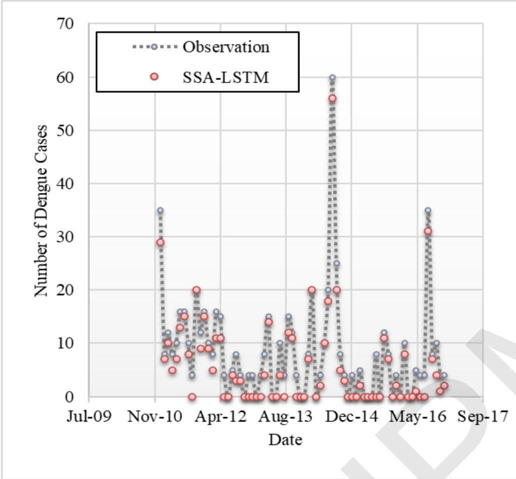
Throughout the analysis, a dataset that contained monthly dengue incidences in Malaysia over the period of 2011 - 2016 was chosen as the training and evaluation datasets. This data set included climatic, geographical, demographic, and landscaping factors, which cover the most comprehensive set of the elements to be accurately predict the number of dengue cases. For this purpose, the models utilized the variety of data sources which enabled them to detect the complex interrelationships coinciding different factors impacting the transmission dynamics of dengue and substantially improved their prediction accuracy. Forecasting is influenced by the important determinant which is the reminiscence about the number of time steps (n period) considered by the models. The comparison among the models by means of the assessment metrics, regarding MAE, MSE and also the maximum and minimum values, shows that the SSA-LSTM yields the smallest average error which is 3. A 17 average mean square error is given by the Keras LSTM model, whereas the NNU pdating model's RMSE is the highest at 4. 15. The fact, that the SSA-LSTM model gives more precise predictions and the SSA-LSTM model is superior because of the greater accuracy in the model. Stacked LSTM layers frequently beat the models that don't incorporate attention mechanisms, having no relevance on their presence or absence. One of the reasons for this might be the additional complexity phenomenon afforded by a stacked LSTM models; this additional feature helps the model to identify more complex patterns and information within data. RMSE comparisons of SSA-LSTM in various Malaysian states are presented in Figure 4. 5 and Figure 4. within the same small age-group, the number of dengue cases recorded in those states compared to actual reported cases. RMSE is one of the most important metrics when it come to measuring the errors of the models that had been deployed, it also means that the models are reliable and effective. The lesser RMSE is interpreted as a sign as the model is doing well. The SSA-LSTM models have a straightforward approach in their performance. They perform well, with most of the RMSE values falling between

2. Usually, when I get home, I find that: 91-4. 55. is the rule. Among all state, Kelantan gets the lowest rMSE, followed by Melaka, Selangor, Johor and Penang as well. Out of all locations, Pulau Pinang presents the highest RMSE. In term of SSA-LSTM, the stat only Kelantan and Melaka show a higher level of performance than the other ones. We should also highlight that the RMSE values are usually lower than 5 meaning that SSA-LSTM models produce predictive data that is within acceptable error standard. If the RMSE decreases, it suggests that the model might be fitted better. Even so, there is always that constant possibility of advancement. Additionally, the data and the models are going to be put together for a later research in order to identify the factors which actually made the variations in the performance and also to estimate the way the performance could be improved. Authors go further and provide extra data in a different Dialogue Section which is not part of the previous one.Table 4.7: Performance of different LSTM models for dengue prediction in Malaysia.

Table 4.7 : Performance of Different LSTM Models for Dengue Prediction in Malaysia

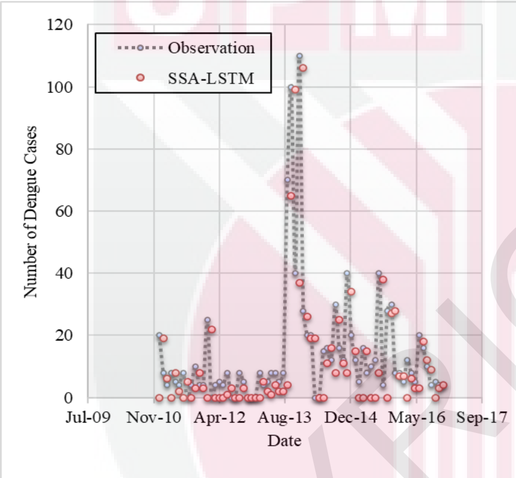
Lookback	Model					
	LSTM	SSA-LSTM	S-LSTM	STA-LSTM	TA-LSTM	SA-LSTM
1	3.75	3.22	3.72	3.26	3.27	3.65
2	3.57	3.07	3.62	3.12	3.10	3.06
3	5.06	3.58	5.11	4.55	4.58	4.95
4	3.74	2.71	3.85	3.42	3.23	3.85
5	3.99	2.65	3.85	3.36	3.42	3.62
6	4.78	3.76	4.62	4.31	4.34	4.11
Mini	3.57	2.65	3.62	3.12	3.10	3.06
Maxi	5.06	3.76	5.11	4.55	4.58	4.95
Average	4.15	3.17	4.13	3.67	3.66	3.87
Std.	0.61	0.41	0.59	0.6	0.63	0.58

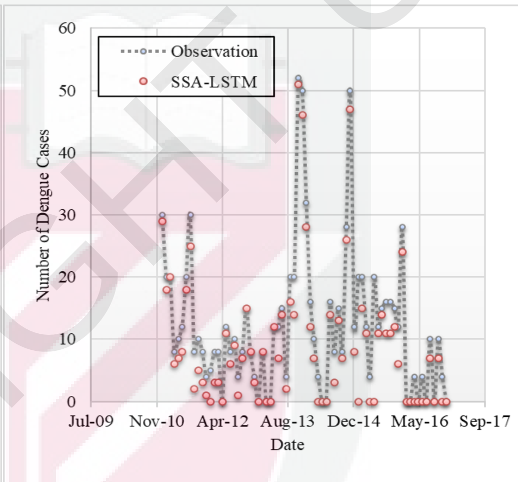




Johor

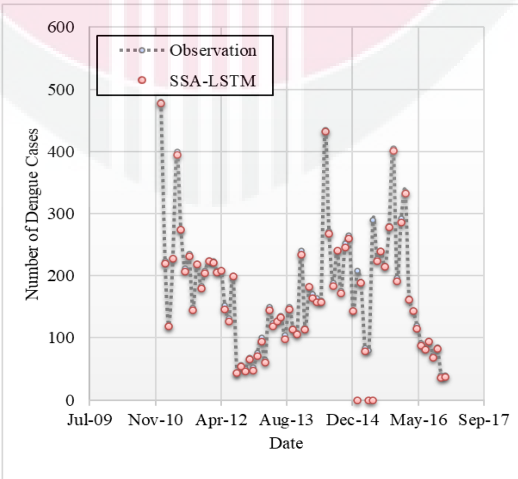
Kelantan





Melaka

Pulau Pinang



Selangor

Figure 4.5 : Performance of SSA-LSTM Model for Dengue Fever Prediction in Five Malaysian States, Measured by RMSE

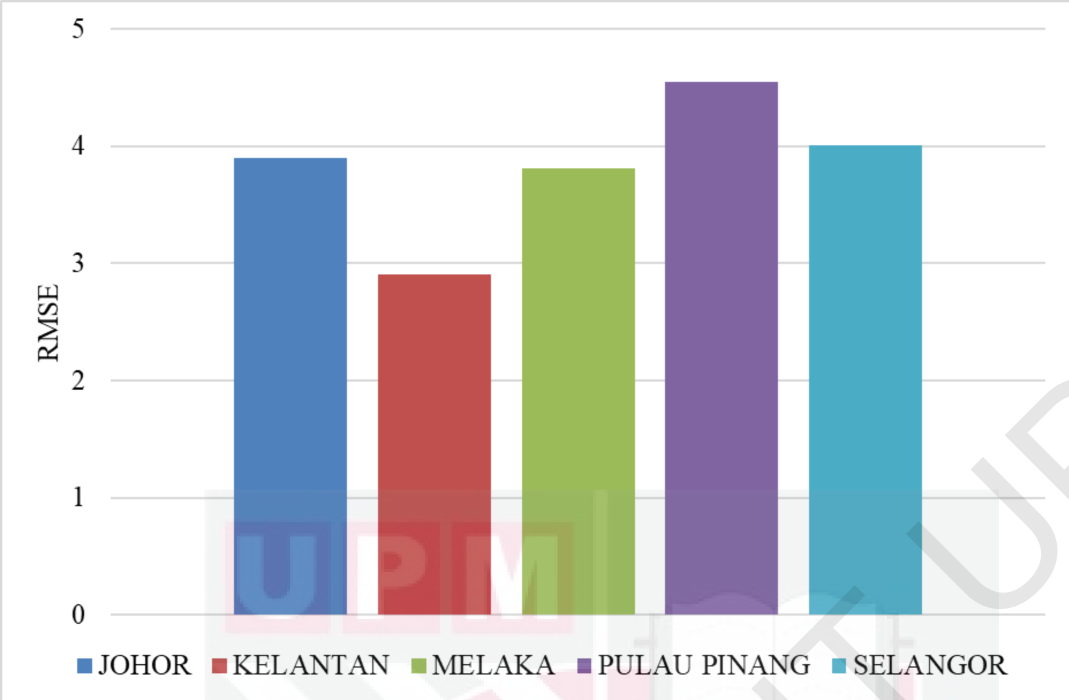


Figure 4.6 : Average Performance of SSA-LSTM Model for Dengue Fever Prediction in Five Malaysian States, Measured by RMSE

4.2.2 Comparison with Benchmark Models

In Table 4.8, the performance comparison of four distinct models—SVM ANN, DT, as well as SSA-LSTM—is presented, evaluating their predictive capabilities across varying lookback periods, with RMSE serving as the performance metric. The lookback periods ranged 1-6 months, providing insights into the models' predictive accuracy over different temporal spans. Notably, the SSA-LSTM model emerges as the frontrunner in this analysis, boasting the lowest average RMSE of 3.17 across all lookback periods. This marks a significant deviation from the average RMSE values observed for the other three models, which stand at 4.59 for SVM, 5.43 for DT, and 4.63 for ANN, respectively. Moreover, the SSA-LSTM algorithm exhibits exceptional performance with lookback periods of 4 and 5 months, achieving RMSE values of 2.71 and 2.65, respectively. On the other hand, a slight decline in performance is observed when the lookback period is reduced, with an RMSE of 3.00. Despite this, the SSA-LSTM model consistently outperforms its counterparts across various lookback periods, showcasing its robustness and efficacy in predicting dengue cases. The background check for a lookback period of three months and a 3. And it's 7 for a period of 2 months prior. The other three models perform better than the proposed model, since the performance of the latter is not consistent at different lookback periods, whereas the performance of the other three models is more stable with relatively same RMSE values.

Table 4.8 : Performance of the Proposed Model (SSA-LSTM) Compared to Three Benchmark Methods Including SVM, DT, and ANN

Lookback	**Model**			
	SVM	**SSA-LSTM**	**DT**	**ANN**
1	4.44	3.22	4.82	4.66
2	4.37	3.07	5.58	4.42
3	4.76	3.58	5.6	4.53
4	4.44	2.71	5.93	4.42
5	4.67	2.65	5.69	4.76
6	4.86	3.76	4.96	5.00
Min	4.37	**2.65**	4.82	4.42
Max	4.86	**3.76**	5.93	5.00
Average	4.59	**3.17**	5.43	4.63
Std.	**0.20**	0.41	0.43	0.22

4.2.3 Impact of Spatial Attention Mechanism

In contrast, when examining LSTM models incorporating both temporal and spatial attention mechanisms across varying lookback periods, spatial models tend to excel in predicting dengue cases. On average, the RMSE for the two temporal models, TA-LSTM as well as STA-LSTM, stands at 3.66 and 3, respectively. Conversely, the average RMSE for the two spatial models, SA-LSTM and SSA-LSTM, is 3.67 and 3.17, respectively, outperforming their temporal counterparts with average RMSE values of 3.87 as well as 3.17, respectively.Notably, the SSA-LSTM model emerges as the top performer with the lowest RMSE across all lookback periods, underscoring its superior predictive capabilities compared to other models. Generally speaking, temporal attention aspects will make the model place importance on particular fragments within the input sequence over time, and spatial attention mechanisms will help the model to emphasize some parts of the input space. These strategies become beneficial at the time of dealing with lengthy, noisy, or non-relevant input sequences or when the input comprises a two-dimensional spatial map; then the model only needs to dwell on demarcated portions of the map that are significant at a given time period. Furthermore, they are a crucial resource when the input sequencing has an impact. The closer look to performance of the spatial models reveals the fact that the result is satisfying only for the shorter lookbacks.As an example, the SSA-LSTM model has a root mean square error (RMSE) of three when the lookback time is one month. This indicates that the SSA-LSTM model is capable of predicting the price of the stock with a reduced error rate. It turns out that the SA-LSTM model is a much more accurate estimation of the magnitude of second hand automobile pricing than CNN followed by a random forest, despite the fact that its root mean square error (RMSE) is 3.65. Compared to the other models, the TA-LSTM model has an RMSE of 3. The student is a senior as well as the STA-LSTM model has an RMSE of 3. 26. Henceforth, this pattern persists for up to a 2-month lookback period, wherein the SSA-LSTM emerges as the top performer with an RMSE of 3.07, closely trailed by the NL-LSTM model requiring an RMSE of 3.06. Notably, as the lookback period extends, the performance of the models becomes increasingly intertwined. Nonetheless, spatial models maintain their superiority over temporal ones across the board. For instance, at a 3-month lookback period, the SSA-LSTM model maintains its lead with an RMSE of 3, followed by the CBL-LSTM with an error rate of 4.58 and the SA-LSTM model with an RMSE of 4.95. In contrast, the TA-LSTM model exhibits an RMSE of 4, coinciding with the implementation of a reduction in the voting age to 58 years old, resulting in the STA-LSTM model yielding an RMSE of 4.55. This trend persists for a 4-month period, during which the SSA-LSTM model secures the second position with an RMSE of 2.71, trailing behind the SA-LSTM model with an RMSE of 3.85, reinforcing the dominance of spatial models in the LSTM framework.In a nutshell, the primary component that plays a substantial impact in the improved prediction accuracy at shorter lookback periods is the concentration of attention on spatial information. With the lowest root mean square error (RMSE) of any model across all lookback periods, the SSA-LSTM, which makes use of both spatial attention and two layers of LSTM, readily succeeds in outperforming other models.

4.3 Results of Third Experiment (LSTM with Integrated Attention)

4.3.1 Results of ST-LSTM and ST-SLSTM with Integrated Attention

Table 4. 9 the performance evaluation of the models for dengue fever prediction in Malaysia is accomplished. The models that were tested in the study comprise of ST-LSTM (spatial-temporal attention LSTM) and ST-SLSTM (spatial-temporal attention stacked LSTM). The levels of the models are appraised through RMSE. The RMSE values for various lookback periods are given in the table. The lookback period is the time that is opted to consider the previous time steps while making predictions.

As for RMSE, the ST-LSTM model led to the lowest value of 2. The students will score 50 for the evaluation of the lookback period of 2 and a maximum value of 4. 79

is given for the lookback period of 3. The ST-LSTM had the average RMSE of 3. 61, with a normal distribution of 0. 57. Although the ST-SLSTM model had a better performance than the ST-LSTM model, the ST-SLSTM model proved to be better than the ST-LSTM. It successfully attained the required minimum RMSE value of 1. 94 for a 5th look behind period and a maximum value of 3. The number 21 is for a lookback period of 6. The average RMSE for the ST-SLSTM model turned out to be 2. The average distance, 66 with a standard deviation of 0, is shown in the picture. 57.

These findings suggest that the ST-SLSTM model was better than the ST-LSTM model in the prediction accuracy. The ST-SLSTM model was enhanced by the stacking of LSTM layers in the ST-SLSTM model which, in turn, resulted in its improved performance. The experimental results show that the LSTM models with the attention-time-spatial mechanisms integrated into it can effectively predict dengue fever in Malaysia.

Table 4.9 : Performance Assessment of the Proposed Models for Dengue Prediction in Malaysia

Lookback	Performance (RMSE)	
	ST-LSTM	**ST-SLSTM**
1	3.58	3.18
2	2.50	3.02
3	4.79	2.61
4	3.85	2.00
5	3.39	1.94
6	3.60	3.21
Min	2.50	1.94
Max	4.79	3.21
Average	3.61	2.66
Std.	0.57	0.57

4.3.2 Impact of Integrated Attention

Table 4. 10 is the one that shows the similarity or difference between the performances of the various LSTM models for dengue fever prediction in Malaysia. The list of models that were evaluated includes LSTM, S-LSTM (stacked LSTM), TA-LSTM (temporal attention LSTM), SA-LSTM (spatial attention LSTM), ST-LSTM (spatial-temporal attention LSTM), STA-LSTM (stacked temporal attention LSTM), SSA-LSTM. The ST-SLSTM got the lowest RMSE score of 3 for a 1 year lookback period. Thus, the LSTM model with the SSA features was the closer in terms of RMSE, with 18 being the closest, followed by the SSA-LSTM with an RMSE of 3. 22. The LSTM and S-LSTM models got an RMSE of 3. 75 and 3. 72, respectively. With a lookback period of 2, the ST-SLSTM model was better than the other models giving the RMSE of 3. 02. The LSTM as well as S-LSTM had the RMSE values of 3. 57 and 3. 62, respectively. For the longer lookback periods of 3, 4, 5, and 6, the ST-SLSTM model was found to be the best among others as it consistently showed the lowest RMSE values, which demonstrates its superior performance. On the contrary, the STA-LSTM, SSA-LSTM, and SA-LSTM models usually got higher RMSE values.

The ST-SLSTM model was the most effective one in the lookback periods of seven, ten, and fifteen. It repeatedly was the best among the other models, even the LSTM and S-LSTM were not able to beat it. These results prove that the integration of spatial-temporal attention and stacked LSTM layers is a successful way of increasing the accuracy of the prediction of dengue fever in Malaysia. The experimental outcomes indicate that the attention mechanisms that are introduced into the models, for instance spatial attention, temporal attention, and stacked attention, disprove the predictive performance. Through the mindful attention to the spatial and temporal features of the data, the models are able to catch the relevant patterns and dependencies in the data thus, making the predicted results more accurate.

Table 4.10 : Performance Comparison of Different LSTM Models for Dengue Fever Prediction in Malaysia

Lookback	Performance (RMSE)							
	LSTM	S-LSTM	TA-LSTM	SA-LSTM	ST-LSTM	STA-LSTM	SSA-LSTM	ST-SLSTM
1	3.75	3.72	3.27	3.65	3.58	3.26	3.22	3.18
2	3.57	3.62	3.10	3.06	2.50	3.12	3.07	3.02
3	5.06	5.11	4.58	4.95	4.79	4.55	3.58	2.61
4	3.74	3.85	3.23	3.85	3.85	3.42	2.71	2.00
5	3.99	3.85	3.42	3.62	3.39	3.36	2.65	1.94
6	4.78	4.62	4.34	4.11	3.60	4.31	3.76	3.21
Min	3.57	3.62	3.1	3.06	2.50	3.12	2.65	1.94
Max	5.06	5.11	4.58	4.95	4.79	4.55	3.76	3.21
Average	4.15	4.13	3.66	3.87	3.61	3.67	3.17	2.66
Std.	0.61	0.59	0.63	0.58	0.57	0.60	0.41	0.57

CHAPTER 5

CONCLUSIONS AND RECOMMENDATIONS FOR FUTURE WORKS

The conclusion chapter serves as the final section of this thesis, summarizing the key findings, implications, and recommendations derived from the research on dengue fever prediction using RNNs with integrated spatial-temporal attention. In this chapter, we provide a comprehensive overview of the research journey, highlighting the significance of the study, recapping the main results and their implications, and outlining the potential avenues for future research and practical applications.

5.1 Conclusions

The following results are the findings of the first experiment, which is aimed at exploring the usage of the temporal attention mechanism for LSTM models in predicting the dengue forecast in Malaysia. The effect was observed that, by this measurement, A-LSTM had the smallest average RMSE value that was 3. 663. the SA-LSTM was the next popular choice with RMSE of 3. 674. While both LSTM and S-LSTM models showed comparable performance, RMSEs of them were 4154 and 4. 133, respectively. The level of correctness of the models with the LSTM also with the S-LSTM was found to increase with the help of the attention mechanism. S-LSTM and LSTM models which utilize attention have been presented as the best in comparison with the models that have been benchmarked. Besides, the fact that the strong impact was due to the connection of each of the characteristics (atmospheric, geographical, and temporal) is also of importance.The four models (LSTM, S-LSTM, A-LSTM, SA-LSTM) could predict dengue cases from 1 to 6 months ahead with a mean absolute error of 4. Thus, for instance, the hypothetical student with 15 points, 4 projects, 13 books, and 3 hours is ranked 7th among the students who have an average of 66 points and 3 points, and 10 students are below them. 67, respectively. The findings present a more precise predictive model for dengue and this model can be used in other similar areas. The results of the second experiment on using spatial attention with LSTM for dengue prediction in Malaysia: Six variations of LSTM models were created and compared for the purpose of dengue prediction-LSTM, S-LSTM, SA-LSTM, TA-LSTM, STA-LSTM, as well as SSA-LSTM. The model with the best performance, using both stacked LSTM layers and spatial attention, had an average RMSE of 3.17 over all lookback intervals. The average RMSE of the SSA-LSTM model was significantly lower than that of the three benchmark models (i. e. , SVM, DT, and ANN). The RMSE values ranging from 2 are shown in the following picture. 91 to 4. 55, the SSA-LSTM model was almost as good as it could be in several Malaysian states. Usually, the spatial attention models turned out to be the better predictors of dengue cases than the temporal attention models. Moreover, it was found that the SSA-LSTM performed well in all the cases of the prediction horizons, the lowest RMSE was got with the 4- and 5-month lookback periods. The final experiment showed that the ST-LSTM obtained the least value of 2. The 50 RMSE for a lookback period of 2 RMSE and a maximum value of 4 can be expressed as the 50 RMSE for a lookback period of 2 RMSE and a maximum value of 4. 79 RMSE for a lookback period of 3 RMS. The ST-LSTM model had the average RMSE of 3. 61 being the most common, having a standard deviation of 0. 57. The ST-SLSTM showed better results than the ST-LSTM model. It managed to obtain the lowest RMSE value of 1. 95 for a lookback window of 5 and a maximum value of 3. 21 for a period of 6 where you can take a retrospection of your life events. The typical RMSE for the ST-SLSTM model was 2. 66, having a mean of 0 twice, why the teacher make it his job to do this

thing that not many can do. 57. The research findings will be useful for the public health authorities in Malaysia and other countries where the dengue fever is a serious health issue. The meantime plan of the suggested method can be useful for the creation of the efficient techniques for the prevention and the curing of the disease and too, will help to the saving of lives.

5.2 Research Novelty and Contributions

The major novelty of this work is the design of an attention-based LSTM for dengue fever prediction that has the capability of remembering long dependences in time series data using spatial, temporal, spatio-temporal attention mechanisms. The proposed model also highlights what portion of time series data has contributed to the disease outbreaks and an increase/decrease of dengue cases. This adds additional advantages to the proposed models as it provides reliability and transparency to the decision makers. This is the very first study that applies attention mechanisms to LSTMs for dengue prediction, and preliminary results show the significance of such attention mechanisms for LSTM-based dengue prediction.

This research contributes to the field in the following ways:

1. Understanding LSTMs for dengue prediction: The research reveals the architecture, hyperparameters, training modes, and the dataset for dengue prediction and LSTM models.
2. Development of attention mechanisms for LSTMs: Several attention mechanisms, like spatial, temporal, and cross spatial-temporal attentions, are designed, and tested for their effectiveness in the process of improving the dengue prediction performance.

3. Testing and comparison of LSTM models with attention mechanisms: The investigation reviews the advantages and disadvantages of the attention mechanisms of the LSTM models for dengue prediction, thereby, providing a clear understanding of the future research areas and the way to go forward.

4. Optimization the dengue prediction via LSTM models: The research deals with the synergy of the optimization of both model hyperparameters and attention mechanisms for the enhancement of the LSTM models for dengue prediction.

5.3 Recommendations

1- Long-Term Forecasting: Although the research was focused on the next 1-6 months, more studies are needed for the long-term forecast of dengue fever cases. Future studies could uncover the performance and limits of LSTM models with attention mechanisms in forecasting dengue incidence over longer time periods, like 1 year or more. This would yield important facts for the public health planning and the resources allocation.

2- Integration of Additional Data Sources: The study used a number of covariates, for example, the climate, the land use, the vegetation, and the GIS factors. Nevertheless, future research could be carried out on the integration of the different data sources, for example, the social and the mobility data to be able to make the dengue fever prediction models more precise. By adding the information on human behavior, travel patterns, and healthcare accessibility, the investigation of the transmission of diseases will be enriched.

3- Comparison with Other Deep Learning Models: The research concentrated on LSTM models with attention mechanisms for the prediction of dengue fever. Later, more studies could be conducted and the performance of other deep learning models, such as the CNN and Transformer models, in the area of dengue disease prediction, will be investigated and compared. This would offer the knowledge on the best and worst deep learning architectures for the said application.

4- Evaluation of Model Uncertainty: It would be good to look for the ways how to estimate and show the uncertainty of the predictions made by LSTM models. Uncertainty estimation can give the decision-makers an idea about the dengue fever cases and also assist them in the assessment of the case's reliability and confidence. The possible methods that could be used for uncertainty estimation include the Bayesian modelling and Monte Carlo dropout.

5- Application in Real-Time Decision Support Systems: The study can be a basis to the real-time decision making systems for dengue fever prevention and control. Subsequent research could concentrate on the practical application of the research data, for example, the integration of the LSTM models with already existing surveillance systems and the development of the public health authority's user-friendly interface. This would result in the fact of that immediate monitoring, early detection of outbreaks, and the timely implementation of preventive measures would be undertaken, thus the dengue fever management would be more effective.

6- Transferability to Other Geographical Regions: Even though the study was concerned with dengue fever prediction in Malaysia, the LSTM models with attention mechanisms proposed in the study could be used in other regions where dengue fever is a common problem. Later research could be conducted to see if the models are transferable and can be generalised to be used in different settings and how they perform in various environmental and socio-economic contexts.

7- Integration of Intervention Strategies: Besides being able to predict dengue fever, further research might also involve the inclusion of intervention strategies in the prediction models. The models will combine the data on the vector control activities, vaccination campaigns, and other prevention measures to give the insights on the effectiveness and the effect of the different interventions on the reduction of the dengue fever cases. This would, in turn, result in proof-based decision-making and resource allocation for dengue fever control programs.

8- Multi-Disease Prediction: The research concentrated on dengue fever prediction, but the LSTM models with attention mechanisms, which were the subject of the research, can be expanded to the prediction of the other vector-borne diseases as well. Later, more research could be done to find out the possibility of the models to be used in predicting diseases such as the Zika virus, chikungunya, and malaria, by taking the same environmental, demographic, and temporal attributes. This would result in the fact that the spatiotemporal dynamics of vector-borne diseases would be understood in a much more extensive way and, therefore, the integrated disease management strategies which are based on these dynamics would be developed.

9- Check how well the models work in the case of the weekly or daily dengue cases prediction and see if they need more modifications to the same performance on these shorter time scales.

10- Making modelling on smaller spatial units like villages or sub-districts is what the author is talking about.

Through the study of these areas which are suggested to the future work, the researchers will be able to, on one hand, the prediction field of dengue fever will be developed further, on the other hand, the accuracy of the models will be improved and the usefulness of the predictions for the public health authorities will be enhanced. This will ensure that the proactive measures that are taken in reducing the impact of dengue fever are successful and therefore it will help in the improvement of the health situation of the people who are affected by it.

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