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A REVIEW OF MALAYSIAN EPIDEMIOLOGICAL DENGUE CONTROL MODELS DATA AND FUTURE DIRECTIONS FOR SUSTAINABLE DENGUE MANAGEMENT

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ABSTRACT

Dengue Fever (DF) remains a major public health concern in Malaysia. Traditional control measures have limitations, making mathematical models essential for optimising interventions. However, a comprehensive review of their advancements in the Malaysian context is lacking. This review analyses advancements in deterministic, stochastic, and agent-based mathematical models for sustainable DF control in Malaysia between 2012 and 2024. Scientifically validated control tactics such as vaccination and Wolbachia-infected mosquito releases were analysed and explained. Key epidemiological trends for environment, incidence rates, geographic distribution, and seasonal patterns were also examined. This review identifies gaps in applying mathematical models to shape sustainable public health policies in Malaysia and proposes directions for improving dengue control strategies. Comprehensive modelling is recommended to enhance efficiency and accuracy with maximum parameter combinations for sustainable dengue control. Additionally, this review offers biologists and public health professionals a clearer understanding of mathematical models' roles in sustainable dengue control, assisting in policymaking.

Introduction

The Dengue Fever (DF) is a widespread tropical illness (Fang *et al*., 1984; Halstead, 2008; Peng *et al*., 2012; Joanne *et al*., 2015) transmitted by *Aedes* mosquitoes (Dieng *et al*., 2012; Mulligan *et al*., 2012; Ogunlade *et al*., 2023). There are four dengue serotypes (DEN-1, DEN-2, DEN-3, DEN-4) that cause DF (St John & Rathore, 2019). *Aedes aegypti*, that primary vector (Lim *et al*., 2010), prefers human habitats (Ng *et al*., 2009; Shepard *et al*., 2014), feeds during the day and can delay egg production, (Dye, 1986; Wekesa *et al*., 2025), increasing likelihood of human interactions (Mulligan *et al*., 2012; Anasir *et al*., 2020). The risk of infection rises with each egg-laying cycle presented in Figure 1.

Since its first major epidemic in 1902, DF has been endemic in Malaysia (Abubakar & Shafee, 2002; Hassan *et al*., 2012; Lee *et al*., 2015; Bujang *et al*., 2017; Basar *et al*., 2018; Saadatian-Elahi *et al*., 2025; Alipitchay *et al*., 2025), with thousands of cases reported annually (Suppiah *et al*., 2018; Sahimin *et al*., 2024). Over time, case numbers have steadily increased (Mazrura *et al*., 2010; Dieng *et al*., 2010; Hii *et al*., 2016; Selvarajoo *et al*., 2020), with periodic outbreaks affecting densely populated

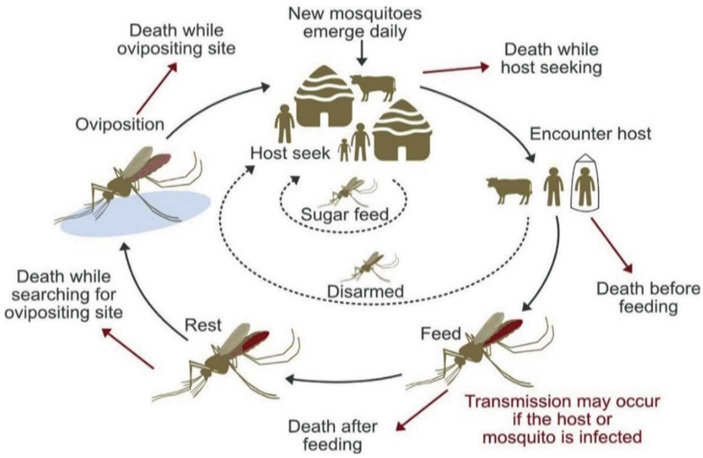

Figure 1: Spread of disease by *Aedes aegypti* mosquitoes (Fairbanks *et al*., 2024)

areas (Hammon *et al*., 1960; Foo *et al*., 2024) and affects people of all ages (Gutierrez *et al*., 2022; Hossain *et al*., 2025). Despite concerted efforts by health officials (Al-Zurfi *et al*., 2015), the number of dengue cases in Malaysia rose from 6,543 in 1995 to 130,010 in 2019 (Pang & Loh, 2016; Tay *et al*., 2022). Figures 2, 3, and 4 show the trends in cases, serotypes, incidence, death rates, and weekly reported cases from 2012 to 2023 (Chew *et al*., 2012; Syafruddin *et al*., 2013; Wong *et al*., 2016; Ahmad *et al*., 2018; Malaysian Society of Infectious Diseases & Chemotherapy, 2023; Saadatian-Elahi *et al*., 2025). An earlier study predicted the incidence rate would increase from 161.5 per 100,000 in 2010 to 940.0 by 2040 (Bujang *et al*., 2017; Abubakar *et al*., 2022). Although dengue incidence decreased due to improved vector control and public awareness (Nuraini *et al*., 2007; Naing *et al*., 2011; Razak *et al*., 2018; World Health Organisation Western Pacific Region, 2025), localised epidemics remained a challenge (Nani Mudin, 2015; Abdelrazec *et al*., 2016; Malaysia MOH, 2021; Azura *et al*., 2021).

DF in Malaysia exhibits significant regional variations (Hairi *et al*., 2003; Yang *et al*., 2009; Esteva & Yang, 2015; Jiao *et al*., 2021; Samsudin *et al*., 2024; Bhanye & Bhanye, 2024). This

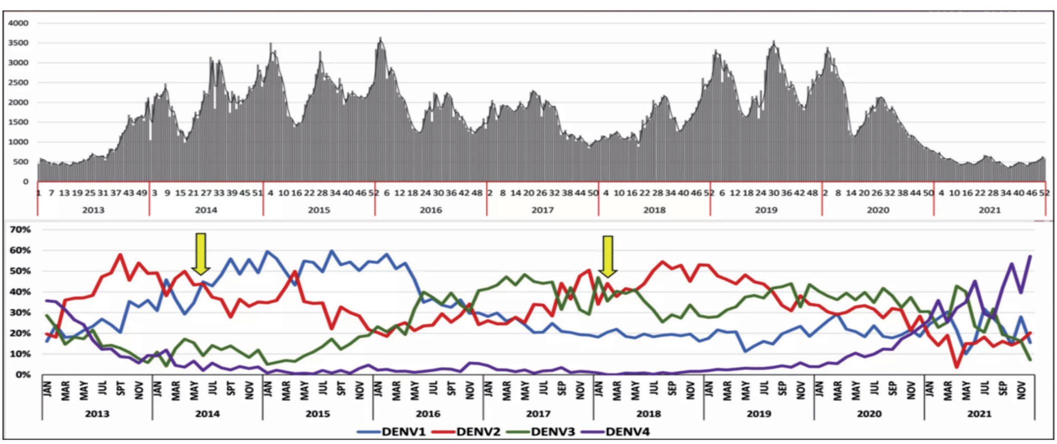

Figure 2: Dengue cases and serotypes in Malaysia (2013–2021)
(World Health Organisation, 2021)

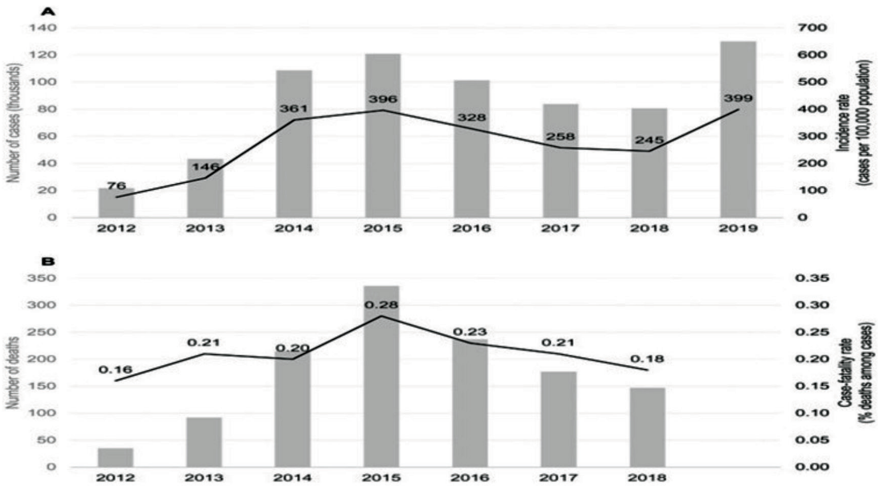

Figure 3: Dengue cases and mortality in Malaysia: (a) Reported cases and incidence rate, 2012–2019 (b) Deaths and case mortality rate, 2012–2018 (Abubakar *et al*., 2022)

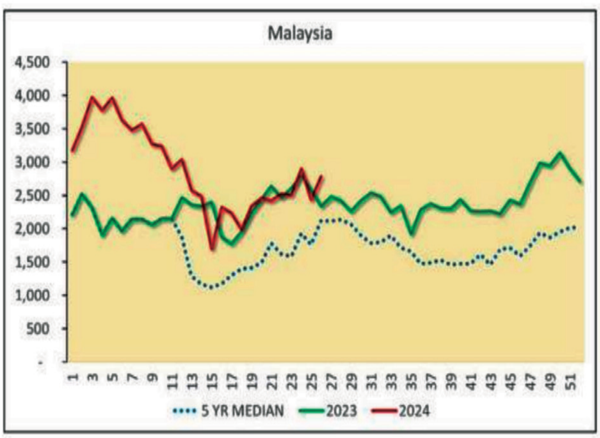

Figure 4: Weekly dengue cases in Malaysia (2023–2024) vs. median (2019–2023), Ministry of Health (Department of Health Malaysia, 2024)

distribution calls for targeted interventions at identified dengue transmission hotspots (Seng *et al*., 2005; Pérez-Guerra *et al*., 2009; Murphy *et al*., 2020; Dom *et al*., 2025) such as Kuala Lumpur (Teo *et al*., 2017), Penang (Yusoff *et al*., 2025), and Selangor (Toha *et al*., 2014; Chew *et al*., 2016; Ali *et al*., 2021; Zaki *et al*., 2021; Khan *et al*., 2024). Climate patterns (Climate history, 2020) are another influencing factor (Oki *et al*., 2011; Cheong *et al*., 2013; Dom *et al*., 2013; Nuraini *et al*., 2021; Wang *et al*., 2022; Wang *et al*., 2023; Mustaffa *et al*., 2024) for the spread of disease as a result of climate change (Abdul Wahid *et al*., 2021) as displayed in Figure 5 and Figure 6. Climate change, particularly through factors such as rainfall, is a critical determinant influencing the life cycles and transmission of infectious agents including malaria, cholera, dengue fever, hand, foot, and mouth diseases, and COVID-19 (Abdul Wahid *et al*., 2021).

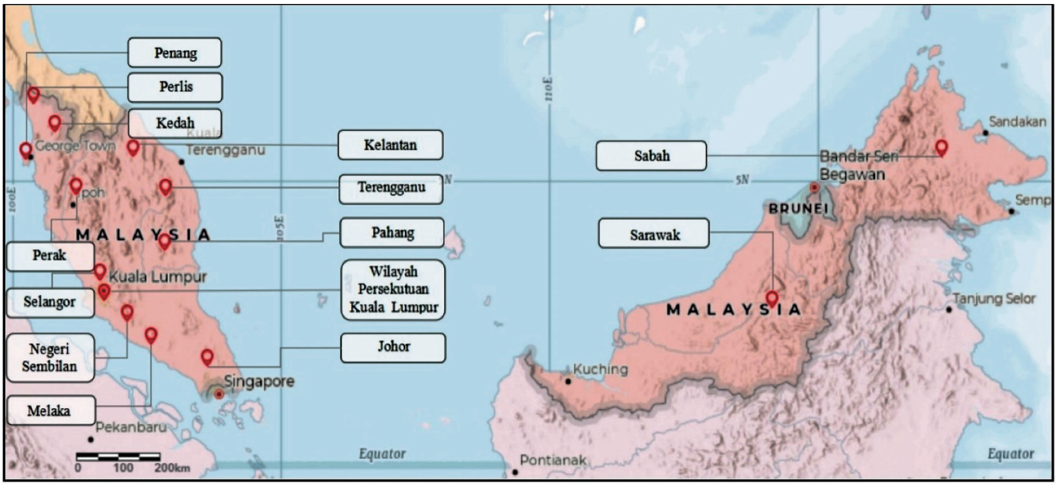

Figure 5: Fourteen study regions with climate pattern influences (Abdul Wahid *et al*., 2021)

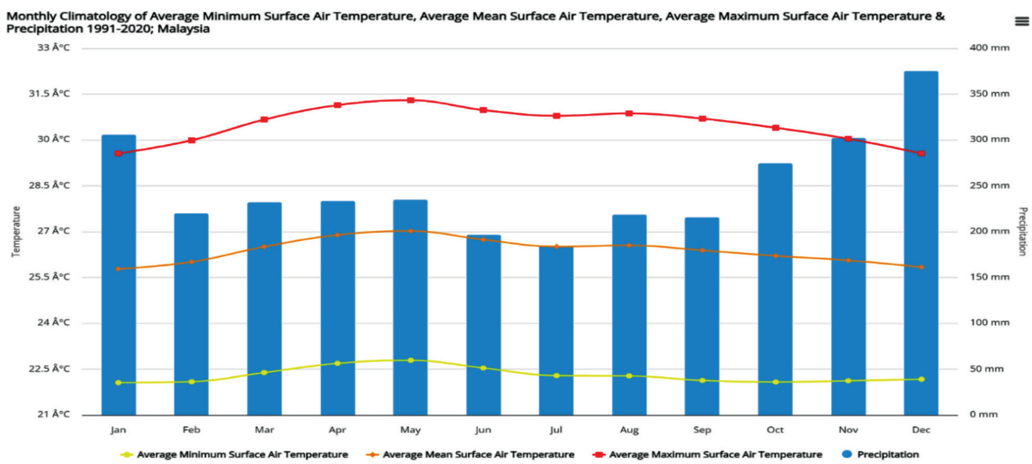

Figure 6: Malaysia monthly climatology (1991–2020) (Climate history, 2020)

Managing vector-borne diseases, like dengue, is crucial in regions with high transmission rates, such as Malaysia (Saadatian-Elahi *et al*., 2021). DF has a major financial, social, and individual impact (Shepard *et al*., 2012; Mohd-Zaki *et al*., 2014) , costing over 359 million Malaysian ringgits annually. Epidemiologic data on its prevalence and incidence by age and time can help track control efforts (Quintero *et al*., 2009; Wong *et al*., 2014; Samat & Pei Zhen, 2017). High-risk areas should be prioritised for resource allocation (Ong, 2016). Figure 7 revealed that about one-third of participants knew dengue could lead to Dengue Haemorrhagic Fever, a severe form DF, and fewer than half understood that there is no specific medicine (Hamdan & Kilicman, 2019; Shafie *et al*., 2024) for dengue (Wong *et al*., 2015).

In epidemiological research, mathematical models (Kermack & McKendrick, 1991; Derouich & Boutayeb, 2006; Manore *et al*., 2014; Sardar *et al*., 2015; Carvalho & Gonçalves, 2021; Emmanuel, 2023) provide frameworks within which to understand the relationships between hosts, vectors and diseases (Syafruddin & Noorani, 2012; Brauer, 2017; Carvalho *et al*.,

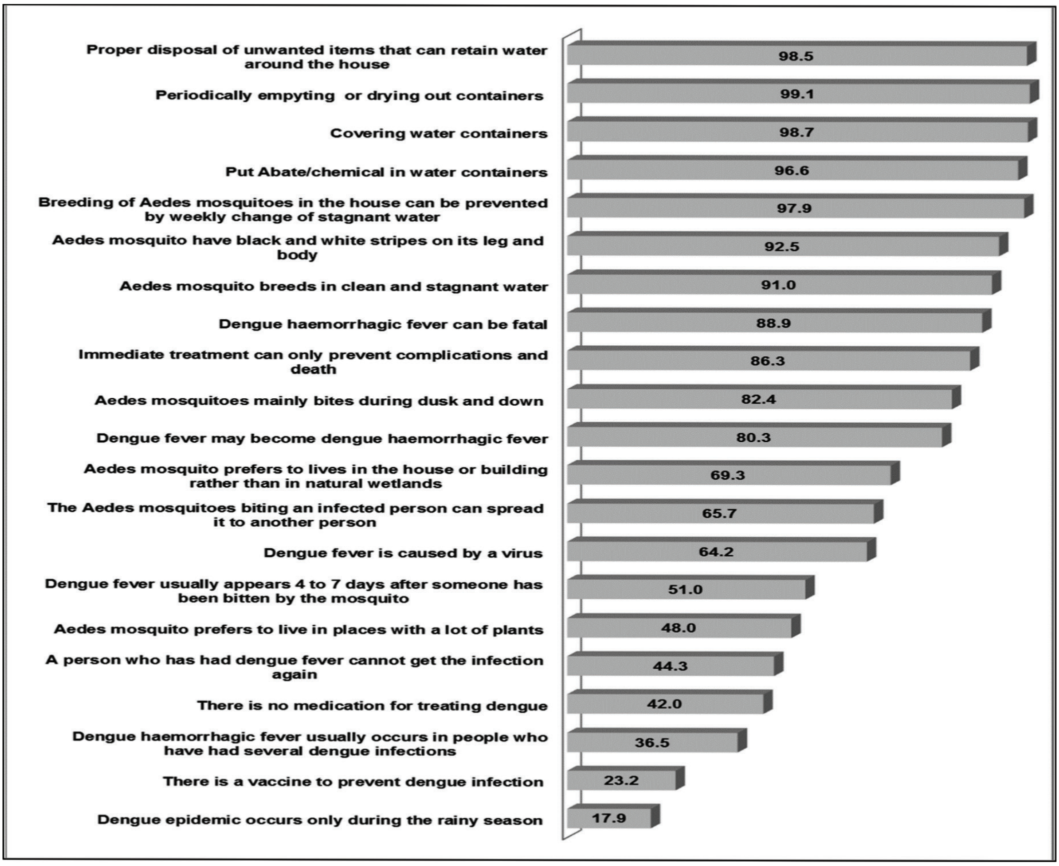

Figure 7: Percentage of knowledge related to dengue (Wong *et al*., 2015)

2019), and to evaluate interventions (Rodrigues *et al*., 2013; van den Driessche, 2017; Hamdan & Kilicman, 2019b) for effective dengue control (Lou & Zhao, 2011; Phaijoo & Gurung, 2017; Mohamed Siddik *et al*., 2020; Hanif *et al*., 2023). This review focuses on studies on DF between 2012 and 2024, reflecting key policy changes that make use of Wolbachia-infected mosquitoes and enhanced surveillance. It aims to evaluate advancements in sustainable mathematical models for DF, assess trends in model selection factors in Malaysia, and examine improvements in accuracy, cost-efficiency, and data integration for better understanding of dengue transmission and sustainable control. It will also highlight model limitations and propose directions for future research to support long-term public health strategies for dengue control.

Mathematical Models

Mathematical models for studying dengue can be broadly classified into three main categories: Compartmental (Esteva & Vargas, 1998; Garba *et al*., 2008; Bhuju *et al*., 2020; Msmali *et al*., 2023), agent-based (Niaz Arifin *et al*., 2014; Tabasi *et al*., 2020; Chong *et al*., 2022), and statistical models (Nur Aida *et al*., 2017; Ariffin *et al*., 2021; Thiruchelvam *et al*., 2021). They are reality simplifications with certain assumptions and limitations (Sanches & Massad, 2016; Puspita *et al*., 2022). Compartmental models (Area *et al*., 2015; Dos Santos *et al*., 2015) started off with SIR-type which are based on ordinary differential equations (ODEs), displayed in Figure 8. The primary goal of these models is to capture the complex interactions between the mosquitoes and humans. This model is then upgraded to SEIR, as shown in Figure 9. SEIR (Msmali *et al*., 2023) models could effectively model the delay between infection and the onset of infectiousness. Studies on the compartmental modelling of dengue in Malaysia between 2012 and 2024 mostly made up of SEIR-type interactions (Wattanasirikoson & Modnak, 2021).

Then, more complex models were proposed such as the SEI-SEIR (Bhuju *et al*., 2020) and ASEI-SEIR (Garba *et al*., 2008) models. This model can be further expanded to include multiple serotypes and interactions between them.

The dengue transmission models have then evolved into more complex equations simulating disease transmission patterns, tracking epidemics (Mohd Salleh *et al*., 2022), forecasting future outbreaks, and assessing the effectiveness of control strategies. Autonomous and non-autonomous systems of ODEs were used to evaluate the effects on the transmission dynamics of DF on various control methods such as therapy, immunisation, human self-defence, vector control using larvicide and adulticide, and awareness (Emmanuel, 2023). Spatial heterogeneity such as geographic distribution and mosquitoes breeding grounds were also incorporated in the models (Keat-Chuan Ng *et al*., 2023). Another advancement is on the impact of climate factors, namely temperature and rainfall on DF transmission (Samat & Ma'Arof, 2016; Mathew *et al*., 2019). These improved models can enhance target control efforts and provide accurate insights into patterns of dengue transmission (Sakellari & Loukas, 2013; Montes de Oca *et al*., 2020).

Agent-based models (ABMs) are developed based on individual (agent) behaviours and interactions, predicting the whole impact using behaviours of some agents like humans and mosquitoes (Niaz Arifin *et al*., 2014). These models capture the dependencies in the behaviour and interactions of the population members (Murphy *et al*., 2019). In our context, agent-based models simulate humans and mosquitoes as individual entities with distinct characteristics (Uribe *et al*., 2024) and behaviours (Chong *et al*., 2022).

Dengue transmission is simulated by monitoring the interactions between people and mosquitoes over time. The movement of

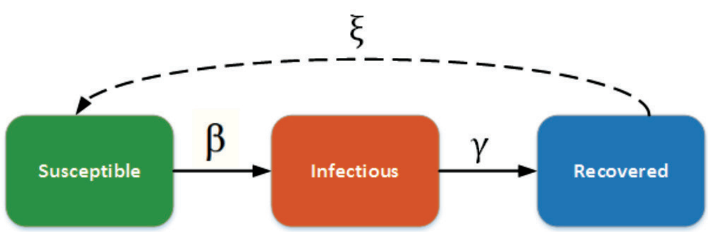

Figure 8: State-flow diagram of SIR-type epidemiological model with parameters β (infection rate), γ (recovery rate), and ξ (waning immunity rate) for a population of N individuals (SIR, 1927)

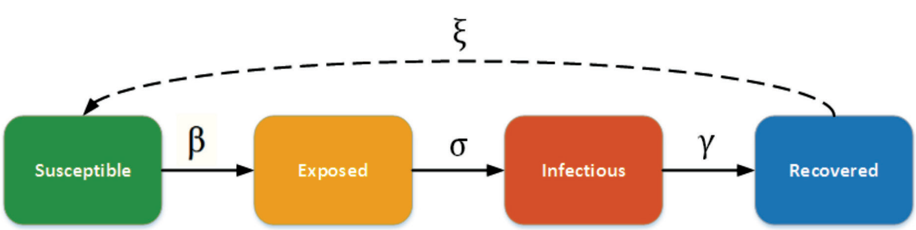

Figure 9: State-flow diagram of SEIR-type epidemiological model with parameters β (expose rate), (infected rate), γ (recovery rate), and ξ (waning immunity rate) for a population of N individuals (Gupta *et al*., 2020)

people and mosquitoes by spatial diffusion across different geographical regions introduces a feature of heterogeneity in Spatial ABMs. Statistical models use historical data to identify patterns and predict future outbreaks (Nur Aida *et al*., 2017). These models do not necessarily rely on the biological mechanisms of disease transmission but focus on correlations and trends in the data. Time series models analyse the temporal patterns of dengue incidence. Regression models explore the relationship between dengue and factors like climate, socio-economic conditions, and control measures.

These models often assume homogeneous mixing (Bansal *et al*., 2007), constant transmission and recovery rates (Masrani *et al*., 2021), a closed population (Kon & Labadin, 2019), permanent immunity (Zeb *et al*., 2024), time-dependent state variables (Fairbanks *et al*., 2024), immediate infectiousness (Gupta *et al*., 2020), and constant population size (Zeb *et al*., 2024). Assumptions by these models will introduce limitations in accurately predicting disease spread. Oversimplified models could overlook crucial components of the spread of illness (Abidemi & Aziz, 2022).

On the other hand, complex models (Abidemi *et al*., 2020) could capture a greater range of dynamics but are more challenging to parameterise and interpret (Hamdan & Kilicman, 2020). Data quality and availability (Woon *et al*., 2018) can also affect the results (Chitnis *et al*., 2008). Many models lack detailed spatial resolution (Keat-Chuan Ng *et al*., 2023), which is important for understanding local transmission dynamics and effectively targeting interventions. Moreover, it is challenging to assess and incorporate human behaviour (Chong *et al*., 2022) and environmental factors (Samat & Ma'Arof, 2016) in models.

Materials and Methods

A literature search on Malaysian dengue epidemiology was performed using PubMed, Scopus, Web of Science, MyCite, and ScienceDirect, as outlined in Figure 10. Keywords included "dengue fever", "mathematical modelling", "epidemiology", "compartmental model", "fractional model", and "Malaysia". The search targeted studies published between 2012 and 2024 to gather recent data, advanced modelling methods, and

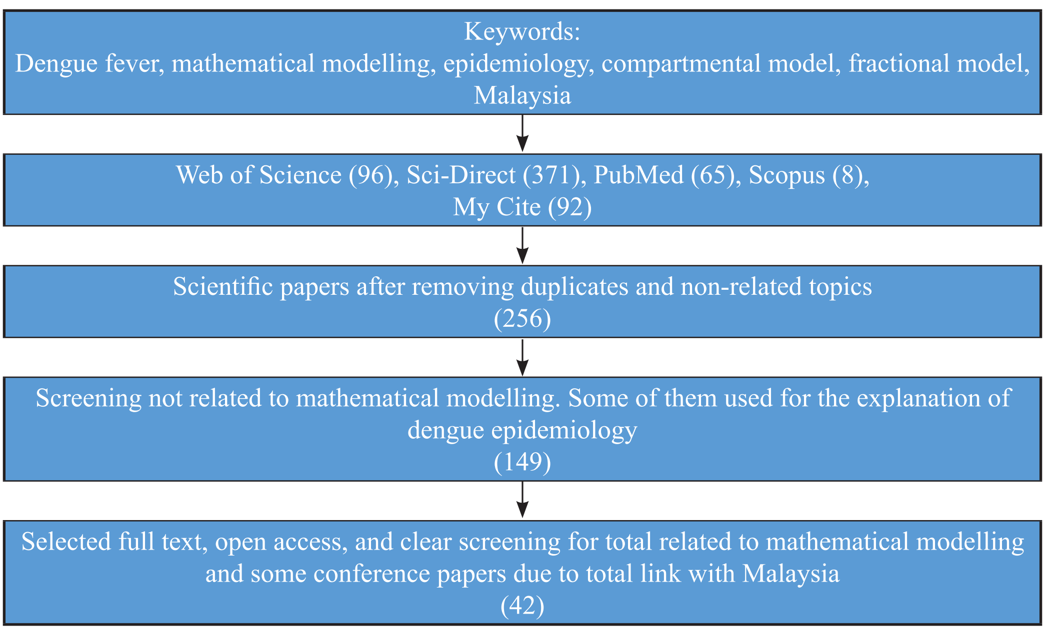

Figure 10: Flow diagram showing the inclusion and exclusion criteria for the selection process

factors like climate change, vector control, and population dynamics. Studies were included if they applied mathematical models to DF in Malaysia or incorporated Malaysian data, especially those with new modelling or intervention approaches. Exclusion criteria ruled out non-peer-reviewed articles, studies not focused on dengue fever, and those with limited use of mathematical models.

Through these criteria, a coherent and specific picture of the advances in mathematical modelling in predicting and sustainable managing the DF epidemic in Malaysia in the last few years is expected. Table 1 presents different mathematical approaches that had been developed and used for sustainable DF control in Malaysia from 2012 to 2024 along with their key findings.

Results and Discussion

From Table 1, researchers have been instrumental in understanding the dynamics of DF transmission, prevention strategies, and impact assessment in Malaysia. There are many risk factors for the occurrence of dengue outbreaks. The environmental factor concerns increased rainfall and temperatures creating optimal breeding conditions for mosquitoes (Hamdan & Kilicman, 2021). The urbanisation factor leads to the presence of artificial water reservoirs that serve as the breeding grounds (Afthanorhan & Aimran, 2020).

This situation is worsened by poor waste management that generates more mosquito habitats. Regions with poor infrastructure of dengue healthcare with relatively slow diagnosis are also associated with more severe outbreaks. Air pollution plays a role in making dengue susceptible, with higher levels of SO_2 associated with a higher incidence of DF (Jamaludin *et al*., 2017; Mohammad *et al*., 2020). Among all, climatic conditions are the main factor influencing dengue transmission.

Disease prevalence is dependent on public attitudes, government policies, and environmental management (Afthanorhan & Aimran, 2020). Various analyses were conducted to evaluate the effectiveness of dengue control measures. The most critical is vector control, which involves reducing mosquito populations through the use of larvicides to kill mosquitoes' larvae, adulticides to kill adult mosquitoes, MHS traps to spread larvicides to other breeding sites, and Wolbachia-infected mosquitoes that reduce the virus' ability to replicate within the vector (Liang *et al*., 2019). Increasing public education and community participation is also effective because individuals could adopt preventive behaviours such as eliminating stagnant water sources and making use of repellents. Proper waste disposal and urban planning can reduce mosquito breeding grounds. Among all vector controls, larvicide and Wolbachia-based biological control was found to significantly reduce dengue incidence (Siddik & Abdullah, 2018).

Vaccination has been explored as a potential control measure (Abidemi, Aziz, *et al*., 2019). Although vaccines provide some level of immunity, they are most effective when combined with vector control strategies. Personal protection measures, such as using insect repellents, wearing protective clothing, and installing mosquito nets can reduce individual exposure but their impact on overall dengue transmission is relatively limited (Abidemi & Aziz, 2020). Lastly, surveillance and early detection methods have been used more and more frequently to predict and prevent dengue outbreaks. Applied ML models to forecast dengue trends and emphasised that real-time monitoring can enable timely interventions (Salim *et al*., 2021).

Mathematical models have been used extensively to gain more insight into the dynamics of DF. Compartmental models are effective in estimating transmission rates and intervention impacts despite their limit in accuracy. Stochastic models are more suitable for low-incidence regions but require extensive data and have high computational cost (Samat & Ma'Arof, 2014). Spatio-temporal models are helpful in identifying high-risk zones but require

Table 1: Selected papers on mathematical approaches used for DF control in Malaysia (2012 to 2024)

References	Contributions	Model Type	Key Findings
(Samat & Percy, 2012)	Research presents a method for estimating dengue risk using a time-space stochastic model that incorporates disease transmission, covariates, and spatial correlations, applied to Malaysia data.	Host-Host and Host-Vector SIR-SI.	The relative risk estimate was better for dengue disease mapping compared to previous studies.
(WHO-VMI Dengue Vaccine Modelling Group, 2012)	The population-wide impact of a tetravalent dengue vaccine was evaluated. The uncertainties in dengue transmission dynamics were addressed. The development of models to assess dengue vaccination strategies was accelerated.	Host-Vector SIR and SEIR.	Research highlights that improving understanding of dengue virology, immunology, and entomology is crucial for accurate modelling. Data sharing, ongoing analysis, and addressing factors like vector control and social outreach are essential for effective dengue control.
(Samat & Ma'Arof, 2014)	The distribution of dengue infections in Malaysia was mapped. The relative risk was estimated. A resource for the creation of efficient methods for prevention and control was offered.	Host-vector SIR-SI.	Areas with varying levels of risk can be determined.
(Samat & Ma'Arof, 2016)	The relative risk of Malaria fever in Malaysia was estimated.	Host-Host SIR-SI.	Sabah and Sarawak are high-risk areas for Malaria fever because of the environmental conditions and breeding sites. The proposed model is effective in estimating risks.
(Ten Bosch *et al*., 2016)	The impact of serotype interactions and seasonal forcing on dengue dynamics, model selection, and vulnerability to control measures were investigated.	Host-Host SIR.	The pattern-oriented modelling approach can be utilised in detecting and fitting disease transmission models based on observed data. Challenges in structural and parameter identifiability were detected, that may go unnoticed if individual patterns were used in isolation.
(Shafie *et al*., 2017)	The effects and cost-effectiveness of dengue immunisation in Malaysia were examined across various vaccination programs.	Host-Host Host-Vector.	The best-value approach is routine immunisation in a population with a catch-up cohort of certain high-risk locations. Vaccine should be used in conjunction with other initiatives.
(Malik *et al*., 2017)	Dengue epidemic behaviour in Gombak, Malaysia was modelled and analysed using a two-mode network approach.	Compartmental model with Host-Vector population.	Bug spray was offered as the control strategy.

(Abd Naeeim & Abdul Rahman, 2017)	The relative risk of DF in Peninsular Malaysia was calculated. The best model was selected. Spatial patterns and temporal trends were visualised.	Bayesian framework Host-vector	Incorporating spatial and temporal trends is important. Systematic vector control prevention programs are needed, especially in hotspot areas.
(Jamaludin *et al*., 2017)	The trends, behaviours, and associations between four pollution-related diseases (asthma, conjunctivitis, URTI, and dengue) were investigated with significant elements in Johor Bahru, Malaysia introduced, including air pollution and climatic variables. The impact of pollutants on disease was determined.	Host-Host Negative Binomial	Sulphur Dioxide (SO_2) is a major contributor to diseases. Effective monitoring and control of air pollutants can reduce diseases. These can be utilised in an early warning system in Johor.
(Lola *et al*., 2017)	The challenges posed by a small number of events per variable (EPV) in data analysis were overcome by Bootstrap Logistic Regression Model (BLRM).	Logistic Regression	The accuracy of estimation is improved. BLRM can enhance the validity of logistic regression models.
(Samat & Mey, 2017)	The relative risk for Malaria and dengue in Malaysia was estimated.	BYM Model Host-Host transmission	This is an alternative method for risk estimation.
(Woon *et al*., 2018)	Dengue percentages and hospitalisation rates in Malaysia were estimated from 2001 to 2013. Essential epidemiologic measures for policymaking and disease control monitoring were provided.	Incidence prevalence mortality Host-Vector	Well-designed seroprevalence studies are important for accurate burden estimation. Regular monitoring should be conducted for effective dengue control and prevention programs.
(Che-Him *et al*., 2018)	The factors influencing DF incidence in Malaysia were investigated.	Negative Binomial GAM Host-Vector	Relationships between the incidence rate of dengue and both climatic and non-climatic factors in Malaysia were significant. Population density was positively related to the monthly dengue incidence rate.
(Hamdan & Kilicman, 2018)	An improved mathematical model of dengue transmission was developed using fractional-order derivatives	SIR Host-Host, Host-Vector	The model is more realistic for dengue transmission than ODEs.
(Tay *et al*., 2018)	Bistable equilibrium criteria in the model of dengue transmission in Malaysia were investigated.	SEI-SVEIR Host-Host Host-Vector	Vaccination is an effective control measure.

(Siddik & Abdullah, 2018)	Optimal control strategies for the transmission dynamics of the DENV were investigated.	Host-Vector	Insecticide spray and biological control are effective control measures.
(Wilder-Smith *et al*., 2018)	Diagnosis, surveillance, prevention, and predictive models related to dengue were improved. Predictive models for the global spread of dengue, mainly focusing on the risk of introduction and establishment in Europe were developed.	Host-Vector Vector-Vector	More implementation research, improved vaccines, and vector control measures are needed. Ongoing vigilance and preparedness for emerging public health threats are important.
(Greenhalgh *et al*., 2018)	The impact of the Mosquito Home Systems (MHS) in high-rise condominiums in Malaysia was analysed.	Ross-Macdonald Host-Vector	MHS effectively reduces the number of dengue cases within the trial sites. There is a limited impact on a broader scale. MHS is a promising strategy for dengue control in specific environments.
(Liang *et al*., 2019)	The impact of a novel autodissemination trap on reducing dengue cases in Shah Alam, Malaysia, then the entire country, was analysed.	Modified Ross-Macdonald Host-Vector	The developed model can help in identifying the required coverage of MHS.
(Naeeim & Rahman, 2019)	Effects of selecting different dependent vectors on the choice of spatiotemporal models were investigated. Various dependency matrices affecting risk assessment and parameter estimations were determined.	Host-Vector Spatio-temporal model	Considering different spatial weight matrices in spatio-temporal modelling is important.
(Kon & Labadin, 2019)	Observed and predicted dengue cases were observed using a generic model.	Host-Host Host-Vector Generic reaction-diffusion	The model is effective in predicting infectious human density in Bintulu, Malaysia, for dengue in week 1. Spatial factors and movement of human and mosquito populations is important.
(Abidemi, Aziz, *et al*., 2019)	The dynamics of dengue transmission and management with two virus serotypes were forecasted with Dengvaxia vaccine and insecticide control strategies.	Two-strain Host-Host	Global stability of equilibrium points was obtained. Time varying controls is optimal.
(Abidemi, Ahmad, *et al*., 2019)	The impact of vaccination, personal protection, treatment, and vector controls on dengue disease transmission was investigated.	With and without intervention. Host-Host Host-Vector	Combining several control measures effectively reduces the proportion of control measures required.

(Hamdan & Kilicman, 2019b)	The optimal strategy for reducing human death and morbidity caused by DF transmission was determined.	Host-Host Host-Vector	Sensitivity of key factors influence the spread of DF.
(Hamdan & Kilicman, 2019a)	The local stability of a dengue model was investigated, considering different memory effects on the host and vector populations.	DF with fractional order system Host-Vector	Different fractional orders assigned to the host and vector compartments affects the dynamics of the disease transmission. Specific order assignments can lead to a decrease in the mosquito population. Considering memory effects is important.
(Koh *et al*., 2019)	A class of parameter-driven state-space models for analysing integer-valued time series data was introduced. The model was applied on real-world data.	State-space	This model has better fit, simpler, easier to employ, and provided better outputs than other models. The first four moments are the closest to the empirical values.
(Liang *et al*., 2019)	The impact of using the MHS in Shah Alam, Malaysia, then the whole of Malaysia, was analysed.	Modified Ross-Macdonald Host-Vector	The MHS has a potential impact on reducing dengue cases in Malaysia.
(Afthanorhan & Aimran, 2020)	Factors of Malaysian dengue infection was recognised to be the environment, population expansion, public opinion, government assistance, and climatic changes by considering the environment as a mediator construct.	SEM	Public attitude and increasing population growth significantly impact on the environment. Government support, public attitude, and environmental factors can significantly influence dengue infection. Population growth is the most important factor affecting DF in Malaysia.
(Abidemi & Aziz, 2020)	Optimal tactics for controlling and minimising the spread of DF in Johor, Malaysia was developed.	Human, aquatic, and female mosquito Host-vector	Human personal protection and vector control using adulticide are effective control measures.
(Abd Naeeim *et al*., 2020)	Two different spatiotemporal models in Peninsular Malaysia in 2017 were compared.	Space-time models Hosts-vectors and vector-vector interactions.	Spatial and temporal variability of dengue disease rates in Peninsular Malaysia for the year 2017 exist.
(Kristiani & Samat, 2020)	The impact of infecting *Aedes* mosquitoes with Wolbachia bacteria was investigated.	SIR-SI Host-Vector	Wolbachia-*Aedes* mosquitoes have potential. Cooperation among stakeholders is important for efficient disease control

(Abidemi *et al.*, 2020)	The transmission dynamics of the DENV in a region where two virus serotypes coexisted was investigated.	SIR Host-Host Host-Vector	Combining Dengvaxia vaccine and insecticide is an effective control measure.
(Hamdan & Kilicman, 2021)	A deterministic mathematical model of dengue transmission in Malaysia that considers the effects of temperature was developed.	Host-Vector	Locally and globally stable disease-free equilibrium point was achieved if the basic reproduction number is less than unity. The backward bifurcation is possible when $R_0 < 1$.
(Salim *et al.*, 2021)	Predicted DF outbreaks in Selangor, Malaysia, using machine learning (ML) models	Classification and Regression Tree, Artificial Neural Network, Support Vector Machine and Naïve Bayes structural model.	The Linear support vector machine (SVM) model excelled in training but overfitted, underperforming in testing.
(Abdul Wahid *et al.*, 2021)	The relationship between Malaysia's climate and the number of cases of hand, foot, and mouth disease (HFMD) was investigated.	GAMM with and without mistakes linked to correlation Host-Host	Considering climate variables with a two-week lag period is important to better understand HFMD events.
(Yip *et al.*, 2022)	An early warning system for dengue outbreaks in the Central Region of Malaysia was constructed by identifying significant covariates and their lagged effects using a Bayesian modelling framework	Spatio-temporal Host-Vector	A six-week gap in dengue incidence coincided with a rise in sea surface temperature in the central equatorial Pacific. Meteorological drivers can aid short-term dengue epidemic detection and support long-term forecasts.
(Tay *et al.*, 2022)	The epidemiological features of dengue in Selangor and Kuala Lumpur, Malaysia were examined. A transmission model to estimate transmission rates and reproduction numbers was developed.	SI-SIR Host-Vector	Dengue remained a public health issue in Malaysia. An effective vector control method is a necessity.
(Wells *et al.*, 2023)	A hybrid stochastic-deterministic model to predict the effects of the MHS in urban settings was formulated. Its efficacy was validated using trial data.	SIR Host-Vector	MHS significantly reduces dengue cases and mosquitoes' populations.

(Abidemi *et al.*, 2023)	DF transmission dynamics were described and validated, R_0 was analysed and computed, and the effects of controls were estimated.	Two-patch Vector-Host	BRDFE is locally and globally asymptotically stable when $R_0 < 1$.
(Lu *et al.*, 2024)	A coupled model forecasting dengue using climate variables and mosquito biting rates was developed, providing real-time forecasts and assessing mitigation measures under varying climate conditions.	SI-SIR Vector-Host	Dengue cases can be forecasted 1-2 weeks in advance with under 6% error, outperforming stand-alone models, especially during outbreaks, and is more robust for evaluating mitigation measures under different climates.
(Jana *et al.*, 2024)	An SIR model was developed and validated. The control measures were developed. was calculated. The dengue transmission dynamics were analysed.	SIR Vector-Host	Insecticides and raising awareness are effective measures.
(Boulaaras *et al.*, 2024)	A mathematical model was developed to understand the dynamics of co-infection of Chikungunya and dengue. Individual models were also investigated.	SIR Vector-Host	The endemic steady state is unique. Optimal control strategies effectively reduced infection levels and managed co-infection dynamics.

large datasets and are highly sensitive to model selection criteria (Abd Naeeim *et al*., 2020). ML methods excel at outbreak prediction but are prone to overfitting and require high-quality training datasets to maintain accuracy (Salim *et al*., 2021).

Fractional differential equation models incorporate memory effects and nonlinear dynamics to provide a more realistic and accurate representation of dengue transmission (Pooseh *et al*., 2011; Diethelm, 2013). The models can capture complex dynamics such as latency and irregular spread patterns and offer a unified framework that bridges different modelling approaches. However, complexity requires numerical methods, parameter estimation is difficult, and simulations are computationally extensive. Additionally, fractional orders are not always biologically intuitive, which may limit their acceptance in applied health sciences.

Other than that, optimal control models are useful for determining cost-effective intervention strategies. Multi-strain dynamics and climate change predictions had been integrated, improving forecasting techniques, providing better real-time insights, and making them more suitable for policy implementation. Effective management of dengue outbreaks requires an integrated approach, combining vector control, environmental management, vaccination, and predictive modelling. Mathematical and statistical models offer valuable insights, but their effectiveness depends on data accuracy and model assumptions.

Future research should focus on integrating multiple modelling approaches or parameters to improve predictions and optimise intervention strategies for long-term disease control. For the large data set, an accurate and High-Performance Computing (HPC) system is highly needed and still scarce in the literature.

Key Parameters and Variables in the Models

Malaysia's dengue modelling commonly considers the following parameters and variables, which include Transmission Rates, Recovery Rates, Incubation Periods, Vector Population Dynamics, Human Demographics, Climate Variables, Control Measures, and Public Awareness. In this research paper, the dengue dynamics in Malaysia is presented based on epidemiological characteristics such as incidence rates, geographic distribution, and seasonal changes. The essential components of the dengue models for this review are shown in Table 2.

Future Design for Health Sustainable Programme

Geographically sensitive variables have been incorporated into models to identify local dengue transmission patterns in Malaysia, highlighting the influence of regional factors like urbanisation, climate variability, and socio-economic conditions on disease dynamics (Nuraini *et al*., 2007; Lye *et al*., 2008; World Health Organisation, 2015; Aguiar *et al*., 2022).

Table 2: Important parameters used in articles related to dengue by mathematical models in Malaysia

Parameter Definition	Values	References
Proportion/percentage of eggs	0-1	(Hamdan & Kilicman, 2018)
Rate of oviposition	0-11.2 per day, 6 per day (per capita)	(Tay *et al*., 2018; Hamdan & Kilicman, 2018; 2019)
Transition rate from aquatic to adult	0-0.19 per day	(Hamdan & Kilicman, 2018; 2019)
Average aquatic mortality rate	0.05, 0.01-0.47, 0.25 per day, per week	(Hamdan & Kilicman, 2018; Tay *et al*., 2018; Mohamed Siddik *et al*., 2020)
Average life span	11-56 days	(Hamdan & Kilicman, 2018; 2019)
The average life span of a human	73-75 years	(Hamdan & Kilicman, 2018; Abidemi & Aziz, 2020)
The rate of biting	0-1 per day, 1, 0.20, per day	(Liang *et al*., 2019; Abidemi *et al*., 2020; Mohamed Siddik *et al*., 2020)
Transmission probability from human to vector	0.375, 0.25 per day	(Tay *et al*., 2022)
Transmission probability from vector to human	0.375,0.1,0.75,0.75 per day	(Liang *et al*., 2019; Tay *et al*., 2022)
The human mortality rate from the disease	10^{-3} per day	(Tay *et al*., 2022)
Human recovery rate	1 per week, 0.1428, 0.083-0.33 per day	(Mohamed Siddik *et al*., 2020; Tay *et al*., 2022)
The natural birth rate of human	per week, 0.00004 per day	(Tay *et al*., 2018; 2022)
The natural death rate of human	0.0000457 per day	(Mohamed Siddik *et al*., 2020)
Dengue extrinsic incubation period	8 days, 7 days	(Liang *et al*., 2019; Abidemi *et al*., 2020)
Per capita birth rate and natural death rate of humans (in days)		(Abidemi *et al*., 2020)

However, sustainable dengue control requires integrating environmental, social, and technological strategies (Anders & Hay, 2012) to minimise long-term ecological and public health impacts (Kamaruddin *et al*., 2021). One key concern is the environmental effects of vector control methods (Lian *et al*., 2006; Karthik Raja *et al*., 2025). Overuse of insecticides leads to ecological imbalances, resistance, and adverse health impacts on non-target species (WHO, 2011; Organisation, 2012; Brady *et al*., 2012; Hamdan & Kilicman, 2019a; WHO, 2021).

Future research should focus on eco-friendly methods such as Wolbachia-infected mosquitoes and dengue traps, which naturally reduce transmission without harming the environment. Plant-based larvicides and microbial insecticides can also provide sustainable alternatives (Karthik Raja *et al*., 2025). Furthermore, climate-adaptive models that account for the impacts of climate change on vector populations are crucial (Mohd Hardy Abdullah *et al*., 2025). Future models should incorporate real-time climate data to predict high-risk areas and help policymakers improve drainage systems, green infrastructure, and water management, mitigating mosquito breeding conditions.

Data-driven decision-making, including real-time data analysis through the use of artificial intelligence (AI), deep learning, and machine learning, can improve resource allocation and timely interventions (Mazhar *et al*., 2024). AI-powered early warning systems that integrate surveillance (Pateras *et al*., 2023), clinical records, and environmental factors can enhance outbreak prediction and response, ultimately reducing the economic burden of dengue (Foluke Ekundayo, 2024). The role of human mobility in disease spread is also critical. Mobility-based predictive models should be explored to assess these factors (Xu *et al*., 2025).

Sustainable urban planning, community-driven sanitation, and the digitalisation of health data could further reduce outbreaks. An integrated approach combining eco-friendly control, climate-adaptive planning, AI-driven surveillance, and community participation is essential for long-term dengue prevention. Future research should promote collaboration across disciplines to develop scalable and sustainable solutions for dengue control.

Co-occurrence Network in Dengue Research Based on Data Without Limit

Figure 11 visualises dengue research in Malaysia (2012-2024) using VOS Viewer, showing keyword co-occurrence to identify key themes. Dominant terms like “dengue”, “female”, “adolescent”, “animal”, and “dengue virus” emphasise clinical, biological, and demographic focus. Thematic clusters include green (public health/epidemiology), yellow (vector biology/mosquito control), red (clinical studies), and blue (virology/immunology). The low prominence of “data analysis” suggests a gap in computational approaches, which could improve dengue modelling and prevention strategies.

Research Needs in Malaysia

Figure 12 displays a VOS Viewer co-occurrence network of Malaysian dengue research (2012–2024), highlighting trends and gaps in mathematical modelling and data analysis. Central terms like “dengue”, “prediction modelling”, and “time series” focus on epidemiological forecasting, with clusters for weather-based modelling (orange) and healthcare analytics (blue). Emerging interest in computational methods is shown by terms like “Bayesian information criterion” and “advanced analytics”, but the small nodes for “regression analysis” and “big data” suggest a limited use of advanced data techniques. This gap hinders modelling accuracy and intervention effectiveness, emphasising the need for more data-driven approaches and interdisciplinary collaboration.

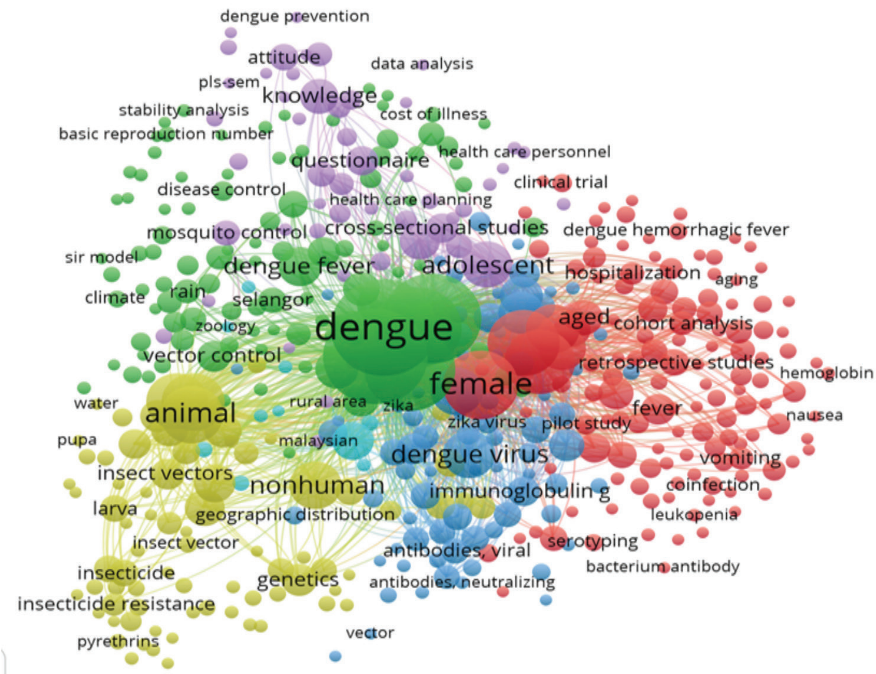

Figure 11: Analysis of dengue research

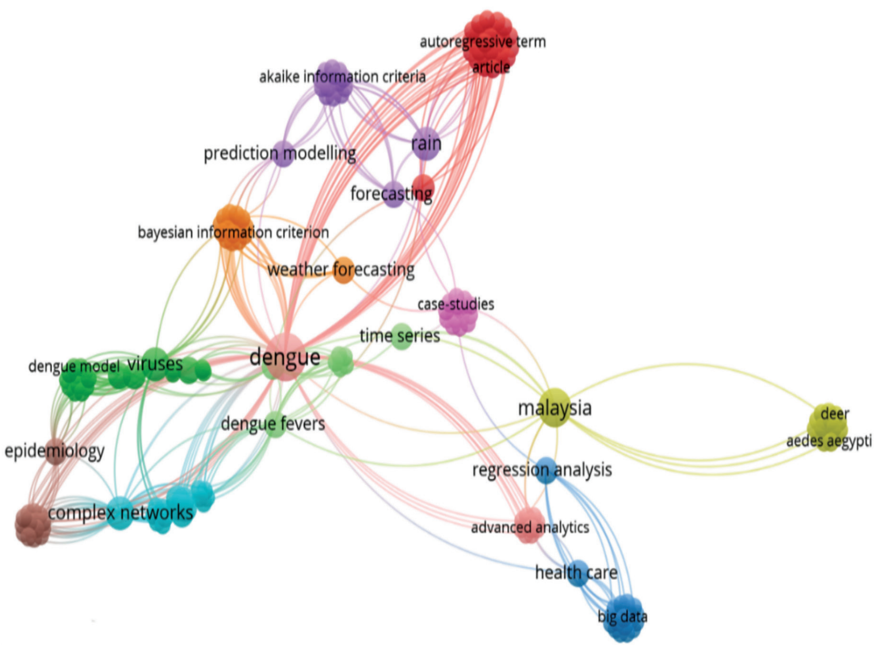

Figure 12: Analysis of dengue research: Gaps and opportunities

High-Performance Computing for Accurate Policy Management

High performance computing (HPC) uses supercomputers and parallel processing to solve complex problems faster than traditional computers, significantly enhancing infectious disease models (Lourenço *et al*., 2018). It's crucial for generating epidemic equilibrium points and optimising control strategies. In Malaysia, HPC can improve dengue forecasting, a current research gap (Hohl *et al*., 2016; Ong *et al*., 2023; Shahrul *et al*., 2025). HPC handles complex simulations, large datasets, and real-time data, such as analysing dengue's spatial spread with geographic, demographic and genetic data, and integrating weather, clinic and vector monitoring data (Díaz-Robles *et al*., 2008; Fiore *et al*., 2018; Keat-Chuan Ng *et al*., 2023). HPC also fosters multidisciplinary collaboration among epidemiologists, biologists, data scientists, and public health experts, enabling data sharing and graphical interfaces (Ismail *et al*., 2022; Jan *et al*., 2024). This collaboration can drive the development of new solutions and improve models for diseases like dengue, malaria, and HIV/AIDS.

Conclusions

Our work provides a complete overview of the efficiencies and limitations of all of the sustainable dengue prevention methods being used, in Malaysia. Since Wolbachia-infected trans-infected mosquitoes would infect their offspring thus preventing dengue from spreading, biological techniques like early identification could be a sustainable form of control. More efforts must be made to model environmental characteristics that includes maintaining functioning drainage systems, ensuring water storage containers are always kept closed, and taking care of the general cleanliness of the area.

Dengue fever outbreaks in Malaysia have the potential for an even greater adverse impact as environmental management approaches are not well researched. Improper waste disposal and stagnant water accumulation in urban areas exacerbate mosquito breeding issues, which highlights the need to address environmental pollution in dengue prevention efforts. Ongoing efforts to improve waste disposal management has Allowed researchers to collect more information on the transmission, prevention, and effects of DF. Additionally, internal heterogeneity and climate change factors have enhanced the dengue transmission model. Since medicine alone cannot reduce the impact of all the different dengue serotypes x, more effort is needed to reduce outbreaks through sustainable vector control methods.

The government can reduce dengue in the long term by providing necessary equipment to hospitals, installing effective surveillance systems for laboratories, and proposing a social mobilisation plan. Delays are also observed in aggregating these data and predicting an outbreak due to the absence of a direct link between hospitals and the Malaysian Ministry of Health (MMOH). Integrating the hospital data with the MMOH databases in real-time would allow for a more significant improvement in dengue control strategies and disease management.

This review adopts a systematic approach, complemented by bibliometric analysis using VOS viewer, to explore the advancements in dengue mathematical modelling in Malaysia from 2012 to 2024. The thematic synthesis identifies modelling trends, while the bibliometric mapping highlights co-occurrence networks and unmet research needs. Real-time data integration and HPC have improved the dengue model's consequentiality and performance for sustainable environmental management. Future research papers may consider the expansion of artificial intelligence (AI) and machine learning (ML) for more accurate predictions, integrating climate controls and change into public health interventions, and stakeholder coordination. These technologies can enhance long-term dengue controls and other epidemiological interventions in Malaysia and other parts of the world.

Using these new technologies investigators would be able to craft more ideal predictive models of dengue infection level and growth rates that would enhance the Malaysian public health systems' ability to better manage future dengue fever outbreaks.

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Conflict of Interest Statement

The authors declare that they have no conflict of interest.

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