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On Temperature-Dependent and Spatially Structured Dengue Transmission Models: A Mathematical Review

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Abstract

Dengue fever continues to expand globally due to complex interactions among climate variability, vector ecology, and human mobility, while mathematical modelling remains an essential tool for understanding these interactions and guiding effective intervention strategies. This review provides a focused mathematical synthesis of dengue transmission models, emphasizing the combined role of temperature-dependent vector dynamics and spatial heterogeneity induced by human movement, which remains insufficiently integrated in the existing literature.We systematically examine deterministic, stochastic, and data-driven modelling frameworks, including SIR–SI, SEIR–SEI, and related compartmental models together with their extensions to multi-patch and metapopulation settings. Particular attention is devoted to the mathematical formulation of temperature-dependent parameters through Brière, quadratic, and Arrhenius-type functions, highlighting their structural characteristics and epidemiological implications. In addition, the review analyzes the incorporation of mobility through patch-based and network formulations and discusses its influence on the basic reproduction number R_0 using next-generation matrix approaches. Across the reviewed studies, a major research gap is identified in the limited development of unified models that simultaneously integrate temperature effects, human mobility, and data-driven calibration. Addressing this gap is important for improving predictive accuracy and strengthening dengue prevention and control strategies.

Keywords: Dengue Transmission Modelling; Temperature-dependent Dynamics; Human Mobility; Multi-patch Systems; Optimal Control.

1. Introduction

Dengue fever remains one of the most important mosquito-borne viral diseases that affect tropical and subtropical regions around the world. The disease is primarily transmitted by *Aedes aegypti* and *Aedes albopictus* mosquitoes, whose geographical distribution and transmission potential are strongly influenced by environmental and climatic conditions. In recent decades, rapid urbanization, population growth, international travel, and climate variability have contributed significantly to the continued expansion of dengue transmission in many parts of the world [1–5].

Mathematical modelling has become an essential tool for understanding dengue transmission dynamics and evaluating intervention strategies. Early dengue models were mainly based on deterministic compartmental frameworks describing host–vector interactions under homogeneous

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assumptions. Over time, these models evolved to incorporate more biologically realistic mechanisms, including seasonal forcing, stochasticity, temperature-dependent vector traits, spatial heterogeneity, human mobility, and optimal control strategies [6–9].

Recent studies have shown that temperature plays a major role in shaping dengue transmission dynamics by affecting mosquito survival, biting behaviour, fecundity, developmental stages, and viral incubation periods [10–15]. Temperature-dependent transmission models demonstrate that even moderate climatic variations may substantially alter mosquito abundance, transmission intensity, and epidemic persistence. Consequently, several mathematical formulations, including seasonal forcing functions, Brière-type thermal response functions, and empirically fitted climate relationships, have been increasingly incorporated into dengue transmission models.

At the same time, increasing attention has been paid to the role of spatial mobility and human movement in the spread and persistence of dengue epidemics in interconnected regions [8, 16–19]. Human mobility has been represented through patch-based systems, network structures, diffusion processes, and mobility datasets derived from transportation and mobile-phone records. These approaches have demonstrated that population movement can strongly influence outbreak synchronization, spatial invasion, and the long-term persistence of dengue transmission.

Several review studies have examined dengue epidemiology, vector ecology, climate-sensitive transmission, and mathematical modelling approaches [9, 15, 20–23]. Nevertheless, many existing reviews focus mainly on climate-related transmission dynamics or general modelling structures without providing a detailed mathematical synthesis of how temperature dependence, spatial mobility, and epidemiological calibration are jointly incorporated into dengue transmission models. This limitation highlights the need for a more integrated mathematical review of temperature- and mobility-driven dengue modelling frameworks.

The present review addresses this gap by providing a structured mathematical synthesis of dengue transmission models developed between 2010 and 2025, with particular emphasis on:

- temperature-dependent vector and transmission dynamics,
- spatial mobility and multi-patch transmission structures,
- reproduction number analysis,
- optimal control formulations,
- and data-informed calibration approaches.

This study systematically compares the mathematical structures adopted across the selected literature, including compartmental formulations, incidence mechanisms, thermal response functions, mobility operators, analytical techniques, and calibration strategies. Particular attention is given to the integration of environmental variability and spatial mobility within mechanistic dengue transmission models. In addition, the review identifies important methodological gaps that remain in the current literature.

Although substantial progress has been achieved in climate-dependent and mobility-based dengue modelling individually, relatively few studies successfully integrate temperature dependence, realistic mobility structures, empirical epidemiological calibration, and rigorous mathematical analysis within a unified framework. Accordingly, this review not only summarizes existing dengue modelling approaches, but also critically evaluates the mathematical development of temperature-dependent and spatially structured dengue transmission models while highlighting important directions for future theoretical and applied research.

The remainder of the paper is organized as follows. Section 2 presents the literature search methodology and study selection process. Section 3 reviews the mathematical frameworks of dengue transmission models. Section 4 provides a comparative analysis of temperature-dependent formulations. Section 5 discusses mathematical and spatial modelling frameworks, including multi-patch systems and reproduction number analysis. Section 6 examines model extensions, while Section 7 reviews optimal control strategies. Sections 8 and 9 address data-driven approaches and comparative synthesis of the reviewed models, respectively. Section 10 discusses current challenges and future research directions, while the conclusion is presented in Section 11. The declarations, including conflicts of interest and acknowledgments, are provided in the final sections of the manuscript.

2. Literature Search Methodology

2.1. Search Strategy and Data Sources

This review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines [24]. A systematic literature search was conducted between January and March 2026 using four scientific databases: Scopus, Web of Science, ScienceDirect, and Google Scholar. The review focused on studies published between 2010 and 2025 concerning mathematical and computational modelling of dengue transmission under temperature variation, environmental forcing, spatial heterogeneity, and human mobility.

The search strategy combined keywords related to dengue transmission, mathematical modelling, climate variability, and mobility processes. Boolean operators were adjusted slightly across databases to ensure compatibility with individual search interfaces. Representative search expressions included:

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(TITLE-ABS-KEY("dengue") AND
TITLE-ABS-KEY("mathematical model" OR "transmission model"))
AND (TITLE-ABS-KEY("temperature" OR "climate") OR
TITLE-ABS-KEY("mobility" OR "spatial" OR "patch"))
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The search identified 412 records, including 96 from Scopus, 84 from Web of Science, 102 from ScienceDirect, and 130 from Google Scholar.

2.2. Study Selection and Screening

Duplicate records were removed manually using article titles, authors, publication years, and DOI information, resulting in 325 unique studies for title and abstract screening after removing 87 duplicates.

The screening process was conducted collaboratively by the authors to evaluate study relevance to the review objectives. Articles were included if they:

- presented mathematical, computational, statistical, or data-driven dengue transmission models,
- incorporated temperature dependence, environmental drivers, spatial structure, or human mobility,
- provided sufficient methodological detail for mathematical interpretation or comparison.

Studies were excluded if they:

- lacked explicit quantitative or mathematical modelling components,
- focused primarily on clinical or laboratory investigations without epidemiological modelling relevance,
- provided insufficient methodological detail,
- were unrelated to dengue transmission dynamics, or
- consisted mainly of commentary or non-research summaries.

Following title and abstract screening, 104 studies were retained for full-text eligibility assessment, from which 35 studies satisfied the predefined inclusion criteria for the final qualitative synthesis.

2.3. Reproducibility and Search Validity

To improve reproducibility and transparency, the search strategy, database sources, inclusion criteria, and screening procedures were documented explicitly. Disagreements regarding study eligibility were resolved through discussion and repeated evaluation of the corresponding full-text articles until consensus was achieved.

The review combined deterministic, stochastic, statistical, data-driven, and spatial modelling studies to capture the broad mathematical landscape of dengue transmission modelling. Particular emphasis was placed on temperature-dependent transmission dynamics, vector ecology, mobility processes, spatial heterogeneity, and epidemiological forecasting.

In addition to identifying commonly used modelling approaches, the review assessed mathematical structures, temperature formulations, mobility mechanisms, analytical methods, calibration strategies, and major modelling limitations across the selected studies.

2.4. PRISMA Flow Diagram

The study identification, screening, eligibility assessment, and inclusion process followed the PRISMA framework and is summarized in Fig. 1. After duplicate removal and screening, 104 studies were retained for full-text assessment, from which 35 studies satisfied the predefined inclusion criteria for the final qualitative synthesis.

The primary reasons for exclusion during the full-text assessment stage included:

- absence of explicit mathematical or computational modelling,
- insufficient methodological detail,
- lack of relevance to dengue transmission dynamics,
- exclusive focus on laboratory or biomedical investigations without epidemiological modelling, and
- commentary-based or non-research publications.

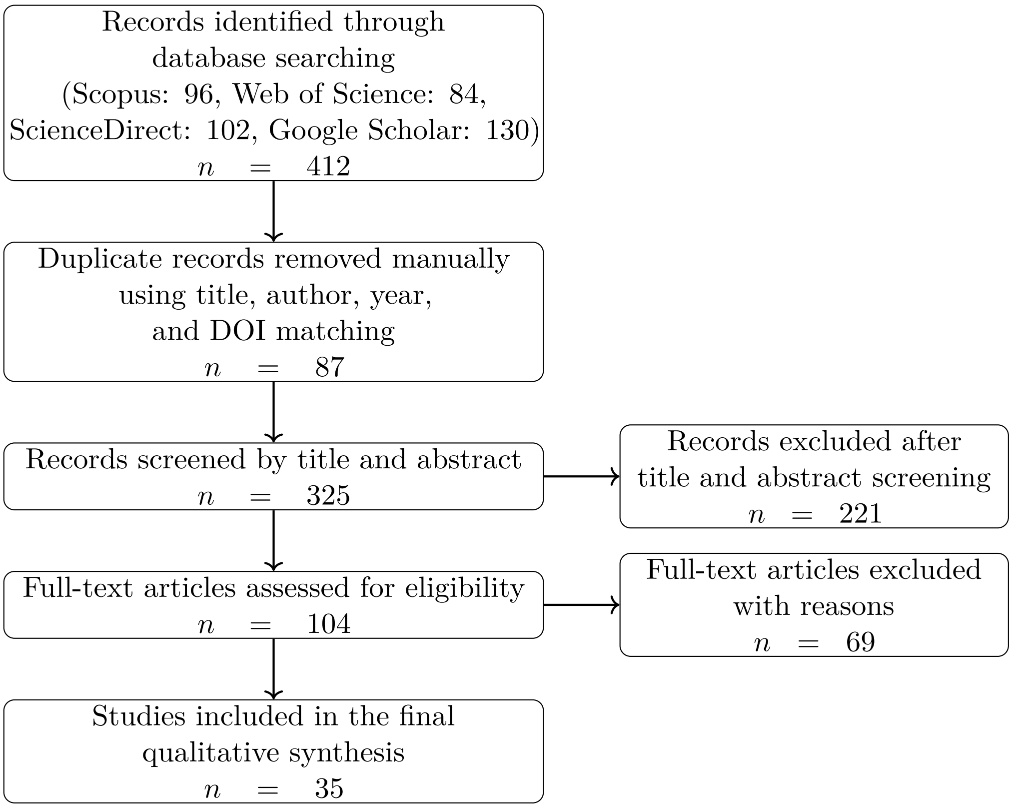

Fig. 1: PRISMA flow diagram illustrating the systematic study selection procedure used in this review.

The selected studies represent a broad range of mathematical and computational approaches for modelling dengue transmission under environmental and spatial influences. To support systematic comparison, the reviewed literature was organized according to key modelling characteristics, including compartmental structure, temperature dependence, mobility formulation, analytical methods, calibration strategies, and major modelling limitations. This organization facilitates clearer evaluation of current modelling trends and remaining methodological gaps in the literature.

A comparative summary of the 35 selected studies is presented in Appendix, i.e. Table 2. The table provides a structured overview of the reviewed models and highlights important directions for future development of temperature- and mobility-driven dengue transmission models.

3. Mathematical Framework for Dengue Transmission Models

Mathematical models of dengue transmission are commonly formulated as systems of nonlinear ordinary differential equations describing interactions between human and mosquito populations. Most studies employ compartmental structures in which humans are divided into susceptible (S_h), exposed (E_h), infectious (I_h), and recovered (R_h) classes, while mosquitoes are classified into susceptible (S_v), exposed (E_v), and infectious (I_v) compartments [8, 25, 26].

A representative deterministic SEI–SEIR model frequently used in the literature is given by

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h - \beta_{hv}\frac{S_h I_v}{N_h} - \mu_h S_h,\\
\frac{dE_h}{dt} &= \beta_{hv}\frac{S_h I_v}{N_h} - (\sigma_h + \mu_h)E_h,\\
\frac{dI_h}{dt} &= \sigma_h E_h - (\gamma_h + \mu_h)I_h,\\
\frac{dR_h}{dt} &= \gamma_h I_h - \mu_h R_h,\\
\frac{dS_v}{dt} &= \Lambda_v - \beta_{vh}\frac{S_v I_h}{N_h} - \mu_v S_v,\\
\frac{dE_v}{dt} &= \beta_{vh}\frac{S_v I_h}{N_h} - (\sigma_v + \mu_v)E_v,\\
\frac{dI_v}{dt} &= \sigma_v E_v - \mu_v I_v,
\end{aligned}$$

where β_{hv} and β_{vh} denote transmission rates between humans and vectors, while the remaining parameters describe demographic and epidemiological processes.

3.1. Incidence Formulations in Dengue Transmission Models

A major distinction among dengue transmission models concerns the formulation of the incidence term. The reviewed studies mainly adopt either standard incidence or mass-action incidence assumptions.

Under standard incidence, the infection process is normalized by the total population size, leading to transmission terms of the form

$$\beta\frac{SI}{N},$$

where S and I denote susceptible and infectious populations, respectively, and N represents the total population size. This formulation assumes that effective contact rates remain bounded as population size increases and is widely used in heterogeneous vector–host systems.

In contrast, mass-action incidence assumes that contact rates increase proportionally with population density, producing transmission terms of the form

$$\beta SI.$$

This formulation is commonly used in simplified theoretical settings or models emphasizing density-dependent transmission effects.

The reviewed studies employed both formulations depending on modelling objectives and epidemiological assumptions. However, temperature-dependent and spatially structured dengue models more frequently adopted normalized incidence because it provides greater stability when population sizes vary across regions or patches. Consequently, the illustrative models presented in this review primarily use normalized incidence terms, consistent with many recent studies incorporating temperature variability and spatial heterogeneity [8, 10, 16].

A fundamental quantity in dengue modelling is the basic reproduction number R_0, defined using the next-generation matrix approach [27] as

$$R_0 = \rho(FV^{-1}),$$

where F represents new infection terms and V describes transition processes such as recovery and mortality. This threshold parameter determines whether the disease can invade ($R_0 > 1$) or die out ($R_0 < 1$) and therefore links model structure with epidemiological outcomes [25, 28].

Temperature-dependent dynamics. In many contemporary dengue models, epidemiological parameters are expressed as functions of environmental temperature rather than treated as constants. Transmission rates, mosquito mortality, and incubation processes are commonly represented by temperature-dependent quantities such as $\beta_{hv}(T)$, $\beta_{vh}(T)$, $\mu_v(T)$, and $\sigma_v(T)$ [10, 11]. These nonlinear dependencies strongly influence the behavior of R_0 and overall transmission dynamics.

Spatial structure and mobility. To represent spatial heterogeneity, classical dengue models are often extended to multi-patch systems in which populations are distributed across interconnected regions. Human mobility is incorporated through movement rates between patches, producing coupled dynamical systems in which transmission depends on both local interactions and spatial connectivity [8, 16].

Analytical implications. The mathematical structure of dengue models strongly influences their analytical behavior. While classical models typically exhibit forward bifurcation with a threshold at $R_0 = 1$, more complex formulations involving temperature dependence or spatial coupling may generate richer dynamics, including multiple equilibria and backward bifurcation [7, 26]. These features emphasize the importance of modelling assumptions in determining epidemiological predictions.

This general framework provides the basis for the subsequent discussions on temperature-dependent transmission and spatial mobility models.

4. Temperature-Dependent Modelling of Vector Dynamics

Temperature plays a fundamental role in dengue transmission because many biological traits of *Aedes* mosquitoes and viral replication processes are strongly influenced by environmental conditions. Consequently, recent dengue models increasingly incorporate temperature-sensitive parameters to represent seasonal variability, climatic suitability, vector survival, and transmission potential more realistically. Several studies have shown that temperature affects mosquito biting rates, development rates, mortality, fecundity, extrinsic incubation periods, and viral transmission efficiency [4, 10–12, 14, 29].

Classical dengue models often assume constant epidemiological parameters, which may oversimplify transmission dynamics in tropical and subtropical regions where climatic variability strongly affects vector populations. To address this limitation, contemporary models incorporate temperature-dependent functions directly into transmission and demographic parameters. A general temperature-dependent dengue system can be written as

$$\frac{dX}{dt} = F(X, T(t), \theta),$$

where X denotes the vector of epidemiological state variables, $T(t)$ represents environmental temperature, and θ is the collection of model parameters.

Common temperature-dependent parameters include the mosquito biting rate $a(T)$, mortality rate $\mu_v(T)$, extrinsic incubation rate $\sigma_v(T)$, recruitment rate $\Lambda_v(T)$, and transmission probabilities between humans and mosquitoes. Consequently, the basic reproduction number also becomes temperature dependent,

$$R_0 = R_0(T),$$

allowing models to capture climatic thresholds under which dengue outbreaks either persist or decline.

4.1. Mathematical Representation of Temperature-Dependent Parameters

Temperature-dependent dengue models commonly use empirical thermal-response functions derived from laboratory or field observations to represent nonlinear relationships between temperature and mosquito or viral traits. One widely used formulation is the Brière-type thermal response function [10, 29],

$$f(T) = cT(T - T_{\min})\sqrt{T_{\max} - T},$$

where T denotes temperature in degrees Celsius (°C), $c > 0$ is a fitted parameter, and $T_{\min}$ and $T_{\max}$ represent lower and upper thermal thresholds.

The Brière function is biologically meaningful only for

$$T_{\min} < T < T_{\max},$$

since the square-root term must remain nonnegative. The formulation exhibits asymmetric thermal behaviour characterized by gradual growth at lower temperatures and rapid decline near the upper thermal limit, making it particularly suitable for modelling mosquito development and viral replication processes.

Several studies also employ quadratic thermal-response functions of the form

$$f(T) = a(T - T_{\min})(T_{\max} - T),$$

where $a > 0$ is a fitted coefficient. Unlike the Brière formulation, the quadratic model is symmetric around its thermal optimum and is mathematically simpler, although it may underestimate rapid declines in mosquito performance at high temperatures. Positivity similarly requires

$$T_{\min} < T < T_{\max}.$$

Arrhenius-type formulations are additionally used to describe biochemical and metabolic temperature sensitivity:

$$f(T) = Ae^{-E_a/(kT)},$$

where A is a scaling constant, E_a denotes activation energy, and k is the Boltzmann constant. In this case, temperature is measured in Kelvin to preserve dimensional consistency. These formulations are particularly useful for modelling metabolic and pathogen developmental processes.

Although mathematically distinct, these thermal-response functions all aim to capture biologically realistic temperature sensitivity in dengue transmission systems. Brière functions are generally preferred for asymmetric thermal responses, quadratic functions for analytical tractability, and Arrhenius-type models for mechanistic temperature-driven processes. Several reviewed studies [4, 8, 10–12, 14, 29] demonstrate that temperature-dependent formulations strongly influence transmission intensity, vector survival, epidemic timing, and estimates of the basic reproduction number.

4.2. Temperature Effects on Vectorial Capacity and Transmission

Many temperature-sensitive dengue models incorporate vectorial capacity, which measures the transmission potential of mosquito populations:

$$V(T) = \frac{ma(T)^2 b(T) c(T) e^{-\mu_v(T)\tau(T)}}{\mu_v(T)},$$

where m denotes the mosquito-to-human ratio, $a(T)$ the mosquito biting rate, $b(T)$ and $c(T)$ the transmission probabilities, $\mu_v(T)$ the mosquito mortality rate, and $\tau(T)$ the extrinsic incubation period.

This formulation illustrates how temperature simultaneously influences multiple biological mechanisms associated with dengue transmission. Increasing temperature may accelerate viral development and biting frequency, whereas excessively high temperatures may reduce mosquito survival. Studies such as Liu-Helmersson et al. [11], Mordecai et al. [10], and Tesla et al. [29] reported that dengue transmission typically reaches a maximum within an intermediate thermal range rather than increasing monotonically with temperature.

4.3. Seasonality and Climatic Variability

Several reviewed models incorporate seasonal forcing to represent periodic climatic fluctuations affecting mosquito abundance and disease transmission. A common formulation modifies mosquito recruitment or biting rates through sinusoidal forcing:

$$\Lambda_v(t) = \Lambda_0 \left(1 + \alpha \cos\left(\frac{2\pi t}{365}\right)\right),$$

where Λ_0 is the baseline mosquito recruitment rate and α denotes the forcing amplitude.

Seasonal temperature variation may generate periodic outbreaks, multi-annual oscillations, or more complex epidemic dynamics depending on the interaction between climate variability and population susceptibility. Aguiar et al. [7] demonstrated that seasonal forcing and disease importation can significantly alter dengue persistence and outbreak periodicity, while Rocha et al. [6] examined the role of seasonality through nonlinear dynamical analysis.

Climate-driven modelling studies further suggest that rising global temperatures may expand dengue transmission into previously unsuitable regions [4, 5, 12, 30]. These findings emphasize the growing importance of incorporating climate-sensitive mechanisms into dengue transmission models.

4.4. Mathematical Challenges and Modelling Limitations

Despite substantial progress, temperature-dependent dengue modelling still faces important mathematical and practical challenges. Thermal-response functions are often estimated from laboratory experiments conducted under controlled conditions and may not fully capture ecological variability in natural environments. Moreover, different studies frequently adopt different thermal formulations, parameter ranges, and calibration strategies, leading to inconsistent predictions.

Additional uncertainty arises from climatic projections and environmental data, since small changes in temperature assumptions may substantially alter predicted reproduction numbers, outbreak sizes, and epidemic persistence. Many temperature-driven models also neglect other ecological factors such as rainfall, humidity, vector adaptation, and human behavioural responses.

From a mathematical perspective, nonlinear temperature-dependent parameters significantly increase model complexity and analytical difficulty. Stability analysis, bifurcation analysis, and parameter identifiability become more challenging when epidemiological parameters vary dynamically with environmental conditions. Nevertheless, temperature-dependent dengue models remain essential tools for understanding climate-sensitive transmission dynamics and supporting public health preparedness under changing environmental conditions.

5. Spatially Structured Multi-Patch Models and Reproduction Number Analysis

Classical dengue transmission models commonly assume homogeneous mixing within a single population. In practice, however, dengue dynamics are strongly influenced by spatial heterogeneity arising from climatic variation, urbanization, transportation networks, demographic structure, and human mobility. These factors have motivated the development of multi-patch dengue models in which geographically separated populations interact through mobility processes [8, 16, 17, 19, 31].

Recent studies have shown that mobility can substantially alter local transmission dynamics and facilitate regional epidemic spread. Movement between connected patches may sustain transmission even when isolated local outbreaks would otherwise decline. Consequently, spatially structured models have become important tools for studying regional persistence, cross-border transmission, and the interaction between climate suitability and human mobility.

5.1. General Multi-Patch SEIR–SEI Framework

Consider a system consisting of n interconnected spatial patches. In each patch, the human population is divided into susceptible, exposed, infectious, and recovered compartments, while the mosquito population is represented by susceptible, exposed, and infectious classes.

For

$$i = 1, 2, \ldots, n,$$

the human compartments are

$$S_i^h,\ E_i^h,\ I_i^h,\ R_i^h,$$

and the mosquito compartments are

$$S_i^v,\ E_i^v,\ I_i^v.$$

The total human population in patch i is

$$N_i^h = S_i^h + E_i^h + I_i^h + R_i^h.$$

Transmission from infectious mosquitoes to humans is defined by

$$\lambda_i^h = a_i \beta_i^{vh} \frac{I_i^v}{N_i^h},$$

where a_i is the biting rate and β_i^{vh} is the vector-to-human transmission probability. Similarly, transmission from infectious humans to mosquitoes is given by

$$\lambda_i^v = a_i \beta_i^{hv} \frac{I_i^h}{N_i^h},$$

where β_i^{hv} denotes the human-to-vector transmission probability.

Consistent with the framework introduced in Section 3, most reviewed spatial dengue models adopt normalized incidence formulations to preserve transmission scaling when population sizes vary across patches or change through mobility.

5.2. Mobility Formulation

To maintain notational consistency, the mobility coefficients

$$M_{ij}, \qquad M_{ji}$$

represent movement rates from patch j to patch i, and from patch i to patch j, respectively.

Under this convention, the total inflow into patch i is

$$\sum_{j=1}^{n} M_{ij} X_j,$$

while the total outflow from patch i is

$$\sum_{j=1}^{n} M_{ji} X_i,$$

where X_i and X_j denote the compartment under consideration in patches i and j, respectively. The resulting net mobility contribution is therefore

$$\sum_{j=1}^{n} M_{ij} X_j - \sum_{j=1}^{n} M_{ji} X_i.$$

This formulation is applied to all mobile human compartments, including susceptible, exposed, infectious, and recovered individuals. Mosquito mobility is neglected because the flight range of *Aedes aegypti* is relatively small compared with typical human travel distances.

A representative multi-patch SEIR–SEI dengue model is therefore written as

$$\begin{aligned}
\frac{dS_i^h}{dt} &= \Lambda_i^h - \lambda_i^h S_i^h - \mu_i^h S_i^h + \sum_{j=1}^{n} M_{ij} S_j^h - \sum_{j=1}^{n} M_{ji} S_i^h,\\
\frac{dE_i^h}{dt} &= \lambda_i^h S_i^h - (\sigma_i^h + \mu_i^h) E_i^h + \sum_{j=1}^{n} M_{ij} E_j^h - \sum_{j=1}^{n} M_{ji} E_i^h,\\
\frac{dI_i^h}{dt} &= \sigma_i^h E_i^h - (\gamma_i^h + \mu_i^h) I_i^h + \sum_{j=1}^{n} M_{ij} I_j^h - \sum_{j=1}^{n} M_{ji} I_i^h,\\
\frac{dR_i^h}{dt} &= \gamma_i^h I_i^h - \mu_i^h R_i^h + \sum_{j=1}^{n} M_{ij} R_j^h - \sum_{j=1}^{n} M_{ji} R_i^h,\\
\frac{dS_i^v}{dt} &= \Lambda_i^v - \lambda_i^v S_i^v - \mu_i^v S_i^v,\\
\frac{dE_i^v}{dt} &= \lambda_i^v S_i^v - (\sigma_i^v + \mu_i^v) E_i^v,\\
\frac{dI_i^v}{dt} &= \sigma_i^v E_i^v - \mu_i^v I_i^v.
\end{aligned}$$

Here, Λ_i^h and Λ_i^v denote recruitment rates, μ_i^h and μ_i^v natural mortality rates, σ_i^h and σ_i^v incubation rates, and γ_i^h the human recovery rate. This framework allows epidemiological and environmental conditions to vary between patches, thereby capturing regional differences in climate suitability and transmission intensity.

5.3. Next-Generation Matrix and Basic Reproduction Number

The basic reproduction number R_0 measures the average number of secondary infections generated by a typical infectious individual in a disease-free population. In multi-patch systems, its derivation becomes more complex because infections may spread indirectly between patches through mobility.

Following the next-generation matrix framework of Diekmann et al. [27], the infected-state vector is

$$x = (E_1^h, \ldots, E_n^h, I_1^h, \ldots, I_n^h, E_1^v, \ldots, E_n^v, I_1^v, \ldots, I_n^v)^T.$$

The infected subsystem is decomposed as

$$\frac{dx}{dt} = F(x) - V(x),$$

where $F(x)$ contains new infection terms and $V(x)$ describes transition, recovery, mortality, incubation, and mobility processes.

At the disease-free equilibrium, the transmission matrix takes the block form

$$F = \begin{pmatrix} 0 & 0 & 0 & F_{hv} \\ 0 & 0 & 0 & 0 \\ 0 & F_{vh} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

where

$$(F_{hv})_{ij} = a_i \beta_i^{vh} \frac{S_i^{h*}}{N_i^h} \delta_{ij},$$

and

$$(F_{vh})_{ij} = a_i \beta_i^{hv} \frac{S_i^{v*}}{N_i^h} \delta_{ij}.$$

The transition matrix is

$$V = \begin{pmatrix} V_h^E & 0 & 0 & 0 \\ -\Sigma_h & V_h^I & 0 & 0 \\ 0 & 0 & V_v^E & 0 \\ 0 & 0 & -\Sigma_v & V_v^I \end{pmatrix},$$

where

$$\Sigma_h = \mathrm{diag}(\sigma_1^h, \ldots, \sigma_n^h), \qquad \Sigma_v = \mathrm{diag}(\sigma_1^v, \ldots, \sigma_n^v).$$

The exposed human transition block satisfies

$$(V_h^E)_{ii} = \sigma_i^h + \mu_i^h + \sum_{j=1}^{n} M_{ji}, \qquad (V_h^E)_{ij} = -M_{ij}, \quad i \neq j,$$

while the infectious human block is

$$(V_h^I)_{ii} = \gamma_i^h + \mu_i^h + \sum_{j=1}^{n} M_{ji}, \qquad (V_h^I)_{ij} = -M_{ij}, \quad i \neq j.$$

Since mosquito mobility is neglected, the mosquito transition matrices remain diagonal:

$$(V_v^E)_{ii} = \sigma_i^v + \mu_i^v, \qquad (V_v^E)_{ij} = 0, \quad i \neq j,$$

and

$$(V_v^I)_{ii} = \mu_i^v, \qquad (V_v^I)_{ij} = 0, \quad i \neq j.$$

The global reproduction number is then defined by

$$R_0 = \rho(FV^{-1}),$$

where $\rho(\cdot)$ denotes the spectral radius.

Because dengue transmission involves sequential human-to-vector and vector-to-human infection processes,

$$(FV^{-1})^2 = \begin{pmatrix} K_{hv}K_{vh} & 0 \\ 0 & K_{vh}K_{hv} \end{pmatrix},$$

which yields

$$R_0 = \sqrt{\rho(K_{hv}K_{vh})}.$$

Here, K_{hv} represents the expected number of infected humans generated by one infectious vector, while K_{vh} denotes the expected number of infected vectors generated by one infectious human. Their product therefore characterizes a complete human–vector–human transmission cycle.

5.4. Mobility Effects and Spatial Heterogeneity

Spatially structured dengue models reveal epidemiological phenomena absent in homogeneous systems. Heterogeneous climatic conditions may create highly suitable transmission patches that act as persistent reservoirs, while human mobility can connect low-risk and high-risk regions and facilitate outbreak propagation.

In highly connected systems, mobility may increase the spectral radius of the coupled next-generation operator even when isolated local reproduction numbers satisfy $R_{0,i} < 1$. Biologically, this occurs because infected individuals traveling between regions may repeatedly reintroduce infection into patches where local transmission alone would be insufficient to maintain endemicity. However, such persistence depends strongly on mobility magnitude, transmission heterogeneity, and network structure.

Several reviewed studies reported that mobility-driven coupling may enhance epidemic persistence, increase outbreak synchronization, and enlarge the spatial extent of transmission [8, 16, 17]. Nevertheless, many existing models still rely on synthetic mobility assumptions rather than empirical movement data and often neglect seasonal travel variation, demographic heterogeneity, or uncertainty quantification.

Despite these limitations, multi-patch frameworks remain essential mathematical tools for understanding dengue transmission under increasing urbanization, climate variability, and large-scale human mobility.

6. Extensions of Classical Dengue Transmission Models

Building on temperature-dependent and spatially structured formulations, many studies have extended classical dengue transmission models to incorporate additional epidemiological, environmental, and intervention-related mechanisms.

Classical dengue models are commonly formulated using compartmental SEIR-type structures for humans and SEI-type structures for mosquitoes. A general representation is

$$\frac{dX}{dt} = F(X, \theta),$$

where X denotes the vector of state variables and θ represents model parameters [27, 32]. Although these formulations provide a useful foundation for studying dengue dynamics, they may not fully capture the biological and environmental complexity of transmission processes.

6.1. Baseline Compartmental Structure

A standard deterministic dengue transmission model under normalized incidence can be written

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h - \beta_{hv}\frac{S_h I_v}{N_h} - \mu_h S_h,\\
\frac{dE_h}{dt} &= \beta_{hv}\frac{S_h I_v}{N_h} - (\sigma_h + \mu_h)E_h,\\
\frac{dI_h}{dt} &= \sigma_h E_h - (\gamma_h + \mu_h)I_h,\\
\frac{dR_h}{dt} &= \gamma_h I_h - \mu_h R_h,
\end{aligned}$$

with mosquito dynamics

$$\begin{aligned}
\frac{dS_v}{dt} &= \Lambda_v - \beta_{vh}\frac{S_v I_h}{N_h} - \mu_v S_v,\\
\frac{dE_v}{dt} &= \beta_{vh}\frac{S_v I_h}{N_h} - (\sigma_v + \mu_v)E_v,\\
\frac{dI_v}{dt} &= \sigma_v E_v - \mu_v I_v.
\end{aligned}$$

Here,

$$N_h = S_h + E_h + I_h + R_h$$

denotes the total human population. The parameters represent recruitment, transmission, incubation, recovery, and mortality processes for both human and mosquito populations.

Because mosquito biting activity is biologically constrained and does not increase indefinitely with host population size, many contemporary dengue models adopt normalized incidence formulations [8, 25, 26].

6.2. Structural Extensions

To improve epidemiological realism, several extensions of the classical framework have been proposed.

(i) Clinical and Epidemiological Extensions. Additional compartments are often introduced to capture disease severity or healthcare-related dynamics. For example, a hospitalized class may be incorporated through

$$\frac{dI_h}{dt} = \sigma_h E_h - (\gamma_h + \delta_h + \mu_h) I_h, \quad \frac{dH_h}{dt} = \delta_h I_h - (\gamma_H + \mu_h) H_h,$$

where δ_h denotes progression to severe infection and γ_H is the recovery rate of hospitalized individuals [26, 33]. Such formulations improve representation of clinical burden and healthcare demand.

(ii) Temperature-Dependent Extensions. Environmental variability is frequently incorporated by allowing key parameters to depend on temperature T. A common formulation is the Brière function

$$\beta(T) = aT(T - T_{\min})\sqrt{T_{\max} - T},$$

which captures nonlinear thermal responses within biologically admissible temperature ranges [8, 10, 11]. These models reproduce seasonal and climate-driven transmission patterns more realistically.

(iii) Spatial and Mobility Extensions. To capture geographical spread, multi-patch frameworks incorporate human mobility between locations. A representative formulation is

$$\frac{dS_i^h}{dt} = \Lambda_i^h - \beta_{hv}\frac{S_h I_v}{N_h} - \mu_i^h S_i^h + \sum_{j=1}^{n} M_{ij}^S S_j^h - \sum_{j=1}^{n} M_{ji}^S S_i^h,$$

where M_{ij}^S represents movement from patch j to patch i, with

$$i = 1, 2, \ldots, n, \qquad j \neq i$$

[8, 16]. These models account for spatial heterogeneity and regional connectivity.

(iv) Integrated Models. More recent studies combine temperature dependence, spatial structure, intervention strategies, and epidemiological extensions within unified frameworks. Although such models provide more realistic representations of dengue transmission, they also increase mathematical and computational complexity [4, 8, 26].

Table 1: Evolution of dengue transmission models with representative mathematical structures

Model Type	Mathematical Representation	Key Advantage	Limitation
Classical SEIR/SEI	$\frac{dX}{dt} = F(X)$	Analytical tractability and threshold analysis	Neglects environmental and spatial effects
Extended compartmental models	Addition of H, control terms, or multi-strain structure	Improved epidemiological realism	Increased model complexity
Temperature-dependent models	$\beta = \beta(T)$	Captures climate-driven transmission	Parameter uncertainty and data limitations
Spatial/mobility models	Movement terms $\sum M_{ij}X_j$	Captures spatial spread and connectivity	Requires mobility data
Integrated frameworks	Coupled system $F(X, T, M, u)$	Realistic and policy-relevant modelling	High computational and analytical complexity

6.3. Comparative Summary of Model Extensions

The evolution of dengue modelling frameworks is summarized in Table 1, highlighting the progression from classical compartmental systems to integrated modelling approaches.

In general, the progression from classical compartmental systems to integrated frameworks reflects increasing efforts to capture the combined effects of biological processes, environmental variability, and human mobility. Nevertheless, relatively few studies simultaneously integrate temperature dependence, spatial dynamics, and empirical calibration within a unified modelling framework, highlighting an important gap in the current literature.

7. Optimal Control Formulation in Dengue Transmission Models

Optimal control theory has become an important analytical framework in dengue epidemiology because it allows intervention strategies to be evaluated while balancing disease reduction against implementation costs. Across the reviewed literature, optimal control approaches have been applied to vaccination programs, insecticide application, public awareness campaigns, environmental sanitation, hospitalization strategies, and vector reduction measures [26, 28, 33–35]. These methods are particularly relevant in dengue-endemic settings where healthcare resources are limited.

In many recent dengue models, intervention strategies such as vaccination, adulticide spraying, larval control, and mobility reduction are formulated within temperature-dependent and spatially structured transmission systems.

Let

$$X(t) = (S_h, E_h, I_h, R_h, S_v, E_v, I_v)$$

denote the SEIR–SEI state vector. A generalized controlled dengue transmission system is written as

$$\frac{dX}{dt} = F(X, u, t),$$

where

$$u(t) = (u_1(t), u_2(t), u_3(t), u_4(t))$$

represents the vector of admissible control functions.

The controls are interpreted as follows:

- $u_1(t)$: vaccination or personal protection,
- $u_2(t)$: vector-control measures such as insecticide spraying,
- $u_3(t)$: treatment or hospitalization interventions,

- $u_4(t)$: environmental management targeting mosquito breeding sites.

A generalized temperature-dependent SEIR–SEI dengue model with controls is given by

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h - (1-u_1)\beta_{vh}(T)\frac{I_v}{N_h}S_h - \mu_h S_h,\\
\frac{dE_h}{dt} &= (1-u_1)\beta_{vh}(T)\frac{I_v}{N_h}S_h - (\sigma_h+\mu_h)E_h,\\
\frac{dI_h}{dt} &= \sigma_h E_h - (\gamma_h + u_3 + \mu_h)I_h,\\
\frac{dR_h}{dt} &= (\gamma_h + u_3)I_h - \mu_h R_h,\\
\frac{dS_v}{dt} &= \Lambda_v(1-u_4) - (1-u_1)\beta_{hv}(T)\frac{I_h}{N_h}S_v - (\mu_v + u_2)S_v,\\
\frac{dE_v}{dt} &= (1-u_1)\beta_{hv}(T)\frac{I_h}{N_h}S_v - (\sigma_v + \mu_v + u_2)E_v,\\
\frac{dI_v}{dt} &= \sigma_v E_v - (\mu_v + u_2)I_v.
\end{aligned}$$

Here, the transmission coefficients

$$\beta_{vh}(T) \quad \text{and} \quad \beta_{hv}(T)$$

depend explicitly on temperature. The control $u_1(t)$ reduces effective transmission, $u_2(t)$ increases mosquito mortality, $u_3(t)$ shortens the infectious period, and $u_4(t)$ suppresses mosquito recruitment and breeding-site availability.

The objective is typically to minimize both disease burden and intervention costs over a finite interval $[0, T]$. A commonly used quadratic objective functional is

$$J(u) = \int_0^T \left[A_1 I_h(t) + A_2 I_v(t) + \frac{1}{2}\sum_{i=1}^{4} B_i u_i^2(t) \right] dt,$$

where A_i represent epidemiological costs and B_i denote implementation costs associated with the controls.

Most reviewed studies apply Pontryagin's Maximum Principle to characterize the optimal controls [26, 33, 35]. The Hamiltonian function is defined by

$$\mathcal{H}(X, u, \lambda, t) = L(X, u, t) + \lambda^T F(X, u, t),$$

where $\lambda(t)$ denotes the vector of adjoint variables and $L(X, u, t)$ is the integrand of the objective functional.

The corresponding optimality system consists of:

- the controlled state equations,
- the adjoint equations
$$\frac{d\lambda}{dt} = -\frac{\partial \mathcal{H}}{\partial X},$$
- and the minimization conditions
$$\frac{\partial \mathcal{H}}{\partial u_i} = 0, \qquad i = 1, 2, 3, 4,$$
subject to admissible control constraints.

Most studies solve the resulting coupled state–adjoint system numerically using forward–backward sweep algorithms. The reviewed literature indicates that optimal intervention strategies can substantially reduce infection prevalence while balancing economic costs. However, many existing studies still rely on simplified assumptions such as homogeneous mixing, constant environmental conditions, or synthetic parameter values.

An important gap in the literature is the limited integration of temperature variability, human mobility, and optimal intervention strategies within unified modelling frameworks. Only a relatively small number of studies simultaneously incorporate climate-driven transmission, spatial mobility, and data-calibrated control policies. Future work would therefore benefit from integrated temperature-dependent and mobility-aware optimal control models capable of supporting region-specific dengue mitigation and public-health planning.

The reviewed studies demonstrate that optimal control methods provide an important bridge between theoretical epidemiology and practical disease-management strategies. Their effectiveness is expected to improve further as future models incorporate richer environmental, demographic, and mobility-related information.

8. Data-Driven Modeling

Recent advances in dengue transmission modelling increasingly rely on data-driven approaches that integrate epidemiological, environmental, and mobility data into mathematical and statistical frameworks. These approaches improve model realism and provide more accurate representations of the complex mechanisms governing dengue transmission.

Epidemiological surveillance data are widely used for parameter estimation and model validation, allowing theoretical predictions to be compared with observed incidence patterns. For example, Götz et al. [25] incorporated real case data to calibrate deterministic transmission models, thereby improving their practical relevance. At larger spatial scales, global burden and risk-mapping studies [2, 36, 37] have utilized large datasets to quantify spatial heterogeneity in dengue transmission.

Environmental data, particularly temperature, also play a central role in data-driven modelling by informing vector-related parameters such as biting rate, mortality, and extrinsic incubation period. Climate-driven studies [10, 11, 14, 29] demonstrate that empirical temperature relationships can reproduce seasonal variability and identify important transmission thresholds.

In spatial modelling frameworks, human mobility data provide important insight into the geographical spread of dengue. Mobility-informed studies [16–19] use transportation and communication data to characterize connectivity between regions, often identifying human movement as a major driver of epidemic propagation.

Despite these advances, data-driven models still face important limitations, including underreporting in epidemiological datasets, uncertainty in climatic projections, and limited access to high-resolution mobility data. Consequently, many studies combine empirical datasets with sensitivity analysis and scenario-based simulations to evaluate model robustness.

Here, data-driven approaches provide an important link between theoretical epidemiology and public-health applications. However, as highlighted in Table 2, relatively few studies successfully integrate temperature effects, human mobility, and real-data calibration within a unified mechanistic framework. These approaches remain particularly important for estimating climate suitability, spatial transmission risk, and mobility-dependent epidemic spread in heterogeneous populations.

9. Comparative Mathematical Synthesis of Reviewed Models

This section provides a comparative synthesis of the 35 reviewed studies summarized in Appendix Table 2. The studies were classified according to model type, compartmental structure, temperature dependence, mobility representation, control strategy, analytical methodology, and calibration approach. These categories were selected to capture the main mathematical and epidemiological features of contemporary dengue transmission models.

The reviewed literature includes deterministic, stochastic, statistical, data-driven, and review-based studies. Model structures ranged from classical SIR–SI and SEIR–SEI systems to climate-driven, trait-based, and spatially structured formulations. Temperature dependence was commonly represented through seasonal forcing or nonlinear thermal-response functions such as Brière-type formulations, while mobility was incorporated through patch-based, network-based, or spatial frameworks. The comparison also considered analytical techniques and calibration procedures based on synthetic, experimental, or real-world datasets.

The classification framework in Appendix Table 2 further allowed qualitative assessment of mathematical depth, epidemiological realism, and data integration across the reviewed studies. In particular, the synthesis distinguishes between purely theoretical models, empirically calibrated mechanistic systems, and data-driven approaches incorporating mobility or epidemiological datasets. This comparison helps identify major modelling trends, analytical strengths, and remaining research gaps.

9.1. Compartmental Structures and Transmission Assumptions

The reviewed studies reveal considerable diversity in compartmental structures and transmission assumptions. Classical dengue models commonly employed deterministic SIR–SI or SEIR–SEI systems under homogeneous mixing assumptions [7, 35]. These models provided tractable frameworks for deriving equilibrium conditions, reproduction numbers, and stability thresholds.

More recent studies extended these formulations by incorporating environmental variability, temporary immunity, vector ecology, and spatial heterogeneity. For example, Phaijoo and Gurung [8] developed a climate- and mobility-driven multi-patch SEI–SEIR framework, while Lourenço and Recker [38] considered multi-strain dengue dynamics. Other studies adopted trait-based approaches in which mosquito life-history parameters depend explicitly on temperature [10, 11].

The review also indicates a gradual transition from purely mechanistic frameworks toward statistical and data-driven approaches. Large-scale spatial studies [4, 36, 39] focused primarily on transmission suitability, vector distribution, and risk mapping rather than explicit host–vector dynamics. Although these approaches improve predictive coverage, they often provide less analytical insight into transmission mechanisms.

Most deterministic models adopted normalized incidence terms of the form

$$\beta \frac{I_v}{N_h} S_h,$$

while others used mass-action incidence formulations,

$$\beta S_h I_v.$$

These assumptions influence transmission scaling and threshold behavior, yet several studies did not explicitly justify their selection. This highlights the need for clearer epidemiological interpretation in future modelling studies.

9.2. Temperature-Dependent Modelling Approaches

One of the major developments in dengue modelling is the incorporation of temperature-dependent vector dynamics. Earlier studies often represented environmental variability through seasonal forcing functions applied to transmission parameters [6, 7]. Although these formulations capture periodic outbreak patterns, they do not explicitly represent mosquito physiological responses to temperature.

More recent studies increasingly employ nonlinear thermal-response functions derived from laboratory and experimental observations. Brière-type functions are widely used because they provide biologically realistic lower and upper thermal thresholds while preserving positivity within the admissible temperature range [10, 29]. Other studies used quadratic or Arrhenius-type formulations to model temperature effects on mosquito survival, biting rates, and viral incubation [11, 12].

The comparative analysis suggests that climate-driven formulations produce more realistic epidemic dynamics than constant-parameter models, particularly in tropical and subtropical regions. However, these models also introduce additional uncertainty because many thermal-response relationships are estimated under controlled laboratory conditions that may not fully reflect field environments.

9.3. Spatial Mobility and Multi-Patch Dynamics

Spatial heterogeneity and human mobility have become central components of modern dengue modelling. Traditional homogeneous-mixing systems neglect the important role of population movement in epidemic persistence and spatial spread. Several reviewed studies demonstrated that mobility between connected regions may sustain transmission even when isolated local reproduction numbers remain below unity [8, 16, 17].

Different mobility formulations appear throughout the literature. Patch-based systems commonly use mobility matrices to describe movement between regions, whereas network-based approaches rely on transportation or communication data. Other studies adopted diffusion-type formulations or mobility inference methods based on travel and mobile-phone datasets.

Patch-based deterministic models remain among the most analytically tractable approaches because they allow explicit construction of block-structured next-generation matrices. However, many studies still rely on simplified mobility assumptions, while only a limited number incorporated empirical movement datasets [16, 18]. Although data-informed mobility models improve realism, they also increase computational and calibration complexity.

9.4. Reproduction Number Analysis and Stability Results

The basic reproduction number R_0 remains the principal threshold quantity across most reviewed models. Many studies employed the next-generation matrix framework of Diekmann et al. [27] to derive transmission thresholds and investigate local stability properties.

For classical deterministic systems, the disease-free equilibrium is typically locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$. Several studies further investigated bifurcation, sensitivity, and persistence properties [6, 7]. Aguiar et al. [7], for example, demonstrated that seasonal forcing may generate oscillatory and nonlinear epidemic behavior.

In spatially structured systems, the derivation of R_0 becomes more challenging because mobility introduces coupled transmission and transition matrices. Consequently, the spectral radius of the next-generation operator depends on both local transmission intensity and inter-patch movement patterns. Despite recent progress, rigorous global stability and bifurcation analyses remain relatively limited in highly heterogeneous mobility systems.

9.5. Calibration Strategies and Modelling Limitations

The reviewed studies also differed substantially in calibration and data integration strategies. Some theoretical investigations relied mainly on synthetic or literature-based parameter values [7, 8, 35], whereas others incorporated observational, experimental, or epidemiological datasets [10, 25, 26]. More recent studies increasingly utilized global climate databases, vector occurrence records, and mobility data to improve predictive performance [4, 36, 39].

Despite these advances, several limitations remain common across the literature. Many models still assume homogeneous mixing within patches, simplified mosquito ecology, or limited environmental coupling. In addition, parameter identifiability and uncertainty quantification are often insufficiently addressed, particularly in highly parameterized climate-driven systems.

The comparative assessment also revealed variation in analytical rigor. Some mechanistic studies derived explicit threshold conditions, stability criteria, bifurcation structures, and sensitivity indices [6, 7, 35], whereas many large-scale climate-driven or spatial investigations relied primarily on simulation and statistical inference [4, 37, 39]. Consequently, although predictive capability has improved considerably, rigorous mathematical analysis of coupled temperature–mobility systems remains limited.

Generally, deterministic compartmental frameworks continue to dominate dengue modelling because of their analytical interpretability and epidemiological relevance. At the same time, there is a clear movement toward integrating climate variability, spatial mobility, and data-driven methodologies into more sophisticated transmission systems. Nevertheless, only a limited number of studies successfully combine temperature dependence, realistic mobility, empirical calibration, and control optimization within a unified mathematical framework.

10. Challenges and Future Research Directions

Despite substantial advances in dengue transmission modelling, important methodological and practical challenges remain, particularly in integrating temperature dependence, spatial mobility, and empirical data within unified mathematical frameworks.

One major challenge concerns the representation of environmental drivers. Although temperature-dependent formulations are widely used, their functional forms and parameterizations vary considerably across studies [10, 11, 14, 29]. This variability introduces uncertainty in model predictions, especially across different ecological settings. Moreover, important climatic factors such as rainfall and humidity are often simplified or neglected, limiting the ability of models to fully capture climate-driven transmission dynamics.

Another limitation involves the modelling of human mobility. While multi-patch and network-based approaches have been developed [8, 16–18], their integration into mechanistic compartmental systems remains limited, as shown in Table 2. Many studies still rely on simplified or synthetic movement assumptions because high-resolution mobility data are often unavailable, particularly in endemic regions. This reduces the ability of models to accurately represent spatial heterogeneity and connectivity.

From a mathematical perspective, increasing model complexity also creates significant analytical challenges. High-dimensional temperature- and mobility-driven systems often prevent explicit derivation of threshold quantities such as the basic reproduction number and restrict rigorous stability or bifurcation analysis. Consequently, many studies depend primarily on numerical simulations with limited theoretical investigation.

In addition, the integration of observational data into mechanistic models remains uneven. Data-driven approaches effectively capture large-scale spatial patterns [5, 22, 37, 39], but they often lack explicit transmission dynamics. Conversely, deterministic compartmental models provide stronger analytical structure but are frequently weakly calibrated against real epidemiological data. Bridging the gap between data-rich statistical methods and mechanistic modelling therefore remains an important research priority.

Future research should focus on developing integrated frameworks that combine climate-dependent transmission, realistic mobility structures, and robust data-assimilation techniques. Advances in epidemiological surveillance, remote sensing, and mobility-data collection provide new opportunities for improved calibration and validation. At the same time, further analytical tools are needed for studying nonlinear and high-dimensional spatial systems.

Future progress in dengue modelling will require stronger interdisciplinary collaboration to ensure that mathematical developments remain closely linked to empirical evidence and public-health needs. Such efforts are essential for improving predictive accuracy and supporting effective, context-specific dengue intervention strategies.

11. Conclusion

This review presented a structured mathematical synthesis of dengue transmission models, with particular emphasis on the combined roles of temperature variability and spatial mobility. The analysis of the 35 reviewed studies demonstrates the continued dominance of deterministic compartmental frameworks together with the increasing incorporation of climate-driven transmission processes and spatial heterogeneity. Overall, the reviewed literature reflects substantial progress in the mathematical understanding of dengue transmission dynamics under changing environmental and spatial conditions.

Temperature-dependent formulations have improved the representation of vector dynamics, thermal suitability, and seasonal transmission patterns, while spatially structured approaches have provided important insights into the influence of human mobility on the regional spread and persistence of dengue. Nevertheless, these developments have largely progressed along separate research directions, with only limited integration within unified mechanistic modelling frameworks, as summarized in Table 2. In particular, the review shows that the simultaneous incorporation of nonlinear temperature dependence, realistic human mobility, empirical calibration, and rigorous analytical treatment remains relatively uncommon in the current dengue modelling literature.

The incorporation of environmental forcing and spatial structure also introduces substantial nonlinearities that generate complex dynamical behaviour, including threshold effects, spatial variability in transmission potential, persistence mechanisms, and intricate stability patterns. These findings highlight the importance of balancing mathematical rigor with biologically and epidemiologically realistic assumptions when developing dengue transmission models. Such integration is essential for improving predictive performance and strengthening the practical applicability of mathematical models in public health planning.

In summary, this review provides a comprehensive comparative perspective on contemporary dengue modelling approaches and clarifies the current state of the field. By systematically organizing and critically synthesizing the reviewed literature, the study establishes a foundation for the future development of more integrated, data-informed, and application-oriented dengue transmission models. Future research should further emphasize the integration of environmental variability, realistic mobility patterns, epidemiological data calibration, and rigorous mathematical analysis within unified modelling frameworks.

CRediT Authorship Contribution Statement

Abdullahi Abdu: Conceptualization, Methodology, Formal Analysis, Investigation, Resources, Data Curation, Writing–Original Draft Preparation. **Admi Nazra:** Supervision, Writing–Review & Editing, Project Administration, Funding Acquisition. **Arrival Rince Putri:** Supervision, Project Administration, Writing–Review & Editing. **Mahdhivan Syafwan:** Supervision, Project Administration, Writing–Review & Editing.

Declaration of Generative AI and AI-assisted Technologies

During the preparation of this manuscript, the authors used ChatGPT Free version (OpenAI) and Grammarly for language refinement, grammar checking, proofreading, and improvement of readability. The authors carefully reviewed and edited the generated content and take full responsibility for the accuracy, integrity, and originality of the manuscript.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix: Comparative Summary of Reviewed Studies

To facilitate a more systematic mathematical comparison of the reviewed literature, the 35 included studies were classified according to model formulation, temperature representation, mobility structure, analytical methodology, calibration strategy, and principal modelling limitations. Deterministic compartmental models were classified as "D", stochastic formulations as "S", data-driven or statistical studies as "DD", and review-oriented studies as "RV". Temperature formulations were categorized based on whether transmission parameters were assumed constant, seasonally forced, empirically climate-dependent, or represented using nonlinear thermal-response functions such as Brière-type formulations. Spatial coupling mechanisms were similarly grouped into patch-based, network-based, diffusion-type, or non-spatial formulations. This classification framework was used to support the comparative mathematical synthesis presented in Section 9.

Table 2: Comparative mathematical assessment of the reviewed dengue transmission models. Abbreviations: MT (Model Type: D = Deterministic, S = Stochastic, DD = Data-driven, RV = Review), MS (Model Structure), TF (Temperature Function: Const, Seasonal, Brière, Climate), MF (Mobility Formulation: None, Patch, Network, Diffusion), CT (Control Type: None, OC = Optimal Control), AT (Analytical Tools: LS = Local Stability, GS = Global Stability, BF = Bifurcation, SIM = Simulation, SEN = Sensitivity, INF = Inference, MAP = Mapping), DC (Data Calibration: Syn = Synthetic, Real, Global, Lit = Literature, Exp = Experimental).

No.	Study	MT	MS	TF	MF	CT	AT	DC	Main Limitation
1	Götz et al. (2017) [25]	D	SEI–SEIR	Const	None	None	LS,SIM	Real	No climate or spatial mobility effects included
2	Rocha et al. (2016) [6]	D	SEIR–SEI	Seasonal	None	None	LS,BF	Syn	Spatial heterogeneity not considered
3	Götz et al. (2014) [34]	D	SEI	Const	None	OC	SIM	Syn	Simplified host–vector interaction structure
4	Aldila et al. (2013) [35]	D	SIR–SI	Const	None	OC	LS,SIM	Syn	Environmental variability not incorporated
5	Aguiar et al. (2011) [7]	D	SEIR	Seasonal	None	None	BF	Syn	No explicit mobility formulation
6	Mordecai et al. (2017) [10]	D	Trait-based	Brière	None	None	SEN	Exp	No explicit compartmental epidemic dynamics
7	Rodrigues et al. (2016) [28]	D	SEIR	Const	None	OC	SIM	Syn	Temperature-dependent transmission omitted
8	Aguiar et al. (2012) [40]	S	SEIR	Seasonal	None	None	SIM	Syn	Significant stochastic variability in outcomes
9	Liu-Helmersson et al. (2014) [11]	DD	Trait-based	Climate	None	None	SEN	Real	Human mobility not considered
10	Khan & Fatmawati (2021) [26]	D	SEIR–SEI	Const	None	OC	LS,SIM	Real	Absence of spatial transmission effects
11	Carvalho et al. (2019) [33]	D	SEIR	Const	None	OC	LS,SIM	Syn	Climate dependence not incorporated
12	Phaijoo & Gurung (2017) [8]	D	SEI–SEIR	Climate	Patch	None	LS	Syn	Limited empirical calibration and validation
13	Diekmann et al. (2010) [27]	D	General epidemic	Const	None	None	LS	Lit	General framework not dengue-specific
14	Ryan et al. (2019) [4]	DD	Statistical	Climate	None	None	MAP	Global	No mechanistic transmission equations
15	Cattarino et al. (2020) [37]	DD	Statistical	Climate	Network	None	INF	Global	Compartmental epidemic structure absent
16	Kraemer et al. (2019) [39]	DD	Spatial	Climate	Network	None	MAP	Global	Focused mainly on vector distribution patterns
17	Wesolowski et al. (2015) [16]	DD	Mobility analysis	Const	Network	None	INF	Real	No mechanistic disease dynamics model

No.	Study	MT	MS	TF	MF	CT	AT	DC	Main Limitation
18	Andraud et al. (2012) [9]	RV	Various	Various	Various	None	RV	Lit	Lack of unified modelling framework
19	Lee & Castillo-Chavez (2015) [31]	D	SEIR–SEI	Const	Patch	OC	LS,SIM	Syn	Limited climate dependence
20	Louis et al. (2014) [22]	RV	Spatial risk mapping	Climate	Network	None	MAP	Lit	Transmission dynamics not explicitly analysed
21	Morin & Comrie (2013) [12]	DD	Climate-driven	Climate	None	None	MAP	Global	No host–vector compartmental structure
22	Brady et al. (2013) [13]	DD	Vector survival	Climate	None	None	SIM	Exp	Human infection dynamics excluded
23	Siraj et al. (2017) [14]	D	Climate-driven	Climate	None	None	SIM	Real	Simplified representation of host dynamics
24	Tesla et al. (2018) [29]	D	SEI–SEIR	Climate	None	None	SIM	Exp	Spatial mobility processes absent
25	Reiner et al. (2013) [23]	RV	Various	Various	Various	None	RV	Lit	Limited comparative quantitative synthesis
26	Stoddard et al. (2013) [17]	DD	Mobility-driven	Const	Network	None	INF	Real	Limited mechanistic compartmental structure
27	Kraemer et al. (2015) [5]	DD	Spatial distribution	Climate	Network	None	MAP	Global	Restricted to vector ecology and distribution
28	Wesolowski et al. (2016) [18]	DD	Mobility analysis	Const	Network	None	INF	Real	Disease transmission mechanism not modelled
29	Perkins et al. (2014) [19]	DD	Mobility simulation	Const	Network	None	INF	Real	Not specifically developed for dengue transmission
30	Stewart-Ibarra & Lowe (2013) [15]	RV	Various	Climate	None	None	RV	Lit	Primarily descriptive review framework
31	Rocklöv & Dubrow (2020) [30]	RV	Climate review	Climate	None	None	RV	Lit	No explicit mathematical modelling framework
32	Lourenço & Recker (2014) [38]	D	Multi-strain SEIR	Const	None	None	SIM	Syn	Spatial coupling not incorporated
33	Bhatt et al. (2013) [2]	DD	Burden estimation	Climate	None	None	MAP	Global	Lacks mechanistic epidemiological dynamics
34	Messina et al. (2019) [36]	DD	Spatial risk	Climate	Network	None	MAP	Global	No explicit transmission model equations
35	Sardar et al. (2016) [41]	D	Multi-strain SEIR	Seasonal	None	None	LS,SEN	Real	No spatial mobility incorporated

Appendix Table 2 provides a structured mathematical classification of the 35 reviewed studies. The table highlights major differences in modelling assumptions, temperature formulations, spatial mobility representations, analytical methodologies, calibration strategies, and modelling limitations across the dengue transmission literature.