INPLASY

Models for Dengue and Chikungunya Virus Transmission Patterns: Protocol for a 10-Year Systematic Review (2015-2025)

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ADMINISTRATIVE INFORMATION

INTRODUCTION

*R*eview question / Objective A) Review Objective
The primary objective of this systematic review is to synthesize and evaluate the modelling frameworks used to characterize and predict the transmission patterns of Dengue (DENV) and Chikungunya (CHIKV) viruses globally with publication dates between January 2015 and July 2025. This review specifically aims to identify research gaps in temporal-spatial coverage, model structure, predictor integration, and validation rigor.

B) Research Questions
1. Data from what geographic areas and date ranges are used to understand the transmission patterns of DENV and CHIKV?
2. What are the predominant modelling frameworks (e.g., system dynamics, agent-based, statistical or machine learning, ecological niche or species distribution) currently employed in DENV and CHIKV research?

3. To what extent are climatic, socioeconomic, and demographic factors integrated as predictors within these models?
4. What is the quality and extent of model validation according to the Kopec et al. (2010) framework?
5. How frequently do models incorporate advanced biological features (e.g., vertical transmission, diapause, memory, etc.) and public health interventions?

Rationale The global burden of Dengue (DENV) and Chikungunya (CHIKV) has increased over the last decade, driven by climate, land use, and demographic changes. Transmission models have become vital tools for public health, providing the predictive frameworks necessary for evidence-based decision-making and the design of effective intervention strategies as well as providing evidence into mechanisms causing observed differences in disease patterns.

Despite the proliferation of these models, there is significant heterogeneity in their structures,

biological parameterization, and validation rigor. To the best of our knowledge, no systematic review has concurrently synthesized and evaluated the modelling frameworks applied to both DENV and CHIKV transmission patterns over the last ten years (2015–2025). This period is particularly critical as it marks a transition toward high-resolution spatiotemporal data, the integration of machine learning, and the increased adoption of the "One Health" approach in infectious disease modelling. Additionally, this group of authors is focused in East Africa where there is a gap in the literature and recent increase in incidence of these diseases, so the perspective of extrapolating existing models to this emerging setting is unique.

The rationale for this study is two-fold:
1. Methodological Synthesis: There is a pressing need to categorize the evolution of modelling frameworks—from traditional compartmental or regression models to complex agent-based, machine learning, and ecological niche models—to understand which frameworks are most common and which are most effective for specific public health objectives. We hypothesize that methods are being underused in the contexts they are most suited for.
2. Quality Assessment: Current literature lacks a standardized evaluation of model credibility. By applying the Kopec et al. (2010) validation framework, this review aims to identify systemic weaknesses in how models are developed, tested, and communicated.

Furthermore, our preliminary search yielded a highly specific eligibility rate of 14.6% (291 included papers from 1,994 records). Few models include the full complexity of these diseases: integration of vertical transmission, larval surveillance data, serotype variability, wildlife reservoirs, and climatic variability, particularly in high-risk regions like the Horn of Africa. This protocol provides the necessary roadmap to address these gaps and improve the reliability of future arboviral transmission models.

Condition being studied The primary conditions addressed in this systematic review are Dengue (DENV) and Chikungunya (CHIKV), which are two of the most significant mosquito-borne arboviral diseases affecting global public health. Both are primarily transmitted to humans through the bites of infected Aedes mosquito species, specifically Aedes aegypti and Aedes albopictus.

Dengue is caused by any of four closely related serotypes (DENV-1–4). It presents a wide clinical spectrum, ranging from mild febrile illness to severe, life-threatening manifestations such as Dengue Hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS). Chikungunya is characterized by an acute onset of fever and often debilitating joint pain (arthralgia), which can persist for months or years, significantly impacting the quality of life and economic productivity in endemic regions.

This review focuses on the transmission patterns and spatiotemporal dynamics of these two diseases and the methods used to estimate relationships and predict risk. The condition of interest extends beyond clinical outcomes to the modelling of disease spread. This includes: 1) The biological parameters governing the transmission cycle between human populations and mosquito vectors; 2) The influence of climatic variability (temperature, precipitation, humidity), land-use, and demographic changes on the suitability and expansion of Aedes mosquitoes; and 3) The geographic and temporal patterns of outbreaks, particularly in the context of increased human mobility and demographic changes.

This study evaluates how various modelling frameworks (such as system dynamics models, agent-based models, statistical models, machine learning models, and ecological niche models or species distribution models) characterize these conditions to support public health interventions and evidence-based decision-making.

METHODS

Search strategy A) Databases and Platforms: A systematic literature search was conducted across six major electronic scientific databases to ensure maximum coverage of peer-reviewed computational and epidemiological literature: PubMed, Web of Science, Scopus, SpringerLink, Nature Portfolio, and Google Scholar.

B) Search Date and Temporal Limits: The primary search was executed on 16th July 2025. The search was limited to articles published between January 2015 and July 2025 to capture the most recent decade of advancements in arboviral disease modelling, high-resolution spatiotemporal data, and machine learning (ML) integration.

C) Search Terms and String: The search employed a combination of keywords and Medical Subject Headings (MeSH) terms. The strategy used three primary thematic clusters (Diseases, Modelling frameworks, and Vectors) joined by the AND operator. The full search string was as follows:

("dengue" OR "chikungunya")
AND ("species distribution model*" OR "SDM" OR "agent-based model*" OR "ABM" OR "rule-based model*" OR "mathematical model*" OR "compartmental model*" OR "mechanistic model*" OR "ecological niche model*" OR "MaxEnt" OR "maximum entropy*" OR "statistical model*" OR "system dynamic*" OR "dynamic model*" OR "metapopulation model*")
AND ("Aedes" OR "Aedes mosquito*" OR "Aedes species" OR "Aedes aegypti" OR "Aedes albopictus" OR "vector-borne" OR "arbovirus" OR "mosquito-borne")

D) Search Strategy Refinement: The search was restricted to English-language, peer-reviewed, full-text journal articles. Initial results were imported into Zotero for deduplication. The search string yielded an initial total of 1,994 records, which were then subjected to multi-stage screening (Title/Abstract and Full-Text) by seven independent reviewers to identify the final 291 eligible studies.

Participant or population The population of interest includes individuals and communities in geographic regions that are either endemic to, or at risk of, DENV and CHIKV transmission. This systematic review includes models of various demographic scales, from individual-level agents in Agent-Based Models (ABM) to aggregated populations in system dynamics models. Specific focus is placed on models incorporating human movement, age-structure, and socioeconomic factors.

Intervention The interventions being evaluated are the various modelling frameworks applied to predict or estimate the transmission patterns of Dengue (DENV) and Chikungunya fever (CHIKV). We define and evaluate four primary categories of modelling interventions: 1) System Dynamics Models: Process-based mathematical models that focus on how host-vector differential equations are structured to capture transmission patterns; 2) Agent-Based Models (ABM): Individual-level simulations that incorporate autonomous agents (humans and/or mosquitoes) to evaluate the impact of fine-scale interactions, human mobility, and household-level characteristics; 3) Statistical and Machine Learning Models: Data-driven approaches, such as Generalized Linear Models (GLMs), Generalized Additive Models (GAMs), Random Forests, eXtreme Gradient Boosting (XGBoost), Support Vector Machine (SVM), Neural Networks, etc., that are used to correlate environmental and socioeconomic predictors with disease incidence; and 4) Ecological Niche and Species Distribution Models (ENMs/SDMs):

Frameworks such as Maximum Entropy (MaxEnt) or Boosted Regression Trees (BRT) used to map the environmental suitability and spatial expansion of Aedes aegypti and Aedes albopictus.

Comparator The comparators are defined by the internal variability of the modelling frameworks and their adherence to established validation standards. The comparison is structured across two dimensions:
A. Inter-Framework Comparison: We compare the performance, structure, and predictor integration of different modelling architectures against one another.
B. Benchmark Comparison: All included studies are compared against the Kopec et al. (2010) validation framework to assess quality across three domains: (1) Model Development Process (accuracy of conceptualization and parameterization); (2) Model Performance (plausibility, internal consistency, and sensitivity analysis); and (3) Consequences of Decisions (the transparency and usefulness of the model for public health policy).

Study designs to be included We include peer-reviewed, full-text original research articles that develop, implement, or validate predictive models of DENV and CHIKV transmission. Eligible designs include system dynamics models, agent-based simulations (ABM), statistical frameworks (GAM/GLM), machine learning, and ecological niche/species distribution models (MaxEnt/SDM). We exclude preprints, conference abstracts, editorials, and purely descriptive observational or entomological studies that lack a formal predictive or structural modelling component.

Eligibility criteria A) Inclusion Criteria
1. Only original research published in peer-reviewed journals is included to ensure a baseline of methodological quality.
2. Full-text articles must be accessible for comprehensive data extraction of model parameters and validation steps.
3. Studies must explicitly present a structural or predictive modelling framework (e.g., equations, agent rules, or statistical algorithms) rather than just descriptive case reports or laboratory studies.
4. Limited to English-language publications to ensure accurate interpretation of complex mathematical notations and technical validation results.

B) Exclusion Criteria
1. Preprints, conference abstracts, editorials, and book reviews are excluded as they often lack the

detailed supplemental data (e.g., code, parameter tables) required for our methodological synthesis.

2. Studies that address arboviruses in a purely clinical (drug efficacy, vaccine trials) or molecular (genomics) context without a population-level transmission component are excluded.

3. Lab-based reports on mosquito biology or simple field-based larval surveys are excluded unless they are integrated into a predictive transmission model.

4. In cases where multiple papers report on the same model and dataset without significant architectural updates, only the primary or most comprehensive study is included to avoid data redundancy.

Information sources The primary information sources for this systematic review consist of six major electronic scientific databases. These were selected to ensure a comprehensive capture of multidisciplinary research across various fields.

A) Electronic Databases

1. PubMed: For biomedical and life sciences literature.

2. Web of Science (Core Collection): For high-impact multidisciplinary scientific research.

3. Scopus (Elsevier): To ensure extensive coverage of computational and engineering-focused modelling.

4. SpringerLink: For access to technical mathematical and environmental science journals.

5. Nature Portfolio: To capture high-resolution studies and recent breakthroughs in disease dynamics.

6. Google Scholar: Utilized as a supplemental source to identify papers potentially missed by formal indexing and for initial citation tracking. Used for supplementary identification of grey literature and manual backward/forward citation tracking.

B) Excluded Sources

To maintain a high methodological standard for the Kopec et al. (2010) quality assessment, we explicitly excluded trial registers, conference abstracts, and non-peer-reviewed grey literature (e.g., policy briefs or preprints), as these sources frequently lack the technical documentation necessary for model validation analysis.

Main outcome(s) The primary outcomes of this systematic review are the methodological quality scores and the thematic distribution of modelling frameworks used for Dengue (DENV) and Chikungunya (CHIKV) transmission between January 2015 and July 2025.

A) Primary Methodological Outcomes

1. Validation Quality Scores: The central outcome is the quantitative Credibility Score (0–2) for each of the 291 included studies, derived from the 17-point Kopec et al. (2010) framework. Studies are being categorized into High (≥70%), Medium (50–69%), and Low (<50%) quality tiers.

2. Model Architecture Prevalence: A longitudinal analysis of the transition from traditional frequentist/compartmental models to advanced Agent-Based Models (ABM) and Machine Learning (ML) integrations over the 10-year period.

3. Spatial and Temporal Coverage: mapping of locations with and without associated data over time to identify differences and gaps in modeling intensity. We also map the spatial focus of modelling studies against actual disease burden. This outcome aims to identify regions with high transmission (e.g., the Horn of Africa) that are currently underserved by high-resolution predictive frameworks.

B) Secondary Outcomes (Thematic Synthesis)

1. Predictor Integration Rates: The frequency and methods by which climatic factors (such as temperature, precipitation, humidity), socioeconomic indicators, and demographic variables are incorporated as model covariates.

2. Biological Complexity Metrics: The proportion of models accounting for advanced features such as vertical transmission in Aedes spp., mosquito diapause, and density-dependent mortality.

2. Public Health Utility: Evaluation of models used specifically for intervention simulation (e.g., vaccination, Wolbachia release, or vector control).

C) Timing and Measures

As the review is currently in the data analysis phase, these outcomes are being synthesized using descriptive statistics (frequencies and percentages) and visualized via Python-based trend analysis. The results will offer a rigorous baseline for identifying systemic gaps in arboviral modelling, specifically regarding spatiotemporal resolution and validation transparency.

Additional outcome(s) 1. Research Collaboration Networks: An analysis of interdisciplinary and cross-institutional collaboration based on author affiliations. This identifies the extent of "One Health" integration between mathematicians, epidemiologists, and entomologists.

2. Data Source Transparency: Evaluation of the types and origins of datasets used for model parameterization, including the use of open-access climate repositories (e.g., ERA5, CHIRPS) versus local entomological surveillance data. Also, assessment of case definitions used in modeling,

given the difficulty in diagnosis based on clinical signs and underreporting of these diseases.

3. Computational Accessibility: Documentation of the software and programming environments (e.g., R, Python, MATLAB) used for model implementation and whether code availability is provided to ensure reproducibility.

These additional outcomes serve to contextualize the added value of this study, moving beyond a simple literature summary to a strategic map of the global arboviral modelling effort.

Data management The data management process for this systematic review is structured to ensure transparency, version control, and multi-user collaboration across the research team. The pipeline consists of three primary stages:

1. Record Organization and Deduplication: All search results from the six electronic databases (PubMed, Web of Science, Scopus, SpringerLink, Nature Portfolio, and Google Scholar) were exported in RIS formats and imported into Zotero reference management software. Initial deduplication was performed using Zotero's automated Duplicate Items function, followed by a manual review by the lead author to remove retracted articles, conference papers, and book sections.

2. Screening and Selection: The screening process (Title/Abstract and Full-Text phases) was managed using a centralized Zotero library shared among seven independent reviewers. Decisions for inclusion or exclusion were recorded using Zotero tags and folders. Discrepancies were resolved via group discussions to reach a consensus, and the final list of 291 eligible studies was locked for data extraction.

3. Data Extraction and Quality Scoring: Extraction was performed using a standardized, multi-tab Excel template. This template was hosted on a secure, collaborative cloud platform (OneDrive) to allow real-time updates and cross-review auditing by the team. The template includes dedicated sheets for Metadata and Affiliations (for bibliometric and collaboration analysis), Technical Parameters (modelling frameworks, predictors, and biological features), Kopec Quality Assessment (a 17-point scoring matrix for validation rigor).

4. Data Analysis and Storage: The finalized dataset was exported as a CSV file for descriptive statistical analysis in Python (via Google Colab). All raw extraction files, the PRISMA flow diagram data, and the Python scripts are archived securely to ensure that the findings can be reproduced or updated in future research cycles.

Quality assessment / Risk of bias analysis The methodological quality and validation rigor of the included studies are assessed using the standardized framework proposed by Kopec et al. (2010). This framework was selected because of its robustness in evaluating population-based disease simulation models across three critical domains:

1. Model Development Process (D1): Assessment of conceptual model clarity, variable definitions, and the transparency of parameter estimation (from literature, expert elicitation, or calibration).

2. Model Performance (D2): Evaluation of output plausibility, internal consistency, parameter sensitivity analysis, and comparisons with external empirical data or other models.

3. Consequences of Model-Based Decisions (D3): Assessment of the model's transparency and its practical usefulness for public health policy and intervention planning.

A) Scoring Mechanism
Each study is evaluated against 17 specific criteria derived from these three domains. For each criterion, the level of reporting is scored on a scale from 0-2, where 0 = Not Reported, 1 = Partially Reported, 2 = Fully Reported, and N/A = Not applicable to the specific model structure.

B) Analysis and Ranking
A cumulative Credibility Score is calculated as a percentage of the maximum possible points for applicable criteria. Studies are then ranked into three quality tiers:
1. High Quality (>= 70%): Robust validation and transparent documentation.
2. Medium Quality (50 – <70%): Moderate validation with some reporting gaps.
3. Low Quality (< 50%): Significant weaknesses in validation or structural transparency.

The assessment is performed by three authors with a verification step by other co-authors to minimize individual subjectivity. These scores are not used to exclude studies but to contextualize the reliability of the findings and identify systemic gaps in current DENV and CHIKV modelling frameworks.

Strategy of data synthesis Due to the significant heterogeneity in modelling frameworks and the diversity of reported outcomes, a formal meta-analysis is not technically feasible for this systematic review. Instead, we employ a Narrative Synthesis and Descriptive Statistical Analysis to characterize the current state of DENV and CHIKV modelling studies.

A) Quantitative Synthesis

We utilize Python (via Google Colab) to perform a descriptive statistical analysis of the included studies. We calculate frequency distributions and percentages across the following variables:

1. Modelling Frameworks: Temporal trends in the adoption of specific architectures (e.g., the rise of Machine Learning vs. traditional ODE-based / regression models from January 2015 to July 2025).

2. Predictor Integration: The proportion of models incorporating climatic, socioeconomic, and demographic covariates.

3. Biological Parameters: Prevalence of advanced features such as vertical transmission, diapause, density-dependent mortality, memory, etc.

4. Validation Quality: Distribution of studies across High, Medium, and Low-quality tiers based on the Kopec et al. (2010) recommendations.

B) Narrative and Thematic Synthesis
We conduct a thematic analysis to identify:

1. Methodological Gaps: Cross-tabulating model types with geographic regions to identify neglected hotspots (e.g., the Horn of Africa).

2. Interdisciplinary Trends: Analyzing author affiliations to assess the extent of collaboration between various departments or disciplines.

3. Model Utility: Synthesizing how models are currently being used to inform public health interventions, such as vector control and vaccination strategies.

C) Visualization
Data synthesis results are presented through structured tables and high-resolution graphical visualizations (e.g., heatmaps of geographic focus, stacked bar charts for framework evolution, and spider plots for validation rigor) generated using Python libraries. This approach ensures a rigorous, transparent baseline for identifying underserved research areas in arboviral disease modelling.

Subgroup analysis To address the inherent heterogeneity in the included studies and to identify specific research gaps, we perform subgroup analyses across four primary dimensions:

1. By Arboviral Disease: We compare the modelling landscape of Dengue (DENV) versus Chikungunya (CHIKV), including a specific subgroup for co-infection models. This allows us to identify whether one disease is disproportionately represented or if modelling frameworks differ significantly between the two.

2. By Modelling Frameworks: We categorize and compare subgroups based on the core modelling framework (System Dynamics models, Agent-Based Models, Statistical/Machine Learning models, Ecological Niche/Species Distribution Models). This analysis evaluates which frameworks are most frequently used for specific public health objectives (e.g., outbreak prediction vs. spatial suitability mapping).

3. By Validation Quality Tier: Using the Kopec et al. (2010) scores, we perform subgroup comparisons between High Quality (score >= 70%) and Low Quality (score < 50%) studies. This helps determine if certain modelling frameworks or geographic regions consistently exhibit higher levels of validation rigor and structural transparency.

These subgroup analyses are conducted using descriptive statistics and visualized through cross-tabulations and frequency distributions to highlight underserved areas in current arboviral research.

Sensitivity analysis As this is a methodological systematic review focusing on model frameworks and validation rigor, sensitivity analysis is applied to the review process itself to ensure the robustness of our qualitative and descriptive findings. We address potential sources of bias and variation through the following mechanisms:

1. Inter-Rater Reliability and Consensus: To minimize individual bias during the screening and extraction of the 1,994 identified records through database search, a subset of papers was independently reviewed by multiple authors. Sensitivity is assessed by comparing the consistency of inclusion/exclusion decisions across the seven-person research team. Discrepancies were resolved through a formal consensus-building process to ensure that the final 291 eligible papers represent a stable and reproducible sample.

2. Validation Scoring Thresholds: Our analysis categorizes models into High (>=70%), Medium (50 - <70%), and Low (<50%) quality tiers based on the Kopec et al. (2010) framework. We perform a sensitivity check by adjusting these percentage thresholds (e.g., ±5%) to determine if the reported systemic weaknesses in arboviral modelling are sensitive to these specific cut-off points or if the trends remain consistent across the 10-year period (2015–2025).

Language restriction Yes, the search is limited to English-language publications only to ensure accurate interpretation of complex notations and technical validation results within the 2015–2025 study period.

Country(ies) involved Kenya, Ethiopia, Somalia.

Other relevant information This systematic review is part of the ARBO-WATCH project (Modelling dengue and chikungunya transmission patterns for improved public health decision-making in the Horn of Africa), which is funded by the Wellcome Trust (Grant Number: 308803/Z/23/Z).

The primary goal of this review is to provide a rigorous, evidence-based baseline for the development of process-based models and decision-support tools specifically tailored for Kenya, Ethiopia, and Somalia. The broader specific objectives for conducting this review are to:
i) Identify high-quality parameter sets for Aedes aegypti and Aedes albopictus population dynamics.
ii) Determine which modelling frameworks are most effective for capturing the unique climatic, socioeconomic, and demographic drivers of the Horn of Africa.
iii) Bridge the gap between theoretical modelling and practical public health surveillance as part of a One Health approach.

This study is being conducted by a multidisciplinary consortium of ten institutions drawn from Kenya, Ethiopia, Somalia, and United States:
1. Ethiopia Public Health Institute (EPHI)
2. Kenya National Public Health Institute (NPHI)
3. Kenya Medical Research Institute (KEMRI)
4. Kenya Meteorological Department (KMD)
5. Somalia's Federal Ministry of Health (FMoH)
6. Jomo Kenyatta University of Agriculture and Technology (JKUAT)
7. Abrar Research and Training Centre (ARACHTI)
8. Ohio State University (OSU)
9. Global One Health Initiative (GOHi)
10. International Livestock Research Institute (ILRI)

The lead institution is ILRI and the project duration is 3 years (starting from February 2025 to January 2028). The findings of this project will directly inform the operationalization of a cross-border, data-driven decision-support ecosystem for arbovirus control. The authors declare no competing interests, and the funder has no role in the design, data collection, data synthesis, or reporting.

Keywords Systematic review; Models; Dengue; Chikungunya; Aedes; Methodological synthesis; Quality assessment; Kopec framework; Transmission dynamics; Arboviruses.

Dissemination plans The findings of this systematic review will be shared through a multi-channel strategy aimed at both academic researchers and public health practitioners in the Horn of Africa:
1. Peer-Reviewed Publication: The primary dissemination vehicle shall be a high-impact, open-access journal article. This will ensure the 10-year methodological synthesis and Kopec validation scores are available to the global scientific community.
2. Conference Presentations: Results will be presented at major international and regional forums.
3. Institutional Reports & Policy Briefs: As a core output of the ARBO-WATCH project, a summary of modelling gaps and best practices will be shared with stakeholders.
4. Digital Repositories: The standardized data extraction template and Python analysis scripts will be made available via open-access repositories (e.g., GitHub or Figshare) to promote reproducibility and support future researchers in arboviral transmission modelling.
5. Capacity Building: The identified High-Quality frameworks will serve as a baseline for training workshops organized for graduate fellows and public health officials within the ARBO-WATCH consortium.

Contributions of each author
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