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To Study and Analyze Existing Decision-Making Techniques for Monitoring of Chikungunya Disease

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Abstract

Chikungunya virus (CHIKV) is a rapidly spreading vector-borne disease that poses significant global health risks due to its recurrent outbreaks, long-lasting arthralgia, and diagnostic overlap with other arboviruses such as dengue and Zika. Effective monitoring and decision-making systems are crucial to improve outbreak prediction, optimize resource allocation, and enhance public health responses. This study explores a wide range of decision-making techniques and time-series models, mechanistic and Bayesian frameworks, machine learning (ML), deep learning (DL), multi-criteria decision-making (MCDM), geospatial and spatiotemporal models, and IoT/edge-enabled decision support. We compare their interpretability, data requirements, real-time suitability, and adaptability to low-resource settings. In addition, we emphasize challenges such as data scarcity, non-stationary dynamics due to climate variability, and the need for explainable and equitable AI-driven systems. By synthesizing state-of-the-art methods and emerging digital health technologies, this paper provides actionable insights for researchers, healthcare practitioners, and policymakers in building robust, scalable, and context-aware monitoring frameworks for Chikungunya disease.

Introduction

Chikungunya virus (CHIKV) is a re-emerging mosquito-borne alphavirus transmitted primarily by Aedes aegypti and Aedes albopictus, which also serve as vectors for dengue and Zika. Since its discovery in Tanzania in 1952, CHIKV has caused recurrent outbreaks across Africa, Asia, and the Americas, affecting millions of people worldwide. Although the infection is rarely fatal, it manifests with high fever, rash, and severe joint pain that can persist for months or even years, causing long-term disability and economic losses [1]. The chronic arthralgia associated with chikungunya has been shown to reduce quality of life, leading to absenteeism and productivity decline, making it a pressing public health concern. The global expansion of chikungunya has been facilitated by increased international travel, urbanization, and climatic changes that favor mosquito breeding. The World Health Organization (WHO) reported ongoing outbreaks in Asia and Africa in 2022, with imported cases spreading to non-endemic regions including Europe [2], [3]. Similarly, the European Centre for Disease Prevention and Control (ECDC) tracks frequent case importation into European countries. This demonstrates that chikungunya is no longer a localized disease but a global health threat requiring transnational surveillance and coordinated control strategies. Figure 1 shows cycle of chikungunya mosquito spread.

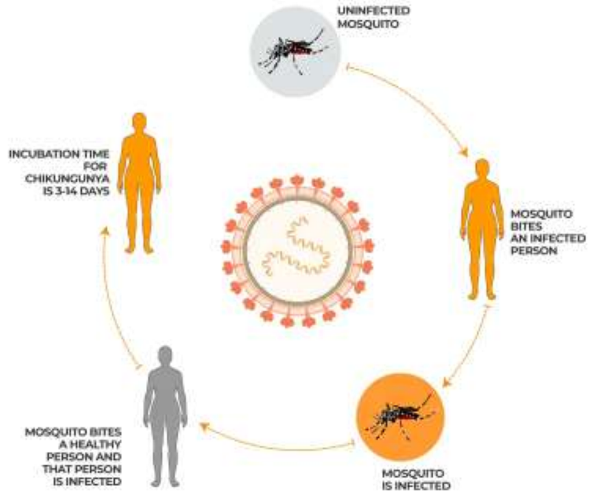

Figure 1. Chikungunya mosquito spread cycle

One of the critical challenges in managing chikungunya is its clinical overlap with other arboviruses such as dengue and Zika. Since these infections share symptoms like fever, rash, and joint pain, misdiagnosis is common, particularly in co-circulation periods [11]. The researchers have employed statistical and mechanistic models to capture the dynamics of chikungunya spread. Statistical methods such as SARIMA have been applied to case data in Brazil, producing reliable forecasts of seasonal incidence trends [8]. Mechanistic compartmental models, such as SEIR variants, have been used to understand transmission dynamics, estimate epidemiological parameters, and evaluate intervention strategies under uncertainty [6]. Bayesian inference further strengthens these models by quantifying uncertainty, allowing policymakers to make evidence-based decisions with explicit confidence bounds. The rise of machine learning (ML) and deep learning (DL) has transformed outbreak forecasting and clinical decision support. Studies have shown that ML classifiers can distinguish between chikungunya, dengue, and Zika with high accuracy when trained on clinical and laboratory features. DL architectures such as LSTMs and CNNs have been applied to arboviral time series, capturing nonlinear dependencies and enabling multi-modal integration with mobility and climate data [12]. These AI-driven approaches provide powerful prediction capabilities but raise concerns regarding interpretability, fairness, and generalizability in low-resource settings.

Parallel advances in geospatial and remote sensing technologies have enabled more precise monitoring of environmental determinants of chikungunya. Satellite-derived indices of temperature, rainfall, vegetation, and urbanization have been used to model mosquito habitat suitability. Bayesian hierarchical spatial models further enhance prediction by accounting for spatial dependence and interaction effects, improving hotspot detection accuracy [4], [5]. These methods highlight the importance of incorporating ecological and environmental signals into outbreak monitoring pipelines. The integration of digital health and IoT-enabled systems marks a new frontier in chikungunya surveillance. Wearable sensors and smart devices have been deployed to continuously monitor symptoms and environmental exposures [14]. IoT architectures allow real-time data collection, edge processing, and cloud-based analytics for outbreak alerts. Moreover, explainable AI ensembles are being designed to ensure transparency and user trust in decision-support systems [19]. These innovations are particularly promising in resource-limited settings, where conventional surveillance infrastructure is weak. Despite this there is an urgent need to systematically study and analyze decision-making techniques for chikungunya monitoring. No single approach is sufficient in statistical models provide baseline interpretability, mechanistic models capture causal structure, ML/DL methods enhance predictive power, and IoT/edge systems ensure real-time adaptability. A layered, hybrid framework that leverages complementary strengths while addressing challenges of data quality, fairness, and explainability will be critical to advancing chikungunya surveillance.

Literature Review

Several studies have explored computational and decision-making techniques for the monitoring and prediction of chikungunya outbreaks. Freitas et al. [4] conducted one of the earliest detailed spatio-temporal analyses during the 2016 outbreak in Rio de Janeiro, applying Bayesian models to identify how socioeconomic and environmental conditions influenced disease spread. Similarly, Santos et al. [5] examined the spatial and temporal dynamics of chikungunya in Brazil between 2017 and 2023, demonstrating that climatic variability and social vulnerability significantly contributed to epidemic intensity.

Mechanistic approaches have also been investigated to capture biological realism in transmission dynamics. Meyer et al. [6] employed a Bayesian SEIR framework to estimate epidemiological parameters while explicitly quantifying uncertainty, offering policymakers more robust decision support. Expanding on this, Vázquez-Peña et al. [7] introduced a relapse-based chikungunya model with Bayesian estimation, highlighting the potential role of reinfection in shaping long-term epidemic trajectories. Complementing these approaches, Yakob et al. [8] demonstrated that SARIMA models could reliably forecast chikungunya incidence in Brazil, showcasing the utility of time-series techniques as baseline forecasting tools. With the rise of digital epidemiology, studies have begun leveraging internet-based data streams for early outbreak detection. Verma et al. [9] showed that Google Trends could predict acute febrile illness signals, including chikungunya, with week-level lead times compared to traditional surveillance. Similarly, Miller et al. [10] validated the use of Google search data as faster outbreak indicators, emphasizing the value of online behavior in enhancing real-time surveillance.

Machine learning (ML) and deep learning (DL) have been increasingly applied for chikungunya detection and diagnosis. Arrubla-Hoyos et al. [11] developed ML classifiers capable of distinguishing chikungunya from dengue and Zika with high accuracy, thus addressing challenges of clinical misdiagnosis. Da Silva Neto et al. [12] conducted a systematic review of ML/DL methods, highlighting their promise in arboviral diagnosis while noting the challenges of data scarcity and model generalization. Abdallah et al. [13] advanced this area by integrating multi-criteria decision-making (AHP) with transfer learning, resulting in a hybrid system for forecasting multiple arboviruses with improved accuracy and interpretability. Beyond predictive modeling, IoT-based systems have emerged as practical tools for real-time health monitoring. Sood and Mahajan [14] proposed a wearable IoT-enabled healthcare system for detecting and monitoring chikungunya symptoms, demonstrating the feasibility of integrating cyber-physical systems in outbreak response. Pley et al. [15] provided a broader perspective, reviewing digital innovations in vector-borne disease management and emphasizing the importance of integrating big data, IoT, and decision-support technologies.

Geospatial and remote sensing approaches further enrich chikungunya surveillance. Palo et al. [17] employed GIS and satellite-derived data to map mosquito risk zones, offering a cost-effective method for large-scale monitoring. Similarly, Nuthammachot et al. [18] integrated MCDM with GIS to generate transparent risk maps, thereby supporting policymakers in targeting high-risk areas. Finally, Cheah et al. [19] emphasized the importance of explainable AI ensembles in infectious disease decision support, ensuring that advanced ML systems remain interpretable and trustworthy for public health applications. Studies demonstrate the diversity of decision-making approaches for chikungunya monitoring. While statistical models such as SARIMA provide robust baselines, mechanistic and Bayesian approaches offer biologically grounded insights. Meanwhile, ML/DL methods deliver high predictive accuracy, MCDM ensures transparency, and IoT/GIS systems extend monitoring into real-time and spatially explicit domains. Table 1 represents a finding of existing approaches.

Table 1. Findings of existing approaches

Author(s)	Method/Model	Key Findings
Freitas et al. [4]	Bayesian Spatio-temporal Models	showed environmental and socioeconomic drivers
Santos et al. [5]	Spatio-temporal Analysis	identified climate and vulnerability factors
Meyer et al. [6]	Bayesian SEIR Models	Estimated epidemiological parameters with uncertainty awareness
Vázquez-Pena, et al. [7]	Bayesian relapse model	Extended SEIR with relapse cases
Yakob et al. [8]	SARIMA Models	Predicted chikungunya incidence reliably in Brazil
Verma et al. [9]	Google Trends Analysis	Forecasted acute febrile illness using online search data
Miller et al. [10]	Google Search Data	Showed faster chikungunya indicators than traditional surveillance
Arrubla-Hoyos et al. [11]	Machine Learning Classifiers	Differentiated chikungunya, dengue, Zika with high accuracy
da Silva Neto et al. [12]	ML/DL Systematic Review	Highlighted performance of AI in arbovirus diagnosis
Abdallah et al. [13]	MCDM + Transfer Learning	Combined AHP and ML for multi-disease outbreak forecasting
Sood & Mahajan [14]	IoT Wearable System	Demonstrated IoT-based healthcare monitoring for chikungunya
Pley et al. [15]	Digital Innovation Review	Reviewed technological innovations for vector-borne disease control
Palo et al. [17]	GIS + Remote Sensing	Predicted mosquito risk zones using GIS-based models
Nuthammachot et al. [18]	GIS + MCDM	Applied multi-criteria GIS methods for risk assessment
Cheah et al. [19]	Explainable AI Ensembles	Discussed role of AI ensembles for infectious disease decision support

Decision Making Techniques

Decision-making techniques for chikungunya monitoring encompass a wide range of computational, analytical, and digital approaches aimed at forecasting outbreaks, guiding interventions, and supporting clinical and public health decisions. Traditional statistical and time-series models such as ARIMA and SARIMA provide baseline forecasts by capturing seasonal incidence trends, while mechanistic and Bayesian models (e.g., SEIR frameworks) integrate biological transmission dynamics with uncertainty quantification to support epidemiological planning. More recently, machine learning (ML) and deep learning (DL) methods have enabled powerful predictive modeling and differential diagnosis using multimodal data sources, though these approaches often face challenges of interpretability and data scarcity. Figure 2, defines the Layered Framework of Decision-Making Techniques

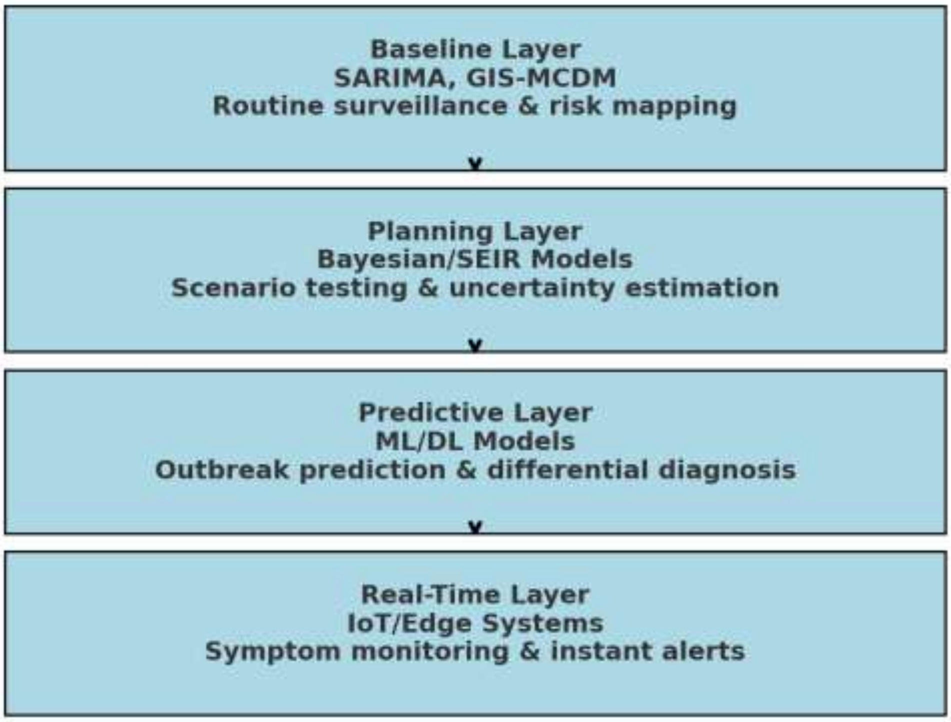

Figure 2. Layered Framework of Decision-Making Techniques

In parallel, multi-criteria decision-making (MCDM) frameworks combined with GIS-based risk mapping offer transparent and stakeholder-oriented tools for hotspot identification and resource prioritization. Furthermore, IoT and edge-enabled systems have introduced real-time surveillance capabilities, integrating wearable sensors and participatory data into outbreak monitoring pipelines.

3.1 Statistical and Time-Series Models (ARIMA/SARIMA): These models use historical case data to forecast future incidence trends. SARIMA, for example, captures both seasonality and temporal autocorrelation, making it useful for arboviruses with seasonal outbreaks. They are simple, interpretable, and effective in low-resource settings but are limited in handling nonlinear dynamics and external covariates [8].

3.2 Mechanistic & Bayesian Models: Mechanistic models (e.g., SEIR) explicitly incorporate biological processes such as infection, recovery, and mosquito transmission. Bayesian inference enhances these models by quantifying uncertainty and integrating heterogeneous data sources. Such models are powerful for understanding disease dynamics and testing intervention scenarios but require large datasets and accurate parameterization [6], [7]. Table 2, shows chikungunya decision-making studies are evaluated, and shows that no single decision-making technique is sufficient on its own.

Table 2. Comparison of Technique for Chikungunya Monitoring

Technique	Strengths	Limitations
Statistical / Time-Series (ARIMA, SARIMA	Simple, interpretable, requires fewer data, effective for seasonal trends	Limited to linear patterns, weak in handling exogenous variables
Mechanistic & Bayesian (SEIR, Bayesian inference)	Captures biological realism, allows counterfactuals, quantifies uncertainty	High data requirements, parameter identifiability issues
Machine Learning (RF, SVM, Gradient Boosting)	Handles multimodal data, strong predictive accuracy	Risk of overfitting, limited interpretability
Deep Learning (CNN, LSTM, Hybrid)	Learns nonlinear patterns, integrates temporal and spatial data	Data-hungry, computationally intensive, black-box nature

Multi-Criteria Decision-Making (AHP, TOPSIS, CRITIC)	Transparent, stakeholder-friendly, integrates multiple indicators	Subjective weighting, static unless updated
Geospatial / Spatiotemporal Models (Bayesian Hierarchical, GIS)	Explicitly models space-time dynamics, integrates satellite/environmental data	Requires high-quality geospatial inputs, complex calibration
IoT/Edge-Based Decision Support	Real-time monitoring, supports smart healthcare, scalable	Data privacy, cost, interoperability challenges

3.3 Machine Learning: ML methods such as Random Forests, Support Vector Machines, and Gradient Boosting can classify chikungunya cases and predict outbreaks using multimodal data—clinical, environmental, and socioeconomic. They provide flexibility and strong predictive performance but risk overfitting when data is limited. Moreover, lack of transparency may hinder adoption in clinical settings [11].

3.4 Deep Learning: DL architectures (e.g., CNNs, LSTMs) can capture complex nonlinear patterns and temporal dependencies. They are effective in integrating large-scale data such as weather, mobility, and mosquito indices. DL has shown promise in arboviral forecasting and differential diagnosis, but its major drawbacks include high data requirements and low interpretability, which limit its direct application in public health decision-making [12].

3.5 Multi-Criteria Decision-Making: MCDM frameworks such as AHP (Analytic Hierarchy Process), TOPSIS, and CRITIC combine multiple indicators—vector density, climate anomalies, population density, sanitation, and healthcare accessibility—into a composite risk score. These methods are transparent and stakeholder-friendly, making them suitable for health authorities. However, they rely heavily on subjective criteria weighting and may need frequent recalibration [13], [18].

3.6 Geospatial & Spatiotemporal Models: Geospatial modelling integrates satellite data, remote sensing, and GIS to produce risk maps and hotspot predictions. Bayesian hierarchical spatiotemporal models account for spatial dependence and improve local intervention planning. These models are valuable for guiding targeted mosquito control but often depend on access to high-quality geospatial datasets [4], [5], [17].

3.7 IoT/Edge-Based Decision Support Systems: IoT-enabled wearables and smart sensors allow real-time symptom monitoring and environmental surveillance. Edge computing reduces latency by processing data locally, enabling immediate outbreak alerts or triage decisions. These systems enhance scalability and personalization but face challenges in data privacy, interoperability, and cost of deployment in low-resource settings [14], [19]. Figure 3, represents the radar chart comparison of various decision-making techniques.

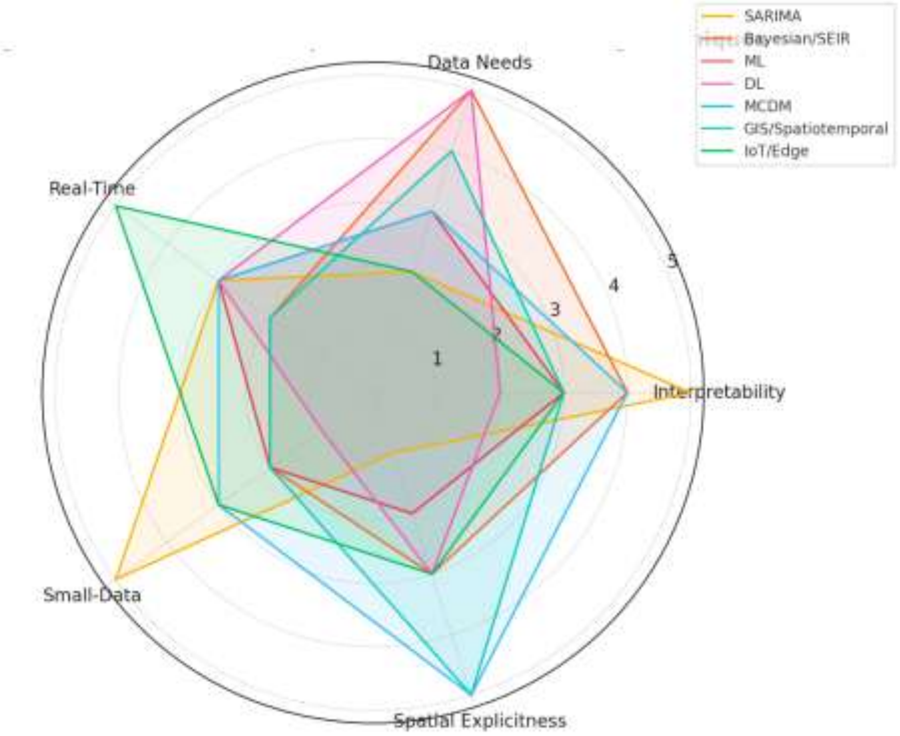

Figure 3. Comparison of Decision-Making Techniques

Evaluation Metrics and Decision Thresholds

Evaluating decision-making techniques for chikungunya monitoring requires a careful balance between accuracy, interpretability, and timeliness. Statistical forecasting models such as ARIMA and SARIMA typically rely on error-based metrics including Mean Absolute Error (MAE) and Root Mean Squared Error (RMSE) to quantify predictive accuracy, while outbreak detection is triggered when incidence rates exceed epidemiological thresholds, often defined as the baseline mean plus two standard deviations [8], [9]. Mechanistic and Bayesian approaches, including SEIR and SIR models with Markov Chain Monte Carlo (MCMC) estimation, employ R^2 values, log-likelihood scores, and Brier scores to measure model fit and probabilistic forecasting quality. In these cases, decision thresholds are set on epidemiological parameters such as the basic reproduction number (R_0); for instance, interventions are initiated if the probability of $R_0 > 1$ exceeds a 95% confidence interval [6], [7].

Machine learning (ML) and deep learning (DL) models, widely applied for chikungunya differential diagnosis and outbreak forecasting, employ classification-oriented metrics such as Accuracy, Precision, Recall, F1-score, and Area Under the ROC Curve (AUC-ROC) [11], [12]. Thresholds for classification are often set at a default cutoff of 0.5 but are adjusted using ROC or Precision-Recall curves to optimize sensitivity and specificity, especially in imbalanced datasets where chikungunya is compared with dengue or Zika. Deep learning architectures such as Long Short-Term Memory (LSTM) and Convolutional Neural Networks (CNNs) demonstrate superior ability in capturing nonlinear temporal-spatial dynamics, but they require large annotated datasets and careful threshold tuning to avoid overfitting [12]. Multi-Criteria Decision-Making (MCDM) frameworks, including Analytic Hierarchy Process (AHP), Technique for Order Preference by Similarity to Ideal Solution (TOPSIS), and CRITIC methods, integrate heterogeneous indicators such as vector density, rainfall, sanitation, and healthcare access to generate composite risk indices [13], [18]. In these studies, decision thresholds are typically defined by normalized risk scores, where values above 0.7 are considered “high risk” zones requiring immediate intervention. Geospatial and spatiotemporal approaches extend this by employing Bayesian hierarchical models and GIS overlays, where evaluation focuses on spatial accuracy, hit rates, and AUC-PR (Area Under the Precision-Recall curve) to validate hotspot predictions. Thresholds in these cases are based on probability cutoffs, for example, labeling a grid cell as a hotspot if its probability of outbreak exceeds 0.8.

Finally, IoT- and edge-based decision-support systems introduce a different evaluation paradigm. Here, latency, response time, and sensitivity are the most critical metrics, as the objective is to provide real-time monitoring and rapid alerts [14]. Thresholds are symptom-driven, such as triggering an alert when wearable sensors detect a fever > 38.5 °C in combination with reported joint pain, thereby translating continuous health data into actionable outbreak warnings [14], [19]. Across all approaches, the choice of metrics and thresholds reflects a trade-off between interpretability, accuracy, and feasibility, underscoring the need for hybrid frameworks that combine statistical rigor, machine learning predictive power, and real-time IoT adaptability. Table 3, represents the comparison of metrics, algorithm and threshold

Table 3. Comparison of metrics, algorithm and threshold

Technique	**Algorithms Used**	**Evaluation Metrics**	**Decision Thresholds**
Statistical Forecasting	SARIMA, ARIMA	RMSE, MAE	Incidence > mean+2SD defines outbreak
Mechanistic & Bayesian	SEIR, SIR + MCMC	R^2, Log-Likelihood, Brier Score	$R_0 > 1$ with 95% CI
ML Classification	RF, SVM, GBT, Logistic Regression	Accuracy, Precision, Recall, F1, AUC-ROC	Optimal cutoff via ROC curve (usually 0.5)
DL Prediction	CNN, LSTM	Accuracy, F1-score, AUC	Probability cutoff (tuned, often 0.5–0.6)
MCDM Risk Mapping	AHP, TOPSIS, CRITIC	Composite Risk Score	Score ≥ 0.7 = High risk
GIS/Spatiotemporal	Bayesian hierarchical models, GIS overlays	Spatial accuracy, AUC-PR	Hotspot probability > threshold (e.g., 0.8)
IoT/Edge Systems	Anomaly detection, lightweight ML	Latency, Response Time, Sensitivity	Symptom triggers (e.g., fever > 38.5°C + pain)

Challenges in Decision Making

Despite advances in statistical modeling, machine learning, and IoT-driven systems, several practical challenges hinder the effective deployment of decision-making techniques for chikungunya surveillance. A major limitation is data scarcity and under-reporting, as many cases go undiagnosed or unrecorded in official health systems, particularly in low-resource regions [15]. This undermines the accuracy of statistical and ML/DL models, which depend on large, high-quality datasets for training and validation. Non-stationarity in disease dynamics, driven by climate variability, urbanization, and human mobility, further complicates forecasting, requiring models to be frequently recalibrated to remain reliable [16]. Additionally, the interpretability gap between advanced AI methods and traditional epidemiological approaches creates barriers for adoption in public health, where transparency and trust are critical. Geospatial and MCDM models, while transparent, often rely on subjective weighting of indicators, introducing potential bias into risk assessments [13], [18]. Finally, infrastructure and ethical concerns challenge the integration of IoT and edge-based systems, as continuous data collection raises privacy risks and requires significant investment in digital infrastructure [14], [19]. Collectively, these challenges emphasize the need for hybrid, context-aware frameworks that are not only technically robust but also ethically sound, resource-sensitive, and adaptable to changing epidemiological landscapes.

Conclusion and Future Scope

Chikungunya remains a significant global health challenge due to its recurrent outbreaks, clinical similarity with other arboviruses, and long-lasting morbidity. This review has highlighted the wide range of decision-making techniques applied to chikungunya monitoring, including statistical and time-series models, mechanistic and Bayesian frameworks, machine learning and deep learning algorithms, multi-criteria decision-making approaches, geospatial and spatiotemporal models, and IoT/edge-based decision support systems. Each method offers distinct advantages, such as interpretability, uncertainty quantification, predictive accuracy, transparency, or real-time adaptability, but also presents limitations in terms of data requirements, computational complexity, and implementation feasibility. A key finding is that no single technique is sufficient on its own; instead, hybrid frameworks that integrate complementary strengths are essential for effective chikungunya surveillance and control. Looking forward, several avenues offer opportunities for advancing decision-making in this domain. First, hybrid modeling frameworks that combine mechanistic epidemiological insights with AI-driven predictive power can enhance robustness and adaptability across diverse epidemiological settings. Second, integration of real-time data streams from IoT devices, participatory surveillance apps, and remote sensing will be crucial for improving outbreak detection and response times. Third, emphasis must be placed on explainable AI and interpretable models, ensuring that healthcare professionals and policymakers can trust and act upon algorithmic recommendations. Fourth, context-aware and resource-sensitive systems are needed, particularly in low- and middle-income countries where infrastructure limitations constrain large-scale deployment. Finally, the future of chikungunya monitoring lies in global collaboration and data-sharing initiatives, where interoperable platforms allow integration of clinical, environmental, and social data to build resilient, scalable, and equitable health surveillance systems. In conclusion, the convergence of statistical rigor, epidemiological modeling, AI advancements, and digital health innovation holds promise for transforming chikungunya monitoring. By addressing current challenges and pursuing hybrid, explainable, and context-aware approaches, researchers and practitioners can develop decision-making frameworks that not only strengthen outbreak forecasting but also support timely, transparent, and effective public health interventions.

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