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A Data-Driven Approach to Dengue Fever Mapping: A Review

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Abstract

Dengue fever remains a pressing public health issue, especially in tropical and subtropical regions where urbanization, climate change, and ineffective vector control contribute to frequent outbreaks. Traditional surveillance methods often fall short in providing timely and accurate insights, necessitating data-driven approaches for improved monitoring and intervention. This review explores various computational methodologies, including Geographic Information Systems (GIS), machine learning, and predictive modeling, to enhance dengue outbreak mapping and risk assessment. Studies from Bangladesh, Thailand, Malaysia, and Reunion Island demonstrate how integrating epidemiological data with environmental and socio-economic factors improves outbreak prediction and control efforts. Advanced techniques, such as dynamic mapping of the basic reproduction number (R0) and deep learning models like Long Short-Term Memory (LSTM) networks, further enhance forecasting accuracy. Additionally, innovative control strategies, such as Wolbachia-infected mosquito releases, show promise in reducing dengue transmission. By synthesizing recent research, this review underscores the critical role of data science in strengthening dengue surveillance, prediction, and intervention strategies.

Keywords: *Dengue Surveillance, Machine Learning, Predictive Modeling*

Abstrak

Demam berdarah masih menjadi masalah kesehatan masyarakat yang mendesak, terutama di wilayah tropis dan subtropis, tempat urbanisasi, perubahan iklim, dan pengendalian vektor yang tidak efektif berkontribusi terhadap wabah yang sering terjadi. Metode pengawasan tradisional sering kali gagal dalam memberikan wawasan yang tepat waktu dan akurat, sehingga memerlukan pendekatan berbasis data untuk pemantauan dan intervensi yang lebih baik. Tinjauan ini mengeksplorasi berbagai metodologi komputasional, termasuk Sistem Informasi Geografis (SIG), pembelajaran mesin, dan pemodelan prediktif, untuk meningkatkan pemetaan wabah dan penilaian risiko demam berdarah. Studi dari Bangladesh, Thailand, Malaysia, dan Pulau Reunion menunjukkan bagaimana mengintegrasikan data epidemiologi dengan faktor lingkungan dan sosial ekonomi meningkatkan upaya prediksi dan pengendalian wabah. Teknik tingkat lanjut, seperti pemetaan dinamis angka reproduksi dasar (R0) dan model pembelajaran mendalam seperti jaringan Memori Jangka Pendek Panjang (LSTM), semakin meningkatkan akurasi perkiraan. Selain itu, strategi pengendalian yang inovatif, seperti pelepasan nyamuk yang terinfeksi Wolbachia, menunjukkan harapan dalam mengurangi penularan demam berdarah.

Kata kunci: Dengue Surveillance, Machine Learning, Predictive Modeling

1. INTRODUCTION

Dengue fever remains a major global health concern, particularly in tropical and subtropical regions where rapid urbanization, climate change, and inadequate mosquito control contribute to frequent outbreaks. Traditional surveillance methods often struggle to provide timely and accurate insights into the disease's spread, leading to delays in response efforts. With advancements in data science, the integration of Geographic Information Systems (GIS), machine learning, and real-time environmental data has opened new possibilities for mapping and predicting dengue outbreaks more effectively. This study reviews various data-driven approaches used for dengue fever mapping, exploring their methodologies, effectiveness, and challenges (Table 1). By analyzing past and emerging techniques, this review aims to highlight the potential of data-driven models in enhancing early warning systems, optimizing resource allocation, and improving public health interventions.

Table 1 – Literatur Study

Study	Background	Approach	Dataset	Method	Result
Understanding the unprecedented 2023 dengue outbreak in Bangladesh: a data-driven analysis [1]	In 2023, Bangladesh experienced an unprecedented surge in dengue fever cases across all administrative divisions.	The study aimed to elucidate the epidemiological characteristics, spatial distribution, and potential contributing factors associated with the 2022-2023 dengue outbreak in Bangladesh.	The research utilized epidemiological data from the 2022-2023 dengue outbreak in Bangladesh, though specific details about the dataset are not provided in the available sources.	For the statistical display of the results, the researchers used ARC Map 10.7 and OriginPro 2024 programs.	The study provided insights into the unprecedented surge in dengue fever incidence across all administrative divisions in Bangladesh during 2023.
Mapping the spatial distribution of the dengue vector Aedes aegypti and predicting its abundance in northeastern Thailand using machine-learning approach [2]	Accurately mapping the spatial distribution and predicting the abundance of Aedes aegypti are crucial for developing effective vector control strategies and early warning systems for dengue prevention.	The study aimed to predict the abundance of female adult Aedes aegypti in northeastern Thailand by analyzing socio-ecological and landscape factors using a machine learning-based system.	Researchers collected a total of 1,066 female adult Aedes aegypti from four villages in northeastern Thailand during January-December 2019.	The study employed machine learning techniques to analyze the collected data, incorporating socioeconomic, climate change, dengue knowledge, attitude and practices (KAP), and landscape factors to predict mosquito abundance.	The machine learning-based approach successfully identified key factors influencing Aedes aegypti abundance, providing valuable insights for targeted vector control interventions.
Application of medical information system to	Dengue is a major global health issue, particularly in hyperendemic	The study aims to analyze dengue case	A total of 18,812 dengue cases recorded from 2012 to	The study applied geoinformatics techniques and	The study found that a rainfall pattern called

identify dengue outbreak factors: Insights from a hyperendemic city in Malaysia [3]	urban areas, where controlling outbreaks requires systematic data collection and analysis.	data from Malaysia's e-Dengue system to improve epidemiological understanding by integrating meteorological, geoinformatics, and socio-environmental factors.	2019 in Ipoh, Malaysia, were retrieved from the e-Dengue system and combined with relevant environmental and meteorological data.	statistical analysis to identify key outbreak triggers, focusing on rainfall trends, socio-environmental conditions, and demographic factors like age.	"wet-dry steps" could be a key outbreak trigger, identified high-risk dengue reservoir zones, and highlighted age-related variations in blood cell.
Dynamic mapping of dengue basic reproduction number [4]	Dengue fever, transmitted by mosquitoes, poses significant public health challenges, particularly in tropical regions like Reunion Island.	The study developed a method to produce time-varying maps for dengue transmission risk by estimating the spatial basic reproduction number (R0) using the Ross-Macdonald framework and differential equations.	The components of the R0 formula were derived partly from a mosquito population dynamics model integrating meteorological and environmental variables, and partly from temperature-dependent functions of vector competence and the extrinsic incubation period.	The method was applied on Reunion Island, where the mosquito Aedes albopictus has been responsible for large dengue outbreaks.	The study found strong agreements between the observed epidemiological patterns and predicted R0 distribution and temporal dynamics, demonstrating the relevance and efficiency of the spatialized R0 to develop an operational dynamic mapping tool
Recent advances in dengue pathogenesis and clinical management [5]	Dengue fever is a significant global health concern, necessitating a comprehensive understanding of its pathogenesis and the development of effective clinical management strategies.	The article reviews recent advancements in understanding dengue pathogenesis, immunity, and clinical research on vaccines and therapeutics.	The review synthesizes findings from various studies on dengue virus infection, immune responses, and clinical trials related to vaccines and treatments.	The authors analyze and comment on recent research, focusing on the role of the dermis in infection, immune response mechanisms, and evaluations of therapeutic interventions.	The review highlights significant progress in understanding dengue pathogenesis and immunity, as well as advancements in clinical research aimed at improving diagnosis, risk prediction, and disease

					classification.
Dense residential areas promote gene flow in dengue vector mosquito Aedes albopictus [6]	Personal care products, such as soaps, introduce plant-derived volatile organic compounds (VOCs) to human skin, potentially influencing mosquito host selection.	The study investigated how different commercial soaps alter human odor profiles and subsequently affect mosquito attraction.	Odor samples were collected from volunteers' forearms before and after washing with four popular soap brands: Dial, Dove, Native, and Simple Truth.	Using gas chromatography-mass spectrometry (GC-MS), the researchers analyzed the chemical composition of the collected odor samples and conducted behavioral assays to assess mosquito responses to these altered odors.	The findings revealed that soap application significantly modifies human odor profiles, with certain soaps increasing and others decreasing attractiveness to mosquitoes, effects linked to specific chemical components in the soaps.
Deconstructing “malaria”: West Africa as the next front for dengue fever surveillance and control [7]	Dengue fever is a significant global health concern, necessitating a comprehensive understanding of its pathogenesis and the development of effective clinical management strategies.	The article reviews recent advancements in understanding dengue pathogenesis, immunity, and clinical research on vaccines and therapeutics.	The review synthesizes findings from various studies on dengue virus infection, immune responses, and clinical trials related to vaccines and treatments.	The authors analyze and comment on recent research, focusing on the role of the dermis in infection, immune response mechanisms, and evaluations of therapeutic interventions.	The review highlights significant progress in understanding dengue pathogenesis and immunity, as well as advancements in clinical research aimed at improving diagnosis, risk prediction, and disease classification.
Leveraging livestock movements to urban slaughterhouses for wide-spread Rift Valley fever virus surveillance in Western Kenya [8]	Extraintestinal pathogenic Escherichia coli (ExPEC) can cause severe infections in humans, and understanding their zoonotic origins is crucial for public health.	The study employed a comparative genomic analysis to identify mobile genetic elements associated with specific sources, aiming to trace the origins of	Researchers analyzed a collection of 3,111 contemporaneous, geographically matched clinical and meat-source E. coli isolates.	By identifying 17 source-associated mobile genetic elements, predominantly plasmids and bacteriophages, the team integrated these findings into a Bayesian latent class model to predict the	The study estimated that approximately 8% of human extraintestinal E. coli infections, primarily urinary tract infections, in the study population were caused by foodborne zoonotic E.

		clinical E. coli isolates.		origins of clinical E. coli isolates.	coli, with certain lineages like ST131-H22 and ST58 exhibiting particularly high virulence potential.
Time series forecasting of Valley fever infection in Maricopa County, AZ using LSTM [9]	Coccidioidomycosis, or Valley fever, is a growing public health concern, and understanding its influencing factors can help improve disease forecasting and management.	This study applies Long Short-Term Memory (LSTM) networks to predict CM cases by analyzing pneumonia cases, weather patterns, air quality, and behavioral changes due to COVID-19.	The study uses daily pneumonia case records from Maricopa County, Arizona, spanning 2020 to 2022, along with meteorological and environmental data such as temperature, precipitation, wind speed, and air pollution levels.	The LSTM model incorporates multiple influencing factors, including climate variables and COVID-19-related lifestyle changes, while considering their correlation and time-lag effects on CM prevalence.	The LSTM model effectively forecasts CM trends with low mean squared error (MSE), though accuracy declines for longer prediction windows, with 10-day and 30-day models showing the best performance.
Establishment of Wolbachia Strain wAlbB in Malaysian Populations of Aedes aegypti for Dengue Control [10]	Dengue fever, transmitted by Aedes aegypti mosquitoes, poses a significant health threat in Malaysia, prompting exploration of innovative control methods.	Researchers introduced the Wolbachia strain wAlbB into local Aedes aegypti populations to assess its potential in reducing dengue transmission.	The study monitored Wolbachia establishment and mosquito population dynamics across multiple Malaysian sites over a specified period.	Field releases of Wolbachia-infected mosquitoes were conducted, followed by regular sampling to evaluate infection frequencies and impacts on mosquito populations.	The wAlbB strain successfully established in the target mosquito populations, indicating its promise as a dengue control strategy in Malaysia.

2. DISCUSSION

The growing threat of dengue fever has led to an urgent need for data-driven approaches to understand its spread and devise effective control strategies. Several recent studies have focused on analyzing epidemiological trends, mapping mosquito populations, and predicting outbreak factors. For example, the 2023 dengue outbreak in Bangladesh was studied using spatial and statistical tools to investigate its unprecedented spread, while a machine-learning approach was used in Thailand to predict Aedes aegypti abundance based on socio-ecological and environmental factors. Similarly, Malaysia's hyperendemic urban areas were analyzed through medical information systems, integrating meteorological and geoinformatics data to identify key outbreak triggers, such as the "wet-dry steps" rainfall pattern. These studies highlight how a combination of advanced computational methods and real-world datasets can help improve surveillance and response efforts.

In addition to epidemiological analysis, research has also focused on modeling dengue transmission and identifying key risk factors. A study on Reunion Island utilized dynamic mapping techniques based on the basic reproduction number (R0) to estimate dengue risk over time, integrating mosquito population dynamics and environmental conditions. Meanwhile, a comprehensive review of dengue pathogenesis examined the latest advancements in immune response mechanisms and vaccine development, shedding light on potential improvements in clinical management and risk prediction. Another intriguing study explored how urbanization influences mosquito gene flow, revealing that high-density residential areas can facilitate the spread of Aedes albopictus, further complicating control efforts. These findings emphasize the importance of both environmental and biological factors in shaping dengue transmission patterns. On the prevention and intervention front, innovative strategies are being explored to mitigate dengue outbreaks. One study demonstrated the successful establishment of the Wolbachia strain wAlbB in Malaysian Aedes aegypti populations, providing a promising biocontrol method to reduce dengue transmission. Additionally, predictive models [11, 12] such as Long Short-Term Memory (LSTM) networks have been employed to forecast disease prevalence, as seen in the case of Valley fever in Arizona, where environmental and behavioral factors were integrated into forecasting models. These advancements illustrate how technology and interdisciplinary approaches can enhance vector control and disease prediction, ultimately aiding public health efforts in managing mosquito-borne illnesses like dengue.

3. CONCLUSION

The integration of data-driven approaches in dengue surveillance and control has demonstrated significant potential in improving outbreak prediction, risk assessment, and intervention strategies. By leveraging Geographic Information Systems (GIS), machine learning, and real-time environmental data, researchers have successfully identified key factors influencing dengue transmission, such as climate patterns, mosquito abundance, and urbanization. Studies from Bangladesh, Thailand, Malaysia, and Reunion Island highlight the effectiveness of spatial mapping, medical information systems, and epidemiological modeling in refining surveillance efforts. Moreover, innovative biocontrol methods like Wolbachia-based mosquito interventions and predictive modeling using Long Short-Term Memory (LSTM) networks further enhance the capacity to mitigate dengue risks. As technological advancements continue to evolve, integrating interdisciplinary methodologies will be crucial in developing more precise and proactive public health strategies to combat the growing threat of dengue fever.

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