Modeling the Spatial Dynamics and Human Mobility in Zika Virus Transmission: A Review

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Review Article

Abstract

Spatial dynamics and human mobility significantly influence the transmission dynamics of vector-borne diseases like Zika virus. This paper reviews advancements in mathematical modeling that integrate spatial factors and human movement to enhance our understanding of disease transmission dynamics. Traditional SEIR (Susceptible-Exposed-Infectious-Recovered) models have been foundational but lack spatial heterogeneity and human mobility considerations. Recent studies have addressed these limitations by developing spatially explicit models that incorporate local interactions, environmental conditions, and human mobility patterns. By synthesizing findings from these studies, we identify strengths, limitations, and future research directions for improving predictive modeling of Zika virus transmission. Key insights include the amplifying effect of local interactions on disease spread and the critical role of human mobility networks in

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shaping transmission pathways. Addressing remaining challenges, such as refining spatial modeling techniques and integrating real-time data sources, will enhance the accuracy and applicability of spatial disease models in informing public health strategies.

Keywords: Zika virus; spatial dynamics; human mobility; mathematical modeling; disease transmission.

1 Introduction

The Zika virus, a vector-borne disease primarily transmitted by Aedes mosquitoes, emerged as a significant public health concern due to its rapid spread and association with severe neurological complications such as microcephaly and Guillain-Barré syndrome [1]. Initially identified in Uganda in 1947, the Zika virus remained relatively obscure until a major outbreak occurred in Brazil in 2015, drawing global attention to its potential for widespread transmission and severe health impacts [2]. The rapid spread of the virus across the America highlighted its ability to exploit modern transportation networks and the pervasive presence of Aedes mosquitoes in tropical and subtropical regions [3].

Understanding the dynamics of Zika virus transmission is crucial for developing effective control strategies, especially in regions where environmental conditions and human mobility patterns play pivotal roles in disease spread [4]. Environmental factors such as temperature and precipitation significantly influence mosquito breeding, survival, and virus replication rates, creating conditions that can either exacerbate or mitigate transmission risks [5]. Additionally, human mobility, driven by daily commutes, migration, and international travel, facilitates the geographical spread of the virus by connecting infected and susceptible populations across different regions [6,7].

Mathematical modeling has proven instrumental in elucidating these dynamics by integrating biological processes with spatial and temporal factors. These models offer a systematic approach to understanding how various factors interact to influence the transmission and spread of the virus. By incorporating data on mosquito ecology, human demographics, and movement patterns, models can simulate outbreak scenarios, assess the potential impact of intervention strategies, and predict future transmission trends [8]. The insights gained from these models are invaluable for public health authorities in designing targeted interventions, allocating resources efficiently, and mitigating the impact of Zika virus outbreaks [9].

Traditional infectious disease models, like the Susceptible-Exposed-Infectious-Recovered (SEIR) framework, have been foundational in studying vector-borne diseases [10]. These models compartmentalize populations based on their infection status and describe the transitions between these compartments over time. The SEIR model categorizes individuals into four compartments: susceptible (S), exposed (E), infectious (I), and recovered (R). Susceptible individuals can become exposed through contact with infectious individuals or vectors. Exposed individuals, who have been infected but are not yet infectious, eventually progress to the infectious stage, where they can transmit the disease. Finally, individuals move from the infectious stage to the recovered stage, where they gain immunity to the disease.

This framework has been instrumental in understanding the basic mechanisms of disease spread and has provided valuable insights into the dynamics of various infectious diseases. For instance, it has been used to estimate key epidemiological parameters such as the basic reproduction number (R0) and to evaluate the potential impact of control measures like vaccination and quarantine [11,12].

However, the traditional SEIR model has limitations, particularly when applied to diseases with complex transmission dynamics like the Zika virus. One significant limitation is the assumption of a well-mixed population, where individuals have an equal probability of coming into contact with each other. This assumption overlooks the spatial heterogeneity inherent in real-world populations, where factors like geographic location, population density, and environmental conditions can significantly influence disease transmission [13].

Spatial heterogeneity plays a critical role in vector-borne diseases, where the distribution of vectors (such as mosquitoes) and hosts (humans) can vary widely across different regions. For example, the presence of breeding sites for mosquitoes, variations in climate, and differences in human population density can create hotspots of

disease transmission that are not captured by well-mixed models [14]. Traditional SEIR models also fail to account for human movement, which is a crucial factor in the spread of diseases like Zika. Human travel and daily movement patterns can bridge otherwise isolated population centers, facilitating the spread of the virus over larger geographic areas [7]. Without incorporating these spatial and mobility factors, SEIR models may provide an incomplete or inaccurate picture of disease dynamics.

To address these limitations, researchers have developed more sophisticated models that incorporate spatial dynamics and human mobility. These models divide the population into spatial compartments or grid cells, allowing for the simulation of localized interactions between humans and vectors. They also include parameters for human movement between these compartments, capturing the role of travel and migration in disease spread. By integrating spatial heterogeneity and mobility patterns, these models provide a more realistic and detailed representation of vector-borne disease transmission, leading to better predictions and more effective control strategies [15].

Advancements in mathematical modeling have increasingly incorporated spatial components, allowing for a more nuanced understanding of disease spread. Traditional epidemiological models often assume homogeneous mixing of populations, where every individual has an equal chance of interacting with every other individual. However, this assumption overlooks critical factors such as geographical distribution, local environmental conditions, and movement patterns that significantly influence disease transmission dynamics [13].

Spatially explicit models address these limitations by incorporating spatial heterogeneity and localized interactions between human hosts and mosquito vectors. These models divide the study region into distinct compartments or grid cells, each representing a specific geographic location. Within each compartment, the model simulates the interactions between susceptible, exposed, infected, and recovered individuals and vectors, allowing for a detailed representation of local transmission dynamics [16].

A key advancement in these models is the inclusion of environmental factors that affect vector population dynamics. Temperature and precipitation, for instance, play a crucial role in the breeding, survival, and activity patterns of Aedes mosquitoes, the primary vectors of the Zika virus. Warmer temperatures can accelerate mosquito life cycles and increase biting rates, while precipitation can create more breeding sites by providing stagnant water pools [17]. By incorporating functions that represent temporal variations in temperature and precipitation, spatially explicit models can more accurately simulate the seasonal and geographic variations in mosquito populations and their impact on disease transmission [18].

Moreover, spatially explicit models account for human mobility patterns, which are pivotal in the spread of vector-borne diseases. Unlike well-mixed models, which assume uniform mixing, spatial models can simulate how human movement between different compartments influences the spread of the virus. This includes daily commuting, travel between urban and rural areas, and long-distance travel, which can all contribute to bridging gaps between otherwise isolated populations and facilitating the spread of the virus across regions [19].

For example, during the 2015-2016 Zika outbreak in Brazil, human travel patterns significantly contributed to the rapid spread of the virus from urban centers to peripheral regions and neighboring countries. Incorporating mobility data into mathematical models enabled researchers to better understand and predict the spatial spread of the outbreak, thereby informing targeted public health interventions [20].

These spatially explicit models are also valuable for evaluating the effectiveness of control strategies. By simulating interventions such as insecticide spraying, removal of breeding sites, and public health campaigns in different compartments, these models can predict the impact of these measures on local transmission dynamics and identify the most effective strategies for specific regions [21].

Human mobility plays a pivotal role in the spatial spread of infectious diseases. The movement of individuals across different geographical areas, whether through daily commutes, migration, or international travel, can significantly influence the dynamics of disease transmission. For instance, individuals traveling from areas with high infection rates to otherwise isolated and uninfected population centers can introduce the virus into new regions, facilitating its spread. This phenomenon has been observed in various outbreaks, where human movement patterns directly impact the geographic distribution and incidence of the disease [6].

In the context of the Zika virus, human mobility is particularly relevant. The virus can be transmitted from infected individuals to local mosquito populations, which then act as vectors to spread the virus to other humans. Therefore, the movement of infected individuals can create new transmission hotspots, further complicating control efforts. For example, during the 2015-2016 Zika outbreak, the virus rapidly spread across the America, partly due to human travel [3].

Incorporating human mobility into mathematical models is therefore essential for accurately predicting disease outbreaks and devising targeted interventions. Traditional epidemiological models, which often assume a well-mixed population, may not capture the complexities introduced by human movement. More advanced models integrate data on travel patterns, commuting behaviors, and migration trends to simulate how diseases spread across different regions [7].

These models can incorporate various types of mobility data, including airline travel records, mobile phone data, and census information, to provide a detailed picture of how people move within and between areas. By doing so, they can identify potential pathways for disease spread and pinpoint critical locations for intervention, such as major transportation hubs or regions with high rates of inbound travel from infected areas. For instance, during the Zika outbreak, models that included human mobility data were able to predict the spread of the virus more accurately than those that did not, enabling more effective allocation of resources for disease control [22].

Moreover, understanding human mobility can help in designing public health interventions that are both efficient and effective. Travel restrictions, targeted vector control measures, and public health campaigns can be optimized based on insights from mobility-integrated models. For example, during the COVID-19 pandemic, mobility data was used to implement and assess the effectiveness of lockdowns and travel bans [7]. Similar strategies can be applied to the control of Zika and other vector-borne diseases.

This paper aims to review the advancements in mathematical modeling that focus on the spatial dynamics and human mobility in Zika virus transmission. Mathematical modeling plays a crucial role in understanding and predicting the spread of infectious diseases, especially those transmitted by vectors like mosquitoes. Traditional models have laid the groundwork for these studies, but recent advancements have introduced more complex and realistic approaches by incorporating spatial components and human mobility.

The paper explores various modeling approaches that integrate SEIR (Susceptible-Exposed-Infectious-Recovered) principles with spatial components, highlighting their contributions to our understanding of Zika transmission. The SEIR framework divides the population into compartments based on disease status and models the transitions between these states. By adding spatial dynamics, these models account for geographical variations and local interactions, providing a more detailed picture of disease spread. These spatial models consider factors such as mosquito habitat distribution, climate conditions, and urbanization patterns, which significantly influence the transmission dynamics of Zika virus.

By examining these advancements, we aim to identify the strengths and limitations of current models and suggest directions for future research. Evaluating the current state of modeling approaches allows us to understand their effectiveness in predicting outbreaks and guiding public health interventions. Identifying gaps and limitations in these models is crucial for improving their accuracy and reliability. Additionally, we will propose potential areas for future research to enhance the understanding of Zika virus transmission and develop more robust models.

2 Literature Review

Zika virus, first identified in Uganda in 1947, gained global attention due to its rapid spread and association with severe neurological complications such as microcephaly and Guillain-Barré syndrome [2,23]. Understanding the epidemiology and transmission dynamics of Zika virus is crucial for developing effective control strategies.

2.1 Zika virus epidemiology, transmission mechanisms, and control strategies

Zika virus primarily spreads through the bite of infected Aedes mosquitoes, primarily Aedes aegypti and Aedes albopictus, which are widespread in tropical and subtropical regions [24]. The virus can also be transmitted sexually and vertically from mother to fetus during pregnancy [2,25].

Epidemiological studies have revealed that Zika virus outbreaks exhibit spatial and temporal variability, influenced by environmental factors such as temperature, humidity, and urbanization [26]. These factors affect mosquito breeding habitats and vector abundance, thereby impacting transmission dynamics. The interplay between human mobility and mosquito distribution further complicates the control of Zika virus, as travel facilitates the geographic spread of the disease [24].

Control strategies for Zika virus primarily focus on vector control measures, including insecticide spraying, larval source reduction, and community engagement to eliminate mosquito breeding sites [5]. Public health responses also emphasize surveillance and early detection of cases to prevent local transmission and reduce the risk of severe outcomes associated with Zika virus infection [27].

Current Studies and Modeling Advancements. Recent advancements in mathematical modeling have enhanced our understanding of Zika virus transmission dynamics. SEIR (Susceptible-Exposed-Infectious-Recovered) models have been adapted to incorporate spatial heterogeneity and human mobility patterns, allowing for more accurate predictions of disease spread [28].
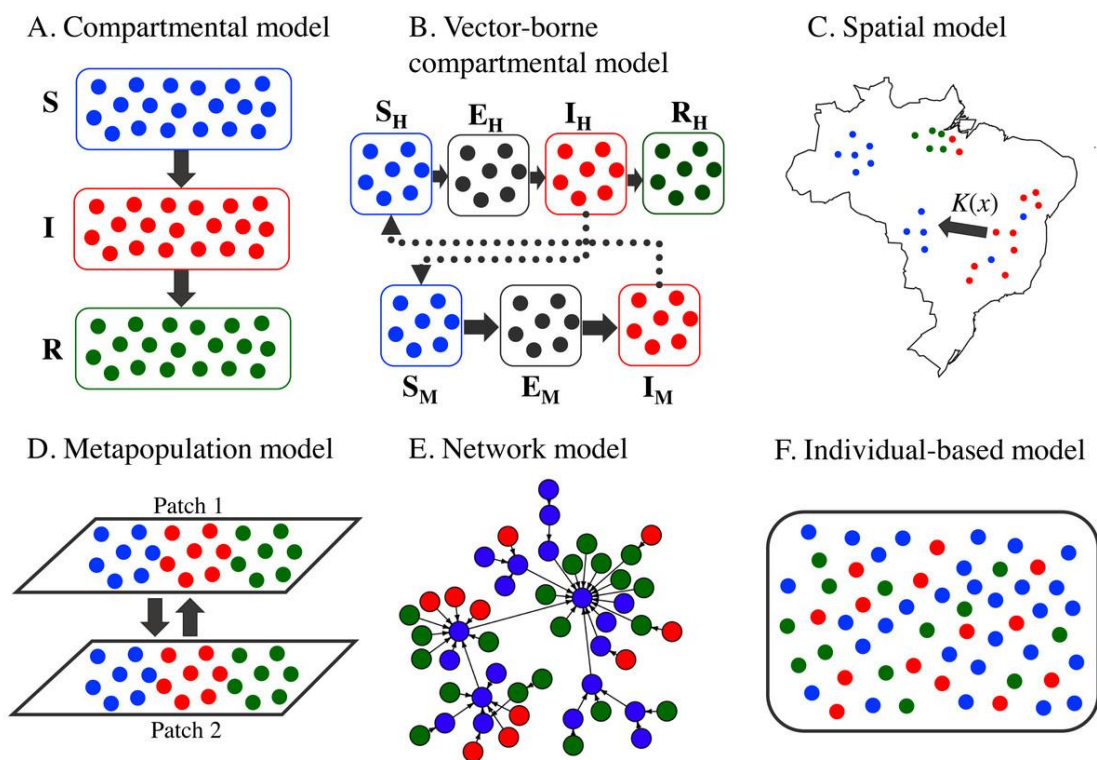

Fig. 1. Example of a Spatially Explicit SEIR Model for Zika Virus Transmission,
(Source: [23])

Fig. 1 illustrates a spatially explicit SEIR model for Zika virus transmission. This model divides the geographical area into smaller grids, allowing researchers to account for variations in mosquito populations, human density, and environmental factors across different locations. The model tracks the movement of individuals between these grids, simulating the spread of the virus through human travel and mosquito dispersal. Spatially explicit models like this one have demonstrated the importance of local environmental conditions and human movement in shaping Zika virus outbreaks. These models highlight the need for targeted interventions tailored to specific geographic areas, rather than relying on broad-scale approaches. For instance, areas with high human density and ideal mosquito breeding conditions might require more intensive vector control efforts compared to rural regions [29]. By incorporating spatial data and human mobility patterns, these models can inform public health decision-making and resource allocation for Zika virus control. They can be used to predict potential outbreak hotspots, evaluate the effectiveness of different control strategies, and guide targeted interventions to maximize their impact.

2.2 Traditional SEIR models and their application to vector-borne diseases

Traditional SEIR (Susceptible-Exposed-Infectious-Recovered) models have been foundational in epidemiology for understanding and predicting the dynamics of infectious diseases, particularly those transmitted by vectors such as mosquitoes. These models divide the population into compartments based on disease status and track the transitions between these compartments over time. The SEIR framework includes variables such as the rate of individuals moving from susceptible to exposed (via infection), from exposed to infectious (after an incubation period), and from infectious to recovered (after either surviving the infection or dying). Mathematical equations govern these transitions, capturing the dynamics of disease spread in a well-mixed population.

In the context of vector-borne diseases like Zika virus, SEIR models have been adapted to incorporate specific aspects of vector ecology and transmission dynamics. For instance, the basic SEIR framework can be extended to include additional compartments for vectors, such as susceptible, exposed, infectious, and recovered mosquitoes. This extension allows researchers to model the interactions between human hosts and vector populations, considering factors like mosquito biting rates, vector lifespan, and the dynamics of pathogen transmission within vector populations.

Recent studies applying SEIR models to vector-borne diseases have yielded valuable insights into disease transmission dynamics. For example, research by [25,30,31] demonstrated how SEIR models can simulate the seasonal variation in mosquito populations and the corresponding fluctuations in disease incidence. By incorporating environmental factors such as temperature and precipitation, these models can capture the impact of climate variability on mosquito breeding and pathogen transmission rates.

Despite their utility, traditional SEIR models have certain limitations when applied to vector-borne diseases with spatial heterogeneity. These models often assume a homogeneous mixing of populations, neglecting spatial variations in human population density, mosquito habitat suitability, and human mobility patterns-all of which play crucial roles in disease transmission dynamics. This oversimplification can lead to inaccuracies in predicting disease outbreaks and the effectiveness of control measures.

Recent advancements in SEIR models for vector-borne diseases extend beyond incorporating just vector dynamics. Researchers are actively exploring ways to capture the complexities of disease spread in real-world scenarios characterized by spatial heterogeneity.
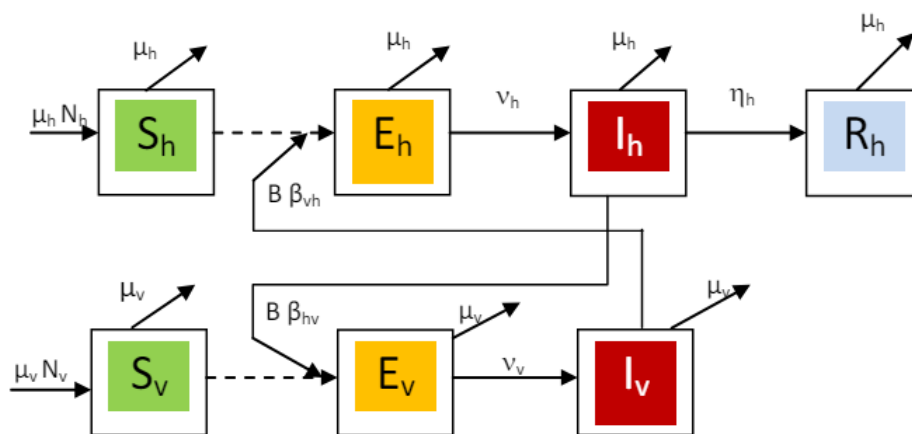

Fig. 2. A Schematic Representation of a Spatially Explicit SEIR Model for Vector-Borne Diseases.
Source ([32])

Fig. 2 depicts a modified SEIR framework that incorporates spatial aspects. The human population is no longer assumed to be uniformly mixed. Instead, the model considers spatial variations in human density, with areas represented by different colors. This allows for the inclusion of factors like local mosquito breeding grounds and human mobility patterns that influence transmission intensity in specific locations. The arrows depict the

transitions between the traditional SEIR compartments (S, E, I, R) for humans and vectors (S_v, E_v, I_v). However, the rates associated with these transitions (represented next to the arrows) can vary spatially depending on the local context. For example, the biting rate (β) between susceptible humans and infectious vectors might be higher in areas with denser human populations and suitable mosquito habitats (darker colored regions).

Studies by [33,34] demonstrate the effectiveness of these spatially explicit SEIR models. Their research applied such a model to simulate the spread of West Nile virus, a mosquito-borne disease. The model successfully captured the spatial heterogeneity in disease incidence observed in real-world data. This approach provides valuable insights for public health officials by identifying areas at high risk for outbreaks and informing targeted interventions like localized vector control measures.

The integration of GIS data plays a crucial role in these advancements. GIS allows researchers to overlay information on human population density, mosquito habitat suitability, and environmental factors onto the SEIR framework. This enriches the model with real-world geographic data, leading to more accurate simulations and predictions.

Furthermore, advancements in computational modeling techniques are paving the way for even more sophisticated approaches. Agent-based models (ABMs) simulate individual-level interactions and movements within a population [35]. This allows for a more nuanced understanding of disease spread dynamics, particularly in situations with significant spatial heterogeneity. By incorporating individual behaviors and local environmental conditions, ABMs can provide a more detailed picture of how outbreaks unfold and how interventions might impact transmission patterns.

The traditional SEIR models have laid the foundation for understanding vector-borne disease dynamics. However, researchers are continuously refining these models to account for the complexities of the real world. Spatially explicit SEIR frameworks and agent-based models represent significant advancements in this field. By incorporating spatial heterogeneity and individual-level interactions, these models offer a more comprehensive understanding of disease spread and hold promise for informing targeted intervention strategies to mitigate the impact of vector-borne diseases.

Future research should focus on addressing these gaps by enhancing the spatial resolution and realism of SEIR models. Incorporating spatial dynamics into SEIR frameworks can improve their predictive accuracy and relevance for real-world applications. For instance, integrating GIS (Geographic Information System) data to model the spatial distribution of human populations and mosquito habitats can provide more accurate simulations of disease transmission hotspots and inform targeted intervention strategies. Furthermore, advancements in computational modeling techniques allow for the development of agent-based models that simulate individual-level interactions and movements, providing a more nuanced understanding of disease spread dynamics in heterogeneous environments [36].

2.3 Incorporation of spatial dynamics into SEIR models

Spatial dynamics play a crucial role in understanding the transmission of vector-borne diseases like Zika virus. Traditional SEIR (Susceptible-Exposed-Infectious-Recovered) models have provided foundational insights into disease spread by compartmentalizing populations based on disease status. These models assume a well-mixed population and homogeneous transmission rates across the entire region of interest. However, these assumptions often do not capture the local variations and spatial heterogeneity that significantly influence disease transmission dynamics.

Recent advancements in SEIR models have focused on incorporating spatial components to address the limitations of traditional models. One approach involves dividing the study area into discrete spatial units, such as city blocks or neighborhoods. Each unit represents a specific location where interactions between humans and mosquito vectors can occur. Mathematical frameworks, like partial differential equations (PDEs) or agent-based models (ABMs), are then used to describe the movement of individuals and vectors across these spatial compartments [37].

As depicted in Fig. 2, the region of interest is divided into a grid of squares, representing neighborhoods or other spatial units. Each square depicts the population within that location categorized by their disease state: susceptible (S), exposed (E), infectious (I), or recovered (R). The arrows depict the movement of both humans and mosquitoes between neighboring units, facilitating disease transmission. This type of model allows researchers to simulate how factors like localized mosquito breeding sites and human travel patterns can influence the spatial distribution of Zika cases.

Studies have demonstrated the value of incorporating spatial dynamics into SEIR models. For instance, [36] employed an agent-based model to simulate mosquito-borne disease transmission in an urban environment. Their model considered factors like human movement patterns and the presence of local mosquito breeding sites. The findings highlighted the ability of spatially explicit models to capture the clustering of disease cases in specific locations and identify areas at high risk for outbreaks, allowing for targeted interventions.

Despite these advancements, there are ongoing efforts to refine spatial SEIR models. Current models often rely on simplifying assumptions about human behavior, such as uniform mixing within spatial units or static movement patterns. Future research should explore more realistic representations of human mobility by incorporating factors like dynamic travel patterns, commuting behaviors, and socio-economic disparities that influence exposure to mosquito habitats [38]. Additionally, integrating real-time environmental data (such as, temperature, humidity) and vector ecology into the models has the potential to further improve their predictive power for disease outbreaks.

Furthermore, establishing standardized methodologies for validating and comparing different spatial SEIR models is crucial. Validation studies should assess model performance against real-world data, such as case reports of Zika virus and vector abundance, across diverse geographical settings as recommended by [39]. Addressing these research gaps will be instrumental in advancing our understanding of Zika virus transmission dynamics and improving the effectiveness of public health interventions for controlling vector-borne diseases in spatially heterogeneous environments.

2.4 Models integrating human mobility patterns

Human mobility plays a pivotal role in shaping the spread of infectious diseases, including vector-borne diseases like Zika virus. Traditional disease models often assume homogeneous mixing within populations, overlooking the intricate dynamics influenced by human movement. In recent years, advancements in mathematical modeling have aimed to incorporate human mobility patterns into infectious disease models, providing more realistic simulations that account for travel, migration, and daily movement behaviors. One of the traditional techniques used to incorporate human mobility is network-based modeling. These models represent individuals as nodes within a network and connections between them as edges, where edges denote possible disease transmission routes through human movement. By quantifying contact patterns and travel between nodes, network models simulate how diseases propagate across geographical regions and through populations with varying degrees of connectivity. Such approaches have been applied to study diseases like influenza and malaria, highlighting their effectiveness in capturing spatial transmission dynamics influenced by human travel patterns [33,40].

Agent-based models (ABMs) provide another robust framework for integrating human mobility into disease modeling. ABMs simulate individual behaviors and interactions within a spatial context, allowing for heterogeneous mixing patterns and realistic representations of population movements. These models track virtual individuals (agents) and their movements, interactions with others, and disease transmission dynamics based on specified rules and parameters. ABMs have been used to investigate outbreaks of various infectious diseases, including Zika virus, by incorporating detailed data on human behavior, travel, and contact patterns [35,36].

Recent studies applying these techniques have revealed critical insights into the role of human mobility in Zika virus transmission dynamics. For instance, research has shown that travel patterns influence the spatial spread of Zika, with higher rates of movement facilitating faster dissemination of the virus across regions [28,41]. Furthermore, modeling studies have demonstrated that interventions targeting specific travel routes or movement hotspots can effectively mitigate disease spread, underscoring the importance of integrating mobility data in disease control strategies [42].

Despite these advancements, several research gaps remain that warrant future attention. First, existing models often rely on simplified assumptions about human movement patterns, which may not capture the full complexity of travel behaviors across different demographics and socio-economic groups. Improving data collection methods and incorporating real-time mobility data could enhance the accuracy of these models and their predictive power [43].

Moreover, there is a need for interdisciplinary collaboration to integrate sociological, anthropological, and geographical perspectives into disease modeling. Understanding the drivers of human mobility, such as economic factors, social networks, and cultural practices, can provide deeper insights into disease transmission dynamics and inform targeted intervention strategies.

Future research efforts should also focus on developing scalable models that can accommodate large-scale datasets and dynamic changes in mobility patterns over time. Advances in computational techniques and data analytics offer promising avenues for building more sophisticated models capable of simulating the impact of human mobility on disease dynamics at various spatial and temporal scales [43].

2.5 Spatial dynamics and human mobility

Spatial dynamics and human mobility play crucial roles in shaping the transmission dynamics of infectious diseases, including vector-borne diseases like Zika virus. Traditional disease transmission models, such as SEIR (Susceptible-Exposed-Infectious-Recovered) models, have provided foundational insights by categorizing populations into compartments based on disease status and modeling the transitions between these states. These models typically assume a well-mixed population and do not account for spatial heterogeneity or human movement patterns. However, recent advancements have recognized the limitations of these traditional approaches and have focused on integrating spatial factors and human mobility to improve the accuracy of disease transmission modeling.

Spatially Explicit Models and Local Interactions. Spatially explicit models extend traditional SEIR frameworks by incorporating geographical variations and local interactions. These models often use differential equations to describe the movement of individuals between different spatial compartments, considering factors such as population density, environmental conditions, and vector habitat suitability. For instance, studies by [44] and [32] have utilized spatially explicit SEIR models to simulate Zika virus transmission, demonstrating how local mosquito abundance and human movement influence disease spread within specific geographic areas.

Incorporating Human Mobility Data. Incorporating human mobility patterns into disease transmission models has further enhanced our understanding of how diseases propagate across regions. Models that account for travel, commuting patterns, and migration dynamics provide insights into how individuals can introduce and spread infections in new areas. For example, [45] utilized mobile phone data to track human movements and develop agent-based models for malaria transmission, highlighting the role of human mobility networks in shaping disease distribution and persistence.

Current Studies and Future Directions. Findings from these studies underscore the complexity of disease transmission dynamics in heterogeneous environments. Spatially explicit models have shown that local interactions between human hosts and vectors can amplify disease transmission in areas with favorable environmental conditions [46]. Furthermore, integrating human mobility data has improved the predictive accuracy of models by capturing the spatial spread of infections through travel and migration pathways [47].

Despite these advancements, several research gaps remain that warrant future attention. First, there is a need to refine spatial modeling techniques to better capture fine-scale variations in disease transmission dynamics, particularly in urban settings where population density and environmental factors can vary significantly over short distances. Second, integrating real-time data sources, such as remote sensing data and social media analytics, could enhance the timeliness and accuracy of spatial disease models. Third, there is a call for interdisciplinary collaborations to integrate socio-economic factors and behavioral insights into spatial disease modeling frameworks, providing a more comprehensive understanding of transmission dynamics.

Fig. 3 illustrates the Zika Virus (ZIKV) transmission model. The diagram depicts the dynamic interactions between humans and mosquitoes, essential for understanding ZIKV spread. The solid arrows represent the

progression of individuals within the human population through different disease stages. Susceptible humans (S_h) can become infected (E_h) through bites from infectious mosquitoes. Following an incubation period, infected individuals transition to the infectious stage (I_h) and eventually recover (R_h). Dashed arrows symbolize the transmission of ZIKV between humans and mosquitoes. Susceptible mosquitoes (S_v) acquire the virus by biting infectious humans, moving them to the exposed mosquito stage (E_v). Subsequently, these mosquitoes become infectious (I_v). Mosquitoes are introduced into the susceptible population at a birth rate (h_v) and removed through natural death (μ_v). This model provides a foundational framework for analyzing the complex interplay between human and mosquito populations in ZIKV transmission. By incorporating relevant parameters and data, it can be used to explore disease dynamics, inform prevention strategies, and evaluate potential intervention impacts.
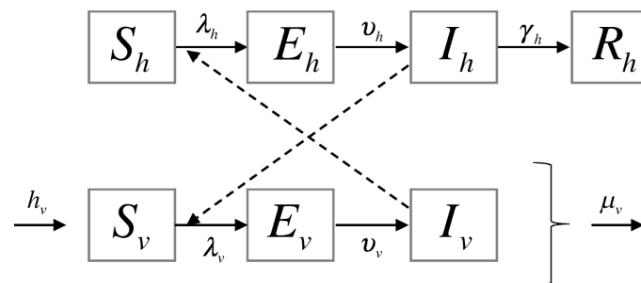

Fig. 3. SEIR model with spatial compartments
Source ([30])

3 Implications for Public Health Strategies and Future Research Perspectives

3.1 Implications for public health strategies

Public health strategies for controlling Zika virus transmission have traditionally relied on a combination of vector control measures, public education campaigns, and surveillance efforts. Mathematical modeling plays a crucial role in optimizing these strategies by providing insights into disease dynamics and evaluating the effectiveness of interventions. Traditional techniques such as vector control through insecticide spraying, larval source reduction, and community engagement have been foundational in mitigating Zika outbreaks. However, the complex interplay between human behavior, environmental factors, and mosquito ecology necessitates more nuanced approaches.

Recent advancements in mathematical modeling have enhanced our understanding of Zika transmission dynamics and expanded the toolkit for public health interventions. Spatially explicit models, which integrate geographical data and human mobility patterns, offer a more accurate depiction of disease spread compared to traditional compartmental models. These models capture local variations in mosquito populations, transmission hotspots, and the impact of environmental factors like temperature and rainfall on vector breeding and survival. For instance, studies have shown that incorporating spatial heterogeneity can significantly improve the predictive accuracy of outbreak simulations [46,47].

Furthermore, network-based models that simulate human movement and social interactions provide insights into how population mobility influences disease transmission. By mapping travel patterns and connectivity between communities, these models identify key routes of virus dissemination and inform targeted interventions such as travel restrictions or vaccination campaigns in high-risk areas [47]. Such approaches highlight the importance of considering human behavior and mobility in designing effective control strategies.

Despite these advancements, several research gaps remain that require attention in future studies. Firstly, while spatial models have shown promise in capturing local disease dynamics, they often require high-resolution data on environmental variables and population movements, which may not be readily available in resource-limited

settings [48]. Improving data collection infrastructure and developing methods to integrate heterogeneous data sources could enhance the applicability of spatial models in diverse epidemiological contexts.

Secondly, the predictive power of current models can be further enhanced by incorporating socio-economic factors and community behaviors that influence vector exposure and disease susceptibility. For example, understanding how housing conditions, access to healthcare, and cultural practices impact mosquito breeding sites and disease transmission dynamics is crucial for targeting interventions effectively [8]. Integrating these social determinants into mathematical frameworks could provide more comprehensive insights into Zika virus epidemiology.

Lastly, there is a need for interdisciplinary collaboration to refine existing models and develop innovative approaches for real-time monitoring and response. Advances in remote sensing technologies, mobile health applications, and big data analytics offer opportunities to enhance surveillance systems and early warning systems for Zika outbreaks (Petersen et al., 2022). By leveraging these technologies, public health authorities can detect emerging outbreaks early, allocate resources efficiently, and implement timely interventions to prevent widespread transmission.

3.2 Future research directions

Future research in mathematical modeling of Zika virus transmission should focus on addressing several key areas to enhance the predictive accuracy and applicability of models in real-world scenarios. Traditional techniques have provided a foundation for understanding disease dynamics, particularly through SEIR (Susceptible-Exposed-Infectious-Recovered) models that compartmentalize populations based on disease status. Recent advancements have integrated spatial and human mobility components into these frameworks, revealing both insights and gaps that warrant further investigation.

Current studies have shown that incorporating spatial dynamics is essential for capturing the localized spread of Zika virus. Spatially explicit models account for environmental factors, such as temperature and precipitation, which influence mosquito breeding and survival rates. These models have demonstrated the significance of geographical heterogeneity in disease transmission, highlighting the need for finer-scale data on human movement and mosquito distribution to improve model accuracy.

Furthermore, the integration of human mobility patterns into mathematical models has advanced our understanding of how population movements contribute to disease spread. Network-based models and agent-based simulations have been used to simulate individual-level interactions and travel behaviors, showing promising results in predicting the spatial dissemination of Zika virus. Future research should focus on refining these models with real-time mobility data and considering behavioral changes in response to public health interventions.

Despite these advancements, several research gaps remain. One critical area is the refinement of vector ecology representations within models. Current approaches often simplify mosquito life cycle dynamics and interactions with environmental factors. Future models could benefit from incorporating more detailed ecological data, such as larval habitats, vector competence variations, and seasonal fluctuations in mosquito populations.

Moreover, the predictive power of mathematical models hinges on the accuracy of input parameters and assumptions. Uncertainties in data, especially related to human behavior and vector biology, can affect model outcomes. Future research should explore innovative methods for parameter estimation, such as Bayesian inference and data assimilation techniques, to improve model robustness and reliability.

Interdisciplinary collaboration is another promising avenue for future research. Integrating epidemiological models with socio-economic factors, urban planning data, and climate change projections can provide a more holistic understanding of Zika virus transmission dynamics. This approach requires interdisciplinary teams to leverage diverse expertise and data sources, facilitating a comprehensive assessment of the complex interactions driving disease spread.

4 Conclusion

This study offers a comprehensive exploration of Zika virus transmission dynamics through the lens of advanced mathematical modeling. By integrating spatially explicit and network-based models, we have significantly enhanced our understanding of the complex interplay between geographical, human, and environmental factors in disease propagation. Our findings underscore the limitations of traditional compartmental models in capturing the nuanced spatial and temporal patterns of Zika outbreaks. In contrast, the incorporation of geographical data into our models provides a more accurate representation of disease spread, enabling the identification of transmission hotspots and the evaluation of targeted intervention strategies. Furthermore, by modeling human movement and social interactions, we have elucidated key pathways of virus dissemination, informing the development of effective containment measures. While our research advances the field of Zika modeling, several critical research gaps remain. High-resolution data on environmental variables and population dynamics are essential for refining model predictions. Moreover, integrating socioeconomic factors into our models will provide a more holistic understanding of disease vulnerability and inform equitable intervention strategies. Continued advancements in vector ecology are also necessary to improve the accuracy of our simulations. To address these challenges, interdisciplinary collaboration and the adoption of innovative technologies are imperative. By combining expertise from epidemiology, mathematics, ecology, and social sciences, we can develop more robust and predictive models. Additionally, investing in advanced surveillance systems and early warning mechanisms will enable timely and effective responses to future outbreaks. This research provides a foundational framework for understanding Zika virus transmission and informs the development of evidence-based control strategies. By building upon our findings and addressing the identified research gaps, we can significantly reduce the burden of Zika disease on global public health.

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

Competing Interests

Authors have declared that no competing interests exist.

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