Proceedings of the 2023 Winter Simulation Conference
C. G. Corlu, S. R. Hunter, H. Lam, B. S. Onggo, J. Shortle, and B. Biller, eds.

USING A HYBRID ABMS TO STUDY THE PROPAGATION OF VECTOR-BORNE DISEASES IN AN URBAN AREA WITH HETEROGENOUS GEOSPATIAL CONDITIONS

Paula Escudero
Mariajose Franco
María Sofía Uribe
Susana Álvarez
Rafael Mateus

School of Applied Sciences and Engineering
Universidad EAFIT
Medellín, 050022, COLOMBIA

ABSTRACT

Agent-Based Modeling and Simulation (ABMS) is a valuable tool for understanding infectious disease propagation. This study presents a hybrid ABMS approach to explore the transmission dynamics of vector-borne diseases (Dengue, Zika, and Chikungunya) in Bello, Colombia, incorporating geospatial characteristics. The model was developed with specific assumptions to validate its alignment with theoretical behavior. Our results demonstrate the temperature's significant impact on disease spread. Particularly, Chikungunya exhibits distinct behavior compared to Dengue and Zika. While major infection peaks occur early in the simulation, subsequent spread diminishes due to the absence of reinfection considerations. This research represents an early stage of a larger project, laying the groundwork for future research to address computational challenges, enabling statistical analysis with multiple runs, and enhancing the model's realism with seasonal temperature variations and geographical distributions. These findings will provide valuable insights for policymakers and disease control strategies in Colombia.

1 INTRODUCTION

Vector-borne diseases are transmitted by blood-feeding arthropods like mosquitoes. Aedes aegypti is the primary mosquito species responsible for transmitting Dengue, Chikungunya, and Zika (Socha et al. 2022). These diseases pose a serious threat to human health since they cause over 700,000 fatalities each year, accounting for more than 17% of all annual deaths (World Health Organization 2018). Countries like Colombia have become increasingly vulnerable to vector-borne diseases due to environmental and geological factors.

This research examines the impact of vector-borne diseases in densely populated urban areas such as Bello, Colombia. Bello's distinct characteristics make it an ideal subject for this investigation, including high population density, social conditions that promote the presence of standing water sources, proximity to other urban centers, and temperature variations, among others.

Mathematical models have played an important role in short and long-term strategic planning for controlling different disease propagation (Brauer et al. 2019). Most of these mathematical models are compartmental epidemic models in which mosquito and human populations are divided into four compartments: susceptible, exposed, infected, and recovered. Specifically, Agent-Based Modeling Simulation (ABMS) is commonly used to study vector-borne diseases from an individual level. However, ABMS models are computationally expensive; therefore, some researchers have proposed using hybrid

ABMS, which integrates Ordinary Differential Equations (ODE) to model mosquitoes and ABMS to model humans. This variation's main advantage is that it significantly improves computing time without sacrificing model specificity (Manore et al. 2014).

The literature review reveals that few studies have investigated the use of ABMS models that include heterogeneous geospatial characteristics of an urban area. Incorporating geospatial characteristics in our ABMS model is important because it captures the spatial context in which individuals live, work, and move, allowing for a more realistic representation of human behavior. This includes factors such as commuting patterns, travel behavior, and daily routines, which significantly influence disease transmission. Including geography enables the simulation to accurately represent human mobility and contact patterns, thus enhancing the understanding of how individuals interact and potentially spread the disease across different geographic areas.

Furthermore, incorporating geospatial characteristics into our agent-based modeling (ABM) helps us understand the spatial distribution of vector-borne diseases in the city, identify high-risk areas, and explore the contributing factors to transmission dynamics. Geospatial data allows us to consider environmental factors, such as temperature, which greatly influence mosquito survival and disease transmission. By including temperature data in our model, we can assess the impact of different temperature scenarios on the spread of Dengue, Zika, and Chikungunya in Bello.

Moreover, using geospatial data can assist Colombian decision-makers in addressing policy implications. For example, in controlling the spread of these viruses, authorities are exploring the use of pyriproxyfen. Pyriproxifen is an insect growth regulator that hinders mosquito reproduction (Fawell, J K 2008). By leveraging geospatial data, decision-makers can optimize the placement of pyriproxyfen stations in high-risk areas, maximizing the effectiveness of vector control efforts.

This research represents the initial stage of a larger project, aiming to provide preliminary modeling of the spread of vector-borne diseases in an urban area. The primary objective is to obtain an initial approximation of the disease dynamics and transmission in an urban area by incorporating geospatial characteristics into our model. However, in the further stages of the project, we will address computational challenges through the use of high-performance computing and the implementation of a system of discrete differential equations. This will enhance the computational efficiency and accuracy of the model and will allow proper calibration and validation. Additionally, we will incorporate targeted control strategies to evaluate their effectiveness in mitigating disease transmission. It is important to note that the current model is not yet ready for decision-makers, but it serves as a valuable tool for validating the overall behavior. By incorporating real data and enhancing computational performance, we aim to develop, in the subsequent stages, a comprehensive and reliable model that can provide actionable insights for policy development and disease control strategies.

This paper is structured as follows: Section 2 reviews the literature on ABMS for modeling vector-borne diseases. Section 3 explains the methodology. Section 4 presents the results. Finally, section 5 concludes the study.

2 BACKGROUND

2.1 Literature Review

Agent-based models (ABM) can be used to understand both the temporal and spatial evolution of vector-borne diseases (Macal 2018). Therefore, ABM has become a widely used tool to model the propagation of these diseases. For example, Maneerat and Daudé (2016) used agent-based modeling and simulation to explore the effects of environmental heterogeneity and mosquito control strategies on mosquito population dynamics. These authors created the agent-based model for a neighborhood in Delhi, India. To model a heterogeneous space, authors consider different porosity coefficients, temperatures, and light levels to portions of the space (patches). In the same way, Miksch et al. (2015) implemented a model to simulate an epidemic in the Philippines in 2010, including some climate characteristics and considering rainy seasons, concluding that

the mosquito population varies between rainy and dry seasons and this has a considerable impact on the dynamics of the epidemic.

In contrast to Maneerat and Daudé (2016), Dommar et al. (2014) represent humans as individual agents. These authors implemented an ABM to investigate the space-temporal heterogeneity of an infectious vector-borne disease outbreak and evaluate the impacts of different policies intended to reduce the propagation of the virus, such as travel restrictions. Additionally, de los Reyes V and L. Escaner IV (2018) performed an analysis to identify the parameters that most influence Dengue transmission in the Philippines. They found that the most important parameters were mosquito biting rate, transmission probability from mosquito to human, respectively, from human to mosquito, and healthcare seeking.

Similarly, Kuhlman et al. (2018) developed a hybrid ABM to simulate the 2016 Zika disease outbreak in Miami, Florida. They integrate Ordinary Differential Equations (ODEs) with an ABM using an SEIR epidemic model for the human population and an SEI model for mosquitoes. To calibrate the model, a variation of the transmission probability was made to determine the actual infection rate during the Miami outbreak. Even though the authors did not consider environmental factors, the model proposed was accurate compared to the actual burst. Nonetheless, the authors found that one of the complications of a hybrid ABMS model was to convert the mathematical expressions of interaction into agent-based interactions. Another example of hybrid ABMS models was proposed by Manore et al. (2014), who implemented a hybrid ABMS using ODEs, allowing a bigger level of detail and better computing performance than if a pure ABMS approach was used. Therefore, mosquitoes are not modeled individually but as an aggregate using ODEs.

The hybrid model proposed by Manore et al. (2014) has made a significant contribution to the study of disease transmission since the model of Mniszewski et al. (2014) is based on the network-patch method described in Manore et al. (2014) also adopted a hybrid ABMS in which they perform different simulations in a hypothetical population of Washington varying parameters such as the probability of transmission, number of mosquitoes and exposure to bites. These last papers served as a reference for our model, where we modeled mosquitoes not individually but as a collective using ordinary differential equations (ODEs).

The literature highlights using ABMS to understand the temporal and spatial evolution of vector-borne diseases. These models consider factors such as environmental heterogeneity, climate characteristics, and human behavior. Some studies focus solely on modeling mosquitoes, while others incorporate individual-level modeling of humans. Hybrid ABMS, combining ABMS with ODEs, has also been utilized to achieve a higher level of detail and better computing performance. These models provide insights into disease transmission dynamics and can inform the development of mitigation strategies. Our research is a case study that represents an important step in understanding the dynamics of vector-borne diseases in urban areas, particularly in the context of Bello. By integrating heterogeneous geospatial characteristics, including human behavior, and utilizing a hybrid ABMS approach, we aim to provide a tool for policy-makers to help the design of effective targeted disease control and prevention strategies.

2.2 Natural History of the Virus

As stated before, the Aedes aegypti mosquito is the principal responsible for propagating viruses such as Dengue, Zika, and Chikungunya (Kakarla et al. 2019). The infection is transmitted by a bite of a female mosquito of this species, so in this research, only female mosquitoes are modeled. The virus infects the mosquito's midgut, and after an incubation period, it extends to the salivary glands, and that is the moment when the mosquito can transmit the virus to other humans (World Health Organization 2020a). These mosquitoes have four life stages: Eggs, Larva, Pupa, and Adult, which are mainly affected by climate factors (Marinho et al. 2016). That is why these diseases are more commonly presented in tropical countries because, with higher temperatures, their development is more rapid, and so is the incubation of the virus in their body (Leung 2020).

The transmission dynamics of vector-borne diseases is very similar for Dengue, Zika, or Chikungunya viruses (Manore et al. 2014). It occurs from vector to human and from human to vector. This is mostly

Table 1: State variables for patches.

Variable	Description
Number of susceptible mosquitoes	Each patch has associated a number of mosquitoes that are susceptible.
Number of exposed mosquitoes	This variable represents the number of exposed mosquitoes located in that patch.
Number of infected mosquitoes	Represents the number of mosquitoes that are infected and are located in that patch.
Temperature (Celsius degrees)	The temperature in each patch changes each day according to data found on the climate of Bello for 2019.
Type	There are four types of patches, residential (type=1), study (type=2), work (type=3), or other (type=4).

of the cases, but for Zika virus, it can occur from human to human (Caminade et al. 2017), but in this project, this way of transmission was not considered.

Humans have four states of infection (Dommar et al. 2014): Susceptible (S) which is when the human does not have the infection in their body and has not been bitten by a mosquito recently. Exposed (E) is when an infected mosquito recently bites a human, but the virus can not be transmitted yet because it has not been incubated in the human body. In this state, the intrinsic incubation period (IIP) is crucial because it indicates the time it takes for the virus to incubate successfully in the human body (Dommar et al. 2014). This time period varies according to the disease and is being modeled using random variables (see Section 3.5.2). The third stage of infection in humans is the Infected state (I), which is when the virus is in the human body and can be transmitted to other mosquitoes. In this state, it is essential to consider the infection period, when the virus will be in the human body. When this time is reached, the human will pass to the last state, Recovered (R), and in most cases, will become immune. The infection period for humans depends on the virus the human is infected with, so it is different for every disease and is explained in Section 3.5.2. The reinfection of humans was not considered in this research, nor were human deaths due to the short simulation time, which is a year (365 days).

The infection in the mosquito occurs when a susceptible mosquito bites an infected human. Unlike humans, mosquitoes can be in only three states (Dommar et al. 2014): Susceptible (S), Exposed (E), and Infected (I), and they never recover because their lifespan is about 2 to 3 weeks (World Health Organization 2020b), so it is not long enough to live until a recover happen. Like humans, mosquitoes also undergo an incubation period to become infected with the virus; this is called the extrinsic incubation period or EIP, which varies depending on the virus and the temperature (Kakarla et al. 2019). This EIP is defined with an equation as a function of the temperature for the Zika and Chikungunya virus, and for Dengue it varies depending on the range of temperatures. This information is explained in Section 3.4.1. Our model did not consider the birth or death of humans due to the simulation time considered.

3 CONCEPTUAL MODEL

The conceptual model in this study was designed using the Overview, Design Concepts, and Details (ODD) protocol (Grimm et al. 2010). The two main entities of our model are humans and mosquitoes. Mosquitoes are modeled as “clouds of mosquitoes" in space because we are not interested in studying their individual behavior. Space represents the territorial extension of the city of Bello in Antioquia, which is 149 km^2 and is modeled using a 2D grid divided into individual squares. Each square contains a patch that is a static agent (entity). The grid dimensions are 32 x 32 patches. Each patch has an associated cloud of mosquitoes that contains several susceptible, exposed, and infected mosquitoes.

On the other hand, humans are modeled as individual mobile entities. In our model, each human agent represents one citizen of Bello. Both humans and patches have state variables that characterize them. The state variables for the patches are presented in Table 1, and for humans are presented in Table 2.

3.1 Process Overview and Scheduling

Each time step of the simulation, also known as a tick, represents one day. The model ran for 365 days. At the beginning of each day, the temperature in each patch is updated, and the numbers of susceptible,

Table 2: State variables for humans.

Variable	Description
Infection state (SEIR)	The infection state of a human can be either susceptible, exposed, infected or recovered.
Time since successful bite	A successful bite is when an infected mosquito bites a susceptible human, resulting in virus transmission. This variable indicates the number of days since the human was bitten and entered the exposed state.
Time since infected	Indicates the number of days since the infection.
Location of the house	Each human is assigned a house located in a residential patch (type 1).
Age	The age of each human remains constant in the simulation because the simulation time is one year.
Activities	There are three types of activities: study, work, or other and each human performs two activities per day. This variable contains the coordinates of the two locations where the human is going to perform each activity.

exposed, and infected mosquitoes in each patch are recalculated. Then, humans move according to their assigned activities, and at the end of the day, they return to their houses. Each time humans move, the following process occurs: First, the probability of each human getting infected is calculated, determining whether this individual becomes infected in their new location. Depending on this, the infection state variable is updated. Next, the number of susceptible, exposed, and infected mosquitoes in the patch where the human moved is recalculated using a new system of differential equations for that patch. At the end of the day, after humans have returned to their homes, the state variables *time since successful bite* and *time since infected* are updated.

3.2 Initialization

For the patches, the following state variables are initialized. The number of susceptible and infected mosquitoes follows a $Uniform(0,100)$ distribution. To set the temperature, we assign a minimum and maximum temperature for each day of the year 2019 in Bello. Finally, the grid is divided into four equal parts, and each patch of the grid receives a type. All the patches in the lower-left section are type 1, in the upper-left section are type 2, in the lower-right section are type 3, and in the upper-right section are type 4. This partitioning is undertaken for the purpose of simplification to facilitate the analysis and modeling of the system within the context of the research.

At the start of the simulation, there are 120,570 susceptible humans and 1,000 infected humans. The low number of initially infected individuals is chosen to maintain a controlled infection rate. When many humans are infected at the beginning of the simulation, the rest of the population quickly becomes infected. The initial number of infected humans was set to a low value to maintain a more controlled infection rate. Additionally, it is worth noting to mention that if the simulation begins with no infected mosquitoes, no humans will become infected throughout the entire simulation. The infected human's *time since successful bite* and *time since infected* variables are initialized as 0, while the susceptible humans start with both variables set to null. Each human is randomly assigned a residential patch (type 1) as a home location. The humans' ages are assigned according to the official demographic data of each age group. Finally, humans under 24 are assigned a place to study, while humans over 24 are assigned a place to work. All humans are assigned one leisure activity different from work or academic activities.

3.3 Parameters and Input Data

The input data for the model consisted of the minimum and maximum temperatures of Bello in 2019, which were used to assign a temperature value to each patch for every day. The model incorporates various parameters, as outlined in Table 3, with values sourced from Manore et al. (2014). To address the inherent parametric uncertainty in individual mosquito models, we adopted the authors' approach, which focuses on addressing heterogeneity in disease spread at the patch level rather than individual mosquito locations.

Table 3: Parameters values from literature.

Variable	Name	Value
μ_v	Per capita mosquito death rate	$\frac{1}{14}$
ψ_v	Per capita natural emergence rate of mosquitoes	0.3
β_{vh}	Probability of transmission from an infectious human to a susceptible mosquito given that a contact between the two occurs	0.333
β_{hv}	Probability of transmission from an infectious mosquito to a susceptible human given that a contact between the two occurs	0.333
σ_v	Maximum number of bites per mosquito per unit time	0.5
σ_h	Maximum number of bites a human can get per unit time	19
K_v	Carrying capacity of the mosquitoes in the patch	1000

3.4 Submodels Patches

In the current version of the model, the temperature and the population of susceptible, exposed, and infected mosquitoes in each patch change daily. However, the temperature assignment to each patch is based on a random selection from a uniform distribution using the minimum and maximum temperatures of Bello in 2019 for that day. Future work will incorporate a more realistic approach by considering seasonal variations and the geographical distribution of temperatures. To calculate the number of susceptible (${S_v}^k$), exposed (${E_v}^k$), and infected mosquitoes (${I_v}^k$) in a patch k in each time step, a system of differential equations for patch k is created and then solved. In the section below, this process is explained in more detail.

3.4.1 Recalculate System of Differential Equations

As mentioned earlier, each patch in the model is associated with a system of differential equations that depend on the number of humans in the patch and the temperature of the patch. Since the temperature of the patch changes each day and humans move continuously, the system of differential equations associated with each patch is constantly changing. The equations used for these systems of differential equations were taken from Manore et al. (2014) and Mniszewski et al. (2014) and are presented below.

$$\frac{d{S_v}^k}{dt} = {h_v}^k - {\lambda_v}^k {S_v}^k - \mu_v {S_v}^k; \qquad \frac{d{E_v}^k}{dt} = {\lambda_v}^k {S_v}^k - {v_v}^k {E_v}^k - \mu_v {E_v}^k; \qquad \frac{d{I_v}^k}{dt} = {v_v}^k {E_v}^k - \mu_v {I_v}^k$$

where the subscript v refers to the mosquito vector, the superscript k refers to the patch, ${h_v}^k$ is the total birth rate of mosquitoes in patch k, ${\lambda_v}^k$ is the per capita rate of infection of mosquitoes in patch k, ${v_v}^k$ is the per capita rate of progression of mosquitoes from exposed state to the infectious state in patch k, and μ_v is the per capita death rate of mosquitoes (parameter). The equations for calculating the total birth rate in patch k (${h_v}^k$), per capita rate of infection of mosquitoes in patch k (${\lambda_v}^k$), and per capita rate of progression of mosquitoes from exposed state to the infectious state in patch k (${v_v}^k$) are described below.

The equation for calculating the total birth rate in patch k (${h_v}^k$) is the following:

$${h_v}^k = {N_v}^k \left(\psi_v - \frac{r_v * {N_v}^k}{K_v} \right)$$

where ψ_v is the natural per capita-emergence rate of mosquitoes (parameter), r_v is the mosquito population growth rate and is defined as $r_v = \psi_v - \mu_v$, K_v is the carrying capacity of the mosquitoes in a patch (parameter), and ${N_v}^k$ is the total number of mosquitoes in the patch k and is defined as ${N_v}^k = {S_v}^k + {E_v}^k + {I_v}^k$.

The equation for calculating the per capita rate of infection of mosquitoes in patch k (${\lambda_v}^k$) is calculated as follows:

$${\lambda_v}^k = {b_v}^k * \beta_{vh} * \left(\frac{{I_h}^k}{{N_h}^k} \right)$$

where the subscript h refers to humans, ${I_h}^k$ is the number of infected humans in the patch k, ${N_h}^k$ is the total number of humans in the patch k, β_{vh} is the probability of transmission from an infectious human to a susceptible mosquito given that a contact between the two occurs (parameter), and ${b_v}^k$ is the number of bites per mosquito per unit of time in the patch k and is defined in the following way:

$$ {b_v}^k = \frac{b^k}{{N_v}^k} $$

where b^k is the total number of contacts between humans and mosquitoes (bites) in the patch k and is defined in the following way:

$$ b^k = \frac{\sigma_v * {N_v}^k * \sigma_h * {N_h}^k}{\sigma_v * {N_v}^k + \sigma_h * {N_h}^k} $$

where σ_v is the maximum number of bites per mosquito per unit of time (parameter) and σ_h is the number of bites a human can get per unit of time (parameter).

The equation for calculating the per capita rate of progression of mosquitoes from the exposed state to the infectious state in patch k (${v_v}^k$) is

$$ {v_v}^k = \frac{1}{{tinc_v}^k} $$

where ${tinc_v}^k$ is the incubation time of the virus in the mosquito in patch k. This time depends on the temperature of the patch (T^k) and varies depending on the virus. This incubation time is modeled differently for each one of the viruses. For Zika, ${tinc_v}^k = 7 + \frac{0.667-0.378(T^k-26)}{0.299+0.027(T^k-26)}$ (Winokur et al. 2020); for Chikungunya, ${tinc_v}^k = 4 + e^{5.15-0.123T^k}$ (Kakarla et al. 2019); and for Dengue: ${tinc_v}^k$ follows a uniform distribution, more specifically $U(10,25)$ if $18 < T^k \leq 21$, $U(7,10)$ if $21 < T^k \leq 26$ and $U(4,7)$ if $26 < T^k < 31$.

For Zika and Dengue viruses, if the temperature of the patch is less than 15 °C, the incubation time of the virus in the mosquitoes is not defined, and the rate of progression of mosquitoes from exposed to infected (${v_v}^k$) is zero. Similarly, for Chikungunya, if the temperature in the patch is less than 12 °C, the mosquito incubation time is not defined in this patch, and the rate of progression of mosquitoes from exposed to infected (${v_v}^k$) is zero. This happens because, at low temperatures, the incubation time of the virus in mosquitoes is really long so mosquitoes reach life expectancy and die before incubating the virus.

The system of differential equations needs to be solved to calculate the number of susceptible (${S_v}^k$), exposed (${E_v}^k$), and infected (${I_v}^k$) mosquitoes in each patch k. To solve this system, the method Runge Kutta of 4^{th} order was implemented with a time step of h=0.1.

3.5 Submodels Humans

As mentioned previously, humans have assigned activities that are performed during the day. The movement of each human is determined by their assigned activities, and during this movement, several variables are updated, including the infection state, time since the successful bite, and time since infection. In the following sections, these submodels will be explained in more detail, providing a comprehensive understanding of their functioning and impact within the model.

3.5.1 Movement

Each day, the human individuals in the model start at their respective homes. To determine their first activity, the coordinates of the activity from their list are selected, and the humans are then moved to those specific coordinates. The probability of infection in each patch is different, so with every movement a human makes, the submodel “update SEIR state" is called to calculate the probability of infection and determine

if the human will get infected in this new place or not. Then, the human is moved to the coordinates of the second activity, and the submodel "update SEIR state" is called again. Then, the human returns to its home location, and the "update SEIR state" is called for the last time.

3.5.2 Update SEIR State

The actualization of the SEIR state is modeled using probabilities. A susceptible human in patch k becomes exposed with a probability of ${p_{SE_h}}^k$. An exposed human becomes infected with a probability of ${p_{EI_h}}^k$, and an infected human becomes recovered with a probability of ${p_{IR_h}}^k$. The probability ${p_{SE_h}}^k$ is obtained by calculating the rate of infection of humans in patch k. On the other hand, both ${p_{SE_h}}^k$ and ${p_{IR_h}}^k$ are obtained by using a random variable approach. A more detailed description of how these three probabilities are calculated is provided below.

The equation for calculating the probability of a human passing from susceptible to exposed in patch k (${p_{SE_h}}^k$) is the following: ${p_{SE_h}}^k = 1 - e^{-{\lambda_h}^k}$ where ${\lambda_h}^k$ is the rate of infection of humans in patch k and is defined as

$$\lambda_h^k = {b_h}^k * \beta_{hv} * \left(\frac{{I_v}^k}{{N_v}^k}\right)$$

where ${I_v}^k$ is the number of infected mosquitoes in patch k, ${N_v}^k$ is the total number of mosquitoes in patch k, β_{hv} is the probability of transmission from an infectious mosquito to a susceptible human given that a contact between the two occurs (parameter), and ${b_h}^k$ is the number of bites a human receives per unit time in the patch k and is defined in the following way: ${b_h}^k = \frac{b^k}{{N_h}^k}$, where b^k is the total number of contacts between humans and mosquitoes (bites) in the patch k (is defined previously) and ${N_h}^k$ is the total number of humans in patch k.

As stated previously, the probability of a human passing from exposed to infected in patch k (${p_{EI_h}}^k$) is calculated by using a random variable approach. In this case the incubation time of the virus in patch k (${t_{inc_h}}^k$) is a random variable that follows a different probability distribution for each virus. For Zika it is $t_{inc_h} \sim Weibull\,(\alpha = 2.69, \beta = 6.70)$ (Krow-Lucal et al. 2017); for Chikungunya it is $t_{inc_h} \sim Lognormal\,(\mu = 1.099,\ \sigma = 0.139)$ (Leung 2020) and (Manore et al. 2014); and for Dengue it is $t_{inc_h} \sim Gamma\,(\alpha = 5.5,\ \beta = 1.12)$ (Chan and Johansson 2012).

${p_{EI_h}}^k$ is obtained by calculating the probability that the random variable(${t_{inc_h}}^k$) is exceeded by the time passed since the human received a successful bite (timeSinceSuccessfulBite) which is a state variable of the human. The equation for this probability calculation is described below.

$${p_{EI_h}}^k = p({t_{inc_h}}^k \leq timeSinceSuccessfulBite)$$

In this manner, every time a human moves, ${p_{EI_h}}^k$ is calculated in the patch k using the human's state variable timeSinceSuccessfulBite. Knowing this probability, it is then used to determine if the human gets infected or not.

The probability of a human passing from infected to recovered in patch k (${p_{IR_h}}^k$) is also calculated by using a random variable approach. In this case, the time of infection of the virus in patch k (${t_{inf_h}}^k$) is a random variable that follows a different probability distribution for each virus. For Zika $t_{inf_h} \sim norm\,(\mu = 6, \sigma = 1)$ (Fontaine et al. 2018); for Chikungunya $t_{inf_h} \sim Uniform\,(a = 3, b = 7)$ (Manore et al. 2014) and for Dengue $t_{inf_h} \sim Uniform\,(a = 2, b = 7)$ (Chan and Johansson 2012).

${p_{IR_h}}^k$ is obtained by calculating the probability that the random variable (${t_{inf_h}}^k$) is exceeded by the time passed since the human got infected (timeSinceInfected) which is a state variable of the human. The equation for this probability calculation is presented below.

$${p_{IR_h}}^k = p({t_{inf_h}}^k \leq timeSinceInfected)$$

3.5.3 Update Times

Both state variables *time since successful bite* and *time since infected* are updated similarly. These variables can either an integer or be null (when the individual has not been bitten). If the variable is not null, it increases by one unit for each tick (day).

4 RESULTS

Due to the large population of Bello and the complexity of the human behavior considered in the model, it is time-consuming to conduct experiments under real-life conditions. Thus, we only present the results for one execution of the model. As part of a larger project focused on vector-borne disease prevention, the next stage addresses computational challenges, allowing for statistical analysis of multiple runs.

This approach will enable further sensitivity analysis and more realistic experimentation with the model; nevertheless, we conducted a simple and exploratory sensitivity analysis for the Chikungunya virus to evaluate how changing the initial number of infected humans affects the total infections that occur in the simulation. We considered three scenarios: a base scenario with 1000 infected humans at the beginning of the simulation and two additional scenarios with 0 and 10000 infected humans, respectively. The second scenario resulted in a decrease of 1.28% of the total number of infected humans at the end of the simulation compared to the base scenario while the third scenario showed an increase of 3.19%.

To ensure accuracy and clarity, separate models were developed for Dengue, Zika, and Chikungunya, considering their unique characteristics. Initially, simulations were conducted using historical temperature data from Bello. Two additional scenarios involving high and low temperatures were explored to demonstrate the influence of temperature on the spread of these viruses. It is important to note that the extreme temperature scenarios did not represent Bello's actual conditions but served as illustrative examples. Future enhancements to the model will focus on incorporating seasonal variations and geographical temperature distributions for a more realistic analysis of mosquito populations and disease dynamics.

As mentioned in the previous section, a total of three scenarios were considered for the simulation of each of the viruses. Figure 1 compares the output of each of the models for Dengue, Zika, and Chikungunya based on the temperature of the municipality of Bello. These plots display how each virus propagates over time in Bello, Colombia; recall that the time horizon used for the simulation is one year with a step size of one day, i.e., one tick represents one day of simulation. It can be evidenced that of all the considered diseases, the Chikungunya's behavior was the most pronounced. Besides, humans infected with Dengue and Zika had similar behavior; they both peaked in approximately the first 50 days of the simulation. This is because infection times differ according to the virus.

In the same way, it is expected for the propagation of the disease to have a peak, just like actual disease outbreaks do. It is evident in Figure 1 that this happens at the beginning of the simulation. However, simulations showed that after this major peak of infections, no further significant spread of these diseases occurred. After approximately 100 days of simulation, human states regarding the diseases vary little to none; one of the factors we consider as the cause for this phenomenon is that we do not contemplate reinfection of the diseases. This means once a human has recovered from a specific disease, it can not suffer it again in the future. Also, it is crucial to understand that all the virus simulations run in a separate environment so that simulation can be more straightforward, meaning agents only experience one disease at a time; they were not exposed to Dengue, Zika, and Chikungunya simultaneously.

To analyze the impact of temperature on the spreading of these diseases, three ranges of temperatures were considered: low temperatures $[T = (12^\circ, 16^\circ)]$, actual temperatures, and high temperatures $[T = (25^\circ, 30^\circ)]$. For these scenarios, the same conditions for the simulation were considered, except for the temperature variation. The results of this experimentation can be evidenced in Figure 2; for visualization purposes, only infected humans were included in the plots since it was the state in which the peak of the disease was more pronounced. These results may be explained by the fact that infection times are temperature-dependent; in Section 3.4.1, a broad explanation for the infection times is presented.

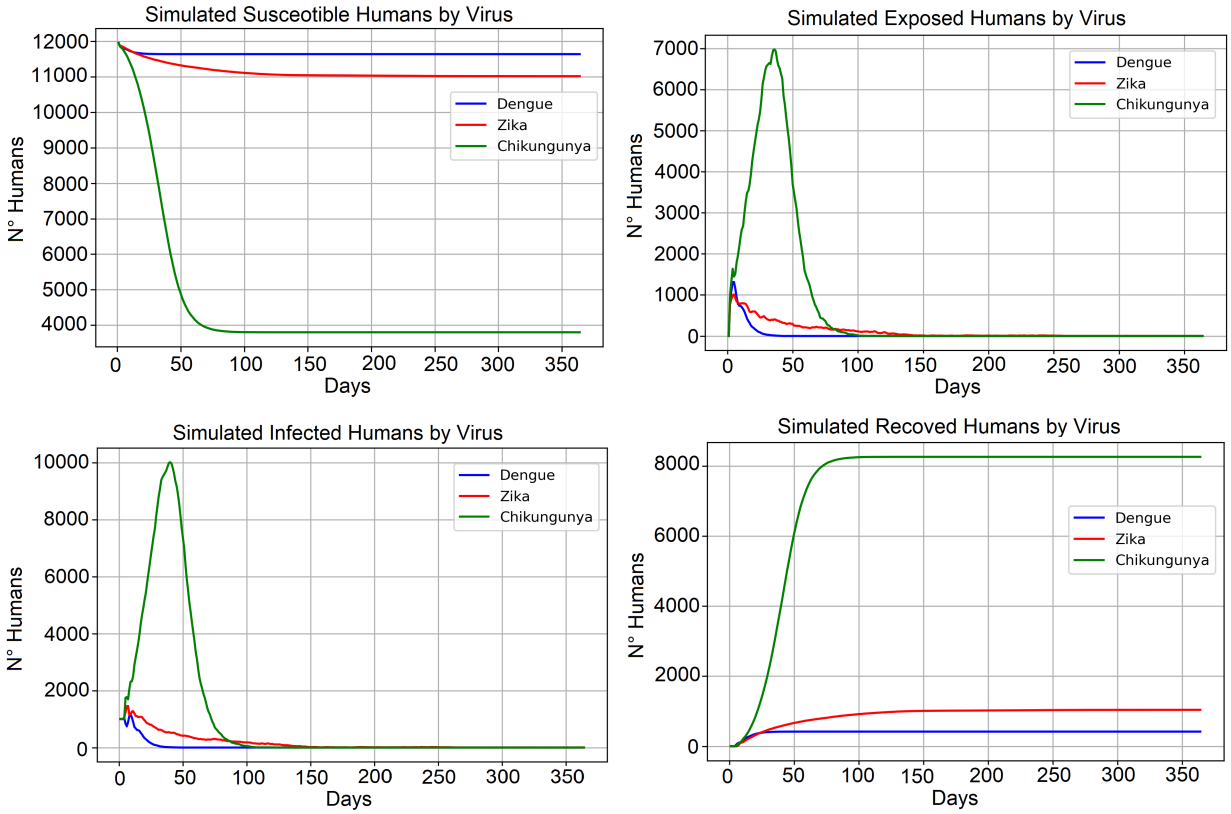

Figure 1: Comparison between simulations for Dengue, Zika, and Chikungunya in Bello, Colombia.

5 CONCLUSIONS

The study demonstrates the utility of a Hybrid ABMS model in simulating the spread of Dengue, Zika, and Chikungunya viruses in an urban area. Integrating geospatial and environmental characteristics differentiates from other models presented in the literature since it allows us to realistically capture the spatial context, human behavior, and disease transmission patterns. While there are assumptions and simplifications in the model that require validation, they generally reflect the behavior of these viruses based on the observed patterns of susceptible, exposed, infected, and recovered individuals.

This research is an essential step in a larger project; subsequent stages will refine the model through high-performance computing, real data incorporation, and addressing computational challenges. The primary purpose of the project at large is to develop a comprehensive and reliable model that informs policy development and targeted disease control strategies. This proposed model would be beneficial to authorities in Colombia who are already experimenting with control strategies such as using pyriproxyfen in different urban areas.

Further work needs to be carried out to validate and calibrate the model with historical data in Bello. Possible improvements include making the model more realistic, like scaling the grid to the actual size of Bello territory and considering the distribution of temperatures per day and per geographic zone in Bello. As well as considering real-scale industrial, educational, living, and leisure zones. These improvements could aid in identifying high-risk areas and evaluating control strategies and targeted interventions.

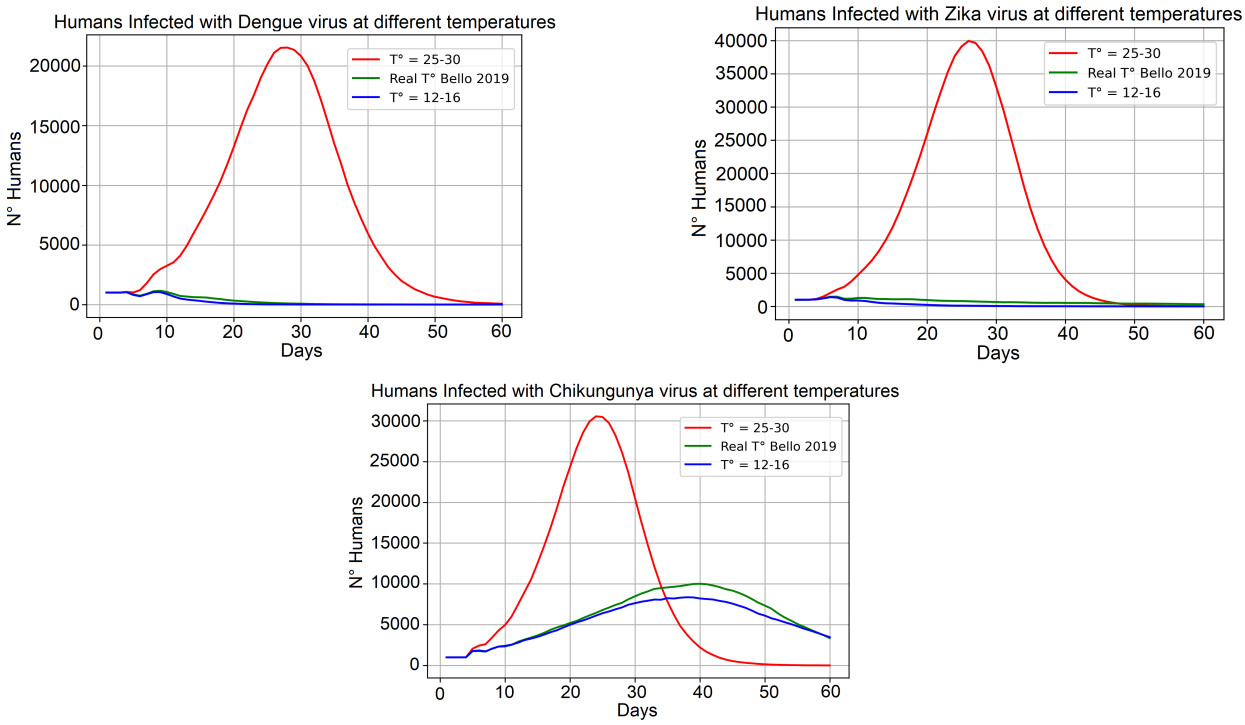

Figure 2: Temperature experimentation for infected humans.

ACKNOWLEDGMENTS

We would like to express our sincere gratitude to the members of the mathematical epidemiology research group at Universidad EAFIT, especially to Professor Maria Eugenia Puerta for her insightful comments and suggestions, which were essential for developing this paper.

REFERENCES

Brauer, F., C. Castillo-Chavez, and Z. Feng. 2019. *Mathematical Models in Epidemiology*, Volume 69, Chapter Introduction: A Prelude to Mathematical Epidemiology, 3–19. Springer.

Caminade, C., J. Turner, S. Metelmann, J. C. Hesson, M. S. Blagrove, T. Solomon, A. P. Morse, and M. Baylis. 2017. "Global Risk Model for Vector-Borne Transmission of Zika Virus Reveals the Role of El Niño 2015". *Proceedings of the National Academy of Sciences of the United States of America* 114(1):119–124.

Chan, M., and M. A. Johansson. 2012. "The Incubation Periods of Dengue Viruses". *PLoS ONE* 7(11):1–7.

de los Reyes V, A., and J. M. L. Escaner IV. 2018. "Dengue in the Philippines: Model and Analysis of Parameters Affecting Transmission". *Journal of Biological Dynamics* 12(1):894–912.

Dommar, C. J., R. Lowe, M. Robinson, and X. Rodó. 2014. "An Agent-Based Model Driven by Tropical Rainfall to Understand the Spatio-Temporal Heterogeneity of a Chikungunya Outbreak". *Acta Tropica* 129(1):61–73.

Fawell, J K 2008. "Pyriproxyfen in Drinking-Water: Use for Vector Control in Drinking-water Sources and Containers". World Health Organization.

Fontaine, A., F. de Laval, D. Belleoud, S. Briolant, and S. Matheus. 2018. "Duration of Zika Viremia in Serum". *Clinical infectious diseases* 67(7):1143–1144.

Grimm, V., U. Berger, D. L. DeAngelis, J. G. Polhill, J. Giske, and S. F. Railsback. 2010. "The ODD protocol: A Review and First Update". *Ecological Modelling* 221(23):2760–2768.

Kakarla, S. G., R. Mopuri, S. R. Mutheneni, K. R. Bhimala, S. Kumaraswamy, M. R. Kadiri, K. C. Gouda, and S. M. Upadhyayula. 2019. "Temperature Dependent Transmission Potential Model for Chikungunya in India". *Science of the Total Environment* 647(1):66–74.

Krow-Lucal, E. R., B. J. Biggerstaff, and J. E. Staples. 2017. "Estimated incubation period for zika virus disease". *Emerging Infectious Diseases* 23(5):841–844.

Kuhlman, C. J., Y. Ren, B. Lewis, and J. Schlitt. 2018. "Hybrid Agent-Based Modeling of Zika in the United States". In *Proceedings of the 2018 Winter Simulation Conference*, 1085–1096. Argonne, IL: Argonne National Laboratory.

Leung, C. 2020. "Estimated incubation period for mosquito-borne disease-related Guillain-Barre syndrome". *Clinical Epidemiology and Global Health* 8(1):244–250.

Macal, C. M. 2018. "Tutorial on Agent-Based Modeling and Simulation: ABM Design for the Zombie Apocalypse". In *Proceedings of the 2018 Winter Simulation Conference*, 207–221. Argonne, IL: Argonne National Laboratory.

Maneerat, S., and E. Daudé. 2016. "A spatial agent-based simulation model of the dengue vector Aedes aegypti to explore its population dynamics in urban areas". *Developments in Environmental Modelling* 9:90–122.

Manore, C. A., K. S. Hickmann, J. M. Hyman, I. M. Foppa, J. K. Davis, D. M. Wesson, and C. N. Mores. 2014. "A network-patch methodology for adapting agent-based models for directly transmitted disease to mosquito-borne disease". *Journal of Biological Dynamics* 9:52–72.

Marinho, R. A., E. B. Beserra, M. A. Bezerra-Gusmão, V. d. S. Porto, R. A. Olinda, and C. A. Dos Santos. 2016. "Effects of temperature on the life cycle, expansion, and dispersion of Aedes aegypti (Diptera: Culicidae) in three cities in Paraiba, Brazil". *Journal of Vector Ecology* 41(1):1–10.

Miksch, F., P. Pichler, K. J. Espinosa, K. S. Casera, A. N. Navarro, and M. Bicher. 2015. "An agent-based epidemic model for dengue simulation in the Philippines". In *Proceedings of the 2015 Winter Simulation Conference*. Huntington Beach, CA, USA: Winter Simulation Conference.

Mniszewski, S., C. Manore, B. C, S. Del Valle, and R. D. 2014. "Towards a Hybrid Agent-based Model for Mosquito Borne Disease". In *Proceedings of the 2014 Summer Computer Simulation Conference*. Monterey, California: Summer Computer Simulation Conference.

World Health Organization 2018. "Zika Virus". World Health Organization. https://www.who.int/news-room/fact-sheets/detail/zika-virus, accessed 07.2021.

World Health Organization 2020a. "Lucha contra el dengue". World Health Organization. https://www.who.int/denguecontrol/mosquito/es/, accessed 07.2021.

World Health Organization 2020b. "Vector-borne diseases". https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases, accessed 07.2021.

Socha, W., M. Kwasnik, M. Larska, J. Rola, and W. Rozek. 2022. "Vector-Borne Viral Diseases as a Current Threat for Human and Animal Health—One Health Perspective". *Journal of Clinical Medicine* 11(11):3026.

Winokur, O. C., B. J. Main, J. Nicholson, and C. M. Barker. 2020. "Impact of temperature on the extrinsic incubation period of zika virus in aedes Aegypti". *PLoS Neglected Tropical Diseases* 14(3):1–15.

AUTHOR BIOGRAPHIES

PAULA ESCUDERO is a Professor of the School of Applied Sciences and Engineering at Universidad Eafit in Medellín, Colombia. Her research is primarily focused on Agent-based and Discrete Event Simulation, with a particular emphasis on healthcare applications such as epidemiology and healthcare management. Her email address is pescuder@eafit.edu.co.

MARIAJOSE FRANCO is a Mathematical Engineering student at Universidad Eafit in Medellín, Colombia. Her email address is mfrancoo@eafit.edu.co.

MARÍA SOFÍA URIBE is a Mathematical Engineering student at Universidad Eafit in Medellín, Colombia. Her email address is msuribec@eafit.edu.co.

SUSANA ÁLVAREZ is a Mathematical Engineering student at Universidad Eafit in Medellín, Colombia. Her email address is salvarezz1@eafit.edu.co.

RAFAEL MATEUS is a Mathematical Engineering student at Universidad Eafit in Medellín, Colombia. His email address is rmateusc@eafit.edu.co.