Agent-Based Modeling and Simulation of Mosquito-Borne Disease Transmission

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ABSTRACT

Mosquito-borne diseases, such as chikungunya, dengue, and malaria, are re-emerging and expanding to new and formerly unaffected places, leading to a need for models which can track their evolution and thus help with public policy and epidemiological studies. Such diseases' evolution is driven by the interactions between hosts and vectors, and is thus heavily dependent on factors like host and vector population distributions and mobility, and geographical and weather conditions. Traditionally used mathematical models fail to capture such issues, thereby creating a gap between what epidemiologists and disease modelers can provide, and what public health policy requires. We give a generalized agent-based model (ABM) which overcomes these limitations by careful integration of geographic information (GIS) and census data to account for the spatial movement of infections, and climate data to capture the temporal nature of an epidemc. It captures the disorganized interactions of hosts and vectors at a micro-scale by explicitly modeling each human and mosquito to simulate the complex trajectories of disease outbreaks (even those have yet to occur), and makes it possible to test the efficacy of various public health policies. This model also suggests that it is possible to estimate hard-to-determine parameters about vectors (e.g., a mosquito's sensing distance), through simple model calibration. Unlike previous solutions, our model is trained and validated using real data from a 2013-14 chikungunya epidemic in the Caribbean and is seen to give accurate results.

Keywords

Chikungunya; Computational Epidemiology; Mosquitoes; Public Health; Simulation

1. INTRODUCTION

Vector-borne diseases, of which mosquito-borne diseases are the largest subset, account for more than 17% of all infectious diseases, and cause more than 1 million deaths every year [49]. Adding to their high fatality rates, they also have high attack rates, and are very prone to mutation, leading to recurrent infections and a lack of single vaccine [50]. This creates the need for more proactive solutions for their containment—particularly, solutions capable of tracking the trajectory of the infection evolution at a very fine granularity. However, modeling the complicated relationships among human-mosquito-pathogen continues to be a challenging problem faced by all epidemiologists and public health experts.

Traditionally adopted mathematical approaches for this purpose are the differential equation models [21] and mean-field type models [30], which fail to track spatial and temporal factors like population density and dynamics, and ignore the spatial implications within the system, thereby creating a huge gap between what epidemiologists can deliver and and what public health policy makers would like [15, 41]. This neglect of spatial and temporal components in epidemic model formulation can be resolved by the use of the agent-based modeling paradigm [44]

We give an agent-based model which overcomes the above limitations of prior mathematical models, to adequately capture the spread of vector-borne diseases at a fine granularity, and show how it can contribute to low-level policy design such as testing intervention strategies in epidemic life-cycle. It captures the complex relationship between humans, mosquitoes, and pathogens by modeling them individually at a micro scale using simple adaptive rules, and letting them interact. The environment is structured using multi-layered GIS data to address the space implications in disease proliferation, is realistically initialized using census data to account for variable population density, and driven by climate (precipitation + temperature) data to correctly capture disease vector dynamics. Each of these three agent populations have been designed to imitate the characteristic behavior of the vector-borne diseases:

1. Our human agent population approximates the mobility patterns across various population sub-groups while being sensitive to the spreading infection to adequately capture the spatial movement of the infection. This overcomes the usual drawback of the aggregated nature of mathematical models and helps us analyze various intervention strategies.
2. To account for the seasonal nature of an epidemic, the mosquito agent population is made to be heavily dependent on precipitation data and availability of resources as these are known to be major factors in disease propagation [17, 4]. This captures the inherently disordered nature of such epidemics. One of our novel contributions here is the incorporation of the climate sensitive complex reproduction cycle of mosquitoes within the mosquito agent. Every stage of

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a mosquito is separately modeled with its age being a linear function of temperature and time to closely resemble the mosquito population in nature.

3. Our infection model is designed as a state machine with variable transition probabilities, making it easily generalizable to a large subset of mosquito-borne diseases.

The epidemic emerging from our model is calibrated and validated using data from the 2013-14 chikungunya epidemic on some Caribbean islands, as a proof of concept. The model predictions are 93.3% accurate on the test data of the reported cases, with the small gap suggesting that there were some cases which went unreported, which matches with reality, where a lot of chikungunya cases go unreported due to the non-fatal nature of the disease. We also show how our model can be utilized to estimate some vector parameters like mosquito sensory range, mortality rate, etc. which are hard to determine directly. Furthermore, we test two prevention strategies, LSM and ITN+IRS, and the results show that for a small urban tropical area, LSM is more effective in terms of cost, mosquito control, and infection elimination. Also, considering that in most cases a mosquito's life cycle is not greatly dependent on the presence or absence of the infection due to their short lifespan [19], our model can be easily adapted for other mosquito-borne diseases with minor modifications. To adopt the model for some other mosquito-borne disease, we only need to modify the values of relevant parameters based on the new vector's and pathogen's behavior, and calibrate others using data from past epidemic of the same disease.

There are some ABMs proposed to model the spread of vector-borne diseases. Dommar et al. [17] developed an ABM to model chikungunya outbreaks, and indicate that topology and precipitation are dominant factors in vector-borne disease propagation. Teng et al. [16] also provide a similar model for simulating dengue spread. However, neither of these accounts for human mobility patterns, thereby neglecting the major source of spatial movement of infections. Arifin et al. [33] provide a framework for effectively using multi-layered GIS data in an ABM-based malaria study. Illangakoon et al. [27] explore the efficacy of ABMs for studying malaria prevalence and transmission, and show how human mobility patterns have a strong affect on disease transmission. Ying et al. [4] study the effect of spatial heterogeneity on mosquito populations. All of these only focus on the spatial nature of the epidemic and are inconsiderate of the climatic conditions, a leading contributor to vector dynamics. Mniszewski et al. [34] leverage the efficacy of differential models by proposing a "hybrid network patch model" to give insights into the effect of variable probabilities in infection model on the ABM; and Isidoro et al. [28] show the utility of ABMs to try out different mosquito control strategies. However, both of these operate on random topologies and thus do not correctly capture the host-vector interactions. Miksch et al. [32] show the potential of ABMs to recreate real life epidemics through model parameterization and calibration but in a manner very limited to a particular disease and location. Our work is a significant improvement over them as most of these models operate at a large scale with granularity ranging from human crowd to cities network [16, 17, 33, 34], making them infeasible for low level policy design. They also focus on a very narrow set of parameters to study disease propagation, disregarding other dominant factors which severely undermines the prediction accuracy of such models. Also, none of these models are validated using real data making their results wildly unpredictable and impossible to compare with other models.

In summary, our novel contributions are:

(i) A framework for incorporating climate sensitive complex reproduction cycle of mosquitoes in the mosquito agent.

(ii) A generalized mechanism for an epidemic ABM's calibration and validation.

(iii) A method for estimating hard-to-determine vector parameters like mosquito sensory range, using ABMs.

(iv) Methods for testing different policies like intervention strategies using our model. (We also have a comparative analysis of existing ABMs for modeling vector-borne diseases and our model.)

In Section 2, we give a detailed explanation of our model design and its intrinsic workings. Here, we also describe our simulation approach and the data-set used for validation. In Section 3, we explain our model parameterization and calibration, and discuss our model's performance on the past epidemic data. In Section 4, we show how our model can be used for policy formulation by comparing two popular mosquito prevention techniques. Finally, we conclude with the current state of our model and some thoughts for future directions in Section 5.

2. MODELING DISEASE TRANSMISSION

The modeling of the effects of climate and topology on vector behavior, and the patterns of human mobility, is a desideratum in the epidemiology of vector-borne diseases. Here, we present our agent-based model which successfully captures these effects in a disease's evolution at an adequate scale. The simulation strategy we adopted to qualitatively analyze our model is also explained here.

2.1 Agent-Based Model

The agent-based model presented here represents the cumulative effects of the behaviors of individual humans and mosquitoes in an urban environment while noting the biological trajectory of the spreading infection. It is composed of three parts: The first is a small modification of the popular SEIR model [43] to describe the infection life cycle. The second describes the vector distribution, interaction capabilities with the immediate environment and their dependency on the climatic conditions. The third presents the laws governing the daily behavior/movements of human agents, and is used to stratify the human population. The scale considered is at city level, and agent granularity is at the level of an individual human and an individual mosquito. The following sections describe the three agents and the environment they interact in.

2.1.1 Infection Model

Mosquito-borne diseases are transmitted human-to-mosquito and mosquito-to-human. Symptoms vary but are generally classifiable into two stages: intrinsic incubation period, and infectious state. Incubation is when a mosquito has successfully infected a human and the pathogen has started multiplying inside the host body. Depending on the disease,

a person may or may not be contagious during this stage. The infectious state is when the pathogen has multiplied and reached a certain threshold, and the human has possibly started to show symptoms. The probability of pathogen transmission is very high during this period. Considering that a lot of vector-borne diseases are known to have significant incubation periods (malaria, dengue, chikungunya, etc.), the SEIR model (Susceptible → Exposed → Infectious → Recovered) was chosen as its exposed state addresses the incubation period. The *susceptible* state is when an individual is vulnerable to infection by the pathogen. An individual is said to be exposed when he is carrying infection but is not yet contagious. The *infected* state is when the individual has started showing symptoms and is ready to infect a mosquito. Once the infection has passed, the individual enters the *recovered* state. Whether a recovered person gains a lifetime immunity is determined by the disease. Figure 1 shows the transition of an individual between the four states and their respective transition probabilities and average time spent in each state. The arrows in Figure 1 represents transition probabilities between connected states. *Chronic recovered* is the state when the person has recovered from the infection and is no longer contagious, but still has symptoms of the disease. It is given as an extension to the recovered state because a lot of mosquito-borne diseases are known to exhibit such behavior [34].

Infection in mosquitoes follows a similar cycle, except they do not recover once they have been infected. When a susceptible female mosquito bites an infected human, it gets infected with a non-zero probability. If the mosquito acquires the pathogen, it multiplies in the mosquito till it reaches enough strength to infect some other susceptible human, thereby completing a cycle. This period is called the extrinsic incubation period.

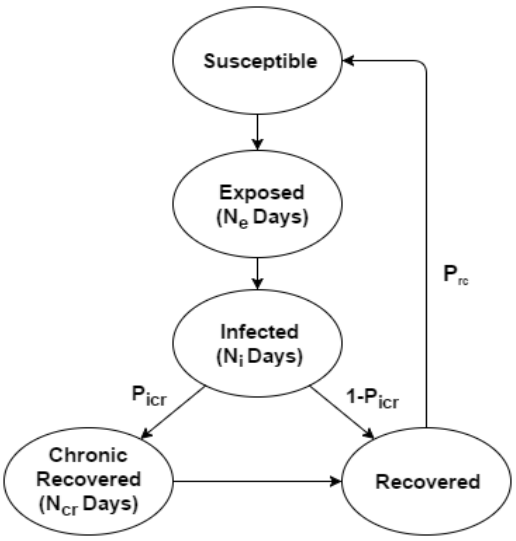


Figure 1: **Infection Model**: Infection progression states in humans

2.1.2 Mosquito Agents

The mosquito agents move through the geographical space and are characterized by the following parameters: flying speed (F_s), maximum distance (F_r), active period (A_s,A_e), maximum number of meals in a day (M_m), mortality rate (M_r), ovipositioning characteristics (P_m,O_c), sex ratio (P_f), and sensory range (S_r). Flying speed and maximum distance bound the spatial movements of a mosquito agent. Target locations are assigned to a mosquito within a circle of radius F_r at the start of the active period, and the mosquito moves from one location to another with speed F_s. The active period A_s to A_e are the hours between which the mosquito is actively searching for a blood meal or ovipositioning sites. Maximum number of meals M_m bounds the number of bites a mosquito is going to take in a day. Mortality rate M_r is the probability of a mosquito dying on a given day due to some natural circumstance. Ovipositioning characteristics include P_m: probability of an adult female to mate successfully; and O_c → [0,1]: whether the mosquito lays egg on a single ovipositioning site or spreads them over multiple such sites. Sex ratio (P_f) is the probability that the hatching egg will be female. The sex ratio is relevant as only female mosquitoes bite humans and lay eggs; males have no direct role in the spread of infectious diseases. Sensory range determines how far a mosquito is aware of its surroundings. If a human agent or a water source comes within a radius of S_r of mosquito agent, only then may a mosquito target it.

All these parameters were determined to be essential to disease propagation (as they directly affect the mosquito population and their behavior relative to the environment) and may vary across mosquito species. For example, female *Anopheles* mosquitoes are generally active during night, while *Aedes* mosquitoes are day-biting. Similarly, *Aedes albopictus* have more meals as compared to *Aedes Aegypti* because of their rapid bites, which generally keep their blood meals short [7, 29].

Figure 2 shows a flow chart of how all the above parameters are connected together. A mosquito agent is created in one of the water sources in the environment. There appears to have been no research with definitive results to mathematically model mosquito movements. Some evidence suggests that simple random walk simulations give remarkably good approximation of real data acquired through mark-release-recapture field trials [45]. Thus, this study models mosquito movements as random walks in a radius of F_r/day with a survival rate of (1-M_r)/day. If it is the active period of a mosquito, it starts moving randomly till a human agent comes within its sensory range. Then it follows a targeted approach and feeds on the human. This is the only stage when the infection propagates between existing agents. If a mosquito bites an infected human then it gets itself infected with a probability β, and when such an infected mosquito bites a susceptible human, it infects the human with probability α. If the mosquito has reached its M_m limit, it rests. Every day, with probability P_m, a mosquito's state is changed to carrying eggs. If the mosquito is carrying eggs, it continues to feed on human agents till its eggs are mature enough to be laid. A mosquito needs at least one meal after mating for the eggs to mature [7]. The maturation period τ is determined as a function of the temperature θ in °Celsius (equation (1)).

$$\tau = 3 + |\theta - 21|/5 \quad (1)$$

Three days is the time taken to mature eggs at the ideal temperature of 21°C [13, 10]. The maturation period was approximated to be decreasing linearly with respect to the difference of temperature from ideal temperature, and the slope was derived from the graph of *Ae. aegypti* (the primary vector in validation case study) at different tempera-

tures [10, 46, 20]. Once a mosquito mates successfully, the time required for the batch of eggs to mature is set to τ as calculated by that day's temperature.

Once the eggs have matured, the mosquito starts looking for ovipositioning sites (water sources) and lays 100 eggs at once or over time at different sites determined by O_c. For simplicity, all the three aquatic stages of mosquito life cycle (egg, larva and pupa) have been modeled as eggs, and will be referred as such throughout this article. The time taken by eggs to turn into an adult mosquito μ, is also a function of temperature θ, but eggs may die before hatching if their water source dries up and is not refilled [13]. The function (equation (2)) was approximated using the average life cycle of *Ae. aegypti* (aquatic phases) [7] and effects of temperature on them [35].

$$\begin{aligned}\mu &= \mu_{egg} + \mu_{larve} + \mu_{pupae} \\ &= (2 + |(\theta - 25)|/2) + (2) + (4 + |(\theta - 25)|/2|) \\ &= 8 + |(\theta - 25)|\end{aligned} \quad (2)$$

Once a batch of egg is laid, the time each egg will spend in aquatic state before evolving into adult mosquito is set to μ, calculated according to that day's temperature.

Due to lack of enough published empirical evidence, both the above equations ((1) and (2)) were derived with the assumption that there is no drastic change of temperature ($< \pm 5^oC$) between consecutive days. Eggs turn into adult female mosquitoes with a probability P_f; male mosquitoes are discarded by the model as they do not directly contribute to disease propagation.

2.1.3 Human Agents

The ABM tries to realistically represent the average daily behavior of an individual in an urban landscape. Considering that mosquitoes move in a relatively short range, the long-distance spatial movement of infection through the city happens mostly as a result of displacement of human agents. Thus, human agents were divided into four general categories based on their mobility patterns, based on where they gather in groups and how often they go near potential mosquito breeding grounds like lakes (as shown in Figure 3):

- Type 1: These human agents leave their assigned buildings at 7:00 a.m. for school and may take up to 30 minutes to reach the school. They stay there till 3:00 p.m. and come back to their respective dwellings. From there, with probability P_{p1} an agent goes to a park at 4:00 p.m. and comes back at 7:00 p.m., after which it stays in place till next morning. Overall commuting takes at most 2 hours.
- Type 2: Similar to Type 1, but the initial destination is office and the probability of going to a park is P_{p2}, which is less than P_{p1}.
- Type 3: These are agents that are continuously on the move. They leave their assigned buildings at 7:00 a.m. and move in between buildings every two hours. They come back to their dwellings at 7:00 p.m. and stay there till next morning.
- Type 4: These are stationary agents who do not involve themselves in any dynamic activity; they stay in their specific buildings throughout the day.

During initialization of the model, each agent is assigned a category and a building. The number of agents in each

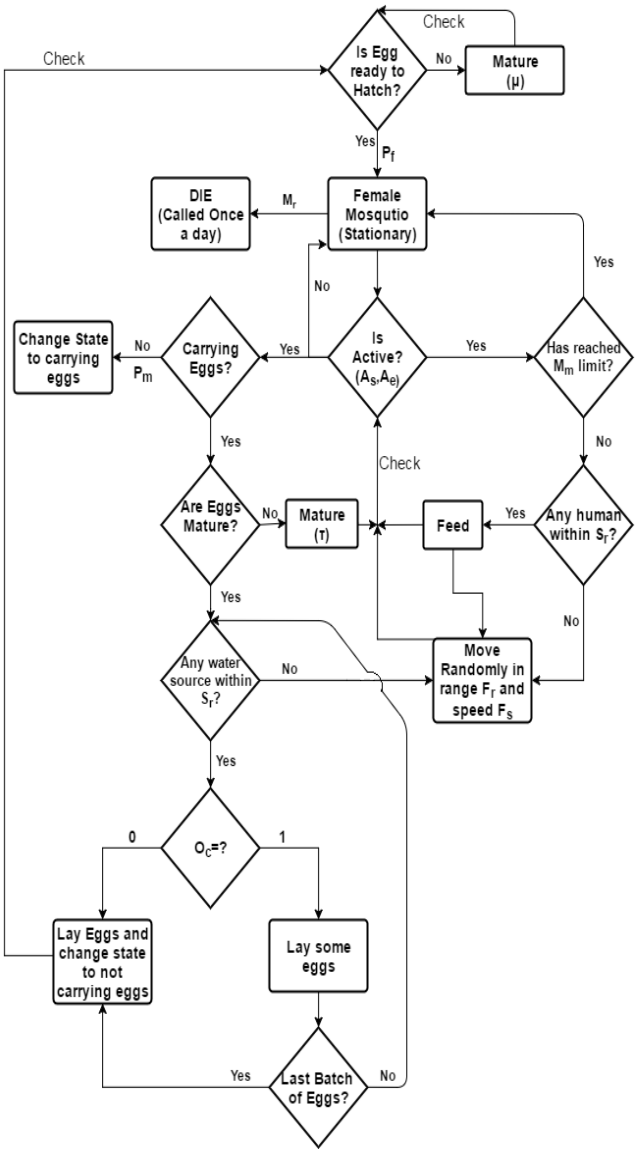


Figure 2: **Mosquito Agents**: Movement, feeding and reproduction behaviors of a mosquito

category is determined from the age distribution in the census data. The agents commute using the road network using the shortest path to their target location. Each agent has an attribute called state which depicts which stage (SEIR) it is in. Once a susceptible agent is bitten by an infected mosquito, it enters the exposed state with probability β. An exposed agent carries on its daily activity and is mainly responsible for the spatial movement of infection through the city. Once the agent has entered the infectious state, it stays in its home till it has recovered. It may stay in recovered (immune) state or move to susceptible state depending on the disease.

2.1.4 Environment

In this model, an infected mosquito is considered to lay infected eggs, as has been observed in the case of dengue and chikungunya [8]. Such infected eggs develop into infected adult mosquitoes. Figure 4 gives a flow diagram to describe the infection propagation among vector and human

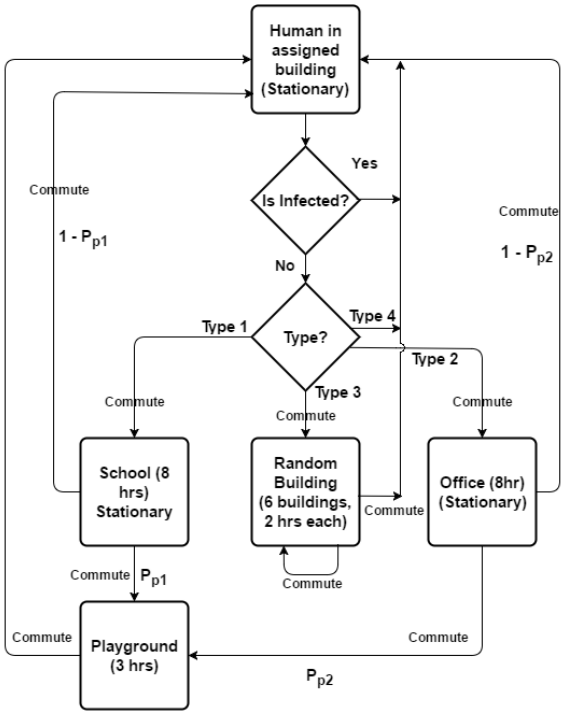
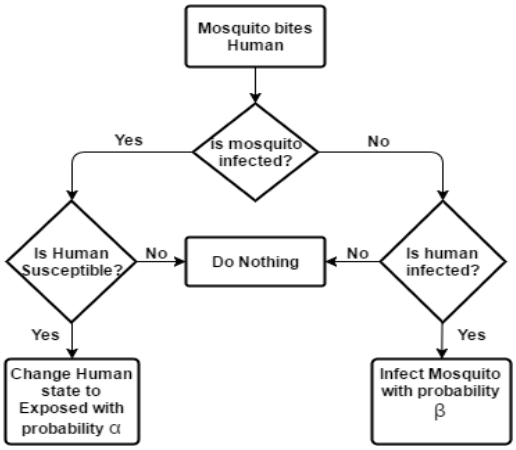
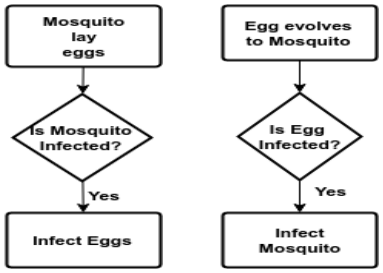


Figure 3: **Human Agents**: Daily activities of human agents

agents. An infection is transferred to a human from an infected mosquito with probability α, and infected human to mosquito with probability β.



(a) Mosquito Feeding



(b) Mosquito Ovipositioning (c) Egg Hatching

Figure 4: **Disease Transmission Cycle**: Possible scenarios of disease transmission

The model uses two-layered geo-referenced GIS data of a city to realistically represent spatial movements of an individual in an urban setting. The first layer consists of buildings which include homes, offices and schools, parks and stationary water sources like lakes which are an integral part of a vector's life cycle. The second layer depicts the road network connecting these buildings, and all human agents move on this network. To simplify the model, the distribution of human agents in first layer is initialized randomly. A small subset of buildings are assigned as schools and offices, and one park with lake/pond is introduced. The model combines these GIS data with the weather information of the location which is integral in the study of vector agents. It consists of daily temperature and precipitation data. Using these parameters, the development cycles of mosquitoes and pathogens are determined. Small water patches, which may serve as mosquito breeding grounds, are introduced after every rainfall and their number depends on the extent of rainfall. (Small puddles cease to exist in less than a week if it does not rain in between, while large water bodies can persist for months or more.)

For the purpose of this study, GIS data of Luneray, a commune in Haute-Normandie region in northern France, was used to model a general urban setting, and was initialized with human population of 1000, mosquito population of 2000, and 500 mosquito eggs. This relatively low ratio of mosquito/human was necessary to keep the model computationally tractable, but was accounted for by tuning the mosquito mortality rate. It was then adapted and scaled to the case studies using the corresponding location's census data, population density, and climate information. A park with a lake was separately added as it was not a part of the available GIS data. For the purpose of subjective analysis of the model, an animated visualization of the simulation was generated using GAMA platform.

2.2 Simulation

As a proof of concept, an application of the model was used for simulation of a case study of a past epidemic of a mosquito-borne disease. The model was used to predict the trajectory of the epidemic and the results were checked against real data. Two intervention strategies were also tested and analyzed. For the purpose of the demonstration, some model parameters needed to be tuned to fit that particular scenario. We used a training data set containing the data from a previous epidemic of the same disease in a similar location to the testing site. Once all parameters are determined which provided reasonably accurate results on training data, the simulation is ran for the testing site.

2.2.1 Case Study

For this study, simulation of outbreak of chikungunya in the Caribbean region is used to illustrate the given framework. For training the model, data from the 2013-14 chikungunya epidemic in Saint Martin was used. Saint Martin, with a population of fewer than 75,000, was the epicenter of the Caribbean epidemic. In December 2013, two laboratory-confirmed non-imported cases were reported for the first time in the Caribbean in the district of Ocean Pond, close to the border of the Dutch side Sint Maarten. The model trained on this data was tested on epidemic data from another Caribbean island, St. Barthélemy. As with the rest of the Caribbean, residents of St Barthélemy had never en-

countered the virus before, and had no existing immunity. The female *Ae. aegypti* mosquito was taken as the vector in the simulation, as it was the primary vector of the 2014 CHIKV outbreak in the Caribbean [36].

2.2.2 Data

Chikungunya epidemic data were taken via the sentinel network in Guadeloupe, Martinique, Saint Barthélemy and Saint Martin [47]. It was compiled together and made publicly available on a weekly basis by PAHO WHO [39]. Most epidemics only last for a few months. Also, only 3 months of data on confirmed cases was made publicly available by PAHO WHO. Therefore, we simulated a duration of 3 months starting from January, 2013 for validation purpose. Weather information was taken from [38] and interpolated to get daily temperature and rainfall data. Lunerays's GIS data were made openly available by GAMA [2]. Census information was taken from [6].

2.2.3 Simulation Toolkit

For the simulation of the ABM, GAMA was chosen as the platform due to its data-driven ability and intuitive agent-based language [42, 23].

3. MODEL VALIDATION AND RESULTS

3.1 Parameterization and Initialization

Summarizing the above model, the following are parameters that drive the model: Mosquito Parameters (F_s, F_r, A_s, A_e, M_m, M_r, P_m, O_c, P_f, S_r), Human Parameters (P_{p1},P_{p2}), Infection Cycle Parameters (N_e, N_i, P_{rc}, P_{irc}) and Infection Transmission Cycle Parameters (α, β). Of these parameters, S_r, M_m, P_f, P_m, α and β were tuned during the training of the model due to the lack of any concrete empirical evidence of their values, while the value of others were compiled together from various sources. Some detailed description of the parameters and their sources is provided as Table 1. The number of schools, offices and households were initialized using census data [6]. Buildings with the largest areas in the GIS data were assigned to be schools and offices randomly.

3.2 Training

Model parameters were tuned using trial and error to give a good fit on training data. The results were animated as a simulation and were graphically represented. Error was derived with respect to the historical/training data. Sensitivity analysis was conducted to determine the effect of each parameter on the model's output and the more sensitive parameters were made sufficiently accurate to reduce the error [25].

A slight error margin was left while training because training data only consists of reported cases, while due to its non fatal nature, some number of chikungunya infections go unreported [1, 3].

The entire population of even a small city cannot be taken into consideration due to computational in-feasibility. The model simulation was accomplished considering 1000 human individuals and 2000 mosquitoes involved in a chikungunya epidemic and interacting at a city scale, in case of training location.

Considering that the population density of the testing location is only about half that of the training location, and the area is likewise smaller, the model was initialized with 500 human individuals and 500 mosquitoes during testing. This relatively low ratio of mosquito/human was accounted for by significantly reducing the mosquito mortality rate to 0.05/day (in comparison to the typically accepted rate of 0.2/day).

Uni-variate sensitivity analysis was conducted, i.e., model outcomes were analyzed with respect to one parameter at a time. The first parameter was a mosquito's sensory range S_r, which was tested for six different values and error in fitting was recorded for each value as shown in Figure 5.

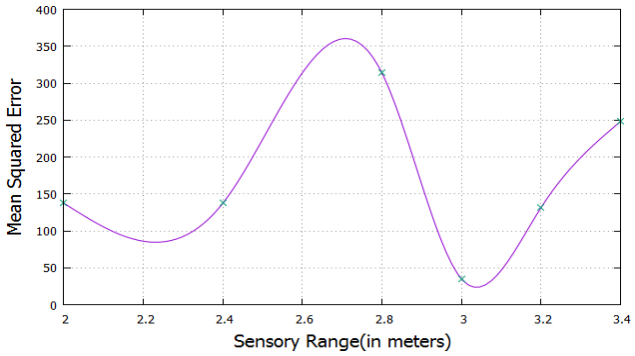


Figure 5: **MSE**: Mean-Squared Error recorded for different S_r values ($M_m = 2$)

The error metric used was mean-squared error Equation 3 (where, n is the total number of epidemiological weeks, i is the current week in simulation, $\bar{Y}_i$ is the number of newly reported cases in real life and Y_i is the number of new cases in simulation).

$$MSE = \frac{1}{n}\sum_{i=1}^{n}(\bar{Y}_i - Y_i)^2 \quad (3)$$

S_r parameter was found to be significantly sensitive, and gave best results when tuned to 3 meters. The second parameter for sensitivity analysis was M_m, a mosquito's maximum number of meals in a day. It was varied for three different values and errors were recorded (Figure 6). M_m was then fixed to 1 to minimize the error. P_m, P_f and M_r were likewise fixed to 0.2, 0.5 and 0.05 respectively as they on average gave approximately constant mosquito population.

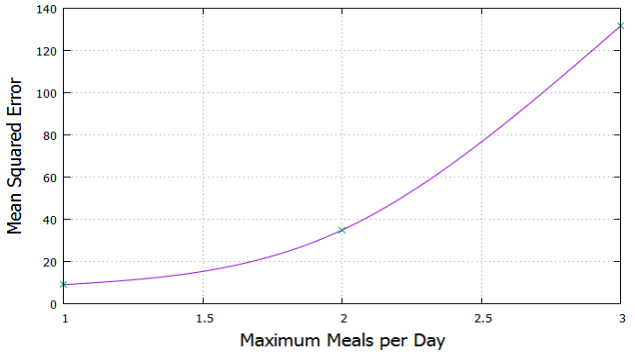


Figure 6: M_m: Mean-Squared Error recorded for different M_m values

Figure 7 shows how the ABM was fit into the historical data. An error of ±9 cases was left to account for unreported cases.

Table 1: ABM Parameters

Parameter	Description	Value	Reference
Mosquito Parameters:			
F_s	Flying speed	0.0...1.0 km/hr	[5]
F_r	Maximum distance	350m	[45]
A_s,A_e	Active period	7:00 a.m., 6:00 p.m.	[8]
M_m	Maximum number of meals in a day	1	Trained
M_r	Mortality rate	0.05/day*	[45]
P_m	Probability of an adult female to mate successfully	0.2	Trained
O_c	Ovipositioning behavior (single (0) or spread over multiple sites (1))	1	[8]
P_f	Probability that the hatching egg will be female	0.5	Trained
S_r	Sensory range	3 m	Trained
Infection Transmission Cycle Parameters:			
α	Transmission probability of infection from mosquito to human	0.6	[17]
β	Transmission probability of infection from human to mosquito	0.275	[17]
Infection Cycle Parameters:			
nb_infected_init	Initial number of infected people	2	[47]
N_e	Number of days a human spends in exposed state	2...6 days	[9]
N_i	Number of days a human spend in infected state	4...7 days	[9]
P_{rc}	Probability of transiting from recovered state to susceptible state	0	[48]
P_{irc}	Probability that passing infection leaves human in chronic state	0.95	[9]
Human Parameters:			
P_{p1}	Probability of a Type 1 agent of going to park at 4:00 p.m.	0.5	Trained
P_{p2}	Probability of a Type 2 agent of going to park at 4:00 p.m.	0.1	Trained

* [45] proposes 0.2/day mortality rate which was reduced considering the relatively low mosquito/human ratio in the model.

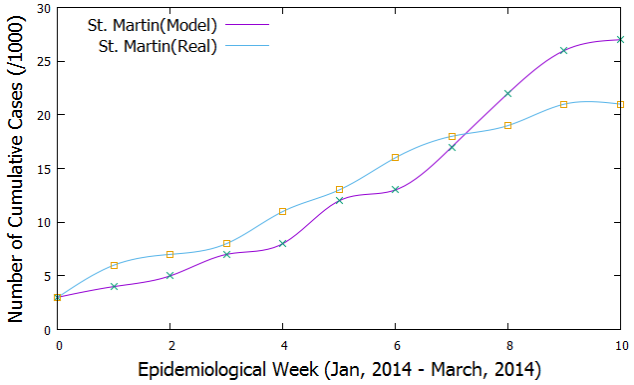


Figure 7: **St. Martin Epidemic (Training)**: Results from training the model on the St. Martin epidemic

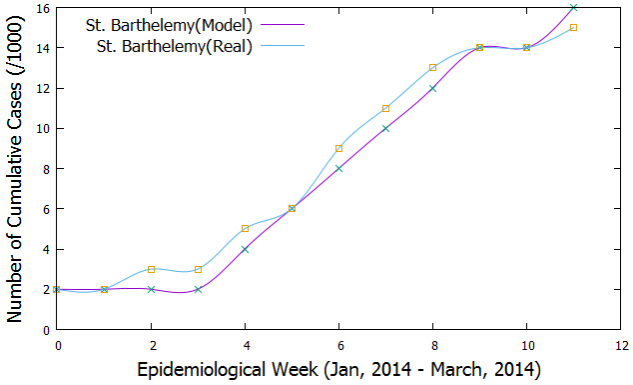


Figure 8: **St. Barthélemy epidemic (Testing)**: Results from testing the model on the St. Barthélemy epidemic

3.3 Testing

Figure 8 shows the results when the trained model was ran to check the effects of a chikungunya epidemic in Saint Barthélemy and results were compared with the actual 2014 chikungunya epidemic of the same. The error encountered was ± 0.54 cases, nearly insignificant, indicating that our model scales well to changing population size. The initial results are a little less than the reported results which may very well be from the fact that by the time the first case was recorded, the infection had already spread through the environment in the real world, while the model is initialized as infection-free. It also suggest estimates on certain *Ae. aegypti* parameters like sensory range (3 meters) and average feeding frequency (1 meal/day).

The results obtained show that ABMs can provide very accurate results when used to model the complex epidemiology of mosquito-borne diseases. They also provide estimates on certain mosquito parameters like sensory range, feeding frequency, etc. which are difficult to measure otherwise.

4. PREVENTION STRATEGIES

As the model performed well in the validation phase, we assumed that it is a reasonably effective representation of the real epidemic and used it for analyses of different prevention strategies on the test location.

4.1 Strategies

No vaccine exists to prevent chikungunya virus infection. It can only be prevented by avoiding mosquito bites either at the individual level or by reducing the mosquito population [12]. Keeping this in mind, two popular paradigms of mosquito prevention were implemented, analyzed and compared using the above model:

1. Centralized Prevention Strategies: In this case, there is a centralized organization dedicated to reducing the mosquito population through methods like detection and elimination of breeding places, proper covering of persistent water sources, and reliable water supply [37]. We choose LSM (Larval Source Management), which is economical and very popular, as a strategy. Its per sq km associated annual cost when adjusted for 2016 prices [11], comes to US$6000 [26].
2. Decentralized Prevention Strategies: Here people adopt prophylactic measures like use of mosquito repellent creams, liquids, coils, mats, etc., or full body coverings

to prevent mosquito bites. One person can be protected for an year at a cost of US$10 with insecticide-treated nets (ITNs); indoor residual spraying (IRS) costs US$180/building [22, 24].

All costs mentioned above are as quoted by private agencies. They may be brought down significantly by conducting large-scale mosquito- control programs, and with relevant government subsidies.

For comparison of the two strategies, the two iterations were initialized with same resources, i.e., the same initial budget of US$ 20,000. Considering it would cost approximately US$ 30,000/year to cover a town of 5 sq km completely for a larvicide program, we assume that only 66% of the larval habitats are found and treated. This is consistent with the fact that larval habitats may be small and widely dispersed, making it difficult to locate all of them [14]. For the second strategy (ITN+IRS), resources worth 20,000 US$ were distributed randomly among the population (220 US$ per household) helping individuals in the population avoid mosquito bites in their households.

4.2 Outcomes

Strategy 1 (LSM) was found to be more effective at completely eliminating the infection from both the human and mosquito populations within 5 weeks. Strategy 2 took 7 weeks to do the same. Not trying to contain the infection kept it going even after 13 weeks (Figure 9). This difference in effectiveness may be from the fact that Strategy 2 is mostly useful during the night time when most individuals are back to their households, while *A. Aegypti* is a day-biting mosquito.

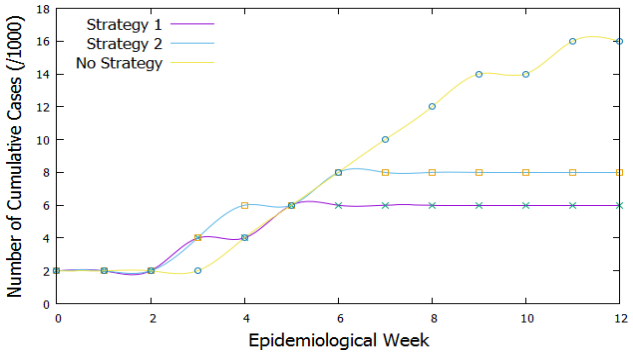


Figure 9: **Prevention Strategies**: Results from testing the two strategies

Strategy 1 also had a much greater effect on mosquito population, reducing it by 70% while Strategy 2 only reduced it by 25% (Figure 10 and Figure 11). The results of both the strategies were found to be consistent with past studies [31, 40].

From the fact that in most cases a mosquito's life cycle is not greatly dependent on the presence or absence of the infection due to their short lifespan [19], it can be reasoned that the above results will hold true for other diseases spread by *A. Aegypti*, like the presently prominent Zika virus.

5. CONCLUSION AND DISCUSSION

Diseases like chikungunya and dengue which currently have no vaccine, need proactive measures to prevent or contain their breakout. Our ABM provides a good mechanism for

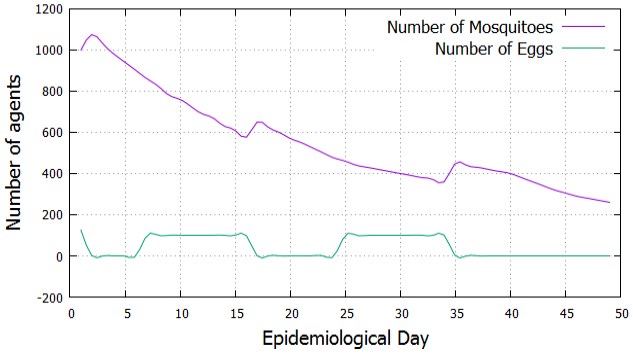


Figure 10: **Mosquito Population (Strategy 1)**: Number of Mosquitoes and Eggs per Day

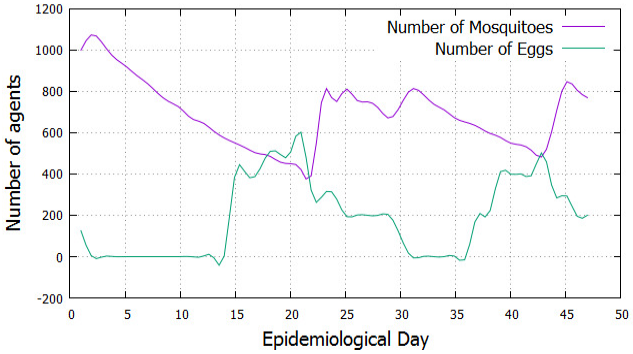


Figure 11: **Mosquito Population (Strategy 2)**: Number of Mosquitoes and Eggs per Day

quantitative analyses of mosquito-borne epidemics. This and other such models carry high practical value as they can be used to quickly try out different combinations of strategies, study the effects of infection on different population groups, find high risk groups, plan vaccination programs, and categorize locations with respect to their seasonal risk factor. They can also be used to arrive at estimates of vector parameters (such as the mosquito's sensing range) that are not easy to measure directly. The case study demonstrated how the model was accurately able to trace the evolution of the infection, given data from a past epidemic in a similar location is provided. It also predicted that on a low budget, centralized strategies like larval source management are more effective compared to individual measures like insecticide-treated bed nets and indoor residual spraying. Though the above model has been tested on tropical climate of Caribbean Islands, it can be easily extended to other locations provided relevant training data are available.

The model can also be extended to consider mutations of infection [18], actual human mobility patterns, multiple mosquito species, and other factors like wind velocity.

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