

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

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This manuscript was compiled on May 16, 2016

Mosquito-borne diseases, such as chikungunya, dengue and malaria are reemerging and expanding to new and formerly unaffected places leading to a need for models which can track their evolution. This evolution is driven by the interactions between hosts and vectors and thus, is heavily dependent on factors like population distribution, human mobility and weather conditions. Capturing these interactions is very complex because of their chaotic nature. We propose a generalized ABM which captures these interactions at a micro-scale by explicitly modeling each human and mosquito to predict the complex trajectory of the infection. The model has been integrated with GIS, census and climate data to effectively model the host and agent behavior and as a proof of concept, is also trained and validated using 2013-14 Caribbean Chikungunya epidemic data. Two popular infection intervention strategies: LSM (Larval Source Management) and ITN + IRS (Insecticide-Treated Nets + Indoor Residual Spraying), were also implemented and analyzed in terms of cost-effectiveness and mosquito control.

ABM | Chikungunya | GIS | Epidemiology

Vector-borne diseases account for more than 17% of all infectious diseases and causes more than 1 million deaths every year [1]. Adding to their high fatality rates, they also have high attack rates and are very prone to mutation leading to recurrent infections. Modeling the complicated relationship between human-mosquito-infection continues to be a challenge faced by all epidemiologists. Though there are quite a few mathematical models proposed for it, they lack the spatial and temporal movement of infection which is inherent to a disease propagation [2]. This study tries to solve this problem of capturing the process of emergence and spread of a large subset of vector-borne diseases viz.: Mosquito-borne diseases, through the use of agent-based modeling (ABM) paradigm.

Agent based modeling is a class of computational models [3] which is used to simulate the behavior and interactions of individual agents in order to improve the understanding of the system as a whole and to evaluate strategies for its operations in a predictive or an explanatory sense [4]. The agents in an ABM, typically in natural systems, follow simple rules and their collective behavior gives rise to complex phenomena which are extremely difficult to be modeled otherwise. ABMs have been applied in numerous fields such as business analysis [5], ecology, biology, computer networking, cloud computing [6] and social sciences [7].

Even with these vast applications of agent-based models, there has been relatively little research done in modeling of vector-borne diseases as ABMs. Though a few such models exist, they either operate at very low agent granularity [8–11], are initialized with random topology [10, 12], lack human mobility network [13–15], or are inconsiderate of changing climate [12, 13]. All these properties are inherent to a disease epidemiology, especially vector-borne diseases where weather

conditions play a significant role in distribution and behaviour of vectors, and in consideration of the same undermines the prediction accuracy of the models. Furthermore, most of these models are not validated which limits their practical value.

We propose an ABM which can be used to predict the trajectory of an infection as well as to test different disease prevention strategies to contain it. The model's environment has been explicitly integrated with GIS, census and climate data to eliminate the above shortcomings.

GIS data added a structure to the topology by introducing buildings and a road network, and helped to model human mobility patterns which are the main source of spatial movement of infection through the city. Census data further augmented the population dynamics by providing realistic initialization of the model. Climate data allowed us to define a detailed behaviour of mosquitoes and their dependencies on the climate, which were compiled together from various sources.

For validation of the model, a proof of concept case study was provided. The model was trained using the 2013-14 chikungunya epidemic in Saint Martin and was tested on epidemic data from another Caribbean island St. Barthélemy. The model predictions were 93.3% accurate on test data of the reported cases and thus showed that there were some cases which went unreported which matches with reality where a lot of chikungunya cases goes unreported due to the non-fatal nature of the disease. Furthermore, two prevention strategies: LSM and ITN+IRS were tested and the results showed that for a small town, LSM is more effective in terms of cost, mosquito control and infection elimination. Though tested on chikungunya, the model is generalizable to other mosquito-borne diseases.

This shows that it is possible to achieve a good accuracy in epidemic predictions using ABMs without sacrificing usability. They also provide means to create a proactive approach to public health and disease control.

Significance Statement

With Mosquito-borne diseases reemerging and expanding to new and formerly unaffected places, the need for modeling of complex human-mosquito-disease trinity has become vital. This study proposes an agent-based model which tackles this problem by studying these interactions at micro-scale and shows that a high prediction accuracy can be achieved using ABMs. It also provides a platform to test different intervention strategies in hopes of promoting proactive approach to public health and disease control.

Materials and Methods

Vector-borne diseases are infections transmitted by the bite of an infected arthropod species (mostly mosquitoes) to an human individual. Arthropod vectors that make part of this transmission cycle are cold-blooded making them very sensitive to climate changes. Weather conditions carries a significant influence over the life-cycle of these vectors (and accompanying pathogens) ranging from survival rates, reproduction rates, spatial distribution/abundance, rate of development of pathogens and temporal pattern of vector activity [16]. Human individuals daily carry out a sequence of activities which maybe static or dynamic. Static activities are done at locations like home, school, workplace or parks. These locations are more likely to have individuals gathering in groups. Dynamic activities involves spatial and temporal movement in between two stationary activities. The modeling of the effects of climate on vector behavior and this population dynamics is inherent to such a disease's epidemiology. This study develops a complex model tries to capture this human mobility information through integration of GIS data of road networks and buildings on a 10-minute basis to simulate the daily activities of different categories of human population. It also uses climate data to determine the spatial distribution of vector population and the pathogenesis of the disease.

The model is composed of three parts: The first is a small modification of popular SEIR model 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. Scale considered is at city level and agent granularity is individual human and individual mosquito.

Agent-Based Model. The model proposed here is an agent-based model which tries to represent the behavior of individual human and mosquito in an urban environment while following the biological trajectory of the spreading infection. The following sections describes the mosquito agent, human agent, model environment and the infection model used to stratify the population.

Infection Model. Mosquito borne diseases are transmitted from human-to-mosquito and mosquito-to-human. Symptoms vary but are generally classifiable into two stages: Intrinsic Incubation period and infectious state. Incubation stage is when a mosquito has successfully infected a human and the pathogen has started multiplying inside the host. Depending on the disease, a person may or may not be contagious during this stage. Infectious state is when the pathogen has multiplied and reached a certain threshold and the human has started to show symptoms. Probability of pathogen transmission is very high during this period. Considering a lot of vector-borne diseases are known to have significant incubation period (malaria, dengue, chikungunya, etc.), the SEIR model (Susceptible → Exposed → Infectious → Recovered) was chosen as its exposed state addresses the incubation period. Susceptible state is when an individual is vulnerable to the infection of the pathogen. An individual is said to be exposed when he is carrying infection but is not yet contagious. 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 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. 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 was added as an extension of Recovered state because a lot of Mosquito-borne diseases are known to have such behaviour.

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 number to infect some susceptible human thereby completing a cycle. This period is called the extrinsic incubation period. This model only considers female mosquitoes as male mosquitoes do not require blood meal exempting them from the disease cycle.

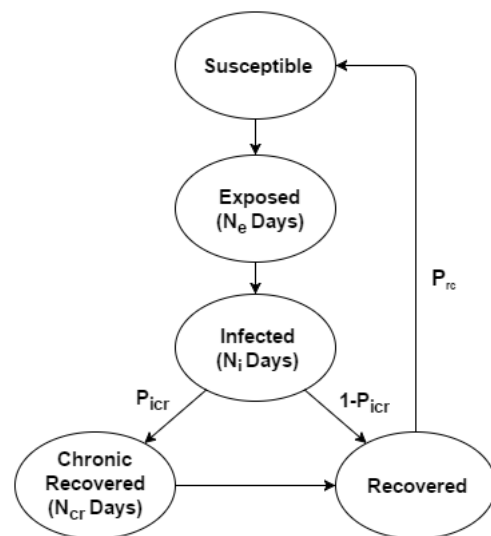


Fig. 1. Infection Model Infection progression states in humans. The arrows represents movement of individuals from one stage to next with given probability.

Environment. The model uses two-layered Geo-referenced GIS data of a city to realistically represent spatial movement of an individual in an urban setting. First layer is buildings which includes homes, offices, schools, parks and stationary water sources like lakes which are an integral part of a vector's life cycle. Second layer depicts the road network connecting these buildings and all human agents move on this network. To simplify the model, 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 this 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, development cycle of mosquitoes and infection is determined. Small water patches which may serve as mosquito breeding grounds are introduced after every rainfall and their number depends on the severity of rain. They expire in less than a week if it doesn't rain in between.

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 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.

Mosquito Agents. The mosquito population represented as agents, move through the geographical space and is 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 determines the spatial movement of the 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 .

Active period A_s to A_e are the hours between which the mosquito is actively searching for 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 everyday due to some natural circumstances.

Ovipositioning characteristics include P_m : probability of an adult female to mate successfully and $O_c \rightarrow [0,1]$: whether the

mosquito lays egg on a single ovipositioning site or spread them over multiple such sites.

Sex ratio (P_f) is the probability that the hatching egg will be female.

Sensory range determines how far is mosquito aware of its surroundings. If a human agent or a water source comes within a radius of S_r of mosquito agent, only then mosquito may target it.

All these parameters were determined to be essential to disease propagation (as they directly affect the mosquito population and their behaviour relative to the environment) and may vary from species to species. For example, female *Anopheles* mosquito are generally active during night while *Aedes* mosquitoes are day-biting. Or how *Aedes albopictus* has higher max meals as compared to *Aedes Aegypti* because of their rapid bites which generally breaks their blood meal short [17, 18].

Figure 2 shows the flowchart of how all the above parameters were connected together. A mosquito agent is created in one of the water sources in the environment. There has been no research with concrete results which mathematically models mosquito's movement. Though some evidence is there which shows simple random walk simulations give remarkably well approximation of real data acquired through Mark-release-recapture field trials [19]. Thus, this study models mosquito movement 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. This is the only stage when the infection propagates between existing agents. If a mosquito bites an infected human it gets infected with a probability P_{thm} and when an infected mosquito bites a susceptible human, it infects the human with probability P_{tmh} . If the mosquito has reached its M_m limit, it rests. Everyday with probability P_m , a mosquito state is changed to carrying eggs. If the mosquito is carrying eggs, it continues to feed on human agents till the eggs are mature enough to be laid. A mosquito needs at least one meal after mating to mature the eggs [17]. The maturation period τ is determined as a function of the temperature θ in °Celsius (equation 1).

$$\tau = 3 + |\theta - 21|/5 \quad [1]$$

3 days is the time taken to mature eggs in ideal condition of 21°C [20, 21]. 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* (primary vector in validation case study) longevity at different temperatures [21–23]. 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, larvae and pupae) have been modeled as eggs and will be referred as such throughout the document. Time taken by eggs to turn into an adult mosquito μ , is also a function of temperature θ though they may die before hatching if their water source dries up and is not refilled in less than 6 months [20]. The function (equation 2) was approximated using the average life cycle of *Ae. aegypti* (aquatic phases) [17] and effects of temperature on them as derived from [24].

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

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

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

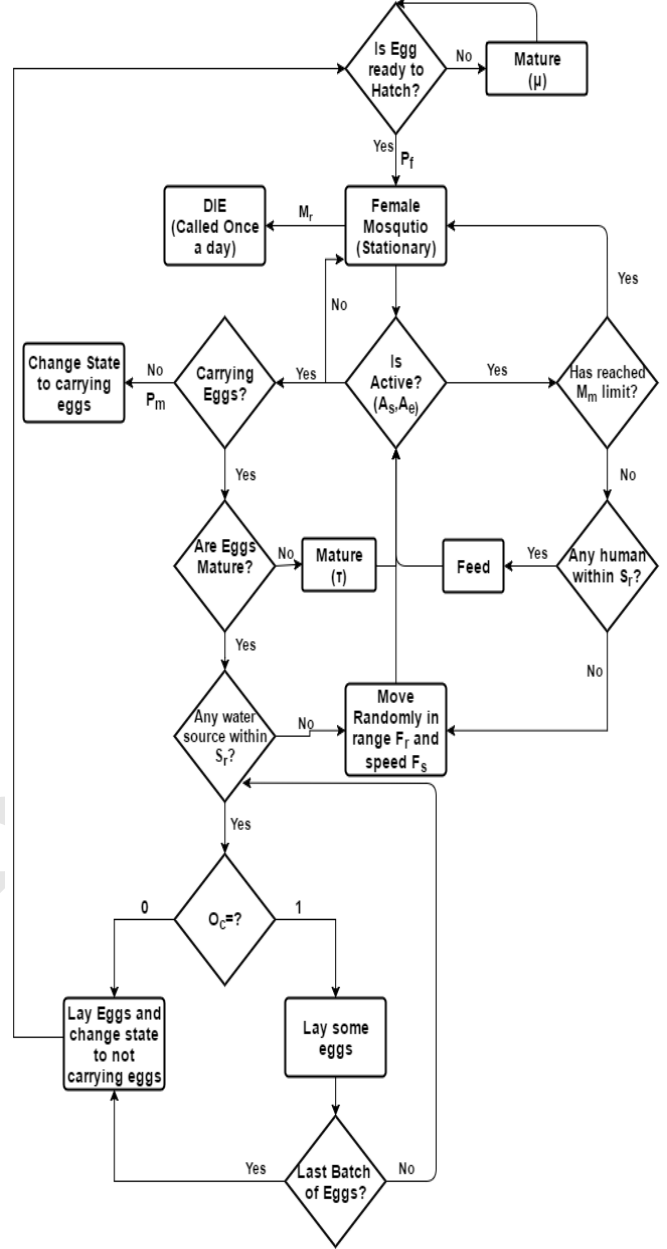


Fig. 2. Mosquito Agents. Movement, feeding and reproduction behavior of a mosquito.

Human Agents. The proposed ABM tries to realistically represent the average daily behavior of an individual in an urban landscape. Considering that the 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 pattern based on where they gather in groups and how often do they go near potential mosquito breeding ground like a lake (as shown in Figure 3):

- Type 1: These human agents leave their house 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 homes. From there with probability P_{p1} the agent goes to park at 4:00 p.m. and comes back at 7:00 p.m. from where it stays at home till next morning. Overall commuting takes at most 2 hours.
- Type 2: Similar to Type 1, but the initial destination is office and their probability of going to park P_{p2} is less than P_{p1} .
- Type 3: These are the agents who are continuously on the move. They leave their house at 7:00 a.m. and move in between houses every two hours. They come back to their homes at 7:00 p.m. and stay there till next morning.
- Type 4: These are stationary agents who do not involve themselves into any dynamic activity and stay in their homes through-out the day.

During initialisation of the model, each agent is assigned a category and a house. Number of agents in each 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) is the agent in. Once a susceptible agent is bitten by an infected mosquito, it enters into exposed state with probability P_{tmh} . 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 into 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.

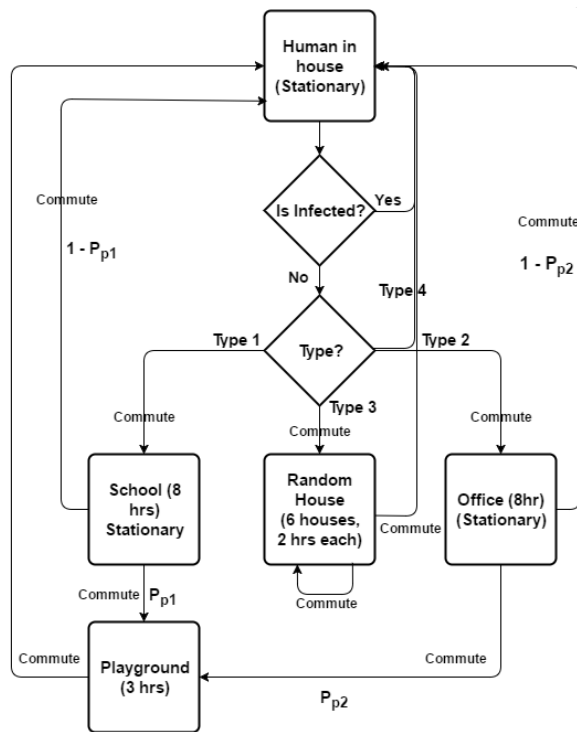


Fig. 3. Human Agents. Daily activities of an human agent.

Interactions. A vector-borne infection only spreads through the interaction between vector and human agents. This happens when a mosquito is feeding on a human. In this model, an infected mosquito was made to lay infected eggs as has been observed in the case of dengue and chikungunya [25], which develop into infected adult mosquitoes. The flow diagram below (Figure 4) describes the infection propagation among vector and human agents. Infection is transferred to a human from an infected mosquito with a probability P_{tmh} and infected human to mosquito with probability P_{thm} .

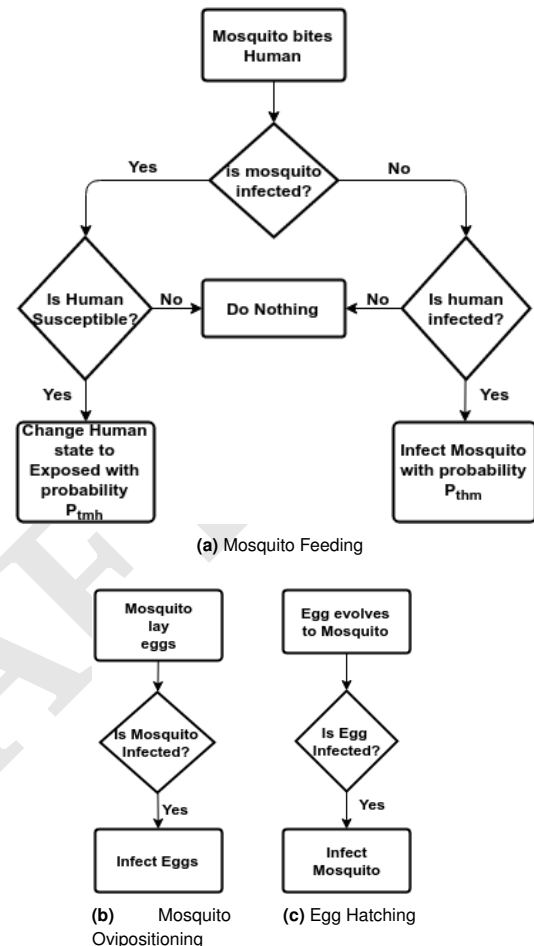


Fig. 4. Disease Transmission Cycle. Infection transmission happens only in the above three cases.

Model Implementation. As a proof of concept, an application of the model was demonstrated on 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 with the real data. Two intervention strategies were also tested and analysed. For the purpose of the demonstration, some model parameters needed to be tuned to fit that particular scenario. To make this feasible, it was decided to use a training data set which is 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.

Case Study. For this study, simulation of outbreak of chikungunya in Caribbean region is used to illustrate the proposed framework. For training the model, data from 2013-14 chikungunya epidemic in Saint Martin was used. Saint Martin, with a population of fewer than 75,000, was the epicenter of Caribbean epidemic. In December 2013, 2 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. Model trained from this data is tested on epidemic data from another Caribbean island St. Barthélemy. As with the rest of the Caribbean, residents of St Barthélemy had never encountered the virus before and had no existing immunity. Female *Aedes aegypti* mosquito was taken as the vector as it is the primary vector of the 2014 CHIKV outbreak in the Caribbean [26].

Data. Chikungunya epidemic data was taken by the sentinel network in Guadeloupe, Martinique, Saint Barthélemy and Saint Martin [27]. It was compiled together and made publicly available on a weekly basis by PAHO WHO [28]. Weather information was taken from [29] and interpolated to get daily temperature and rainfall data. Lunerays's GIS data was made openly available by GAMA [30]. Census information was taken from [31].

Simulation Toolkit. For the implementation of the ABM, GAMA was chosen as the platform due to its data-driven ability and intuitive agent-based language. [32, 33]

Results and Validation

Model Parametrization and Initialization. Summarizing the above model, following are the parameters that drives 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 (P_{tmh}, P_{thm}). Out of these parameters, $S_r, M_m, P_f, P_m, P_{tmh}$ and P_{thm} were tuned during the training of the model due to the lack of any concrete evidence of their values, while the value of others were compiled together from various sources. Detailed description of the parameters and their sources is provided as a table in the Supporting Information.

Training the Model. 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 [34].

A slight error margin was left while training because training data only consists of reported cases while due to its non fatal nature, a large number of Chikungunya infections go unreported [35, 36].

The entire population of the city cannot be taken into consideration due to computational reasons. The model implementation is accomplished by using 1000 human individuals and 2000 mosquitoes involved in a chikungunya epidemic and interacting at a city scale, in case of training location. Considering the population density of testing location is half of training location's and quarter the area, 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 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 Mosquito's sensory range S_r which was tested for six different values and error in fitting was recorded for each value. The error metric used was mean-squared error. S_r parameter was found to be significantly sensitive and was tuned to 3 m. The second parameter for

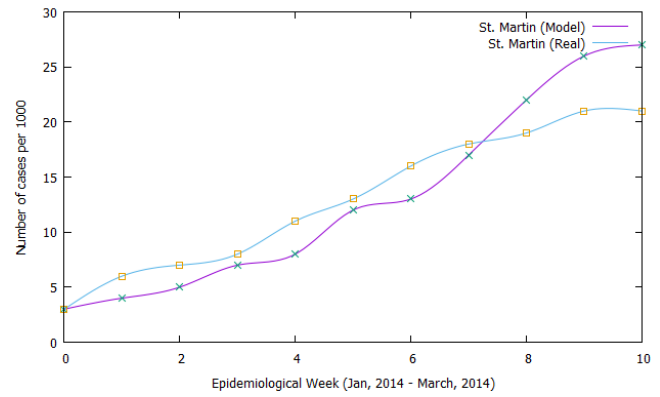


Fig. 5. St. Martin epidemic (Train). Results from training the model using St. Martin epidemic (Number of cases/week)

sensitivity analysis was M_m , mosquito's maximum number of meals in a day. It was varied for three different values and errors were recorded. M_m was then fixed to 1 to minimize the error. P_m, P_f and M_r were fixed to 0.2, 0.5 and 0.05 respectively as they on average gave approximately constant mosquito population. More detailed description of the techniques used and the results obtained is provided as a part of Supporting Information.

Figure 5 shows how the ABM was fit into the historical data. An error of ± 9 cases was left to account for unreported cases.

Testing. Figure 6 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 2014 chikungunya epidemic of the same. The error encountered was ± 0.54 cases. The initial results are a little less than the reported results which may very well be from the fact that by the time first case was recorded, the infection had already spread through the environment in physical world while the model is initialized as infection free (infection contained in the infected individuals).

The obtained results show that ABMs can provide very accurate results when used to model the complex epidemiology of mosquito-borne diseases.

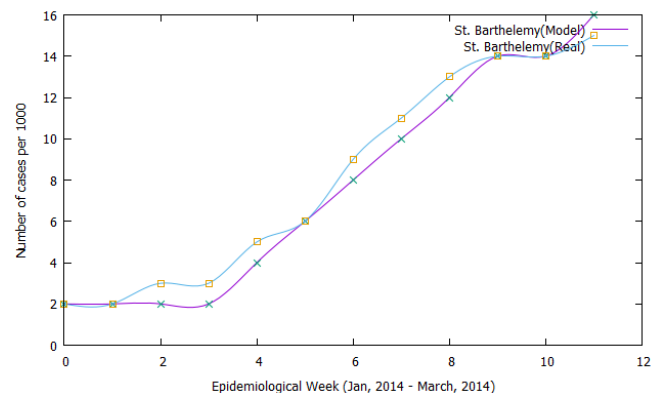


Fig. 6. St. Barthélemy epidemic (Test). Results from testing the model using St. Barthélemy epidemic (Number of cases/week)

Prevention Strategies

As the model performed reasonably well in the validation phase, we assumed that it is a good representation of the real epidemic and used it for practical purposes like analysis of different preventions strategies on the test location.

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 [37]. 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 mosquito population through methods like detection and elimination of breeding places, proper covering of persistent water sources and reliable water supply [38]. We choose LSM (Larval Source Management) as test strategy which is economical and very popular. Per sq.km associated annual cost when inflated to 2016 [39], comes to US\$6000 [40].
2. **Decentralized Prevention Strategies:** Here people adopts 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) and US\$180/house with indoor residual spraying (IRS) [41, 42].

All the costs mentioned above are as quoted by private agencies. It can be brought down significantly by conducting large-scale mosquito- control programs and government subsidies.

For comparison of the two strategies, the two iterations were initialized with same resources i.e. same initial budget of US\$ 20,000. Considering it will take approximately US\$ 30,000 to cover the town (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 find all of them [43]. For the second strategy (ITN+IRS), resources worth 20,000 US\$ were distributed randomly among the population (220 US\$ per household) making the chosen population immune to mosquito bites in their household.

Outcomes. Strategy 1 (LSM) was found to be more effective completely eliminating the infection from both the human and mosquito population 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 7). This difference in effectiveness maybe 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.

Strategy 1 also had a much greater effect on mosquito population reducing it by 70% while Strategy 2 only reduced it by 25% (graphical results available as Supporting Information). The results of both the strategies were found to be consistent with the past experiments. [44, 45].

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 [46, 47], it can be reasoned that the above results will hold true for other diseases spread by *A. Aegypti* like presently prominent Zika virus.

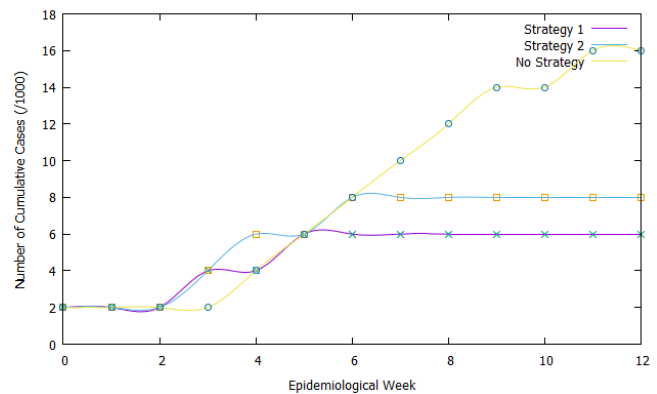


Fig. 7. Prevention Strategies Results from testing the two strategies

Conclusion and Discussion

Diseases like chikungunya and dengue which currently have no vaccine needs proactive measure to prevent or contain their breakout. The proposed model shows that ABMs provide a good mechanism for modeling complex phenomenons like epidemics. These models carry high practical value as they can be used to quickly try out different combination of strategies, study the effects of infection on different population groups, find out high risk groups, plan vaccination programs and categorize locations with respect to their seasonal risk factor. The case study above 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 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 is available.

As a future scope, the model can be improved to handle mutation of infection [48], actual human mobility patterns, multiple mosquito species and other important climate factors like wind velocity. One can even collaborate with field researchers to get better constraints on the model parameters.

ACKNOWLEDGMENTS. The authors would like to thank Dr. Barbara A. Han for her invaluable input on mosquito and infection life-cycle.

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Supporting Information (SI)

The following section contains detailed description of the techniques used for model implementation.

SI Figures. For the purpose of subjective analysis of the model, an animated visualization of the simulation was generated using GAMA platform. Figure S1 is a snapshot of the simulation of the case study where the model was initialized with Luneray's GIS data and climate and census information of St. Martin. The lines are the roads connecting the gray buildings, dots are human agents and triangles are mosquito agents.

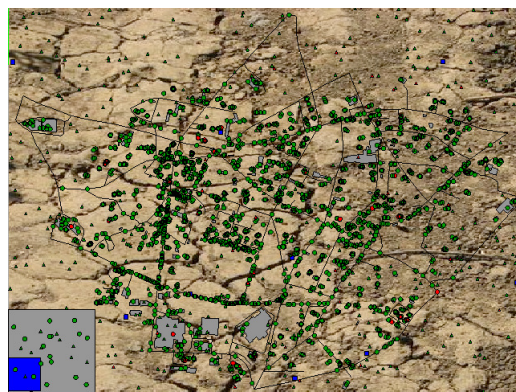


Fig. S1. ABM Environment GUI of environment created using GAMA.

For the purpose of training the model parameters, uni-variate sensitivity analysis was conducted i.e. model outcomes were analyzed with respect to one parameter at a time. The first parameter was Mosquito's sensory range S_r which was tested for six different values and error in fitting was recorded for each value (Figure S2). The error metric used was mean-squared error. S_r parameter was found to be significantly sensitive and was tuned to 3 m.

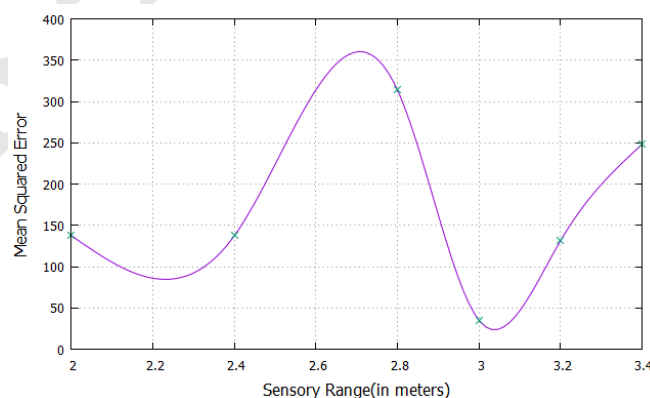


Fig. S2. MSE. Mean-Squared Error recorded for different S_r values. ($M_m=2$)

The second parameter for sensitivity analysis was M_m , mosquito's maximum number of meals in a day. It was varied for three different values and errors were recorded. M_m was then fixed to 1 to minimize the error. The results obtained are given by Figure S3

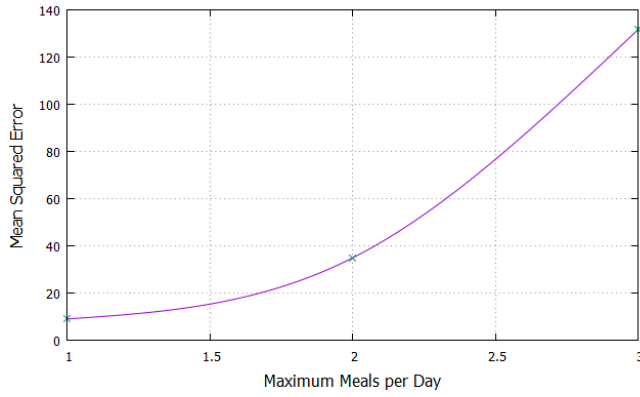


Fig. S3. M_m . Mean-Squared Error recorded for different M_m values.

P_m , P_f and M_r were fixed to 0.2, 0.5 and 0.05 respectively as on average they gave approximately constant mosquito population as show in Figure S4.

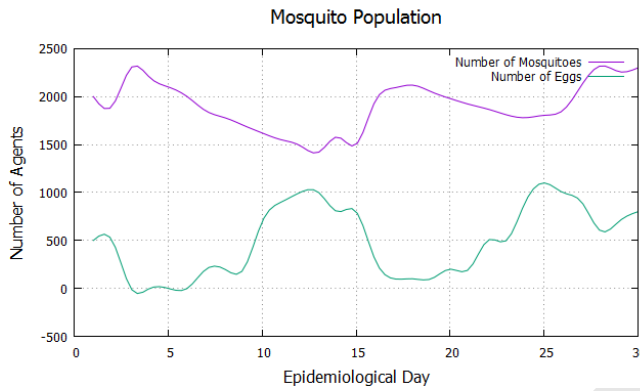


Fig. S4. Mosquito Population. Number Mosquitoes and eggs per day

When the model was tested for the effectiveness of two intervention strategies (LSM and ITN+IRS) in controlling mosquito population, Strategy 1 had a much greater effect reducing their population by 70% while Strategy 2 only reduced it by 25%(Figure S5 & Figure S6).

SI Tables. Table S1 describes all the parameters used in proposed model and how their value was decided. Reference column cites the sources where the values of the respective parameter was referred from. 'Trained' implies that the respective parameters were tuned during the training phase either due the lack of concrete evidence of their values or high sensitivity in different environment.

Appendices. The model source code is made to be publicly available at: [\[github-link\]](#)

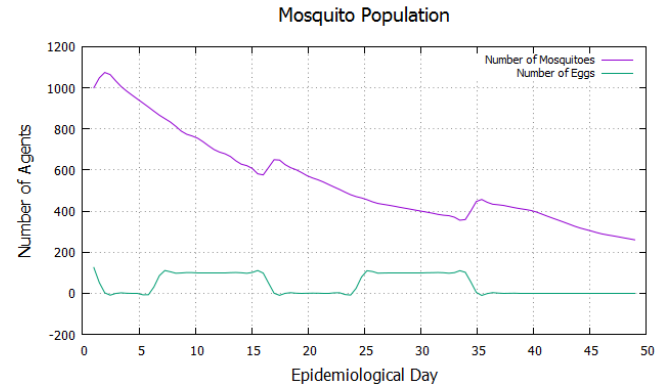


Fig. S5. Mosquito Population (Strategy 1). Number Mosquitoes and eggs per day

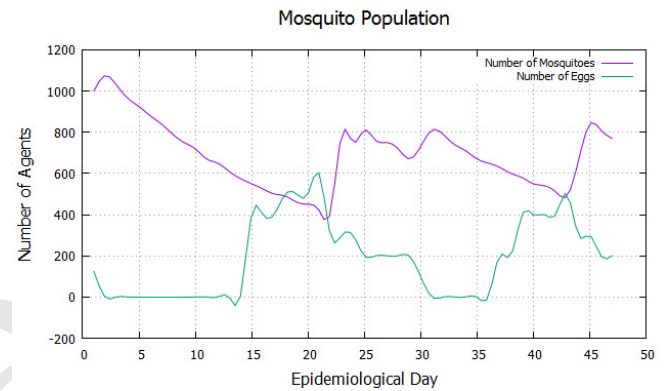


Fig. S6. Mosquito Population (Strategy 2). Number Mosquitoes and eggs per day

Table S1. ABM Parameters

Parameter	Description	Value	Reference
Mosquito Parameters:			
F_s	Flying speed	0.0...1.0 km/hr	[49]
F_r	Maximum distance	350m	[19]
A_s, A_e	Active period	7:00 a.m., 6:00 p.m.	[25]
M_m	Maximum number of meals in a day	1	Trained
M_r	Mortality rate	0.05/day*	[19]
P_m	Probability of an adult female to mate successfully	0.2	Trained
O_c	Ovipositioning behaviour (single(0) or spread over multiple sites(1))	1	[25]
P_f	Probability that the hatching egg will be female	0.5	Trained
S_r	Sensory range	3 m	Trained
Infection Transmission Cycle Parameters:			
P_{tmh}	Transmission probability of infection from mosquito to human	0.6	[8]
P_{thm}	Transmission probability of infection from human to mosquito	0.275	[8]
Infection Cycle Parameters:			
nb_infected_init	Initial number of infected people	2	[27]
N_e	Number of days a human spends in exposed state	2...6 days	[50]
N_i	Number of days a human spend in infected state	4...7 days	[50]
P_{rc}	Probability of transiting from recovered state to susceptible state	0	[51]
P_{irc}	Probability that passing infection leaves human in chronic state	0.95	[50]
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

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