Mathematical modeling and simulation of the Chikungunya spread in Veracruz Mexico

Gerardo M. Ortigoza Capetillo

Facultad de Ingeniería
Universidad Veracruzana

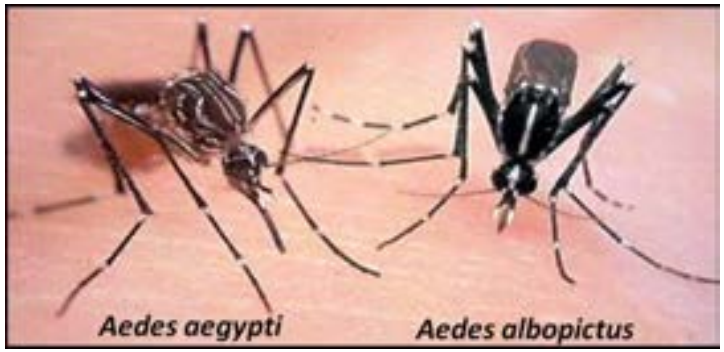
gortigoza@math.ubc.ca

October 31, 2018

Index

Index

Chikungunya Chikungunya is a viral disease transmitted to humans by infected mosquitoes: Aedes aegypti and Aedes albopictus. It causes fever and severe joint pain. Other symptoms include muscle pain, headache, nausea, fatigue and rash. Joint pain is often debilitating and can vary in duration.



Malaria	Anopheles
Dengue	Aedes aegypti
Chikungunya	Aedes aegypti, Aedes albopictus
Zika	Aedes aegypti, Aedes albopictus
Mayaro	Aedes aegypti,Aedes albopictus
Yellow Fever	Aedes, Haemagogus
West Nile virus	Culex: pipiens, tarsalis, and quinquefasciatus
La Crosse encephalitis	aedes triseriatus

Table: Diseases transmitted by mosquitoes

The disease was first detected in 1952 in Africa. Numerous chikungunya re-emergences have been documented in Africa, Asia (India), and Europe, with irregular intervals of 2-20 years between outbreaks. **Reunion Island 2005-2006**

Figure: Geographic distribution and spread of Chikungunya

Index

Mathematical modeling of the spread of Chikungunya: Achievements and Challenges

Temporal	76.66 %
Spatial	28.33 %
Probabilistic	13.33%
Deterministic	61.66 %
Statistical	25%
theoretical/hypothetical	38.33%
fitting data	35%
vector control	23.33%

Total papers review 60,

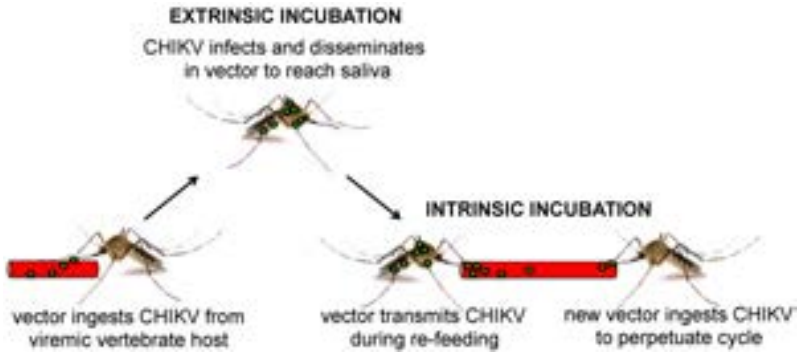
Index

SIR_si	31.7 %
SEIR_sei	26.8 %
SEIIaR_sei	21.95%

Total compartmental papers 41, SI ignores incubation period.

Index

Typical lifecycle of Chikungunya infection



1. Adult female mosquito bites infected person.
2. Incubation of virus within mosquito (extrinsic) ranges from 2 to 9 days, average 3, (temperature dependent).
3. Infectious mosquito bites susceptible person.
4. Virus incubates within person average (intrinsic) ranges 4-5 days, average human infectious period 4-5 days

$$
\begin{aligned}
S' &= -\beta_1 S i_v \\
E' &= \beta_1 S i_v - \lambda_1 E \\
I' &= \lambda_1 E - \gamma I \\
R' &= \gamma I \\
s_v' &= \mu - \beta_2 s_v I - \mu s_v \\
e_v' &= \beta_2 s_v I - \lambda_2 e_v - \mu e_v \\
i_v' &= \lambda_2 e_v - \mu i_v
\end{aligned}
$$

β_1 rate at which mosquitos infect humans,β_2 humans infect mosquitos, λ_1 inverse of the latent period of infection in humans,λ_2 in mosquitos γ rate of recovery, μ mortality rate of mosquitos (1/20days). Yakob et.al.2013

$$
\begin{aligned}
S' &= -\beta S \frac{i_v}{n_v} \\
E' &= \beta S \frac{i_v}{n_v} - kE \\
I' &= kE - \gamma I \\
R' &= \gamma I \\
s_v' &= \mu n_v - \beta_v s_v \frac{I}{N} - \mu s_v \\
e_v' &= \beta_v s_v \frac{I}{N} - \eta e_v - \mu e_v \\
i_v' &= \eta e_v - \mu i_v
\end{aligned}
$$

β rate at which mosquitos infect humans,β_v humans infect mosquitos, k inverse of the latent period of infection in humans,η in mosquitos Brauer et.al.2016

Basic reproductive number: average number of secondary infections that result if a single infectious individual is introduced into an entirely susceptible population.

$$R_0 = \frac{\beta_1 \beta_2 \lambda_2}{\gamma \mu (\mu + \lambda_2)}$$

When $R_0 < 1$ the infection will die out in the long run. But if $R_0 > 1$ the infection will be able to spread in a population. Generally, the larger the value of R_0, the harder it is to control the epidemic.

critical mortality rate $\mu^* = 0.5 \left(\sqrt{\lambda_2^2 + \frac{4\beta_1 \beta_2 \lambda_2}{\gamma}} - \lambda_2 \right)$

Reunion β_1, β_2 fitted

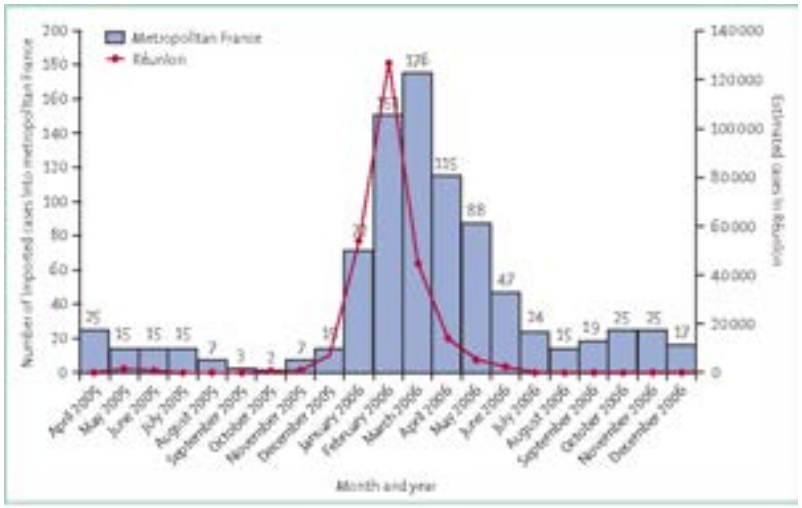
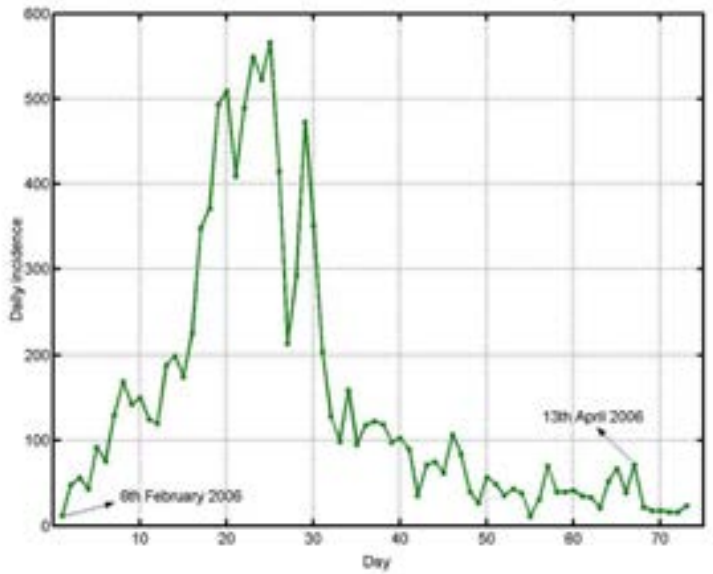
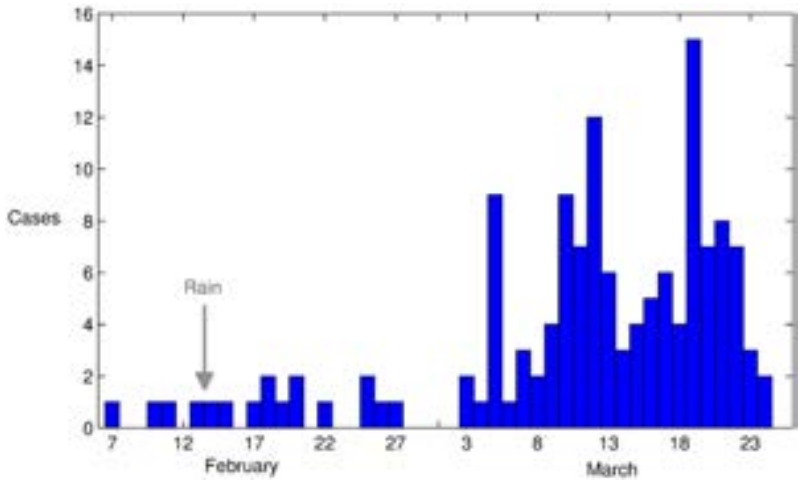


Figure 3: Chikungunya cases in Réunion and imported cases into metropolitan France, April 2005-December 2006
Weekly notifications based on an estimated mathematical extrapolation (http://www.invs.sante.fr and

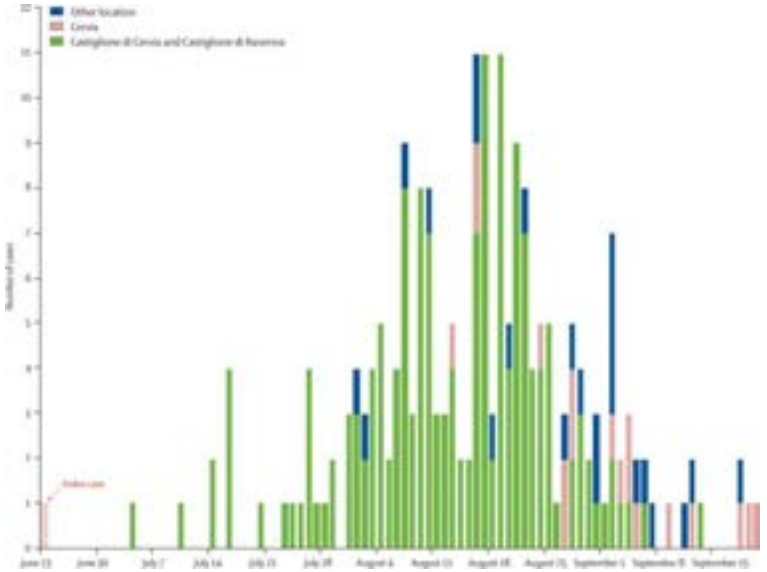
Mauritius SIR_si simulations



Camboya β_1 fitted



Italy statistical analysis



Some vector control

1. Quarantine
2. mechanical control reduce breeding
3. larvicide adulticide
4. sterile insect technique
5. infect mosquitoes with wolbachia reduce: egg laying rate, transmission abilities and lifespans.

Moulay et.al. 2012

Dynamics of the mosquito population

$$\frac{d\mathcal{E}(t)}{dt} = b\mathcal{A}(t)\left(1 - \frac{\mathcal{E}(t)}{K_E}\right) - (s+d)\mathcal{E}(t)$$
$$\frac{d\mathcal{L}(t)}{dt} = s\mathcal{E}(t)\left(1 - \frac{\mathcal{L}(t)}{K_L}\right) - (s_L + d_L)\mathcal{L}(t)$$
$$\frac{d\mathcal{A}(t)}{dt} = s_L\mathcal{L}(t) - d_m\mathcal{A}(t)$$

$\mathcal{E}(t)$ eggs, $\mathcal{L}(t)$ larvae, $\mathcal{A}(t)$ adult, b ovipation rate, K_E, K_L carrying capacities, d,d_L, d_m mortality rates.
$s_m + e_m + i_m = \mathcal{A}$

Control prevention effort

$$\frac{d\mathcal{E}(t)}{dt} = b\mathcal{A}(t)\left(1 - \frac{\mathcal{E}(t)}{K_E}\right) - (s + d + \epsilon u_2(t))\mathcal{E}(t)$$
$$\frac{d\mathcal{L}(t)}{dt} = s\mathcal{E}(t)\left(1 - \frac{\mathcal{L}(t)}{K_L}\right) - (s_L + d_L + d_c u_2(t))\mathcal{L}(t)$$
$$\frac{d\mathcal{A}(t)}{dt} = s_L\mathcal{L}(t) - d_m\mathcal{A}(t)$$

ϵ, d_c eggs and larvae mortality rates induced by chemical intervention.

$$S' = -\beta(1 - u_1(t))S\frac{i_v}{n_v}$$
$$E' = \beta(1 - u_1(t))S\frac{i_v}{n_v} - kE$$
$$I' = kE - \gamma I - qI$$
$$R' = \gamma I + qI$$
$$s_v' = s_L\mathcal{L}(t) - \beta_v(1 - u_1(t))s_v\frac{I}{N} - \mu s_v$$
$$e_v' = \beta_v(1 - u_1(t))s_v\frac{I}{N} - \eta e_v - \mu e_v$$
$$i_v' = \eta e_v - \mu i_v$$

Index

Cellular automata is a discrete model studied in computer science, mathematics, physics, complexity science, theoretical biology and microstructure modeling. It consists of:

- A tesselation of the space (cells).
- A finite number of states.
- For each cell, a set of cells called its neighborhood.
- A local update rule, a mathematical function that determines the new state of each cell in terms of the current state of the cell and the states of the cells in its neighborhood.

Discrete time space dynamical system. An initial state (time $t = 0$) is selected by assigning a state for each cell.
A new generation is produced by applying the local update rule.

Index

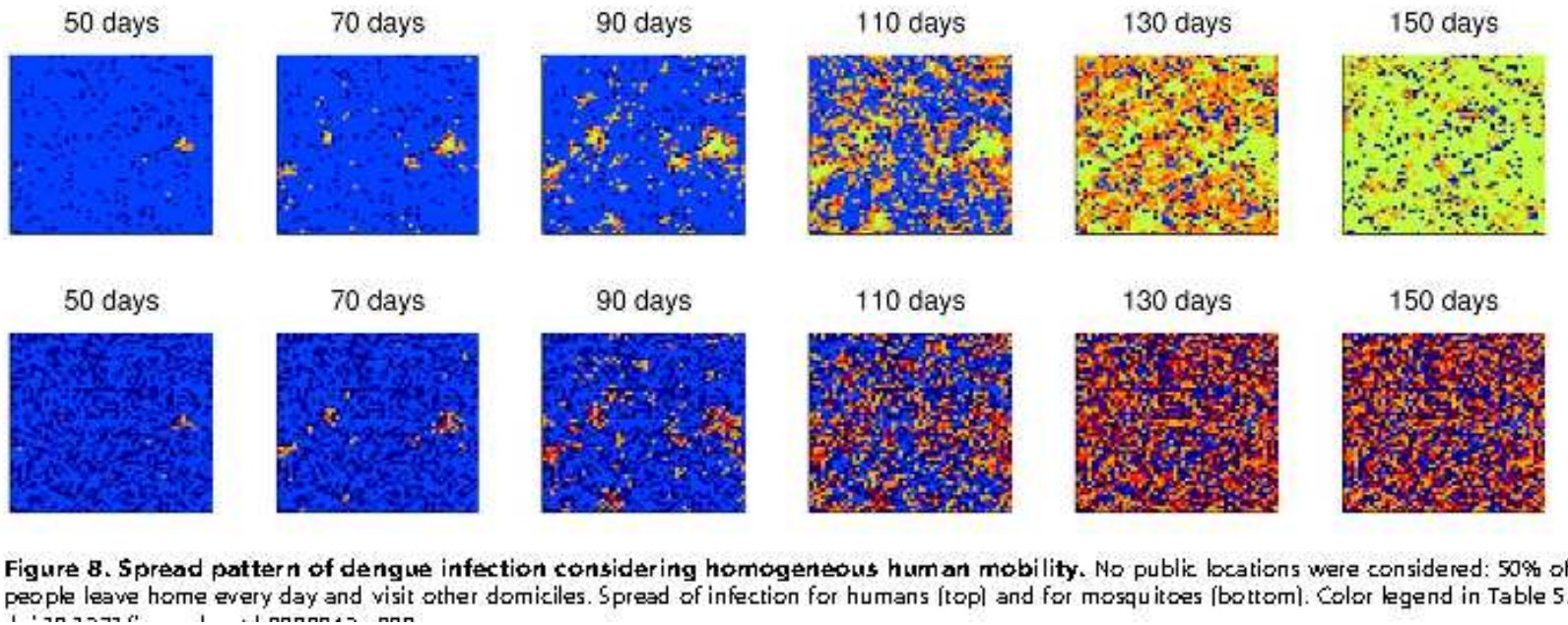


Figure 8. Spread pattern of dengue infection considering homogeneous human mobility. No public locations were considered: 50% of people leave home every day and visit other domiciles. Spread of infection for humans (top) and for mosquitoes (bottom). Color legend in Table 5.

Figure: Modeling the Dynamic Transmission of Dengue Fever: Investigating Disease Persistence, Castro et. al. 2011

parameters are given 'good' values in the habitat that species is adapted to, and 'bad' values in the other habitat:

For the simulations, the landscape was set up by randomly distributing 'good' and 'bad' cells that occurs in equal frequency with $E_s^+ = 1.5$ and $E_s^- = 0.5$. We give in Fig.(2) b, the global evolution of the infection in a vector and competent host population and in Fig.(3), the spatial evolution in the vector.

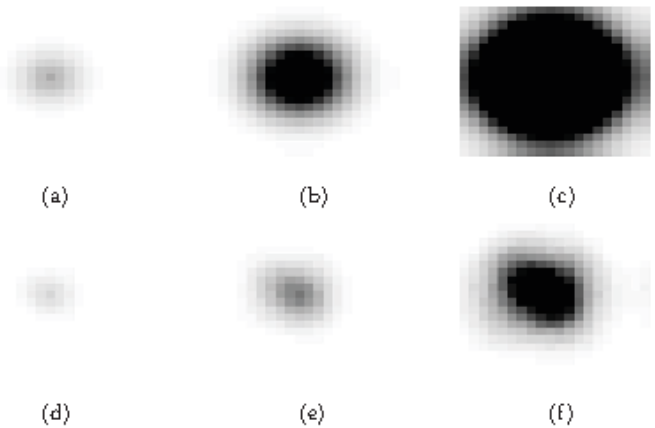


Fig. 3. Spreading of the disease with Moore neighborhood in homogeneous (a-c) and heterogeneous (d-f) environments for vector species at times t=400, t=600 and t=800 respectively

Figure: The Basic Reproduction Number for Chagas Disease Transmission Using Cellular Automata, Cisse et. al. 2014,

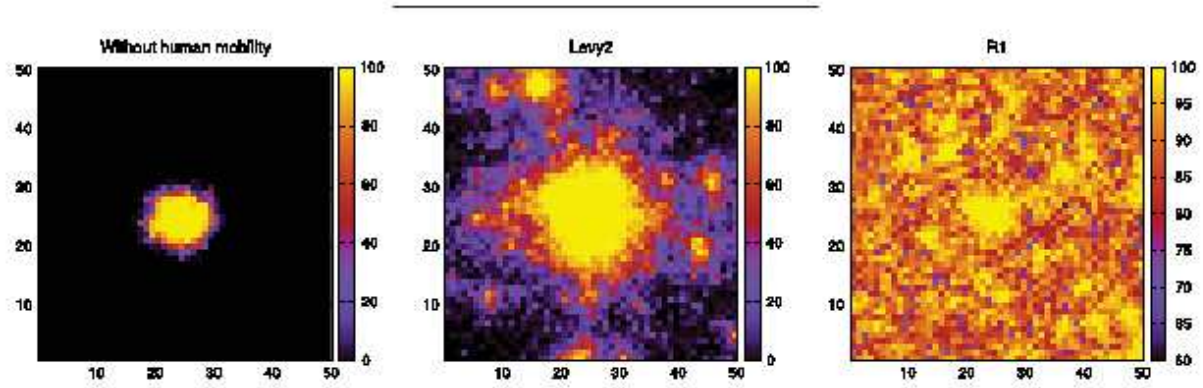


Fig. 1. Spatial distribution of recovered individuals for three different conditions: No human mobility (left panel), a human movement pattern according to a Levy-flight distribution with parameter $\beta = 2.00$ (central panel) and a human movement pattern according to a uniform random distribution R1 (right panel) for $t = 350$ (after the end of the epidemic outbreak) and a grid size of 50×50 blocks.

Figure: Modelling dengue epidemic spreading with human mobility, Barmak et.al. 2016

Index

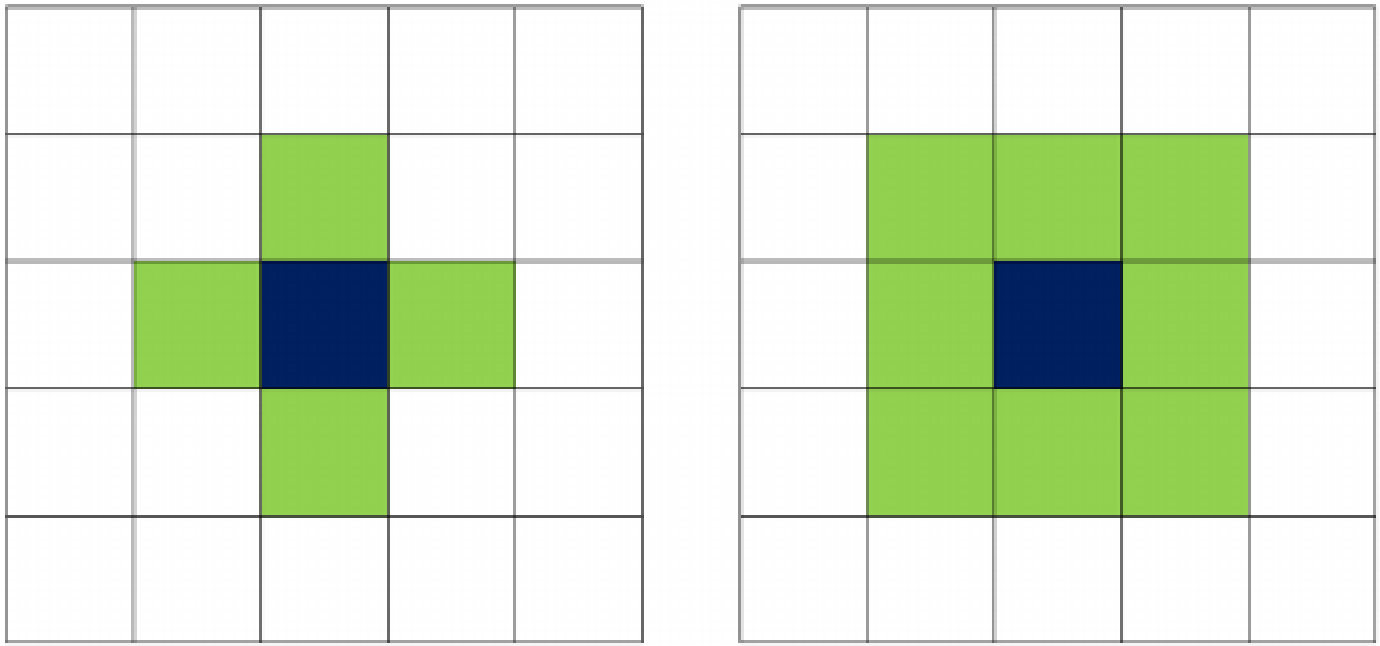


Figure: Rectangular neighborhoods

Neumann

Extended Neumann

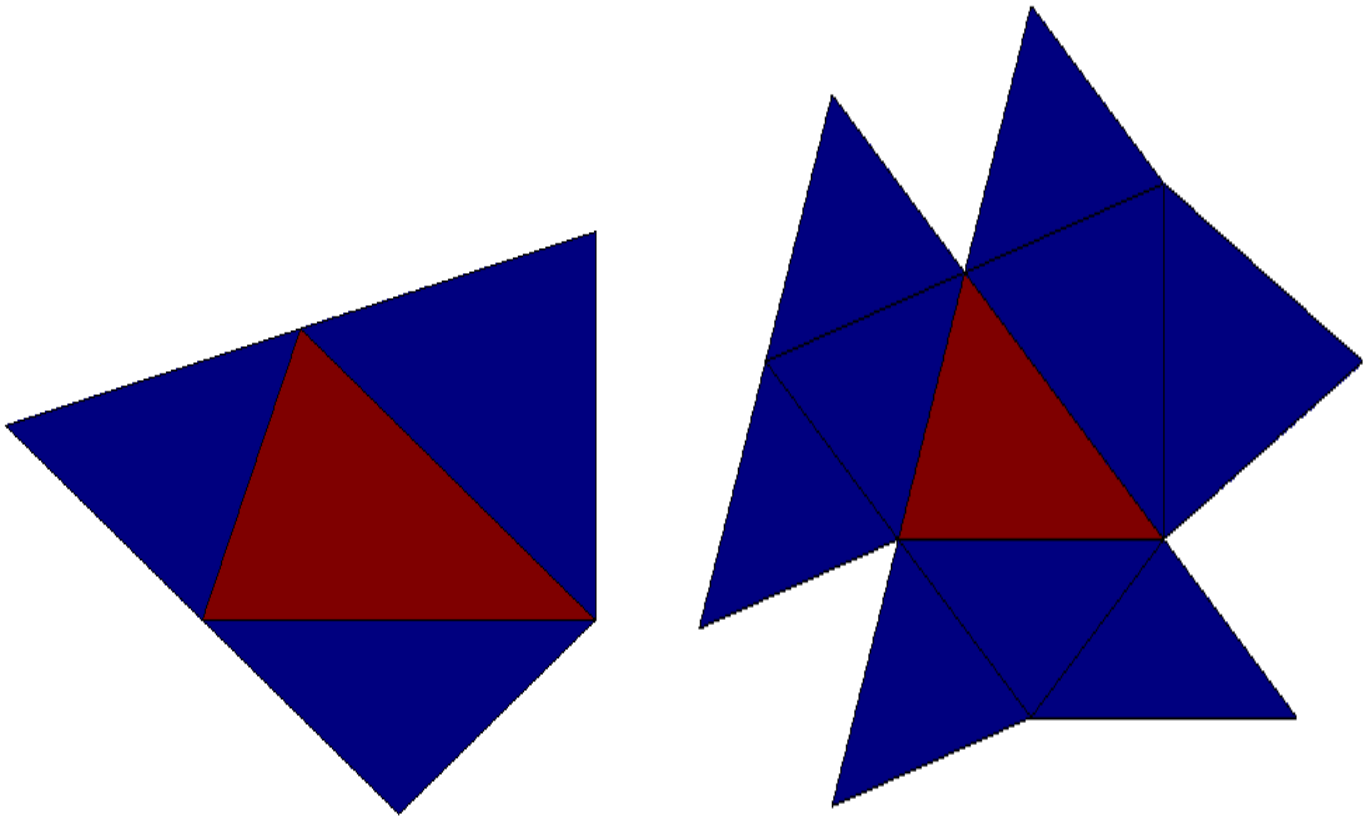


Figure: unstructured triangular neighborhoods

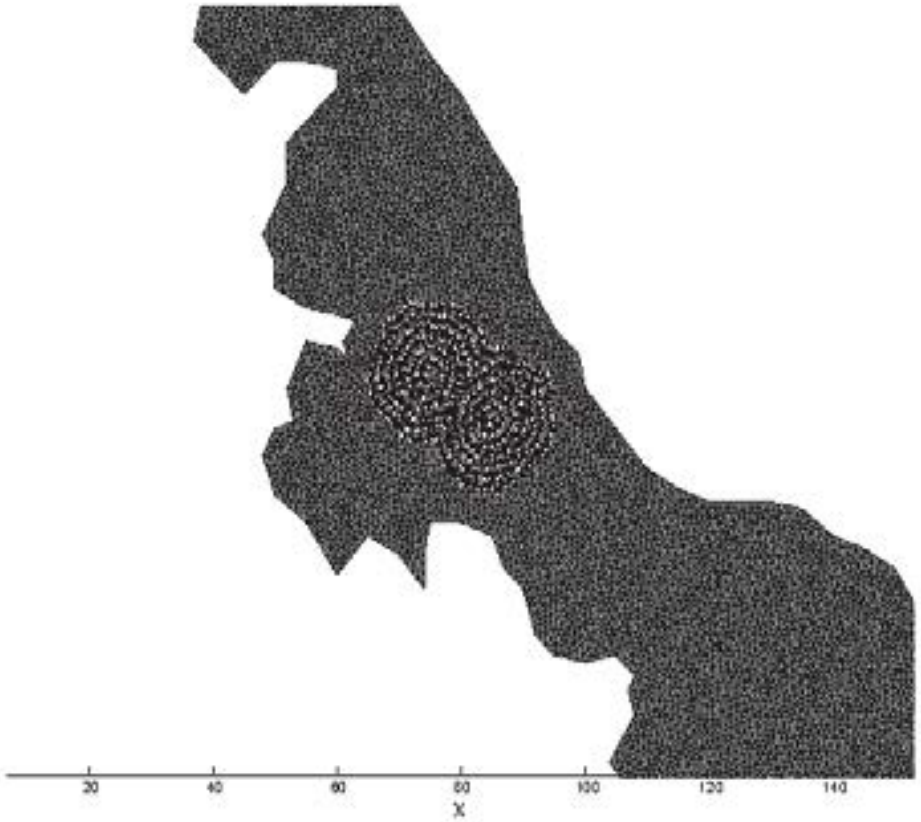


Fig. 15. Two spreading trains of fronts (infected defoliated) after 20 iterations they interact with one another.

Figure: Unstructured triangular cellular automata for modeling geographic spread, Applied Mathematics and Computation Volume 258,G.Ortigoza 2013

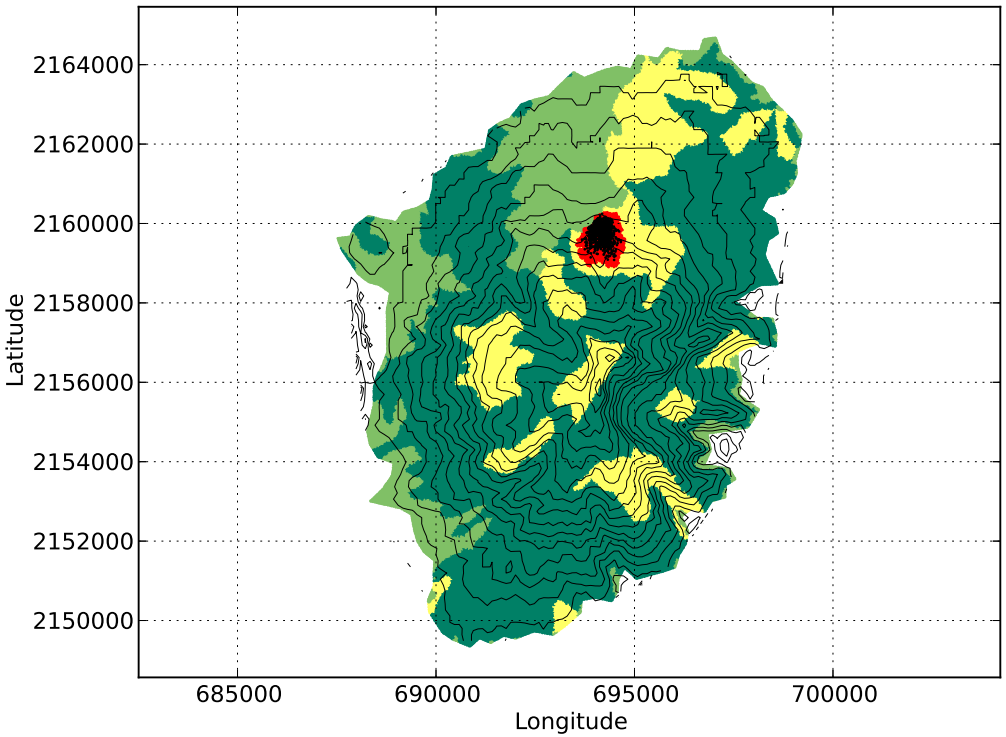


Figure: ACFUEGOS: An Unstructured Triangular Cellular Automata for Modelling Forest Fire Propagation, International Conference on Supercomputing in Mexico ISUM 2015: G. Ortigoza

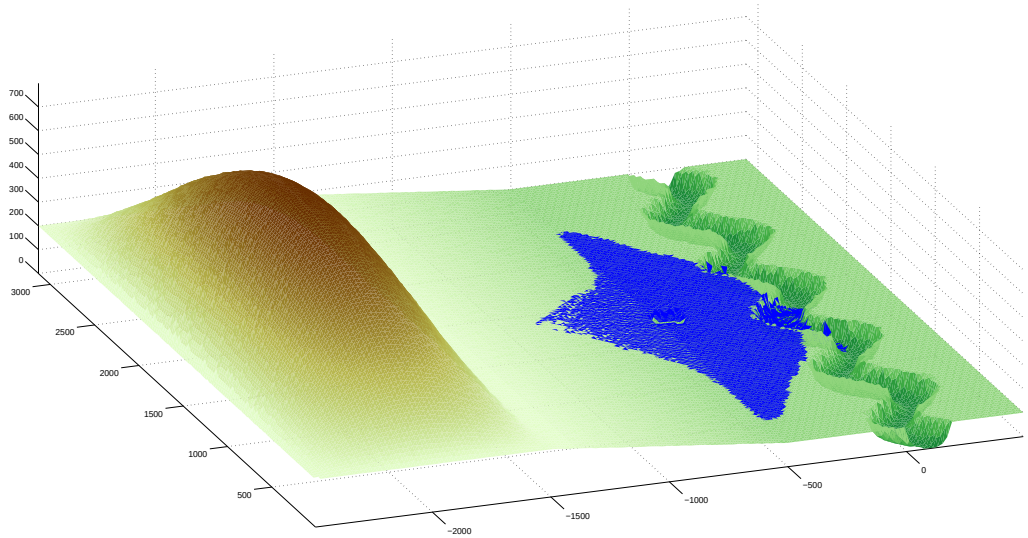
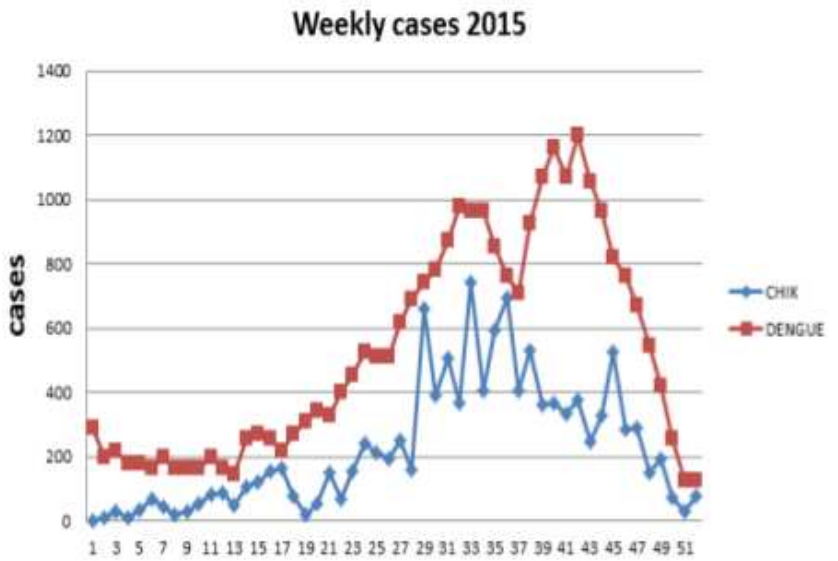


Figure: Modelo matematico para simular inundaciones basado en un automata celular triangular no estructurado, retos y perpectivas de las ciencias ambientales, G. Ortigoza et.al 2017

Chikungunya in Mexico 2015



Veracruz

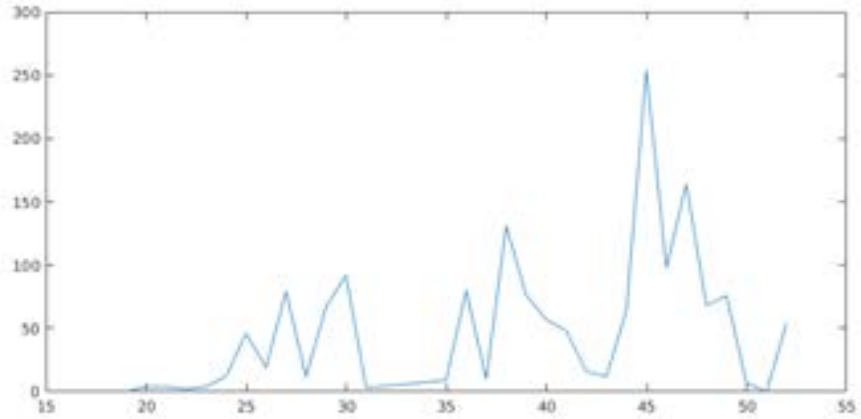


Figure: Study area

	Population	Area km^2
Veracruz	609,964	247.9
Boca del Rio	142,207	42.8
Medellin	75,346	398.2

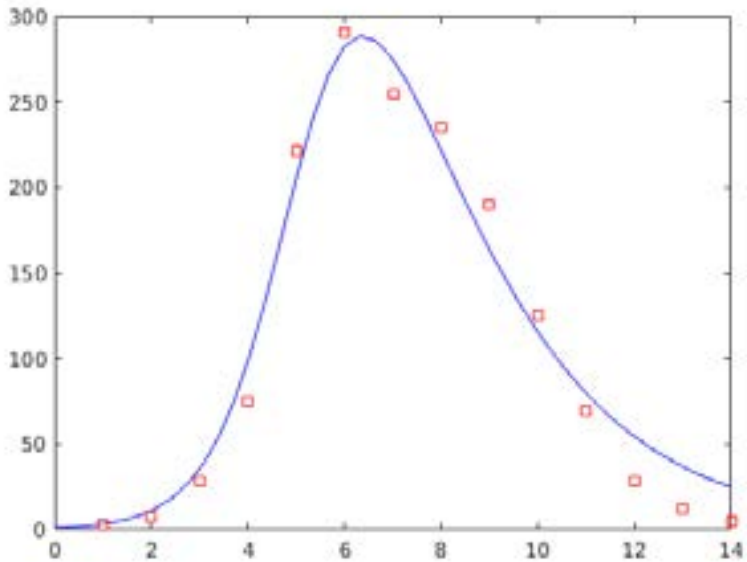
Influenza Epidemic in an English Boarding School, 1978

1	2	3	4	5	6	7	8	9	10	11	12	13	14
3	8	28	75	221	291	255	235	190	125	70	28	12	5

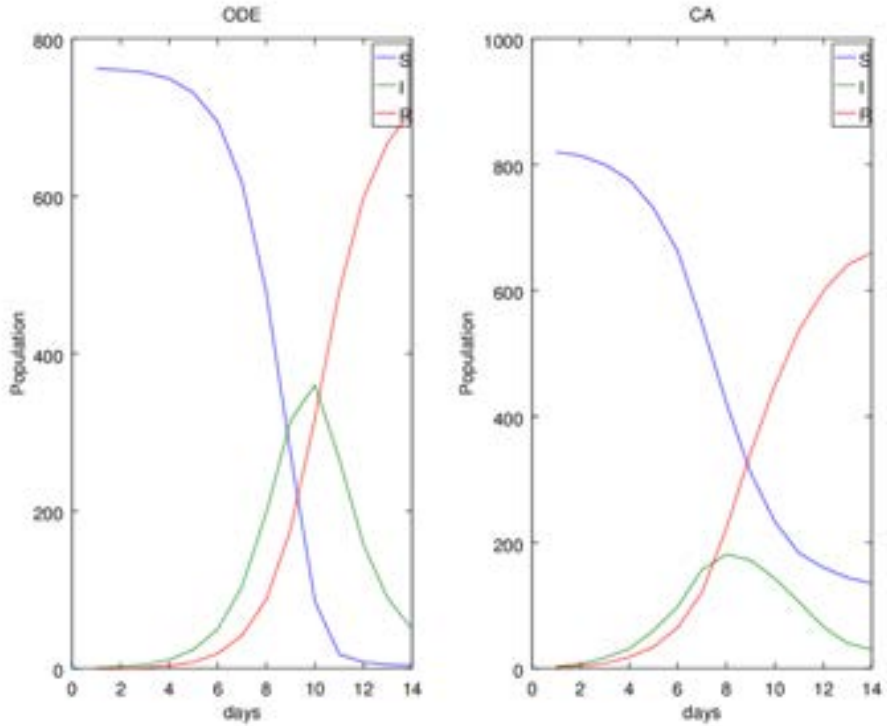
$$\frac{dS}{dt} = -\beta SI, \quad \frac{dI}{dt} = \beta SI - \gamma I, \quad \frac{dR}{dt} = \gamma I$$

Population 763, $S(0) = 762, I(0) = 1, R(0) = 0$, fitting
$\beta = 0.0028, \gamma = 0.448$, $R_0 = \frac{S(0)\beta}{\gamma} = 3.7079$

Fitting



Comparison



Miksch et. at 2013, Comparison of differential equations and cellular automata for epidemic simulation.

Index

Discussion

- Unstructured Cellular Automata provides an opportunity to model spatio-temporal spread Chikungunya
- Translate SEIR_sei model into cellular automata
- Consider vector control
- Include heterogenous populations, and moving population
- Include gis
- Include wheather variables: rainfall, temperature, relative humidity
- Parallel code OpenMp

Index

References

- Moulay, et.al. *Optimal control of chikungunya disease: larvae reduction, teatment and prevention*,mathematical Biosciences and Engineering Vol 9,num 2, 2012
- Yakob L., Clements A., *A mathematical model of Chikungunya Dynamics and Control: the major Epidemic on Réunion island*, plos one, vol 8, is 3, 2013.
- G. Ortigoza, *Unstructured triangular cellular automata for modeling geographic spread*, Applied Mathematics and Computation Vol 258, 2015.
- Brauer F., Castillo-Chavez C., Mubayi A., Towers S, *Some Models for Epidemics of Vector-Transmitted Diseases*, Infectious Disease Modelling Vol 1, Iss 1, 2016

THANKS A LOT