Proceeding Series of the Brazilian Society of Applied and Computational Mathematics, Vol. 5, N. 1, 2017.

Trabalho apresentado no CNMAC, Gramado - RS, 2016.

Proceeding Series of the Brazilian Society of Computational and Applied Mathematics

Propagation Dynamics of an epidemic of Flaviviridae arbovirus in Complex Networks of Human Beings and *Aedes aegypti*

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Abstract. In this work, we propose a new epidemics diffusion model to evaluate the migration behavior of dengue in the populations of its hosts and transmitters (man and mosquitos *Aedes*) to facilitate the search for combat actions to this disease. As a result, an algorithm that takes into account local characteristics (such as the initial number of infected entities or the probability of infection for the spread of the epidemics) and incorporates mobility to the final model was produced, following the simple or compound contact between transmitters and target entities. This paper explores the human and mosquito factors that interact and contribute to the global spread and persistence of dengue in modern societies and the results obtained may yield new understanding of epidemic spreading and the corresponding immunization strategies in dual communities.

Keywords. Disease spreading, Diffusion Model, Epidemics, Dengue, Scientific Computing.

1 Introduction

A great number of social, technological or even environmental systems can be described more properly as complex networks whose nodes represent organizations or individuals and whose edges correspond to links or interactions between them. Recently, a great number of papers has been published studying the characteristics of such systems, which recognize the significance of *local clustering* between its component entities. Particularly interesting examples of this behaviour can be found in cellular metabolic networks [1], in the web of human sexual contacts [2] and, most notably, in the Internet and the World Wide Web [3]. In this work, motivated by recurrent studies about the spread of certain diseases in modern society, we will study a phenomenon of government interest in the public health sector: the propagation dynamics of the dengue virus in two interacting populations distributed according to complex networks.

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Dengue is an infeccious disease caused by four closely related serotypes of a *flavivirus* of the family *flaviviridae* [4] also designated as arbovirus (abbreviation of *arthropod-bornvirus*), which occur mainly in tropical and subtropical regions of the world. The vertebrate hosts are generally primates but only man has clinical manifestation of the disease, with a longer viremia of about seven days. It is a serious illness transmitted by several mosquito species of genus *Aedes*, mainly by *A. Aegypti*.

1.1 Dengue Epidemics

Dengue is a viral disease that spreads rapidly worldwide. Its main vector has origins in Africa and has been spreading in through tropical and subtropical regions since the 16th century during the Navigation Era. Looking at the recent developments of the disease, numbers surprise: at least in the last 50 years, the number of infected individuals has increased 30 times with increased geographic expansion to new countries, and during 2010, more than 1.7 million dengue cases were reported [5].

In Brazil, the first reports of the existance of the virus date from the late 19th century in Curitiba (PR) and early 20th century in Niterói (RJ) and São Paulo (SP), in Brazil. Even after having eradicated the mosquito in 1955 (as effect for the control of a yellow fever epidemic), a few years later the disease comes back on the scene with the relaxation of preventive measures [6].

1.2 Simulation approaches

In the literature, it is possible to find several models that study the disease propagation in a network of agents. For example, in [7], a mathematical model for dengue transmission composed by the mosquito and human factors is studied. Analyzing two real dengue outbreaks that occurred in Salvador (Brazil) in 1995 and 2002, this paper shows that control mechanisms applied only on the adult mosquito form are not able to prevent dengue propagation, laying emphasis on control measures applied on the aquatic mosquito form.

In [8] epidemics spreading is studied in different network structures, but only considering the hosts population, established on a *static* network topology. In this fashion, the result is naturally bounded by the simulation framework, and a different approach is naturally demanded in order to predict the complex dynamics of disease outburst.

The existing epidemic diffusion models can be divided in several classes, of which the most appropriate for the analysis of dengue spreading will be based on the one described hereinafter: the SEIR model, in which it is not only possible to represent a healthy and an infected person, but also individuals that are in *conditions* of infection (which does not mean they will necessarily get it).

2 The SEIR Epidemic Diffusion Model

In this scheme, each agent can belong to one of the following classes:

DOI: 10.5540/03.2017.005.01.0386

- $S(t)$: depicts the fraction of individuals not yet infected with the disease (i.e. susceptible to it) at a given time t;
- $E(t)$: denotes the fraction of entities exposed contracting the disease at any given time t;
- $I(t)$: represents the fraction of individuals infected by the disease and able to transmit it to those belonging to $S(t)$;
- $R(t)$: characterizes the compartment of individuals who were infected and then removed from $I(t)$, either due to its immunization or its death. It is an *absorbing* set (there is no transition to any other category from it).

In this work, we consider a new model to study the spreading dynamics of an epidemics of *Flaviviridae* arbovirus that takes into account its spread in *two coupled complex networks*: one of human beings (hosts) and another of *Aedes* mosquitos (transmitters). It is a modified version of the model given in Section 2, which we will call SEIR*.

3 The Studied Model: SEIR*

To study the evolution of a dengue epidemic, we consider in our model the issue of *mobility*: both people as mosquitoes move in accordance with a random motion in a given area. In such a case, we consider that the transmission of the disease from an infected entity (whether a mosquito or a person) to a healthy one (person or mosquito, respectively) takes place with a defined probability (p_{trans_1} for the first case and p_{trans_2} for the second) when an entity occupies the same position as the other.

Therefore, the transition to the Exposure state (from the Susceptibility one) may be reversed, that is, it is possible to return to the Susceptibility state if dengue is not contracted (note that the transition between the first two states is bi-directional):

$$S_h \longleftrightarrow E_h \longrightarrow I_h \longrightarrow R_h \tag{1}$$

Considering the population of *Human Beings*, we have that a person can belong to one of four states regarding the disease: the Susceptibility state (S_h), which represents people who have not contracted dengue, the Exposition state ((E_h), which lists people who had contact with mosquitos (in general), the Infection state (I_h), that depicts individuals who contracted the disease and the Recovery state (R_h), which groups people who already passed by the infection. As the objetive is to study the *transmission* of dengue in a population, we do not consider the recurrence of the disease in individuals (i.e. the infecction can only be contracted once by each person).

As for the mosquitoes population, it was simplistically divided it into three other compartments: the Susceptibility State (S_m) representing mosquitoes that have not contracted the disease, the Exposition state (E_m) which groups insects that have bitten at least one person (which can therefore contract the disease if it is infected) and the Infection one (I_m), which characterizes the infected insects, transmitters of the disease. In this case, we do not consider the case of reproduction of infected mosquitoes.

Thus, the life cycle of each mosquito can be represented by the following state sequence:

$$S_m \longrightarrow E_m \longrightarrow I_m \tag{2}$$

3.1 Simulation Parameters

In order to simulate the spreading effects of a dengue outbreak, we assume some quantities as constants: the maximum lifetime for a transmitter is assumed to be $t^M_{life} = 30\ days$ and for a host it is assumed to be $t^H_{life} = 68\ years$. The exposure time (both for transmitters and hosts) was assumed to be $t^M_{expos} = t^H_{expos} = 7\ days$, and the healing time for human beings was also assumed to be constant ($t^H_{heal} = 7\ days$).

We assumed also the initial age distribution and the movement pattern in the simulation area as random, both for the mosquito and human populations, with *contact* between the transmitter and the host (a "bite") whenever they occupied the same position in the simulation environment.

Finally, among the user-controlled variables we can mention the following: initial quantity of *transmitters*, reproduction probability of a *transmitter*, probability of a susceptible *transmitter* becoming infected (after the contact with an infected host), probability of an exposed *transmitter* becoming infected, initial amount of hosts, probability of a susceptible *host* becoming infected, probability of an exposed *host* becoming infected;

4 Results

4.1 Simulation Scenario

To analyze the results we used the *Netlogo 5.2* tool [10]. In total, 571 *humans* were inserted in the simulation, which was executed for a period of $t_{sim} = 15.000\ hours$ (corresponding to 625 days). In Figure 1 we have a representation of the simulation map during a typical execution, in which both the humans as the insects (represented by the image of birds) may belong to one of the following states: Susceptible, Exposed, Infected or Recovered (which are represented by the *white, yellow, red* and *green* collors, respectively).

Larger simmulations (with more realistic settings) could not be carried out by computational limitations of both the equipment and the software used, imposing a limit to the environment size and to the amount of entities in the setup.

4.2 Simulations and Experiments

The following parameter set was used in the tests here related. Considering the transmitters, the initial number of vectors was assumed as $N^V_0 = 4$, the average lifetime of a vector was set as $t^V_{life} = 30\ days$, their reproduction probability was assumed as $p^V_{reprod} = 0.02$ and the probability of a Susceptible vector becoming Infected was chosen as $p^V_{SEI} = 0.03$, while the probability of an Exposed vector becoming Infected was set as $p^V_{EI} = 0.15$. The average lifetime of a human was set as $t^H_{life} = 68\ years$, while the Healing time t^H_{heal} of a human as the Exposure time from both a vector t^V_E and a human t^H_E were set as $t^H_{heal} = t^V_E = t^H_E = 7\ days$;

DOI: 10.5540/03.2017.005.01.0386

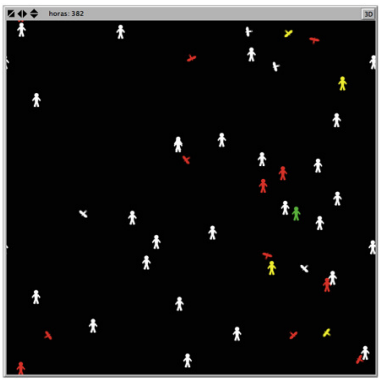

Figura 1: *Excerpt of the simulation map adopted.*

4.2.1 Test 1

In the first test, we adopted the following parameter set, with small values for the transmission probabilities p_{SEI} of a and p_{EI}:

- Probability of a Susceptible human becoming Infected: $p^H_{SEI} = 0.02$;
- Probability of an Exposed human becoming Infected: $p^H_{EI} = 0.15$;

The evolution of N^H_{inf} and N^H_{rec}, the number of Infected and Recovered humans, can be seen in Figure 2, on the left. In not shown values, at the end of the dynamics, approximately 1.05% of the human population was infected, while 21.6% contracted the disease along the interaction.

On the right of Figure 2 we can see the relation between N^H_{inf} and N^V_{inf}, i.e. the number of infected humans and infected vectors for Test 4.2.1. As we can see, the percentage of infected vectors falls after a maximum of 46.8% in the beginning of dynamics and oscillates approximately around 26.1%, its final value.

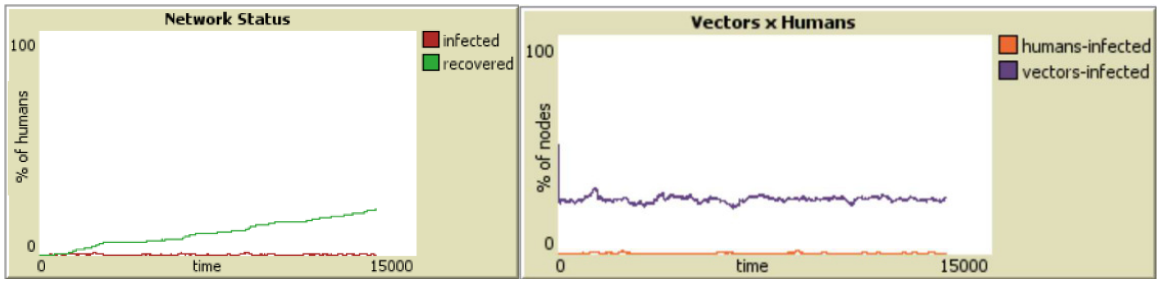

Figura 2: (N^H_{inf}, N^H_{rec}) *and* (N^H_{inf}, N^V_{inf}) *for* $p^H_{SEI} = 0.02$ *and* $p^H_{EI} = 0.15$

Some information can be inferred from the analysis of Figure 2. The first is that during the entire simulation period there is a considerable percentage of infected vectors. The second one, as a consequence, is that a small portion of the population remains infected

throughout the whole dynamics, which reveals an endemic characteristic for the adopted parameters. Besides, it is possible to see that these results occur both due to the short lifespan of the mosquitos as to the rapid recovery of the infected men (only 7 days). Finally, as expected, it can further be seen the gradual growth of the number of recovered human beings which, for the models used in this work, cannot contract the disease again, reducing the chance of human infection.

4.2.2 Test 2

Studying the dynamics of a case with high values for the transmission probabilities p_{SEI} and p_{EI}, the following parameter set was adopted in the second test:

- Probability of a Susceptible human becoming Infected: $p^H_{SEI} = 0.60$;
- Probability of an Exposed human becoming Infected: $p^H_{EI} = 0.91$;

The evolution of N^H_{inf} and N^H_{rec} can be seen on the left of Figure 3. At the beginning of the interaction, infection spreads and reaches its maximum (affecting 8.56% of the human population) in $t_{max_2} \approx 1.175\ h \approx 49\ days$ of disease spreading. Simulation ends with 0.62% of the population with the disease, while 91.5% of the humans are recovered, after acquiring the infection.

In not shown values, it is possible to see on the right of Figure 3 that the number of infected vectors declines from a peak at the beginning of the interaction and oscillates around 26.6%, its final value (similarly as in Test 4.2.1, since the disease parameters are the same in both situations).

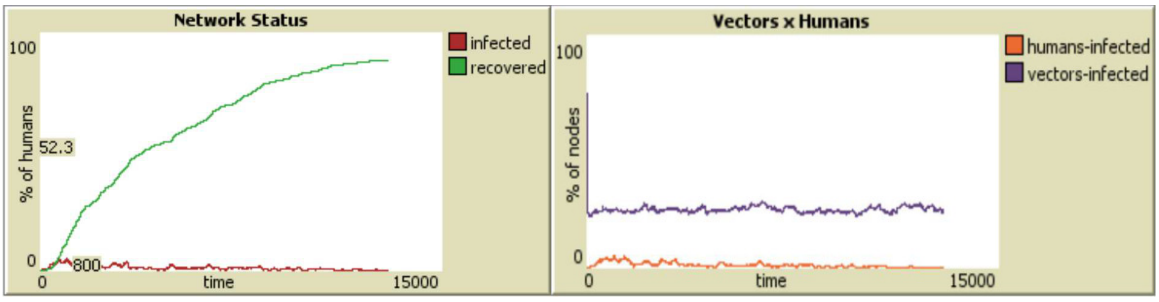

Figura 3: (N^H_{inf}, N^H_{rec}) *and* (N^H_{inf}, N^V_{inf}) *for* $p^H_{SEI} = 0.60$ *and* $p^H_{EI} = 0.91$

In the second test, it is possible to see that even increasing the chance of human infection (from $p^H_{SEI_1} = 0.02$ to $p^H_{SEI_2} = 0.60$), only a small portion of the population is infected at any given time, just like in Test 4.2.1. Despite being small, however, the amount of infected entities in Test 4.2.2 is greater than the amount displayed in Test 4.2.1, what can be noticed by the amount of recovered persons at the same time.

This can be explained by the diffusion feature of the of the SEIR model adopted: after the Infection state, it is assumed that an individual enters into the state of Recovery and does not contract the disease again.

DOI: 10.5540/03.2017.005.01.0386

5 Conclusions

In this work a variant of the SEIR epidemiological model was proposed to simulate the spread of dengue in a given population sample, with good ability to predict the number of cases infected throughout the simulation time.

As future work, we can mention: incorporating time delay to the SEIR epidemic model to study its effects on disease transmission, improvements in the mobility model (for both humans and vectors) to evaluate the effect of displacements or concentration (also for both humans and insects) in the disease propagation or even consider the possibility of *recurrence* of the disease, using a SEIS model (characterized by the evolution among the states Susceptible, Exposed, Infected, Susceptible), for example.

It is important to remember that a more elaborate work has great relevance for assisting public agencies in assessing the most appropriate measures to combat the spread of this disease, whose impact is growing in modern society.

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