Explaining the high number of infected people by dengue in Rio de Janeiro in 2008 using a susceptible-infective-recovered model

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An epidemiological model for dengue propagation using cellular automata is constructed. Dependence on temperature and rainfall index are taken into account. Numerical results fit pretty well with the registered cases of dengue for the city of Rio de Janeiro for the period from 2006 to 2008. In particular, our approach explains very well an abnormally high number of cases registered in 2008. A phase transition from endemic to epidemic regimes is discussed.

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Dengue is an arboviral human disease that has a large impact worldwide [1–3]. It is caused primarily by the mosquito *Aedes aegipty* and it affects mainly those who live in the tropical and subtropical countries, where warm temperatures and water provide the needed conditions for mosquito proliferation. In recent years dengue has become an international health problem that has both social and economic aspects [3–7]. Great attention is being given to the spread of the disease because the number of people living in the infection risk areas is around 2.5 to 3.5 billion [3,4,8,9], with a yearly total of 50 million new cases [8,10,11]. Of these, 500 000 result in hemorrhagic dengue or shock syndrome [3,11]. Due to global warming, dengue is spreading and has reached many countries that have a moderate climate [8].

We stress that understanding the dynamics of epidemic models is of major importance and can be used to control the spread of the disease in many cases. Including the work of Bailey [12], the approaches already used in the literature include complex network description [13,14], scale-free network [15], mean-field descriptions [16,17], field theory and percolation [18], and cellular automata [19–21].

In this Brief Report we construct and discuss an epidemiological model for dengue disease using a cellular automata. The model takes into account rainfall index and temperature dependence. The main goal is to reproduce, quantitative and qualitatively, the historical data of dengue disease registered in the city of Rio de Janeiro, Brazil, for the period from 2006 to 2008, where a large number of cases of infected people were observed. We characterize some statistical properties of the model, in particular a possible phase transition from endemic to epidemic regimes. On the construction of the model, we stress that *deep* biological or virological aspects of the disease will not be considered but rather only the most basic and important epidemiological aspects.

Some of the important considerations are as follows: (i) Dengue disease is a seasonal epidemic with peak outbreaks in the summer, mainly because of the higher levels of rainfall and high temperatures. These are the appropriate conditions for the mosquito to reproduce and therefore to proliferate. (ii) The mosquito usually makes its flights near the area where it was born, but, depending on the wind conditions or some other external factors, it can make longer flights, reaching areas that are further away. (iii) A healthy person may acquire the disease (infection) through a bite from an infected female mosquito. (iv) A female mosquito becomes infected after biting an infected person. (v) The person remains infected for an average period of 7 days [19]. At the end of this period, the person becomes immune to such a serotype and does not transmit the disease when bitten by another female mosquito.

We considered a two-dimensional square lattice of size $L \times L$ that represents a particular city or area of the city (see also Refs. [19,22–24] for different approaches). For simplicity, each site of the lattice corresponds to a lot or house in the city which contains a limited number of persons N_{ps} and each site has a constant density of flying mosquitos from it. Each flight is described by using a Lévy flight distribution [25–27], which is characterized by an exponent σ, and a time-dependent probabilistic rule $\lambda(t)$, which indicates that the disease stops spreading (because of the seasonality of the dengue epidemic).

Each person in the house is represented by a variable $\zeta_{i,j,k}$, where $i,j = 1,2,\ldots,L$ and $k = 1,2,\ldots,N_{\mathrm{ps}}$. The condition $\zeta_{i,j,k} = 0$ represents a person k in site i,j who is healthy; this person is put into group S. The variable $\zeta_{i,j,k} = 1$ denotes a person k who is infected; this person is put into group I, whereas $\zeta_{i,j,k} = 2$ means that person k is immune (has already been infected and become immune) and belongs to group R. We make no distinction among the different serotypes of dengue disease. Other serotypes or the coexistence of different serotypes will be considered in a further work.

Since there exist a range of days needed for an infected person to become immune, we introduce a residence time of a person in the state $\zeta_{i,j,k} = 1$, denoted as τ'. The variable $\delta_{i,j,k}$ accounts for the time that a person k, located at the site (i,j), is infected (it means $\zeta_{i,j,k} = 1$). When $\delta_{i,j,k} = \tau'$ the person becomes immune, reaching the state $\zeta_{i,j,k} = 2$. We considered as fixed $\tau' = 7$.

We now describe the evolution rules for the model as follows:

(i) Starting from a site that contains $0 < n \leqslant N_{\mathrm{ps}}$ infected persons of type $\zeta_{i,j,k} = 1$, n mosquitoes (transmitter) could in principle fly, with probability $\lambda(t)$ [see (ii) below], randomly to another site located within the range r according to a Lévy

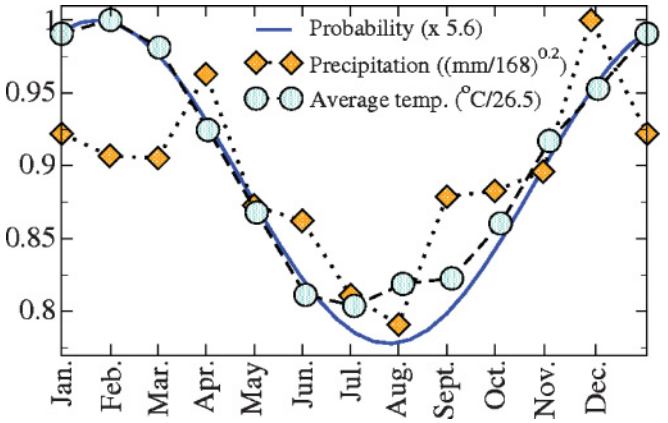

FIG. 1. (Color online) Rainfall index (dotted line) and average temperatures (dashed line) for the city of Rio de Janeiro [29] and probability of the disease transmission (line).

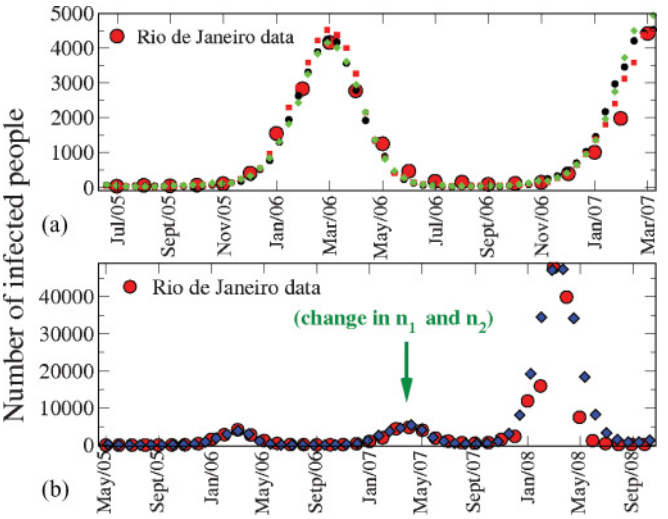

FIG. 2. (Color online) Plot of N_f versus t for the city of Rio de Janeiro, obtained from Ref. [34]: (a) black bullets, green diamonds, and blue squares are obtained from individual simulations of the model for $n_1 = 0.158$ and $n_2 = 0.025$; (b) diamonds and square were generated from our simulations. The phase transition was triggered with changing $n_1 = 0.158$ and $n_2 = 0.025$ before the phase transition to $n_1 = 0.1625$ and $n_2 = 0.025$ in May 2007.

flight whose distribution is given by $P(r) \sim r^{-(1+\sigma)}$, where the exponent σ is a free parameter that controls the shape of the distribution. It is used to investigate long-range interactions in several cellular automata [25,28]. We have considered periodic boundary conditions.

(ii) The probability of infected mosquitos (n) which may leave an infected site (i, j) each day, denoted as the spread probability of the disease $\lambda(t)$ for each of the n mosquitos, dependends on the temperature (and rainfall index). It is written as $\lambda(t) = n_1 + n_2 \sin(2\pi t/T + \phi)$, where n_1 denotes a probability related to the average temperature while n_2 corresponds to the increase (decrease) of the probability related to the variation in temperature. T is the period of the sine function set as $T = 365$ (one year) and ϕ is related to an arbitrary phase. Each unit of time is measured in terms of Monte Carlo steps and corresponds to 1 day. A comparison of the meteorological date with the approximation used can be seen in Fig. 1, where $T = 365$ and $\phi = 1.5$, thus supporting our hypotheses of seasonality.

(iii) If a target site, say (i', j'), contains at least one healthy person ($\zeta_{i',j',k} = 0$), then a random number p is chosen and the person k will be infected as per the following rule: $\lambda(t) \geqslant p \rightarrow \zeta_{i',j',k} = 1$ or $\lambda(t) < p \rightarrow \zeta_{i',j',k} = 0$.

(iv) For an infected individual at site (i, j), the countervariable is updated so $\delta_{ijk} = \delta_{ijk} + 1$ at each Monte Carlo step. If $\delta_{ijk} = \tau'$, the infected individual becomes immune, $\zeta_{ijk} = 2$.

To illustrate the dynamics of the model, we will set the control parameters according to the data from the city of Rio de Janeiro. The results lead us to discuss the high number of registered cases of dengue in March 2008 [30,31]. The parameters were set according to demographics data like population and occupied area which were obtained from *Instituto Brasileiro de Geografia e Estatística* (IBGE) [32]: permanent private house = 1 742 667; resident families = 1 918 177; resident people = 5 857 904; and city area = 1 182 296 km^2. Dividing the number of people living in Rio de Janeiro by the number of families, we found there are, on average, three people per family, leading to a fixed $N_{ps} = 3$. Dividing the total population living in Rio de Janeiro by $N_{ps} = 3$ gives the number of sites of the square lattice as $L = 1397$. The control parameters were set as $\sigma = 2.0$, $n_1 = 0.158$, $n_2 = 0.025$, and $\phi = 0.7$. Using $\sigma = 2.0$ produces an average flight distance of 100 m [33].

Figure 2(a) shows the behavior of the number of infected people, N_f, plotted against the time measured in months. The large red bullets correspond to the registered cases obtained by the health council of Rio de Janeiro [34]. The other smaller symbols (bullet, square, and diamond) are numerical data obtained for different ensembles. One can see that the model fits the data fairly well for about 20 months (almost 2 years).

Adjusting the control parameters properly in the appropriate time, our model fits both typical and atypical cases of dengue, including the data from 2008 in Rio de Janeiro. The rise in dengue observed in March 2008 may be the result of two different scenarios: (i) the average lowest temperature and consequently the average temperature could be higher as compared to same period of previous years and (ii) reduced activity to control the mosquito by public organizations and the population, and so on. Let us elaborate a bit more on this increase of temperature. We show in Fig. 3 that the lowest, as well as average, temperatures for April in both 2006 and 2007 varied from one year to the other [see Fig. 3(a)]. However, this variation was substantial for the following months. We show the variation for June in Fig. 3(b) for the years 2007 and 2006. As we will argue, this variation may have triggered a phase transition, thus explaining the large number of infected people registered in the year 2008. The increase in the lowest and the average temperature were also observed for, at least, December 2007, as shown in Fig. 3(c).

We consider that the parameters n_1 and n_2 varied from one year to another to account for the variation in the temperatures described above. For the period previous to May 2007, the parameters used were $n_1 = 0.158$ and $n_2 = 0.025$, whereas for the period after May 2007 they were $n_1 = 0.1625$ and $n_2 = 0.025$. We found a possible phase transition in the

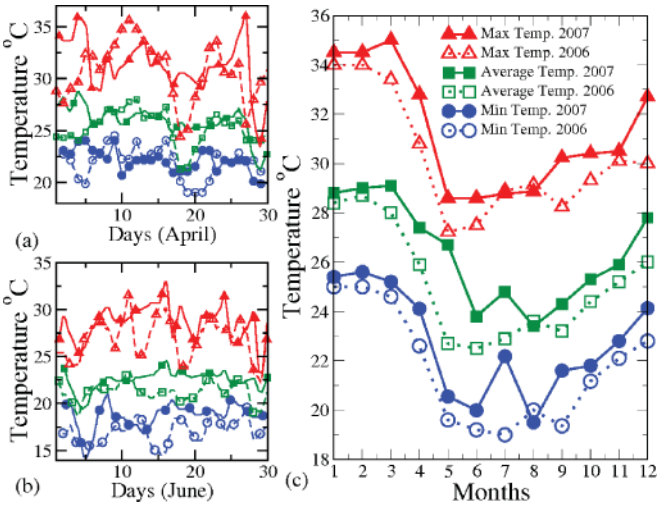

FIG. 3. (Color online) Daily temperature for the period of (a) April and (b) June. Solid lines represent the temperature for 2007 while dotted lines correspond to those for 2006. Red denotes the maximum, blue is the average, and green is the minimum. (c) Maximum, average, and minimum temperature for the years of 2006 and 2007. Data were obtained from Ref. [35].

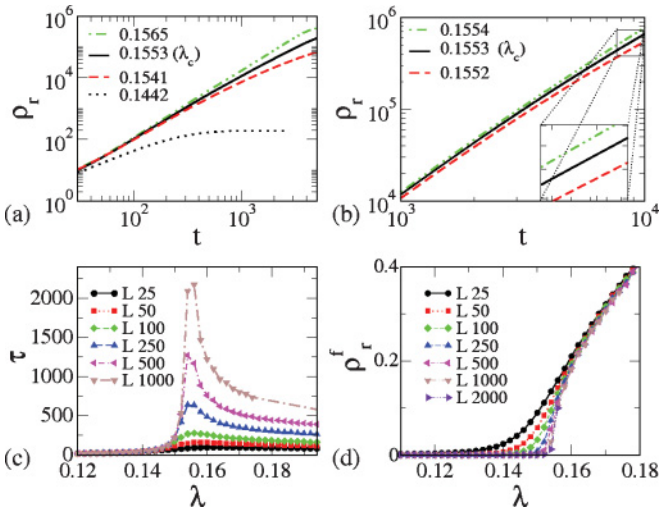

FIG. 4. (Color online) (a) Plot of ρ_r versus t for $L = 1000$ and different values of λ, as labeled in the figure; (b) ρ_r versus t for $L = 5000$ and three different λ as shown in the figure; (c) τ versus λ for different values of L; (d) plot of ρ_r^f versus λ for different values L. For all $\sigma = 2$.

system that can explain what happened in 2008, as shown in Fig. 2(b). Because of a small increase in temperatures, a phase transition was triggered and that would make the dynamics of transmittance of the disease very high, leading to a disaster for the population.

To study a possible phase transition from endemic to epidemic regimes in the model, several different aproaches in the literature were considered, including an analytical description of phase transition [18], numerical investigations [25,36], and a combined analytical and numerical approach [26,37]. To proceed with the simulations we make a simplification in the model. Since the epidemic phase is observed for $\lambda(t) > \lambda_c$, we consider n_2 as fixed, i.e., $n_2 = 0$. With this simplification an order parameter can be defined just as the density of active sites, which we denote it as ρ_r and represents the number of recovered people. At the criticality of $\lambda = \lambda_c$, we have that ρ_r is a power law of the time (see Ref. [38]), as shown in Figs. 4(a) and 4(b). The investigation is carried out for extensive numerical simulations and considering the network size from $L = 25$ to $L = 5000$ and assuming now that $N_{ps} = 4$. The parameter σ was set as $\sigma = 2.0$. At the start, only one infected person in the center of the network was considered.

Figures 4(a) and 4(b) show the behavior of ρ_r versus t for several different values of λ. The larger the network, the more precise the value of λ_c. For $L = 1000$ we found that the critical control parameter $\lambda_c = 0.1553(5)$ leads to a phase transition. For a large $L = 5000$, we obtain $\lambda_c = 0.1553(1)$, thus a more accurate parameter. A phase transition is characterized by the behavior of the survival time τ, which diverges for values of $\lambda \to \lambda_c$ (see Ref. [38]) as shown in Fig. 4(c). τ is the average of the maximum time where the disease still exists in the dynamics for an ensemble of initial conditions. The behavior of the final density of recovered persons, ρ_r^f, can also be obtained. We stress that $\rho_r^f = 0$ denotes the absorbing state. On the other hand, when $\rho_r^f > 0$, one has an active state. Therefore for $\lambda > \lambda_c$ there is a transition from the absorbing to the active states [38]. Figure 4(d) shows a plot of ρ_r^f versus λ where the endemic phase is shown to be above the curve (where the infection disappears, i.e., $\lambda < \lambda_c$), whereas below it the epidemic dynamics are shown ($\lambda > \lambda_c$).

The numerical evidence of a phase transition is a possible explanation for the large number of registered cases of dengue in the city of Rio de Janeiro for the year 2008. We assume that, due to fluctuations of the control parameters, the model entered an epidemic regime characterized by $\lambda > \lambda_c$, thus leading to an explosion on the number of infected people. Such a time evolution was then described in the regime of epidemic dynamics. When λ decreased to $\lambda < \lambda_c$ the epidemic again came under control. Our extensive numerical simulations show us that the transition observed for the city of Rio de Janeiro is $\lambda_c = 0.161(1)$.

Considering other values of σ, our numerical results lead also to a possible phase transition. To illustrate, we show in Fig. 5 a plot of λversus σ where there is a clear separation from two phases which we denote as the endemic (below the curve) and epidemic phases (above the curve). The border of the curve

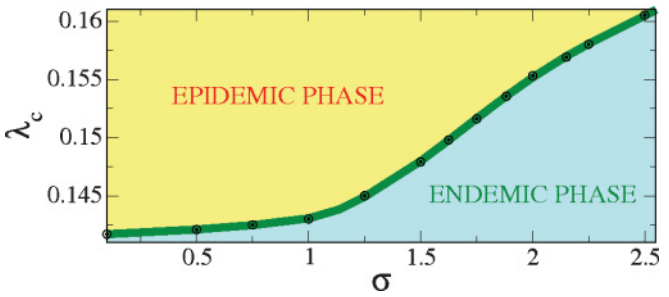

FIG. 5. (Color online) Plot of λ versus σ showing a clear separation of the epidemic and endemic phases.

identifies the critical λ_c where the phase transition takes place. We emphasize that along the endemic phase, occurrence of the disease is observed but at a low level, contrary to the epidemic phase, where an explosion of cases are observed. This kind of investigation on the parameter space λ vs σ may have applicability to other models discussing epidemic diseases [25].

Our model takes into account parameters which are biologically and demographic motivated. The obtained results fit the cases obtained from the health council for the city of Rio de Janeiro fairly well, both qualitatively and quantitatively, for the period from 2006 to 2008 and the epidemic observed in the year 2008. The seasonality of dengue disease is related to a transition of a parameter, $\lambda(t)$, where λ assumes values along the epidemic ($\lambda > \lambda_c$) and endemic phases ($\lambda < \lambda_c$). Our results claim that the large epidemic observed in the city of Rio de Janeiro in 2008 was a consequence of the epidemic phase, $\lambda > \lambda_c$, when then led to an explosion in the number of infected people, causing enormous inconvenience to the population, which, unfortunately, resulted in death for many. One of the possible strategyies that could be used to control an epidemic is to try to keep the parameters within $\lambda < \lambda_c$. This is possible through more direct control of the most infected areas, specifically by controlling the mosquito population. For our model specifically, results indicate that controlling a site will likely result in the mosquito population leaving that site (i, j).

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