

Spatial and temporal dynamics of infected populations: the Mexican epidemic

Mario A. Rodríguez-Meza
Departamento de Física,
Instituto Nacional de Investigaciones Nucleares,
Apdo. Postal 18-1027, México D.F. 11801, México
e-mail: marioalberto.rodriguez@inin.gob.mx
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Recientemente apareció en México y en otras naciones la pandemia asociada al virus A/H1N1-2009. Presentamos un estudio de esta pandemia en el caso de México usando el modelo SIR de epidemias. Este modelo es uno de los modelos más simples pero ha tenido éxito en epidemias para poblaciones cerradas. Consideramos los datos para México y usamos el modelo SIR para hacer algunas predicciones. Después consideramos la generalización del modelo SIR para obtener adicionalmente el comportamiento espacial de la epidemia. Hacemos el estudio de la propagación espacial y temporal de la epidemia con parámetros que son consistentes con los obtenidos de ajustes del modelo SIR temporal al caso de México.

Descriptores: Dinámica de epidemias; modelo SIR espacial; ecuaciones de razón no-lineales.

Recently the A/H1N1-2009 virus pandemic appeared in Mexico and in other nations. We present a study of this pandemic in the Mexican case using the SIR model to describe epidemics. This model is one of the simplest models but it has been a successful description of some epidemics of closed populations. We consider the data for the Mexican case and use the SIR model to make some predictions. Then, we generalize the SIR model in order to describe the spatial dynamics of the disease. We make a study of the spatial and temporal spread of the infected population with model parameters that are consistent with temporal SIR model parameters obtained by fitting to the Mexican case.

Keywords: Epidemic dynamics; spatial SIR model; non-linear rate equations.

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I. INTRODUCTION

The human being has suffered several pandemics along its history. In the last century one of the most devastating was the spanish flu that killed more people than the world war I itself. It is important to know its dynamics to take appropriate health measures in order to diminish the effects of the pandemics. By using population dynamics methods we can model the spatial and temporal dynamics of the disease[1].

The purpose of this work is to present a simple model to study the epidemic dynamics based on rate equations of the populations dynamics. The model was developed by Kermack and McKendrick[2] and it is known as the Susceptible-Infected-Released (SIR) model. We have used the SIR model and one of its possible extensions to take into account the oscillatory behavior of the infected population to study the A/H1N1-2009 pandemic in the case of Mexico[3]. One of the disadvantages of the SIR model is that it does not take into account for the fact that the infected people have the greatest influence on the healthy people that are spatially closest to them. This also means that the SIR model ignores the possibility that populations are spread over a spatial region and that it takes time for an infection to spread across that region. We extend the SIR model in order to study the spatial behavior.

In the following section, Sec. II, we review very briefly

the SIR model and apply it to the case of the Mexican epidemic in Sec. III. Then in section IV we improve the SIR model in order to take into account for the spatial behavior and apply it to the Mexican epidemic, using the SIR parameters values found previously in the simple SIR model. Our conclusions are in Sec. V.

II. THE SIR MODEL

This model considers that the population is divided into susceptible people (S), healthy people that can be infected, the infected people (I), and the released people (R), persons that were ill and then died or cured and then become immune. The released people, also named, removed people can be those infected people that are isolated. We follow Ref. [3] and refer the reader to this reference for more details.

The basis of the model are: (a) There is only one infection responsible to produce an infection in a host. (b) The end of the disease is the death or a complete immunity. (c) The rate at which the disease propagates is proportional to the product of susceptible and infected people, the proportionality factor is a , its value will give us the infection period (see below). (d) All individuals are equally susceptible. (e) The system is closed, i.e., there are no births or migrations. (f) The total population N is large enough in order to have a deterministic

description, i.e., based on its history. (g) The incubation period is short, i.e., a susceptible that become ill can pass the virus to another susceptible. (h) The decreasing speed of the infected people is proportional to its size, with the proportionality factor b , the inverse of the released period. The model also assumes that all the populations are homogeneously mixed, they have equal probability to be in contact between each other, except the isolated or dead people.

Taking into account all these considerations and using normalized variables to the total population N , $s \equiv S/N$, $i \equiv I/N$, $r \equiv R/N$, the model is described by the non-linear differential equations:

$$\frac{ds}{dt} = -s(t)i(t), \quad (1)$$

$$\frac{di}{dt} = s(t)i(t) - \rho i(t), \quad (2)$$

$$\frac{dr}{dt} = \rho i(t), \quad (3)$$

where the constant $\rho \equiv b/aN$. Time is in units of $1/Na$, i.e., gives us the time in units of the infection period.

The first equation above indicates the rate at which the susceptible population diminishes due to that they are being infected, according to assumption (c). The second equation gives us the speed at which the infected grows according to assumptions (c) and (h). The negative term in this equation is the one we have to subtract according to assumption (h), when some members of the compartment i are being move to compartment r . Finally, the increasing rate of the removed people is contemplated in the third equation according to assumption (h).

The mathematical formulation of the epidemiological model is complete when we fix the initial condition of the populations, for example, at time $t = 0$, that mark the start of the epidemic: $s(t = 0) = s_0 > 0$, $i(t = 0) = i_0 > 0$, $r(t = 0) = r_0 = 0$. We also add the condition that the system is closed, $s(t) + i(t) + r(t) = 1$, i.e., the total population is constant. This condition, the initial values of the populations, and Eqs. (1-3) mean that we need only the values of two parameters, s_0 and ρ .

We should notice that this is a very simple model. The SIR model has been modified or improved after it was proposed, in order to be applied to specific situations [4–7]. The models mainly have relaxed the (e) and (g) assumptions, given above, introducing more complicated dynamics. For example, latency period of the VIH virus is very variable. There are ill people that show their first symptom a few years later after they were infected and there exist cases where there is no manifestation ever. Besides, in an epidemic like AIDS there are births of infected and non-infected children and so the total number of the population is changing.

Other variations of the standard SIR model consider the case of epidemics where the populations is heterogeneous with very susceptible groups as can be the very young children or the very old people (see for instance [8]).

Even though the standard SIR model is simple, it allows us to make some predictions about the initial behavior of the spread of an epidemic. When a population is isolated or it is very weakly interacting with its surroundings, the SIR model gives appropriate results[3].

III. PANDEMIC BY THE A/H1N1-2009 VIRUS

In the spring of 2009 it appeared a new epidemic with unknown origin. One of the first cases was reported on april 12th, a woman 39 years old. She died the next day. By the end of april the Mexican government announced that emergency measures have to be taken and schools were closed.

We applied in this section the SIR model to study the pandemic by A/H1N1 using the available data for Mexico. We show the results we obtained using the simplest SIR model[3]. The data we used were obtained from the web page of the Secretaría de Salud de Mexico[9]. In Fig. 1 we show the fitting results using the data published on may 8th. The fitted parameters are: $Na = 62$, $\rho = 0.9928$, $s_0 = 0.99999988$. The onset of the epidemic is determined by parameter ρ (see [3] for details). This parameter is the most important in the SIR model and not only determines the onset of the epidemic, it determines the maximum of the infected people, i.e., how drastic is the epidemic. As we defined this parameter $\rho = b/aN$, i.e., is the ratio of infection period over released period. If we diminish its value the maximum of infected people, i , will be augmented.

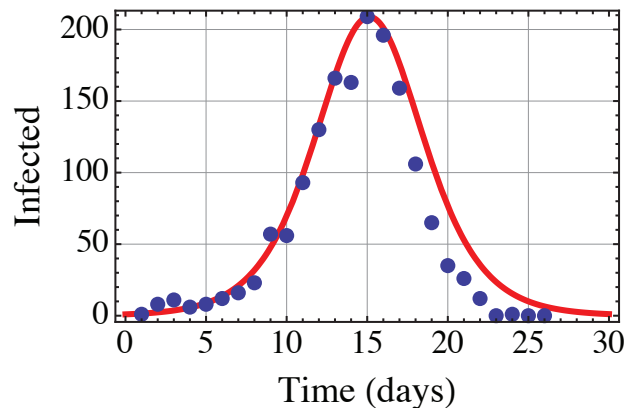


FIG. 1. Fitting of data reported on the 8th of may.

We see that the fitting is good and this gives us confidence in the model so far with the available data up to that date but we should be aware that the system is open and so we will be careful with the conclusions. However, as it is shown in [3] a maximum value of infected people was predicted that is in agreement with the first observed maximum value. In the next section we improve the model to study the spatial behavior in addition to the temporal behavior.

IV. DYNAMICS OF POPULATIONS: THE SPATIAL BEHAVIOR

Let us assume that the infection can be spread over a city or a spatial region that occupies a region in the xy -plane. We write

$$\begin{aligned} S &= S(x, y; t) \\ I &= I(x, y; t) \\ R &= R(x, y; t) \end{aligned} \quad (4)$$

to indicate that now the populations have a spatial and temporal behavior and we say that $S(x, y; t)$ is the density of susceptible population in persons per square kilometer, for example, in a small square centered at (x, y) . The same interpretation is for $I(x, y; t)$ and $R(x, y; t)$.

The basic idea to obtain the equations of the new SIR model that govern the spatial and temporal behavior of the populations is to use also all the assumptions that lead us to Eqs. (1–3) to build up the temporal behavior. We model the spatial behavior by adding a diffusion term in such a way that we take into account the fact that populations are spread over the region and it takes time for an infection to spread across that region (see Ref. [1] for other possible diffusion models). The evolution equations then are

$$\frac{\partial s}{\partial t} = -is - (\nabla^2 i)s \quad (5)$$

$$\frac{\partial i}{\partial t} = is + (\nabla^2 i)s - \rho i \quad (6)$$

We may notice also that the infected people have the greatest influence on susceptible persons that are spatially closest to them. We are assuming that infected individuals recover at the same rate at all places. Spatial coordinates are in units of $(d/Na)^{1/2}$ where d is the diffusion constant and the time is again in units of $1/Na$, the infection period. The diffusion effects of the released people do not have any effects on the spatial dynamics of susceptible population or infected population and its equation is given by Eq. (3) but with the new meaning of the populations. We note also that again parameter ρ is the most important parameter of the model.

Let us assume that the city is a square region with sides of size l and we solve Eqs. (5) and (6) with the boundary conditions:

$$\frac{\partial s(0, y; t)}{\partial x} = \frac{\partial s(l, y; t)}{\partial x} = \frac{\partial i(0, y; t)}{\partial x} = \frac{\partial i(l, y; t)}{\partial x} = 0, \quad (7)$$

$$\frac{\partial s(x, 0; t)}{\partial y} = \frac{\partial s(x, l; t)}{\partial y} = \frac{\partial i(x, 0; t)}{\partial y} = \frac{\partial i(x, l; t)}{\partial y} = 0. \quad (8)$$

This means that there is no migration through the boundaries consistent with assumption (e) of Sec. II.

In Fig. 2 we show snapshots of the spatial and temporal evolution of the infected populations for several times. Time is in units of $1/Na$ and the spatial length is in units of $(d/Na)^{1/2}$. The infected population are given in units of i_0 , which is the density of the initial infected people.

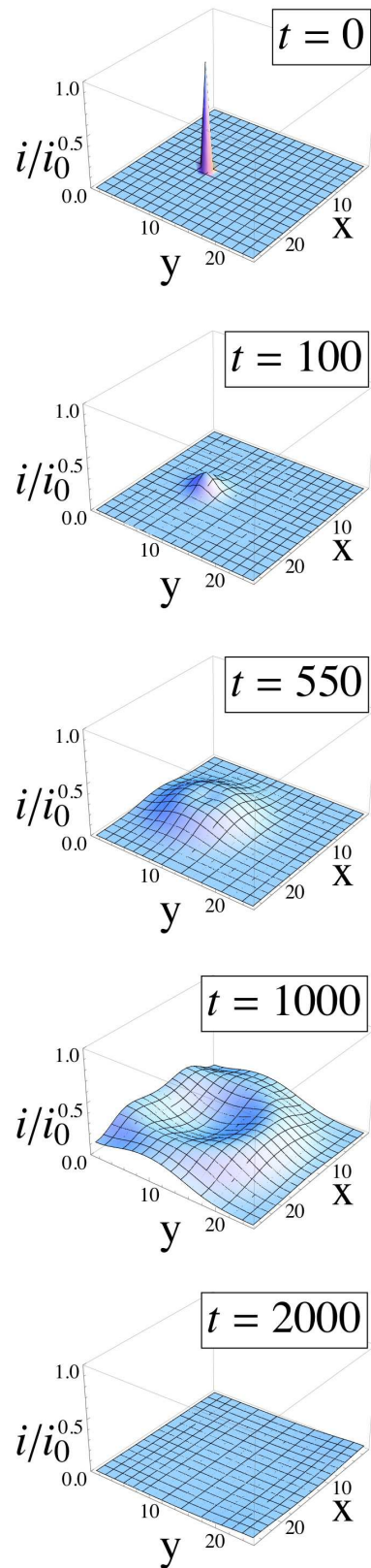


FIG. 2. Snapshots of the evolution of the infected density over a region of size $l = 25$ in units of $(d/Na)^{1/2}$. We have used $\rho = 0.9928$ and $i_0 = 10^{-4}s_0$.

Close to the center we introduce an infected population $i_0 = 10^{-4}s_0$, one person in ten thousand is ill in a small area, and by solving numerically Eqs. (5) and (6) we evolve the infected and susceptible populations (see Refs. [10] and [11] for details about how to solve numerically a partial differential equation). Parameter $\rho = 0.9928$ which is the value we obtained by fitting the Mexican data shown in Fig. 1. Also we recall that the other parameters values were for the temporal behavior $Na = 62$ and $s_0 = 0.9999988$. Then, if we consider that the city is Mexico city modeled with a square region of sides $l = 55$ km in length, we can obtain that the diffusion constant has the value $d = 300.08$ km²/day. In addition, the population of Mexico city is around 8 million people, which gives us a mean density of 12,800 people per square unit length. That is way we have used $i_0 = 10^{-4}s_0$ for the initial infected density. The spatial and temporal behavior of the infected population depend on this value or on the s_0 parameter. We have selected i_0 density in a consistent way with the value of s_0 we obtained by fitting the temporal data of the Mexican case.

The infected peak spreads initially, then in a later time diminishes and it forms an infected wave that propagates to the boundary to finally disappears. It is important to recall that the diffusion constant is contained in the scaling length $(d/Na)^{1/2}$ so the spatial behavior should be generic. If ρ were greater than s_0 no epidemic develop and the peak diminishes until it vanishes. But if $\rho < s_0$ the infected density increases and an epidemic develops.

V. CONCLUSIONS

We have applied one of the simplest model to describe epidemics, the SIR model. In this work we use it to model the pandemic by the virus A/H1N1-2009 in the case of Mexico. One of the main assumptions of the model is to consider that the population is closed or that it interacts very weakly with its surroundings. Also, it does not consider that the disease can spread spatially over a region and that it takes time to spread across that region.

We have improved the SIR model in order to take into account spatial behavior of the infected populations by adding a diffusion term to the equations and we obtain Eqs. (5) and (6). The diffusion effects of the released people do not have any effects on the dynamics and we do not consider its equation given by (3). We have used this spatial and temporal SIR model to study the spatial dynamics of the epidemic in Mexico and assume that the population is closed which is a very stringent condition but however can give us insight in the spatial and temporal behavior of an epidemic. That the system is closed is given by the boundary conditions, Eqs. (7) and (8). The parameters we use are consistent with the ones obtained by fitting the Mexican data. The diffusion coefficient is absorbed in the scaling of the spatial length. Diffusion can be diminished by public health measures like the ones the Mexican government took in april 2009. Finally, the main purpose of this work was to make a first study of an epidemic outbreak when we have the first data and make predictions about the spatial and temporal behavior of the epidemic. We think that at this stage we can apply the SIR model or its variants in spite of their limitations. The model have to be modified in order to study the oscillatory long term behavior of epidemic. A possible model to study this oscillatory stage was presented already in Ref. [3].

One of the main disadvantages of the spatial SIR model we presented in this work is that there is no migration. To improve our model we need to consider that people travel and therefore are moving between cities. Possible models are considered in Ref. [6] and references therein. A possibility is a mobility model for residents of n cities who may travel between them to study the spatial spread of infectious[12]. In contrast to our model this is a kind of spatially discrete model.

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