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The spreading of Covid-19 in Mexico: A diffusional approach

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ABSTRACT

In this work, we analyze the spreading of Covid-19 in Mexico using the spatial SEIRD epidemiologic model. We use the information of the 32 regions (States) that conform the country, such as population density, verified infected cases, and deaths in each State. We extend the SEIRD compartmental epidemiologic with diffusion mechanisms in the exposed and susceptible populations. We use the Fickian law with the diffusion coefficient proportional to the population density to encompass the diffusion effects. The numerical results suggest that the epidemiologic model demands time-dependent parameters to incorporate non-monotonous behavior in the actual data in the global dynamic. The diffusional model proposed in this work has great potential in predicting the virus spreading on different scales, i.e., local, national, and between countries, since the complete reduction in people mobility is impossible.

Introduction

The coronavirus disease 2019 (Covid-19) epidemic began in Wuhan city, China, in December 2019 [30]. Due to its rapid spreading all around the world, the World Health Organization (WHO) officially declared it as a pandemic in early March 2020.

The scientific community turned its attention to the challenges inherent in understanding, describing, and formulating solutions to contain this problem’s social and economic damage. In the beginning, in all countries, the goal was to avoid hospital saturation since there is no country, even the developed ones, with the installed capacity to support the demand generated by the critical sick people if the pandemic is out of control. Then, once the goal above was partially achieved, investigations directed the attention to develop strategies and models for future pandemics so that the response of authorities is more effective and the social and economic impact minimized. The pandemic did not spread at the same rate to all the countries; there was a time delay associated with the degree of connection not only inside each country but also with neighboring countries; the most communicated, the faster the virus arrived and spread.

In Mexico, the first case of Covid-19 was detected on 27th February 2020 [27]. Due to the early containment measures, the epidemic curve in Mexico reached a maximum point in week 28 and later had 12 weeks of continuous reduction. However, from week 40 an increase in cases was registered. This behavior is a clear fingerprint of a new outbreak with consecutive reduction (wave of the Covid-19), and indicates that the mobility effects become relevant.

The Covid-19 pandemic has placed epidemic modeling at the forefront of worldwide public policy-making [4]. The international scientific interest on Covid-19 is of great proportions, as indicated by the large number of publications in specialized journals of medicine, biology, mathematics, physics and chemistry, mainly (e.g. [5,6,10–13,20,22,24,29,31]). The epidemic risk of each region is a function of factors such as geographic proximity, the population spatial distribution [32], the economic development [3] and the migration index. Such information based on the geographic economy matrix and the migration index well could predict the spatial spread of the epidemic [5]. A novel model that considers quarantined and hospitalized individuals effects, produce a SEQHR (susceptible – exposed – quarantined –infected –hospitalized –recovered) compartmental model, was proposed by Kabir and Tanimoto [15]. The SEQHR epidemic dynamics model is coupled with the concept of behavioural dynamics from evolutionary game theory (EGT). In a recent work these principles and approaches were applied to study prosocial behavior of wearing a mask

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different approaches have been developed that can be grouped in predicting the behavior of the spread of Covid-19: mathematical models (deterministic and stochastic), network models, physical quantity diffuses from site to site under the specific rules set.

Through a Fickian-law type. This model is called dSEIRD, which was considered for susceptible and exposed populations. The main feature of the stochastic model is that the number of people being infected was modeled by a Poisson distribution with the parameter RT, which could be different in different stages of observation.

Dos Santos-Gomes and de Oliveira Serra [10] developed a computational tool for real-time forecasting the Covid-19 dynamic propagation, which is based on a machine learning approach with the integration of Kalman filter and interval type-2 fuzzy systems for adaptive tracking. Liu et al. [18] adopted a forecasting model for economic applications to forecast active Covid-19 infections, which is based on the SIR model [7]. Aspri et al. [2] present a deep study on mortality containment concerning economics opening; for this, they propose a SEIARD model (susceptible (S)- exposed (E)- asymptomatic (A)- infected (I)- recovered (R)- Covid-19 related deceased (D)- natural deaths (DN)) model, which is composed of a set of seven ordinary differential equations. The SEIARD model is highly coupled with several feedbacks (S with I-E-A; E with I-E-A; A with I; I with D; R with A-I; DN with S-E-A-I-R). The feedback and causality of the SEIRD model are analyzed and discussed by Santana-Cibrian et al. [25]. The self-organization model that describes diffusion over a given lattice was introduced to describe Covid-19 dynamics in Europe [8]. According to these authors, the proposed model is very simple in terms of the specific diffusion rules. The procedure consists of each lattice site, a quantity called charge (in general is any physical quantity: energy, electric charge, stock market charge) is placed. Therefore, the researchers investigated how the physical quantity diffuses from site to site under the specific rules set.

According to the literature, we observe that for understanding and predicting the behavior of the spread of Covid-19, various models with different approaches have been developed that can be grouped in mathematical models (deterministic and stochastic), network models, lattice models and among others as signal processing techniques (time series). One year after the WHO officially declared the Covid-19 pandemic, waves and third waves of Covid-19 or outbreaks had been recorded in most countries. The mobility effect of important population density scales has not been explicitly considered in most mathematical models. In this work, we proposed a diffusion impact in the SEIRD model to consider the spreading of Covid-19 among regions with population at small, medium, large, and very large scales. The diffusive mechanism is considered for susceptible and exposed populations through a Fickian-law type. This model is called dSEIRD, which was applied to predict the spreading of Covid-19 in Mexico. The 32 States or regions with which the geo-politics of Mexico is divided were analyzed with the dates of INEGI census 2020 [14]. We found that the scaling coefficient DT (diffusion coefficient type) is a crucial parameter to predict the spreading of Covid-19. The dSEIRD model can be applied practically to any scale of the population density, therefore, it can be applied from very small localities (neighborhoods or colonies, small and large towns), passing through geopolitical divisions of countries and between countries.

### The diffusional SEIRD model

The mathematical modeling helps in understanding how a virus spreads within a population. The mathematical model solutions can be refined and improved with information already known about the virus spread [21]. However, modeling the spread of Covid-19 remains a challenge due to its novel appearance in the world. Its dynamic behavior depends on multiple factors in the affected country or geographical zone, such as i) Public health system response, ii) economic development, and iii) population mobility. From the beginning of the Covid-19 pandemic up to date, governments and public health systems have collected information and knowledge regarding spreading the disease. They found that mathematical modeling is a powerful tool to support public policy. In this context, we base our study on a standard mathematical model that considers compartmental sectors of populations, i.e., the SEIRD model. The SEIRD epidemiologic model given by the following set of ordinary equations has been used to interpret, control, and manage epidemic events departing from registered data of different variables [17,22]:

\[
\frac{dS}{dt} = -\beta \frac{S}{N} I \\
\frac{dE}{dt} = \beta \frac{S}{N} I - aE \\
\frac{dI}{dt} = aE - \frac{1}{T_I} I \\
\frac{dR}{dt} = \frac{1}{T_I} I \\
\frac{dD}{dt} = f \frac{1}{T_I} I
\]

where S is the susceptible, E the exposed, I the infected, and R the recovered populations. D represents the dead people. In the above equations \( \beta \) represents the infection rate, while \( a \) is the incubation rate to pass from the exposed to infected condition. \( T_I \) is the average infectious period and \( f \) represents the fraction of infected people who have unfortunately died. These equations can be written for the \( j \)-th State of Mexico and divided by the State surface area \( A_j \) to get:

\[
\frac{dS_j}{dt} = -\beta \frac{A_j}{N_j} I_j, \quad j = 1, \ldots, 32 \\
\frac{dE_j}{dt} = \beta \frac{A_j}{N_j} I_j - aE_j, \quad j = 1, \ldots, 32 \\
\frac{dI_j}{dt} = aE_j - \frac{1}{T_I} I_j, \quad j = 1, \ldots, 32 \\
\frac{dR_j}{dt} = \frac{1}{T_I} I_j \\
\frac{dD_j}{dt} = f \frac{1}{T_I} I_j, \quad j = 1, \ldots, 32
\]

where the new variables per State surface area defined by:
\[ s_j = \frac{S_j}{N_j}, \quad j = 1, \ldots, 32 \]  
\[ e_j = \frac{E_j}{N_j}, \quad j = 1, \ldots, 32 \]  
\[ i_j = \frac{I_j}{N_j}, \quad j = 1, \ldots, 32 \]  
\[ r_j = \frac{R_j}{N_j}, \quad j = 1, \ldots, 32 \]  
\[ d_j = \frac{D_j}{N_j}, \quad j = 1, \ldots, 32 \]  

In Eqs. (6) and (7) \( N_j \) is the population of the \( j \)-th State. Each one of Eqs. (6)–(10) governs the dynamics of pandemic inside each State of Mexico as a homogeneous region with no interaction with other states or surrounding geographical inhabited zone. In this sense, each State is isolated from the surrounding States (or a neighboring country or the sea). Here, it appears convenient to introduce new terms quantifying the interaction through state boundaries and the fact that a portion of the sea). Here, it appears convenient to introduce new terms quantifying the isolated from the surrounding States (or a neighboring country or the Mexico as a homogeneous region with no interaction with other states or.

- The susceptible population is all the people inside each state. This population is able to travel through State boundaries.
- The exposed population can travel inside and outside the States.
- Infected persons do not travel anymore; they are in a hospital or at home.
- The mobility of susceptible and exposed people is proportional to its home.

We postulate that mobile populations follow a Fickian law, allowing to rewrite the Eqs. (6) and (7) as:

\[ \frac{d s_j}{d t} = -\beta_j \frac{A_j}{N_j} s_j i_j + D_j \nabla^2 s_j, \quad j = 1, \ldots, 32 \]  
\[ \frac{d e_j}{d t} = \beta_j \frac{A_j}{N_j} s_j i_j - \alpha e_j + D_j \nabla^2 e_j, \quad j = 1, \ldots, 32 \]  

Here the diffusion coefficient for each State is linearly approximated as a function of the initial density population:

\[ D_j = D_0 \rho_j^2, \quad j = 1, \ldots, 32 \]  

At this point, the scaling coefficient \( D_0 \) remains unknown, but it can be inversely inferred from daily infected data reported by the public health authorities of Mexico. The basis of Eq. (18) is that more populated states must present major mobility (diffusion) of people. It is consistent with the fact that the most populated states show the most active epidemic. Eventually, if one state shows exposed people, they can infect healthy people inside and outside the state by diffusive mechanisms.

From the point of view of the dynamics of the epidemiological system, an important interaction is established between susceptible (S), exposed (E), and infected (I) people. From the mathematical model, it can be observed that there are feedback effects between exposed (E) and infected (I), which are crucial in the prediction of epidemiological parameters, including the diffusive effects proposed in this work. The recovered (R) and Deaths (D), do not influence the dynamics of S-E-I. However, they are essential as epidemiological parameters, important in making decisions about public health policies. According to the above, the SEIR and SEIRD models can be applied indistinctly to describe diffusive processes epidemiological [dSEIRD model, given by Eqs. (8–10) and (16,17)]. Another reason for including the death rate in the epidemiological model is that the available records of this variable have the lowest level of uncertainty compared to the information of infected or exposed people. Although, it should be said, the model for the deaths rate is very simplistic, as demonstrated further from the numerical predictions, and that better proposals are needed.

Application to the Mexico case

With the end to be implemented, the dSEIRD model requires the population density for each State. This information is summarized in Table 1. Such data were used as the initial condition for the susceptible population, i.e., \( s_j = S_j^0 \) at \( t = 0 \). At this point, we noticed that the actual infected data per State reported by the Mexico government could be employed to solve (in retrospect) the set of differential equations, on the fact that the infection variations per day are known, i.e.

\[ \frac{d I_j}{d t} = \text{known}, \quad j = 1, \ldots, 32 \]  

Other parameters are approximated based on known facts. For instance, we use one average period of 21 days for the recovery of infected people (\( T_r = 21 \) d), and one incubation period of about 15 days (\( \tau = 0.067 \)). With this, the degrees of freedom of the mathematical model are reduced to just 2: the scaling coefficient for diffusion (\( D_0 \)) and the infection rate (\( \beta \)). The fraction of people who died (\( I \)) can be calibrated further as it is a direct function of the infected people.

The dSEIRD model was numerically solved in the commercial software Comsol Multiphysics, which is based on finite element numerical routines. In this software, the solution domain is discretized into numerous subdomains, where each unknown variable is solved at each time step. In our calculations, we ensure that model results develop a weak dependency with the number of subdomains. This condition was found with the grid mesh depicted in the Fig. 1.

We investigate and analyze the effect of the scaling coefficient over the evolution of daily new infected people in the whole country. This parameter could directly be related to some massive government policies implemented to contain the epidemic, such as lockdown of public activities and reducing the non-essential activities in the economic and productive sectors. This hypothesis needs to be confirmed with the available information and it is a matter of a future work to understand the impact of massive policy on the epidemic evolution. In our work, we define different values for this scaling parameter, \( D_0 = 1 \times 10^{10}, 1 \times 10^{10}, 1 \times 10^{10} \), \( 1 \times 10^{20} \), and \( 1 \times 10^{40} \text{ km}^2/\text{day} \), and show how the numerical results of the dSEIRD model compare against actual data, see Fig. 2. In such a figure \( t = 0 \) corresponds to the date of the first case of Covid-19 in Mexico, i.e., 19th February of 2020. We observe that the larger the coefficient, the more pronounced the predicted curve amplitude for the first infection peak (first 200 days approximately). Regardless of the parameter value, the model cannot accurately predict the first maximum value or when it took place, as we note delays in the first peak. However, it predicts reasonably well the second maximum and its respective date.

On the other hand, at late times, some scaling parameters values overpredict infected people maximum values. In general, the theoretical model predicts well the average trend of infections per day. In specific, the maximum values of infections per day are better predicted rather than the minimum ones.

As depicted in Fig. 2, there is no linear relation between the diffusion coefficient and the predicted infection curves. To identify the optimal value of \( D_0 \), we define an error function that depends on the difference between the real data and model predictions according to:

\[ \text{error} = \int_0^T (I_{\text{real}} - I_{\text{model}})^2 dt \]  

Note that we evaluate the error function for the whole time interval as a result of the estimation of infected people in all the States (sub-domains) in Mexico. It requires the solution of the coupled ordinary differential equations given in (8–10) in conjunction with the partial
differential equations given in (16) and (17). In this way, the estimation of the error function in terms of the scaling parameter is a computationally expensive procedure.

For the theoretical cases shown in Fig. 2, the Fig. 3 collects the error computed as a function of the scaling coefficient \( D_0 \) (including additional values of the diffusion coefficient). The error function has local and global minima hidden in an extensive interval of the scaling parameter. However, we found the optimal value that better estimates the dynamic behavior of the infected population. The optimum value that minimizes the error function is \( D_0 = 1 \times 10^{-24} \text{ km}^4/\text{day} \) (error = \( 6.1452 \times 10^{13} \)), and such a case is also plotted in the Fig. 2 (continuous solid blue line). We assumed that all the other parameters are constant and known so that the error function has only one unknown or fitting parameter. With this information and considering the definition (18), we found for Mexico that the diffusion coefficient ranges from \( 1.08 \times 10^{-23} \text{ km}^2/\text{day} \) (for Baja California Sur State) up to \( 6.1633 \times 10^{-21} \text{ km}^2/\text{day} \) (for Ciudad de México State). As the country has zones with low and high population density, this variability of the diffusion coefficient indicates significant differences in the dynamic evolution of the epidemiologic processes due to the local mobility of people.

In Fig. 4 we present predictions of the infected and exposed populations in Mexico based on the optimum value of diffusion coefficient. It is interesting to note that the number of exposed people is much larger than the infected people. This numerical result unveils the degree of transmissivity of the virus in a susceptible population, and shows that the basic reproduction number in Mexico, not evaluated in this work, is moderated compared to others obtained for viruses like measles or smallpox [23]. For the first 150 days, the exposed people reach almost 100,000 new cases per day, while for the second maximum period (about 350 days from the beginning of pandemic), the number is close to 180,000 new cases per day. Here comes the discussion about what is the real number of infected people in the whole population at a given time.

We must recall that the curve of infected people reported by the Mexican government is based on lab tests to detect Covid-19. However, many people do not take the lab test for some reason (i.e. they do not develop symptoms, live in places far from medical centers, insufficient lab tests,

### Table 1

Population density for each State of Mexico. From the INEGI Census 2020 [14].

| State                | Population density, persons/km² | State                | Population density, persons/km² |
|----------------------|---------------------------------|----------------------|---------------------------------|
| Aguascalientes      | 253.9                           | Ciudad de México     | 6163.3                          |
| Baja California     | 52.8                            | Durango              | 14.9                            |
| Baja California     | 10.8                            | Guanajuato           | 201.5                           |
| Campeche            | 16.1                            | Guerrero             | 55.7                            |
| Coahuila            | 20.8                            | Hidalgo              | 148.1                           |
| Colima              | 130.0                           | Jalisco              | 106.2                           |
| Chiapas             | 75.6                            | Estado de México     | 760.2                           |
| Chihuahua           | 15.1                            | Michoacán            | 81.0                            |
| Durango             | 14.9                            | Guanajuato           | 201.5                           |
| Estado de México    | 760.2                           | Hidalgo              | 148.1                           |
| Guanajuato          | 201.5                           | Jalisco              | 106.2                           |
| Hidalgo             | 148.1                           | Jalisco              | 106.2                           |
| Jalisco             | 106.2                           | Estado de México     | 760.2                           |
| Michoacán           | 81.0                            | Hidalgo              | 148.1                           |
| Mexico              |                                  | Guanajuato           | 201.5                           |
| Mexico              |                                  | Jalisco              | 106.2                           |
| Nuevo León          | 90.2                            | Veracruz             | 112.3                           |
| Oaxaca              | 44.1                            | Yucatán              | 58.7                            |
| Puebla              | 191.9                           | Tlaxcala             | 336.0                           |
| Quintana            | 41.6                            | Tabasco              | 97.1                            |
| Real data           |                                  | Real data            |                                  |

Fig. 1. Grid mesh employed to discretize the Mexico map.

Fig. 2. Comparison of new infected data per day for Covid-19 and the model results varying the scaling coefficient \( D_0 \).
false negative cases, etc.). The “meaning” of exposed people is that they have been in contact with infected people. One exposed person can, in turn, get the Covid-19 virus or not, and eventually, there are two other options: develop the symptoms or not. Thus, only one fraction of people with symptoms is confirmed through the lab test. In this sense and following this line of reasoning, the curve of exposed people plotted in Fig. 4 serves as the limit case where all those people being in contact with infected persons get Covid-19 and develop symptoms. In other words, it is the worst-case scenario of the pandemic.

Once the mathematical model has predicted the national cases of new infections per day, other derived information can be computed. On one hand for instance, the Fig. 5 presents the variations of new infected and exposed people per day for the States: Ciudad de México, Nuevo León, Jalisco, Querétaro, and Tabasco; these States have developed a significant number of infections and deaths. Undoubtedly, the Ciudad de México is the most affected community in Mexico since the number of infected and exposed people can be one order of magnitude larger than other states. One interesting result from the numerical simulations is that the number of new infected and exposed people in States different to the Ciudad de México depends weakly on the population density. The dynamic evolution of such variables depends, among other factors, on the local policies implemented by the state governments and how they attach to the federal guidelines. For instance, the dynamic behavior of the States Nuevo León and Querétaro, where the latter has more than twice the density population than the former, the number of infected and exposed is almost one order of magnitude less for Querétaro than for Nuevo León.

Besides, in the Fig. 6 we present the number of deaths and recovered people calculated as a function of time. We emphasize that the mathematical formulation for computation of death and recovery people of the SEIRD model is somewhat simplistic, according to Eqs. (4) and (5). The model assumes that recovered people have life-long immunity. Also, it neglects the fraction of the population that dies for other causes different to Covid-19. The parameter \( f \) depends on multiple factors, including comorbidities in some population sectors and uneven distribution of hospitals in the country. Also, this parameter \( f \) can present dependency with time mainly by i) periods when the hospitals are fully saturated, ii) the usage of disuse of certain drugs, iii) the beginning of vaccination application, iv) when there are not available hospitals then the shortage of medicinal oxygen for in-house treatment becomes critical. In this sense, the postulation of a constant rate of deceased people (constant \( f \)) is unrealistic, very restrictive, and it is not enough to capture the complex national dynamics.

We understand the need for robust epidemiologic models that accurately describe the measured dynamic information. However, the available models and their parameters are calibrated to well-known epidemics. If one uses such models, additional investigation of the proper parameters is required since the virus is new to humanity and it is not yet well understood its transmission mechanisms or how the immune system responds to invasion. A straightforward approach that we followed in this work is considering all the model parameters constants. As previously stated, the rate of mortality \( f \) has high uncertainty as it depends on multiple factors. In the Fig. 6, left graphic, we show the diffusional dSEIRD model’s numerical solution for various values of \( f \). The national cases of deceased people are included for comparison. As long as \( f \) increases, the curve of death people substantially increases in one exponential manner. As said before, the simple Eq. (5) is not enough to follow, at least quantitatively, the scenario of mortality in Mexico. The right graphic of Fig. 6 presents the computed estimation of recovered people from the state of infection. In general, we see that practically this sector remains invariant regarding the fraction of death people.
The inter-State spreading of exposed people

In this section, we focus on estimate the mobility of exposed people between adjacent States in Mexico. It is a critical feature of the Covid-19 pandemic since this sector of the population eventually yields the beginning of infections in places with no cases. The reduction of the mobility of exposed people would help to a rapid descent of Covid-19 cases. Nevertheless, this sector of the population is unknown; thus, defining public policies oriented to reduce mobility is challenging. In this sense, to contain the rapid spread of the Covid-19 virus, some countries have decreed a curfew or, even worse, closed their boundaries for a certain time with devastating economic and social consequences. In the Fig. 7, we present the logarithm of density of exposed people (the logarithm operation is to contrast the values between States) for States of Mexico at four moments of the pandemic: at 100, 200, 300, and 350 days from the beginning. It is clear that the central region of the country has been the most affected zone including mainly: Guanajuato, Querétaro, Hidalgo, Estado de México, Ciudad de México and Tlaxcala. Other States have presented consistently low degrees of exposed people, for instance: Campeche, Chihuahua, Chiapas, and Durango. These latter States present up to 5 orders of magnitude lower exposed people than the Ciudad de México.

One characteristic of the diffusional dSEIRD model is the ability to predict the movement of certain population sectors (susceptibles and exposed) in the country. In this case, only those equations including the diffusive term, i.e., Eqs. (16) and (17), allow the computation of transport of susceptible and exposed populations through State boundaries. The susceptible population in Mexico is large (more than 120 million) compared to the exposed and infected people, and for this reason, the susceptible population over time practically remains constant. However, the dynamic of exposed people is interesting and it includes the magnitude and direction of this sector between the States of Mexico.

With the aim to understand the movement of exposed people, in the Figs. 8 and 9 we have plotted cone vectors for two regions of Mexico concerning the quantity:

\[
\text{Movement of exposed people} = -D_j \nabla e_j, \quad j = 1, ..., 32
\]
This quantity has units: persons/(km d). In the Fig. 8 we focus on the States surrounding Ciudad de México. The length of cone vectors relates to the magnitude of movement of exposed people [persons/(km d)]. To a better visualizing, places with the smaller activity have been logarithmically magnified to contrast with the zones with major movements. In our approach, we considered the States as homogeneous regions with constant diffusivity regardless of the real distribution of cities and small communities; hence, the most important phenomenon occurs at boundaries between States. According to Fig. 8, it is clear that migration of exposed people occurs from Ciudad de México to Estado de México and Morelos. Eventually, Estado de México diffuses exposed people to surrounding States as Guerrero and Hidalgo, but with a much smaller quantity. As long as time passes, the migration of exposed people increases, and it is notoriously major at 350 days which coincides with one of the critical periods of Covid-19 infections in Mexico (December 2020-January 2021).

This type of analysis is also applied for the central region of Mexico, where a large number of exposed people is calculated according to Fig. 7. Thus, the movement of this sector of population is inferred through the cone vectors plotted in Fig. 9. For this region of the country,
there is not a clear predominancy as the Ciudad de México case. But however, one can infer that the zone including Querétaro, Hidalgo, and Estado de México is the most affected concerning the transmission of COVID-19 to healthy people. Guanajuato and Querétaro act as source of exposed people to surrounding States as San Luis Potosí, Jalisco and Michoacán. The mobility of exposed and susceptible populations plays a crucial role in the virus spreading. We observe that even the pandemic and its effects are pronounced in Mexico, certain part of the population travels between States; they do not stay at home as the authorities recommend. The reason for this is that it is not sustainable the lockdown for a long time.

Mexico’s government announced a monitoring system for each State of Mexico to regulate the use of public spaces in accordance with the risk of COVID-19 contagion, called traffic light of epidemiological risk, which is made up of four colors: red, orange, yellow and green [1]. The red color represents the highest epidemiological risk where only essential economic activities are allowed, meanwhile in the green color all the activities are allowed. The traffic light color is evaluated each 15 days. Including epidemiological interaction between regions (States of the Republic) in the traffic light criteria would represent a benefit. The results generated with the diffusional-based model may support decisions in public health policies inasmuch as the intensity and direction of migration flow through inter-States boundaries is a natural result in our simulations. The government may establish timely schedules for transit through States with major infection rate so the infection spreading to neighboring States with minor infection rate be delayed and/or damped.

In the same line of reasoning to outline control measures, Liu et al. [19] characterized the Sichuan epidemic outbreak and estimated the impact of interventions in limiting SARS-CoV-2 transmission, which allowed the adoption of measures control to reduce the duration of the pandemic. Later, Liu and coworkers [20] presented the development of a computational model based on SARS-CoV-2 transmission data to investigate the effect on COVID-19 outbreaks of school closure strategies based on syndromic surveillance and antigen detection in the students.

Conclusions

We propose a diffusional model to describe the spatial spreading of Covid-19 through Mexico, taking into account daily information reported by the federal authorities regarding infected and death cases. We use the epidemiological compartmental SEIRD model with constant parameters, and including diffusional coefficients depending on the population density of each geo-politic State. Furthermore, we assume that exposed and susceptible populations may displace proportionally to the population density in their corresponding States. In this way, we determine the mobility of susceptible and exposed populations in the center of Mexico. As the pandemic advance in Mexico, the number of infected people increases their displacement from States with high cases to those States with lower infection cases. This is evident when we analyze the mobility at the Ciudad de México boundaries.

Understanding the mobility of susceptible and exposed populations is highly relevant for i) implementing public policies in the case of new Covid-19 variants coming from abroad and ii) to contain the spreading of virus by specific local and regional vaccinations strategies. This diffusional model may be adapted to more complex epidemiological models, to encompass hospital saturation, cases of reinfection, and the federal campaign of vaccinations. The diffusive (dSEIRD) model is more realistic than lumped models and unveils valuable information like intensity and direction of the migration flow between States relevant to implement some containing campaigns.

The results suggest the need for time-dependent coefficients in the dynamics governing the infected and the dead people. The solution is a combination of exponential functions with maxima values located at different time intervals, so it is not possible to capture this non-monotonous dynamic behavior with constant model coefficients. In a future work, we will tackle the problem of incorporating time-dependent parameters in a diffusive model.

CRediT authorship contribution statement

Carlos G. Aguilar-Madera: Methodology, Software, Formal analysis, Validation, Writing – original draft. Gilberto Espinosa-Paredes: Investigation, Formal analysis, Validation, Writing – original draft. E.C. Herrera-Hernández: Formal analysis, Validation, Writing – original draft. Jorge A. Briones-Carrillo: Conceptualization, Resources. J. Valente Flores-Can: Conceptualization, Resources. Víctor Matías-Pérez: Conceptualization, Resources.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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