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A lattice gas model for infection spreading: Application to the COVID-19 pandemic in the Mexico City Metropolitan Area

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**Abstract**

In this work, we propose a 2D lattice gas model for infection spreading, and we apply it to study the COVID-19 pandemic in the Mexico City Metropolitan Area (MCMA). We compared the spatially averaged results of this model against the MCMA available data. With the model, we estimated the numbers of daily infected and dead persons and the epidemic’s duration in the MCMA. In the simulations, we included the small-world effects and the impact of lifting/strengthen lockdown measures. We included some indicators of the goodness of fit; in particular, the Pearson correlation coefficient resulted larger than 0.9 for all the cases we considered. Our modeling approach is a research tool that can help assess the effectiveness of strategies and policies to address the pandemic phenomenon and its consequences.

**Introduction**

The COVID-19 disease, first identified in December 2019 in Wuhan (China), has spread worldwide with devastating health consequences, producing a growing number of fatalities and a significant disruption in the social, economic, and educational organizations in all countries. The World Health Organization (WHO) formally declared the COVID-19 outbreak as a Global Pandemic on March 11, 2020. See [1,2] for a general review. Since then, trying to control the dynamics of the infection spread, most countries in the world, following the spirit of China’s disciplinary measures, have applied strict or gentler rules for social distancing. It is estimated that more than half of the entire humankind has been affected by drastic restrictions in their movements and social relationships. Surprisingly, although it was globally known that an impending pandemic would occur, governments, social policies, and health systems all over the countries were not prepared to manage this situation [3].

The spatial and temporal evolution of the infection spreading is critical for the battle against the pandemic. The responsibility of defining and implementing the spread containment strategies lies in the policymakers, who have to make critical decisions with limited factual information. After the pandemic outbreak, the decision-makers require reliable information for detailed planning, such as the pandemic’s peak arrival, the number of hospital beds needed at worst times, and deciding on lifting or strengthening the lockdown, finally for returning (if possible) to usual living.

On a large scale, the spread of viral pathogens should be considered one of the main threats to humanity and society. Consequently, there is an urgent and immediate need for the scientific community to act together and provide novel and better methods, strategies, forecasting techniques, and models, which allow to understand and mitigate the effects of the present and future pandemics [3]. In public health, epidemiological modeling approaches play decisive roles in producing evidence in response to novel viral outbreaks (Ebola, SARS, MERS, and currently COVID-19) and eliminating chronic infections (as with HIV, viral hepatitis, and tuberculosis). In the case of SARS-Cov-2, mathematical models that project disease outbreaks and the potential effects of interventions have played a critical role and have become ubiquitous as proactive governance tools [4].

Modeling and predicting the outbreak’s evolution in each region can help manage and hold the disease spread and balance public health’s impact versus the economic crisis. However, based on limited information on the COVID-19 cases, it is quite challenging to predict how the pandemic will evolve. It is related to many issues that one has to consider, such as the spread dynamics, virus incubation time, transmission rates, demographics, restrictions of social mobility, individual protection measures such as using protective masks and hygiene procedures, meteorological factors, among others. Even so, promising modeling approaches can reveal reliable aspects of pandemic evolution and serve as tools for decision-makers in any country to study how the different strategies are changing the evolution of the COVID-19 pandemic [5].

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Fig. 1. Two and three-particle collisions. Collisions do not depend either affect the color of the involved particles.
This situation leads the community of mathematical epidemiologists to search for diagnostic and prognostic models of outbreak dynamics during the active phase [4]. With these models, scientists try to estimate the future impact of COVID-19 on the population and evaluate the measures required from the public health system and the effectiveness of different quarantine strategies. They are proposing various models to achieve this goal, ranging from the very simple to the complicated. However, in general, detailed models include many variable parameters and require a large amount of detailed statistical data for validation that is not available in most countries. Maybe the prominent example is the Chinese outbreak, where the more extensive specification of affecting factors and decease statistics is available [6–8], but for the rest of the world, the available data variety is quite limited. It speaks in favor of simple models, mostly regression and compartmental ones, such as the SIR and SEIR models and their variants [5,9–14].

Deterministic models have a long history of application to the study of infectious disease epidemiology. Roberts et al. [15] discussed the uses and limitations of deterministic models as approximations to stochastic systems. Spatially extended stochastic processes in epidemiology lead to the classical reaction-diffusion process when an infection spread only locally. However, epidemiological spreading happens not only from person to neighboring person but often over vast distances when infected but asymptomatic persons travel and carry infection to others far away. Fractional derivatives [16,17] generalize this notion, especially fractional Laplacian operators, leading to Lévy flights and sub- or super-diffusion. Mainly, super-diffusion is a more realistic mechanism of spreading epidemics than ordinary diffusion [18,19]. Fractional calculus is a field in which many models have yet to be introduced, debated, and applied to real-world applications in many science and engineering branches, where non-locality plays a crucial role [20].

Numerous recent works illustrate the use of fractional calculus in epidemiology. In [21], the authors illustrate the fractional approach with an outbreak of dengue disease recorded in 2009 in the Cape Verde islands off the coast of West Africa. The numerical simulations showed that the fractional models fit better the reality than the standard differential models. In [22], the authors developed a fractional MSEIR model involving the Caputo fractional derivative and computed the equilibrium points and the basic reproduction number. Additionally, they carried out numerical simulations of the varicella outbreak among Shenzhen school children, China. Qureshi [23] proposed a new

Fig. 2. Infection dynamics at the lattice sites.

Fig. 3. Screenshot of the simulation of the infection spreading phenomenon using the lattice gas model here proposed.
epidemiological system for the measles epidemic via the Caputo fractional order operator, a nonlocal operator with all the epidemic characteristics concerned with memory. Singh et al. [24] use a new Caputo-Fabrizio [25] fractional derivative with a non-singular kernel in a modified epidemiological model for the computer viruses and discussed the exactness and uniqueness of the solution by applying the fixed-point theorem. Danane et al. [26], motivated by previous works on the hepatitis B virus and fractional derivative equations, include a memory term represented by a fractional derivative in each component of the hepatitis B viral dynamics. They proved the solutions’ positivity and boundedness and established that their model has three steady states: the disease-free equilibrium, the infection steady state without humoral immunity, and the infection steady state with humoral immunity. Uçar et al. [27] analyzed the contribution of the Atangana-Baleanu derivative [28] on the smoking model introduced by Zaman [29]. In [30], Ali et al. reported a numerical and analytical study of the HIV-1 infection of CD4+ T-cells conformable fractional mathematical model. They studied the model analytically by Kudryashov and modified Kudryashov methods [31] and numerically by finite difference method, and discussed how accurate the solutions could be obtained from analytical and numerical methods.

On the other hand, the cellular automata techniques constitute a conceptually straightforward constructive method for modeling dynamical systems where self-organization patterns, which arise from simple rules, are revealed in complex phenomena in a wide range of research fields in mathematics, physics, economics, and social sciences. The books of J. L. Schiff [32] and A. Ilachinski [33] provide excellent introductions to cellular automata. The book of B. Chopard and M. Droz [34] and the work of F. Bagnoli [35] illustrate the application of cellular automata to model physical and other systems.

This paper proposes and applies a data-driven modeling approach based on the 9-velocities lattice gas cellular automata [36] to simulate the spread of the COVID-19 infection in the Mexico City Metropolitan Area (MCMA). Several efforts have been made for building cellular automata [37–45] or agent-based [46–49] models for epidemics; however, to the best of our knowledge, the present work is the first attempt done for using the lattice gas cellular automata to predict the COVID-19 spreading in the MCMA.

Fig. 4. Delegations of Mexico City and municipalities of the State of Mexico constituting the Mexico City Metropolitan Area, as considered in this work.
Methods and data

We propose and apply a lattice gas approach to model the spread of COVID-19 infection in the Mexico City Metropolitan Area (MCMA). Here, we describe the cellular automata model and the available data on the pandemic evolution of the COVID-19 disease in the MCMA.

The lattice gas model

The lattice gas models are dynamical systems consisting of a regular lattice where any site has several states representing the directions of motion of the gas particles and evolve in discrete time steps obeying homogeneous local rules, which must warrant conservation of mass, momentum, and energy during the propagation and collisions of the particles. Lattice gas models constitute an efficient way to simulate viscous flows at moderate Mach numbers in complex boundary conditions. The most straightforward lattice gas with thermal properties is the nine-velocities model defined on a square 2D lattice where the particles may be at rest or traveling to the nearest or next nearest neighbors [36,50–53].

Our lattice gas model is a cellular automaton defined on a 2D Cartesian grid of unit squares, whose vertices are points (sites) on the nine-velocities model defined on a square 2D lattice where the particles may be at rest or traveling to the nearest or next nearest neighbors [36,50–53].

The state at any lattice site \( x \) may be at rest or traveling to the nearest or next nearest neighbors [36,50–53].

Here, we describe the cellular automata model and the available data on

\[
\psi(x, t) = \begin{bmatrix} S(x, t) \\ E(x, t) \\ I(x, t) \\ H(x, t) \\ R(x, t) \end{bmatrix}
\]

\[
\psi(x, t + 1) = X^C M[\psi(x' . t)]_{x', c_V}
\]

Here \( V \) is the neighborhood of site \( x \) that includes the site \( x \) itself and the nearest and next-nearest neighbor sites of site \( x \). When necessary, we can introduce additional operators to consider boundary conditions

The particles that arrive at one site may collide with each other, but the collisions are constrained to conserve the number of particles, momentum, and kinetic energy. The collisions do not affect the particles’ colors, although the particle color may change according to given color transition probabilities.

Three transition operators express the model dynamics: streaming (M), collision (C), and color change (X):

Table 1

Mexico City and the Surrounding Municipalities [56,57].

| Name                  | Entity      | MCMA Quadrant | Population | Area [km²] | Mean Density [hab/km²] |
|-----------------------|-------------|---------------|------------|------------|------------------------|
| Cuautepec CDMX        | Downtown    | CDMX SW       | 548,606    | 32.5       | 16880.2                |
| Cocula de            | EDOMEX NE   | 310,743       | 35         | 8878.4     |
| Berriozabal CDMX     |             |               |            |            |                        |
| Cuautitlan EDOMEX NE |             | 175,004       | 40.8       | 4289.3     |
| Ecatepec de           | EDOMEX EDOMEX NW | 1,707,754  | 156.2      | 10933.1    |
| Morelos EDOMEX NE    |             |               |            |            |                        |
| Gustavo A             | EDOMEX NE   | 1,176,967     | 87.9       | 13389.8    |
| Madero Tecamac       | EDOMEX NE   | 500,585       | 169.9      | 3190.5     |
| Xochicalco           | EDOMEX NW   | 262,015       | 428.1      | 710.2      |
| Venustiano            | CDMX NE EDOMEX NW | 433,231     | 33.9       | 12779.7    |
| Carranza Atizapan de | CDMX NW     | 557,108       | 92.9       | 5996.9     |
| Zaragoza Azcapotzalco| CDMX NW     | 408,441       | 33.5       | 12192.3    |
| Cuautitlan            | EDOMEX NW   | 577,190       | 110.1      | 5242.4     |
| Iztacalco             | EDOMEX NW   | 910,187       | 157.9      | 5764.3     |
| Naucalpan de          | EDOMEX NW   | 441,064       | 232.6      | 1896.2     |
| Josefa Ramirez        | EDOMEX NW   | 756,537       | 80.4       | 9409.7     |
| Nicholás Romero       | EDOMEX NW   | 556,493       | 70.8       | 7860.1     |
| Tlatelolco de         | EDOMEX NW   | 379,624       | 46.4       | 8118.6     |
| Iztapec              | EDOMEX SE   | 397,344       | 225.2      | 1764.4     |
| Chimalhuacan          | EDOMEX SE   | 226,911       | 42.1       | 5389.8     |
| Ixtapalapa            | EDOMEX SE   | 1,819,551     | 113.2      | 16038.4    |
| La Paz                | EDOMEX SE   | 309,596       | 36.6       | 8458.9     |
| Milpa Alta            | CDMX SE     | 139,371       | 298.2      | 467.2      |
| Nezahualcoyotl        | EDOMEX NW & SW | 1,135,786  | 63.3       | 17942.9    |
| Tlalnique             | CDMX SE     | 366,586       | 85.8       | 4272.6     |
| Valle de Guadalupe    | CDMX SE     | 419,700       | 46.6       | 9064.4     |
| Solidaridad Xochimilco| CDMX SE     | 418,060       | 114.1      | 3664.0     |
| Alvaro Obregon        | CDMX SW     | 755,537       | 95.9       | 7878.4     |
| Benito Juarez         | CDMX SW     | 433,708       | 26.7       | 16243.7    |
| Coyocac              | CDMX SW     | 621,952       | 53.9       | 11539.0    |
| Cuajimalpa de         | CDMX SW     | 199,809       | 71.5       | 2974.5     |
| Morelos Xicomanio     | EDOMEX SW   | 290,231       | 140.9      | 2059.8     |
| Chimalhuacan          | CDMX SW     | 245,147       | 63.4       | 3868.7     |
| Cuautitlan            | CDMX SW     | 682,234       | 314.5      | 2149.3     |
| Total                 |             | 19,824,134    | 3989.4     | 4969.2     |
The streaming operator (M) explores the neighborhood $V_x$ and move to site $x$ all the particles with velocities pointing toward the site $x$, respecting the colors. If one particle is at rest at site $x$, it remains there. The collision operator (C) takes the streaming operator’s output and performs the collision among the particles that arrived at the site $x$. Operator C conserves the number of particles at the site, the number of particles of each color, momentum, and kinetic energy. Dynamically, the collisions are independent of the color of the particles.

Fig. 1 presents the possible two and three-particle collisions with outputs different from the inputs [36].

In this Figure, the arrows, which were colored just for illustrating the presence of several particle species, represent the moving particles; a small circle represents a particle at rest. In this Figure, we can observe that the collision configurations presented in any box exhibit the same number of particles, total momentum, and total kinetic energy.

The color operator (X) changes the color of the particles arriving at any lattice site according to given transition probabilities: $p_{SE}$ (susceptible become exposed), $p_{EI}$ (exposed become infectious), $p_{IH}$ (infectious become hospitalized), $p_{HR}$ (hospitalized become recovered), $p_{IA}$ (infectious become ambulatory), $p_{AR}$ (ambulatory infectious become recovered), and $p_{RS}$ (recovered become susceptible again). The probability that hospitalized people die is $p_{ID} = 1 - p_{HR}$, and the probability that ambulatory people die is $p_{AD} = 1 - p_{AR}$. Fig. 2 illustrates this transition process with a compartmental scheme.

In the computer simulation model, we implemented the transition probabilities between species with the possibility of changing their values as a function of time and position, which may be useful for considering control strategies such as lockdown or exit of lockdown conditions. We also introduced the possibility of effects like the small-world phenomenon during the simulation. Small-world effects helped to consider the possibility of speedy displacement of infectious people between sites far away from each other [37]. Fig. 3 shows one screenshot of the infection spreading simulation with the proposed lattice gas model.

**The Covid-19 data in the Mexico City Metropolitan Area**

The Secretaría de Salud (Ministry of Health) of the Mexican Federal Government, through its Dirección General de Epidemiología (DGE) and based on the applicable regulations in the matter of open data, makes available to the general population the information from the Sistema de Vigilancia Epidemiológica de Enfermedades Respiratorias de México (Epidemiological Surveillance System for Viral Respiratory Diseases), reported by the 475 viral respiratory disease monitoring units throughout the country of the entire health sector regarding cases associated with COVID-19, to facilitate all users who require it, access, use, reuse, and redistribution of it [54, 55]. In particular, the open data associated with COVID-19 confirmed infections and deaths in Mexico City (CDMX) and the Mexico City Metropolitan Area (MCMA), including population, can be obtained through the web site of CentroGeo-GeoInt [56].

For the present work, we assumed that MCMA comprises only Mexico City (CDMX) and the nearest and next-nearest municipalities of the State of Mexico (EDOMEX) that surround it (Fig. 4 and Table 1). This region comprises near 20 million inhabitants distributed over an area of 3,989 km$^2$ (on average, this is equivalent to 4.5 inhabitants living in a 30 m-side squared space). Naturally, the population density in urban areas is larger than the mean density reported in Table 1.

In Fig. 5a, we presented the time series of the daily confirmed COVID-19 infections detected in the MCMA (and in its NE, NW, SW, and SE quadrants) from March 9 to August 31, 2020. In Fig. 5b, we show the fast Fourier transform of the time series of MCMA infections. It displays a 7-day periodicity, reflecting incomplete data recording during the weekend days (Saturday and Sunday). Therefore, we excluded the COVID-19 data reported during the weekend for the present work. In the graphs of Fig. 5a, we see that although the number of daily infections is decreasing significantly in the NW, NE, and SE quadrants (cyan, red, and green vertical bars), it continues to grow in the SW quadrant (yellow bars), although somewhat slowly.

In Fig. 6, we present MCMA time-series graphs (daily and cumulative) of reported COVID-19 data for confirmed infections and deaths from March 9 to August 31, 2020. These graphs do not include the reported data for the weekends. In these plots, it is interesting to note that
Fig. 6. COVID-19 data reported in the MCMA for confirmed infections and deaths (daily and cumulative) from March 9 to August 31, 2020. The graphs do not include the weekend days data.
the number of daily deaths has been consistently decreasing over the last three months (June, July, and August), although the number of confirmed daily infections has remained practically moving on a plateau. It indicates that the fraction of people recovered from the COVID-19 disease increases in the MCMA, reflecting an increasingly better medical management of the COVID-19 disease by the Ministry of Public Health.

The data reported on August 28, 2020, for the MCMA [4], show that 27% of the confirmed infectious people got hospitalized, while the rest (73%) remained ambulatory or confined at home. The fraction of the exposed people that result confirmed positive with COVID-19 was 0.45, on average. The fraction of deaths due to the COVID-19 disease was around 0.16. In Fig. 7, we present the time series (from March 9 to August 31, 2020) of the fractions of cumulative infectious over cumulative exposed people (CI/CE) and cumulative deaths over cumulative infected (CD/CI).

Results and discussion

For carrying out the computer simulations with the lattice gas model described above, we used a 300x300 lattice with periodic boundary conditions. As the initial condition, we assumed that all the particles represent susceptible people distributed randomly over the lattice with a mean density of 4.5 particles per site, with velocities randomly selected. We introduced a tiny number of infectious people (0.001 particles per site, on average) randomly distributed in the lattice.

We defined the transition probabilities as follows: pSE = 1, that is, we assumed that all susceptible particles arriving at one site become exposed if one or more infected particles are present there; 0.46 < pEI < 0.50, not all the exposed particles at any site become infectious (Fig. 7); pH = 0.27, as in the MCMA, we assumed that 27% of the infected particles went to the hospital; 0.12 < pID < 0.14, a small fraction of the infected particles die (Fig. 7), the rest get recover from the disease; and pRS = 0, we assumed no reinfecctions. To select the probabilities pEI and pID, we used the data reported in Fig. 7. We repeated ten times the computer simulation and averaged the results.

The computer simulation with the lattice gas model produced numerical solutions for the state field \( \psi(x,t) \) described in Section 2.1 (Equation (4)). For the collective state, we report the average behavior of the system in terms of the mean-field given by

\[
\Psi(t) = \frac{1}{L} \sum_{i=1}^{L} \psi(x_i,t) = \frac{1}{L} \sum_{i=1}^{L} \begin{bmatrix}
S_i(x_i,t) \\
E_i(x_i,t) \\
I_i(x_i,t) \\
D_i(x_i,t)
\end{bmatrix} = \begin{bmatrix}
S(t) \\
E(t) \\
I(t) \\
D(t)
\end{bmatrix}
\]

The corresponding cumulative series is given by

\[
\Omega(t) = \Psi(t) + \Omega(t-1), t = 1, 2, 3, \ldots
\]

with \( \Omega(0) = \Psi(0) \) In Eq. (6), we denoted with \( L \) the number of lattice sites.

In what follows, we presented and discussed only the daily confirmed infections \( I(t) \), the cumulative infections \( I_c(t) \), the daily deaths \( D(t) \), and the cumulative deaths \( D_c(t) \). We expressed the results for every million inhabitants; we divided the properties \( I_c, L, D, D_c \) by the number of gas particles in the system, and then we multiplied them by \( 10^6 \).

We applied the Nelder-Mead simplex optimization method [58,59] with three parameters to perform a best-fitting procedure of the numerical solution to the actual MCMA data. We assumed linear scaling between the cellular automaton times and the real times (2 fitting parameters), and between the amplitudes of the numerical and actual numbers of cases (1 fitting parameter).

For example, if the \( F(t) = \{ (t, D_k) | k = 1, 2, \ldots, N \} \) is the data series registered for the daily deaths due to COVID-19 disease in the MCMA during \( N \) days of the pandemic evolution, and \( G(t) = \{ (t, D_k) | k = 1, 2, \ldots, M \} \) is the series of \( M > N \) estimations obtained with the lattice gas model, we used the simplex optimization method to find the values of the parameters \( A, B, \) and \( M \) that minimize the functional

\[
\Lambda(A, B, M) = \sum_{i=1}^{N} |AG(Mt + B) - F(t_i)|^2.
\]

In Figs. 8–11, we present the results of the best fittings of the lattice gas simulations to the daily confirmed infections, cumulative infections, daily deaths, and cumulative deaths in the MCMA due to the COVID-19 disease. We included three indicators of the goodness of fit.

Daily and cumulative COVID-19 infections in the MCMA

Figs. 8a and 9a show the daily confirmed and the cumulative COVID-19 infections in the MCMA (open circles) from March 9 to August 31, 2020. The same Figures present the corresponding estimations made with the lattice gas model (solid line), which we extended until the end of 2020. In the Figs. 8b–d and 9b–d, we have included three indicators of the goodness of fit: plot of the adjusted lattice gas estimations versus the observed data, the frequency distribution of the deviations, and the plot of the normal probability of the deviations, respectively.

We defined the MCMA COVID-19 pandemic’s horizon as the number of days elapsed between the dates where the number of confirmed infections is 10% of the maximum. According to this definition, the intersections of the curve of the lattice gas estimations with the dotted
straight line shown in Fig. 8a, the horizon of the pandemic in the MCMA will be of 218 days (from April 2 to November 5, 2020), with a reduction to 150 daily confirmed infections, approximately.

On the other hand, the estimations of the cumulative COVID-19 infections in the MCMA (Fig. 9a) show that by November 5, 2020, there will be occurred around 170,000 confirmed infections.

For September 10, 2020, the numbers of daily and cumulative infections reported in the MCMA were 1195 and 154,212. The predictions made by the model for this date were 727 and 152,329 daily and cumulative infections on average, showing point underestimations around 39% in the first case but around 1% in the second one.

From March 9 to August 31, 2020, the medians of the absolute percent deviations between the model estimations and the MCMA data were 8.8% for the daily infections and 2.2% for the cumulative infections.

It is convenient to remember that the region we call MCMA is smaller than the actual MCMA. In this work, we only considered the 16 Delegations of CDMX and 19 Municipalities of the EDOMEX, comprising 19,824,134 inhabitants. The complete MCMA includes its 16 Delegations and 60 Municipalities of EDOMEX, with 21,942,666 inhabitants. Then, the region we considered contains 90% of the actual MCMA population. If we count this observation, the cumulative infected cases could be 189,000 in the complete MCMA by the beginning of November.

Fig. 8. Daily confirmed infections in the MCMA from March 9 to August 31, 2020. (a) Lattice gas model estimation (solid line) and data (open circles). The optimization procedure gave the following values for the fitting parameters and the Pearson Correlation Coefficient: A = 0.003133, B = 0, M = 2.54, and PCC = 0.9574. (b) Estimation vs. Data. (c) Frequency distribution of deviations. (d) The plot of the normal probability of deviations.

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Daily and cumulative deaths in the MCMA during the COVID-19 pandemic

Figs. 10a and 11a show the records (open circles) and estimations (solid line) of the daily and cumulative deaths due to COVID-19 infections in the MCMA. Figs. 10b–d and 11b–d show the adjusted lattice gas estimations’ plot versus the observed data, the frequency distribution of the deviations, and the plot of the deviations’ normal probability.

About the daily deaths by the COVID-19 disease (Fig. 10a), the lattice gas model predicted a horizon of 172 days (from April 4 to September 22, 2020), with 20 daily deaths on average by the end of September. On the other hand, the model estimation of the cumulative deaths (Fig. 11a) gave 16,060 for the same period and predicted 16,300 dead people for November 5, 2020. In the complete MCMA, the number of deaths could be 18,200 by the first days of November.

For September 10, 2020, the numbers of daily and cumulative deaths reported in the MCMA were 50 and 16,609. For this date, the model predictions were 30 and 15,844 daily and cumulative deaths on average, which correspond to point underestimations around 40% in the first case, and around 5%, in the second one.

From March 9 to August 31, 2020, the medians of the absolute percent deviations were around 17% and 2.6% for the daily and cumulative deaths.

Conclusions

In this paper, we presented a nine-velocities lattice gas model with
six species of particles dynamically equivalent. We identified the species by colors and made to represent susceptible (S), exposed (E), infectious (I), hospitalized (H), recovered (R), and dead (D) individuals. The particles move on a square 2D lattice, collide with each other, and change from one species to another according to given transition probabilities, which may vary as functions of time. Also, we introduced small-world effects during computer simulations. We applied this model to estimate the numbers of infected cases and deaths due to the COVID-19 pandemic disease in the Mexico City Metropolitan Area. We used the COVID-19 data (from March 9 to August 31, 2020) made public by the Health Ministry of the Mexican Government. The simulations produced results that we fitted to the data using the simplex optimization method, with Pearson correlation coefficients larger than 0.9. The medians of the absolute percent deviations between the model estimations and the MCMA data were 8.8% for the daily infections, 2.2% for the cumulative infections, 17% for the daily deaths, and 2.6% for the cumulative deaths. We estimated that the horizon of the COVID-19 pandemic in the MCMA could extend until November 2020, with around 200,000 confirmed infections and 19,000 deaths. Although the simulations reported in this paper were restricted to obtain the mean time-series of infected and deaths, we can use the model to investigate other aspects of the phenomenon, such as the people’s mobility influence on the pandemic development. This model could shed some light on the different behavior observed for the infected and deaths in the MCMA quadrants. This study was carried out based on the MCMA available data (March 9 to August 31, 2020), which allowed to estimate the transition

![Fig. 10. Daily deaths due to COVID-19 disease in the MCMA from March 9 to August 31, 2020. (a) Lattice gas model estimation (solid line) and data (open circles). The simplex optimization procedure gave the following values $A = 0.00692$, $B = -0.165$, $M = 2.04$, and $PCC = 0.9428$, for the fitting parameters and the Pearson correlation coefficient. (b) Estimation vs. Data. (c) Frequency distribution of deviations. (d) The plot of the normal probability of deviations.](image)
probabilities from exposed to infected (0.46 < pEI < 0.50), from infected to dead (0.12 < pID < 0.14), and hospitalizing infected individuals (pIH = 0.27), as reported in Fig. 7. The model did not consider the number of unreported symptomatic infectious neither other factors such as the possibility of the virus spreading through interspecies transmission or the transfer of the virus from the reservoir to people. These possibilities were recently underlined and discussed by Gao et al. [60–62] within the Caputo fractional derivative framework.

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**CRediT authorship contribution statement**

Alejandro Salcido: Conceptualization, Methodology, Software, Investigation, Data curation, Formal analysis, Validation, Visualization, Writing - original draft.

**Declaration of Competing Interest**

The author declares that he has no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.
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