Spatial Scale Effects in COVID-19 Spread Models

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The COVID-19 pandemic has highlighted epidemiological models as important forecasting methods and planning strategies, with studies conducted using a wide variety of analytical and computational techniques. Knowing that more pandemic episodes may occur, it is essential that epidemiological modeling present increasingly credible results. From this perspective, this paper aims to highlight the influence of spatial distribution on an epidemic dynamic, using agent-based modeling. To calibrate the behavioral profile of the population, data was taken on mobility, population pyramid, individual behavior and government policies of a real population during the pandemic. Two different initial spatial distribution scenarios are tested and the robustness of the infection is analyzed. Totalistic rules were designed to assess the influence of infected individuals in the vicinity of an agent, a factor that must not be ignored in modeling respiratory diseases with viruses capable of spreading by aerosols, such as SARS-CoV-2. It is shown that the scenario with nonuniform distribution of agents is much more robust, generating an epidemic process even when uniform distribution, for the same parameters, did not propagate the infection. Our results also suggest that herd immunity is attained in different levels of recovered individuals, showing higher values in denser regions. In conclusion, it is reinforced that the nonuniform feature of the spatial distribution of individuals plays a key role in the infection dynamics and should receive more attention when building epidemiological models.

Keywords: complex systems; epidemiological modeling; spatial scale effects; spatial distribution in power laws; COVID-19

1. Introduction

Currently, the COVID-19 pandemic has placed the discussion about the spread of epidemics on the agenda of academia, research
institutions and society in general. Since 2020, human life on Earth has changed due to the COVID-19 pandemic, consequently leading to an explosion of epidemiological studies and also changing how and what scientists study [1]. In this sense, understanding the mechanisms underlying the dynamics of virus dissemination is essential to reduce the impact of this health problem on the population and help public agents to manage it, providing basic guidelines to mitigate the pandemic [2–4]. Early work at the start of the pandemic showed that social isolation and spatial distancing play a key role in flattening the infection curve [5], a decisive issue to protect countries’ health systems. This relevant conclusion based on a simple model illustrates the power of mathematical modeling to furnish valuable insights and solutions for real-world problems.

Agent-based modeling (ABM) consists of a particularly interesting approach to exploring spatiotemporal dependence and heterogeneity in the population, which are very important aspects of epidemics spreading [6–9], allowing tests of government policies on social stratification, age distribution [9] and population mobility [10] to be performed, also offering the possibility to combine social networks, epidemic compartmental algorithms and population behavioral aspects.

Epidemiological theory combined with network theory (joining social sciences and graph theory) has provided powerful techniques and tools for analyzing epidemics in human populations [11]. Most of these studies consider networks with uniform distribution of individuals (e.g., using random plots [12]), nonuniform distributions (e.g., using the lattice Boltzmann method network [13]) or an initial uniform distribution with inhomogeneous infection rates [14]. Defining the distribution of individuals is as important as establishing the other parameters of the model, since it strongly influences the likelihood of the results.

In a historical contribution, Zipf [15] found that, despite countries having different cultural and economic structures, people organize themselves into clusters [16, 17], and the size distribution of the population is efficiently approximated by power laws (known as Zipf’s law). These power laws are often interpreted as the macroscopic behavior of systems consisting of micro units [18]. Thus, the real population presents different scales (macro and micro) of interactions, a crucial factor for understanding social phenomena. Recently, the role of power law in population heterogeneity was reported as a key factor for epidemic propagation [19].

In this paper, we show how the pandemic spreads in a hypothetical country composed of nine hypothetical Federative Units (FU 1 to FU 9), considering an ABM [20] relying on an algorithm based on the
Barabási–Albert model [21, 22] to generate a power law distribution of individuals and a second scenario with a uniform distribution of individuals using random scattering. The population parameters, displacement rules and spatial and social characteristics of this hypothetical country are based on empirical data from the Brazilian FUs. Our goal is to clarify how spatial characteristics, taking population density as the main factor, could change an epidemiological process, emphasizing that we use an identical population calibrated from real data to analyze infection robustness in two different scenarios of spatial distribution.

2. Methodology

We performed extensive Monte Carlo simulations considering a network composed of nine square lattices with linear extension $L = 300$, periodic boundary conditions in both directions and sites with 10 m$^2$ of area. A simulation step is equivalent to 1 hour. Each simulated FU is characterized basically by its density. Daily, 20% [23] of the total population is transferred among the FUs, featuring a global scale of interactions (Figure 1): Most FUs send and receive agents (double

![Figure 1](https://doi.org/10.25088/ComplexSystems.32.1.71)

Figure 1. Interstate flows among FUs. Most FUs send and receive agents (double edges), whereas the single edge between FU 8 and FU 9 means that only FU 8 sends travelers in a direct flow. Also, we considered a bidirectional flow to keep the population size constant. 20% of the FUs population is tagged a priori as a potential interstate traveler, but a portion of these individuals is replaced by new individuals periodically. Daily, individuals were transferred between the FUs, respecting the empirical average quantities of air and road trips. Thicker edges indicate a more intense flow between the FUs.
edges), counting on bidirectional flows to keep the population size constant. In turn, individuals move through space performing Lévy flights [24], whose occurrence rate is directly linked to the age of each individual, considering smaller mobility for older individuals [25]. Those internal displacements comprise the local scale of interactions.

Identifying and understanding the virus spreading pathways is of crucial importance [3]. A key point of interest is the complexity of the airport system and how it is related to the spread of the virus during a pandemic process. Larger air networks, like Brazil’s air network [26], play a crucial role in the virus spread dynamics, since closer cities to airports were most affected by the transmission of the virus [27]. In each lattice of the model, the capital region concentrates about 70% [28] of departures and arrivals of travelers on interstate flights. The remaining trips were performed by road, in which the individuals can arrive (or leave) at any site of the lattice. Additionally, up to 25% of travelers are replaced periodically, configuring a process of traveler renewal (a method used to diversify the group of travelers among the FUs during the dynamic).

As stated in the previous paragraphs, only density is taken into account in the model to design spatial characteristics, having seen the computational limitations to reproducing the population and territorial extension of the states. Thus, the number of agents $N$ (Table 1) in each FU is based on the empirical population densities. The maximum number of individuals simultaneously occupying the same site is $Y = 7$ (this value corresponds to twice the average number of inhabitants per household in Brazil [29] in 2010). Once again, these values were chosen to make the simulations as credible as possible within the computational limitations.

<table>
<thead>
<tr>
<th>Federation Unit</th>
<th>Number of Agents $N$</th>
<th>Agent/Site</th>
</tr>
</thead>
<tbody>
<tr>
<td>FU 1</td>
<td>1537</td>
<td>0.017</td>
</tr>
<tr>
<td>FU 2</td>
<td>2644</td>
<td>0.029</td>
</tr>
<tr>
<td>FU 3</td>
<td>2120</td>
<td>0.024</td>
</tr>
<tr>
<td>FU 4</td>
<td>6728</td>
<td>0.075</td>
</tr>
<tr>
<td>FU 5</td>
<td>14785</td>
<td>0.164</td>
</tr>
<tr>
<td>FU 6</td>
<td>18000</td>
<td>0.200</td>
</tr>
<tr>
<td>FU 7</td>
<td>1004</td>
<td>0.011</td>
</tr>
<tr>
<td>FU 8</td>
<td>1351</td>
<td>0.015</td>
</tr>
<tr>
<td>FU 9</td>
<td>277</td>
<td>0.003</td>
</tr>
</tbody>
</table>

Table 1. Number of agents $N$ and population density in each FU.

Additionally, the model considers the period of individuals’ resting: two periods of 12 hours (day and night) were defined. During the night, only 10% [30] of the population (night workers) can move,
infect and become infected by the virus while the other 90% rest, staying as isolated individuals. During the day, the night workers rest and the remaining population can move, spread the virus and become infected by this pathogen.

### 2.1 Epidemiological Process Modeling

We built an epidemiological model in a scenario without vaccination and proven effective drugs, but considering non-pharmacological measures to combat the spread of the virus. Based on the SEIR model [31], after an agent has contact with the virus, during the first two days it is marked as “Exposed,” carrying the virus but not acting as a spreading agent. After two days, it becomes infected and can spread the virus, infecting other people for eight days and recovering 10 days after the first contact. Simulations were performed considering the first infected individual appearing in the epidemiological “week 0” (here, an epidemiological week does not follow the epidemiological calendar in its stricto sensu, having a chronological feature solely).

The mobility of agents and personal non-pharmacological adoption in the model is based on the pattern verified for the individuals during a period of the pandemic, behaviors resulting from individual opinions and adopted governmental policies. The data used in the model to stratify the population into groups with different levels of protective masks adoption and mobility is available in public repositories [32]. Individuals may change their opinion occasionally [33], thus altering their adherence to the use of protective masks, their level of mobility and switching the group to which they belong. The quantities of individuals in each group change over time, according to the epidemiological scenario divided into epidemiological phases [34–36]. In our model, the epidemiological scenario is composed of three epidemiological phases named blue, red and purple (Figure 2).

![Figure 2. The SMA is computed every 15 days. Then, σ is defined as the difference between the current SMA and the previous (15 days ago) SMA. If σ is less than or equal to −15%, the system regresses one epidemiological phase, for example, from purple to red. If σ is greater than or equal to +15%, the system progresses to the next more restrictive phase. If −15% < σ < 15%, the scenario is stable and the system remains in its current epidemiological phase.](https://doi.org/10.25088/ComplexSystems.32.1.71)
The epidemiological phases are switchable, with a switching process following a turnstile system (Figure 2): We evaluate the simple moving average (SMA) [37] of infection cases in 7 days every 15 days. Take $\sigma$ as the percentage difference between the actual value of SMA and the previous SMA’s value evaluated 15 days ago. $\sigma$ provides a quantitative measure for changing the epidemiological phases according to the intervals shown in Figure 2. If $\sigma$ is greater than or equal to $+15\%$, the system migrates to the next more restrictive phase (e.g., if the system is in phase red, it migrates to phase purple). If this difference is less than or equal to $-15\%$, the system migrates to the less restrictive epidemiological phase, going to phase blue if it was in phase red or to phase red if it was in phase purple. Finally, if this difference is greater than $-15\%$ and less than $+15\%$, the scenario is considered stable and the system remains in its current epidemiological phase, without changes. FUs can be simultaneously in different epidemiological phases. These population dynamics are identical in both scenarios of spatial distribution.

Our model has two infection probabilities: $p_1$ and $p_2$. The probability of infection $p_1$ is due to the infected individuals present on the same site $i$ as the agent under analysis. The probability of infection $p_2$ is due to the infected individuals situated in the eight sites $j$ of Moore’s neighborhood. These probabilities were obtained from transformations applied to a normalized random variable (the portion inside the square brackets in equations (1) and (2)) that deals with the variation in the number of infected people, considering the use of protective masks. A limiting parameter $p_g \in [0, 1]$ is implemented as a control parameter of the virus transmissibility [38]:

$$p_1 = \left[ \frac{(T_n)_i \cdot w_n + (T_m)_i \cdot w_m}{(T_I)_i} \right] \cdot p_g,$$

$$p_2 = \left[ \frac{\sum_{j=1}^{8} ((T_n)_j \cdot w_n + (T_m)_j \cdot w_m)}{\sum_{j=1}^{8} (T_I)_j} \right] \cdot p_g \cdot \phi.$$ (1) (2)

$T_m$ and $T_n$ are the quantities of infected individuals with and without protection masks in a determined site, respectively. The total of individuals in a specific site is given by $T_I$; $w_n$ and $w_m$ represent the statistical contribution of the infected individuals, considering protection mask usage: For an individual without a mask, $w_n = 1$, and $w_m = 1 - \epsilon$ for an individual with a mask. The protection mask efficiency is given by $\epsilon$. We considered $\epsilon = 68.5\%$ [39–41] in our analysis.

$p_1$ is associated with the probability of direct contamination over short distances [42] and, observing the size of the sites, $p_2$ represents the probability of infection by aerosol particles (the virus can spread
for a long distance in special atmospheric conditions as aerosol [43]). $p_2$ is also related to the occasional individuals’ movements from a site to a neighboring site between two successive simulation steps, configuring an important artifact that, indirectly, takes into account the eventual movements between two steps of a simulation with discrete time evolution. The parameter $\phi \in [0, 1)$ establishes the magnitude relation between $p_1$ and $p_2$, since it is expected that the probability of becoming infected at its own site $i$ is greater than becoming infected at a neighboring site $j$ ($p_1 > p_2$).

In the thirtieth epidemiological week, the parameter $p_g$ increases 1.6 times [44], with the intention of representing the new gamma $\gamma$ variant emergence in Brazil.

### 2.2 Uniform and Nonuniform Distribution of Agents

Uniform distribution of individuals was performed by assigning random positions to the agents, using a pseudorandom number generator [45]. To scatter the agents nonuniformly, the lattices have been divided into a grid with 16 subregions. Each of these subregions received an initial amount of agents proportional to the empirical intermediate and immediate geographic regions’ [46] population densities. Then, the agents were scattered using a technique based on the Barabási–Albert model [21, 22] to make a location with more individuals within itself and its vicinity more likely to receive new individuals. Therefore, the individuals are spatially distributed nonuniformly in clusters whose sizes have a power law distribution at the end of the process.

With a focus on maintaining the nonuniform distribution during the simulation time $T$, a statistical weight was assigned to the sites with more individuals, so the individuals are steered to stay in denser regions and shift if they are in a sparsely populated site. In the scenario with uniform distribution of individuals, the probability of moving does not depend on the population density of the sites, solely respecting the sites’ capacity $\Upsilon$.

### 3. Results and Discussion

Here, we present our results and discuss relevant remarks, mainly including the observation of how local and global interactions can interfere in the dynamics of spreading infections, making analyses to compare uniform and nonuniform (power law) distribution of individuals.

It is important to discuss in more detail the influence of parameters $p_2$ and $\phi$ used to model the transmission of the virus by aerosol particles, a substantial factor in airborne diseases like COVID-19. Figure 3
Influence of $\phi$ variation in the curves of infected ((a) and (c)) and recovered ((b) and (d)) for uniform (top) and nonuniform (bottom) distributions with $p_g = 0.06$. In both cases, $\phi$ has evident importance in the curves generated by the model, creating different qualitative and quantitative scenarios when individuals are nonuniformly distributed, (c) presenting rebounds. Furthermore, when $p_g = 0.06$ and $\phi = 0.0$, only nonuniform distribution presented an active spreading process. Figure 3 shows how $\phi$ can determine the duration and amplitude of the epidemiological waves. Considering $\phi = 0.0$, $p_g = 0.06$ and the individuals uniformly distributed, the epidemic process does not succeed, unlike the result obtained when considering the nonuniform distribution of individuals for the same values of $p_g$ and $\phi$, since this case presented an infection process with even lower values of these parameters. In turn, an intermediary value of $\phi$ ($\phi = 0.40$) culminates in an explosion in the number of new infections. In a scenario with individuals nonuniformly distributed, increasing $\phi$ also substantially increases the number of new cases; additionally, the waveforms showed rebounds (Figure 3(c)) due to spatial characteristics. Considering the same parameters in both cases, the epidemiological curves referring to the nonuniform distribution of individuals saturate much faster than when the individuals are uniformly distributed.
Choosing the amount of initially infected individuals and their locations influenced the epidemic models’ results tightly. Figure 4 shows the influence of different definitions of the initial number of infected individuals $I_0$ and their location considering uniform and power law distributions of individuals. Distinct initial localities provided different herd immunity levels (consider herd immunity the saturation level of the curves of recovered individuals). In a scenario of uniform distribution of individuals, when the first infected individual arrived in the FU with a lower density (FU 9), the infection process vanished. The same did not succeed when the individuals were nonuniformly distributed, showing an active infection process even when the first infected individual had arrived in FU 9.

Figure 4. Varying the initial number of infected individuals $I_0$ and the place of pandemic onset with uniform ((a) and (b)) and nonuniform ((c) and (d)) distribution of individuals. Parameters: $p_g = 0.06$ and $\phi = 0.30$.

Figure 5 shows the results of analyses performed to evaluate the influence of the renewal period of interstate travelers on the epidemiological curves and the number of infected individuals, using the curves

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Figure 5. Curves of recovered individuals, considering different periods of travelers’ renewal (up to 25% of travelers are periodically replaced by other individuals), considering uniform (a to d) and nonuniform (e to h) distributions of individuals. Periods of travelers’ renewal: (a and e) monthly, (b and f) every two months, (c and g) every three months and (d and h) every four months. In the uniform case, the number of infected increased when the renewal period went from (b) two to (c) three months, showing the importance of observing the epidemiological scenario before deciding to open borders and encouraging interstate travel. Results when distributing individuals nonuniformly endorsed the conclusion provided by the previous case, showing a greater number of infections for a (g) three-month renewal than when renewing (f) every two months. Parameters: $p_g = 0.06$ and $\phi = 0.30$. 

of accumulated cases obtained from simulations within a fixed period of traveler replacement (one to four months) considering uniform (Figures 5(a–d)) and nonuniform (Figures 5(e–h)) distributions of
individuals. In both cases, the non-monotonic variation of the curves is evident: an increase in the travelers’ renewal period should imply a decrease in the number of cases, since we do not consider the loss of immunity of the recovered. However, the number of infected individuals increases when the renewal period goes from two to three months, decreasing when the renewal period of traveler replacement increases from one to two and from three to four months. These non-monotonicities indicate the importance of observing the epidemiological scenario before deciding to open borders and encouraging interstate travel. Inserting new travelers during a period of growth in cases of infection contributes to the emergence of new cases and the consequent worsening of the epidemiological scenario.

The results shown in Figure 5 also suggest that herd immunity can occur at different levels (higher for denser FUs). This difference is more evident when we scattered the individuals nonuniformly, showing a visible gap among the curves of recovered individuals (Figures 5(e–h)).

Figure 6 shows a graphic representation of infected individuals’ dispersion over time, considering uniform (Figures 6(a–c)) and

![Figure 6](https://doi.org/10.25088/ComplexSystems.32.1.71)

**Figure 6.** The infection gradually spread across the subregions, reaching different areas at different times ((d) to (f)) with nonuniform distribution of individuals. This gradual infected individuals dispersion through the space looks more like the real scenario than the scenario with uniform distribution ((a) to (c)) that showed the capital as the unique subregion of concern (a region where the virus circulates fastest) during the total simulation time. Parameters: $p_g = 0.10$ and $\phi = 0.40$. 
nonuniform (Figures 6(d–f)) distribution of individuals. In both cases, the capital region agglomerated many infected individuals. When the individuals were uniformly distributed, most of the infected individuals emerged in the capital region, highlighting this locality as the principal area of contagion during the total simulation time (Figures 6(a–c)). The spatial disposition of infected individuals changed when individuals were nonuniformly distributed. For this case, beyond the capital region, other regions were affected in different epidemiological weeks (e.w.), as shown in Figures 6(d–f). This result makes clear that denser subregions are regions with higher virus transmission, so measures to contain the virus need to be strengthened in these regions. Similarly, subregions with lower chances of infection could have the containment rules relaxed.

### 4. Conclusions

In this paper, we have investigated the spatial scale effects in epidemic spread models, mainly COVID-19 spread models. Using an agent-based model (ABM) and Monte Carlo simulations, we performed simulations considering two spatial scales of interaction (local and global) with uniform and nonuniform (power law) distribution of individuals. We performed uniform distribution by randomly scattering the agents in the lattice, whereas the power law distribution of agents was executed by scattering the agents on the lattices’ sites using an analog method of the Barabási–Albert algorithm.

We observed that herd immunity occurs at different levels (higher for denser Federative Units (FUs)). Furthermore, periodic renewal of interstate travelers without considering the current epidemiological scenario increased the number of infected individuals, reinforcing that opening borders and increasing mobility must respect the epidemiological conditions.

Distributing individuals uniformly in the lattices, the capital region (unique agglomeration region in this case) emerged as the foremost region with a higher number of infections, regardless of epidemiological week. However, when the individuals were distributed nonuniformly, other subregions beyond the capital gradually emerged as areas of concern. This spatiotemporal evolution shown by the power law distribution is more like what happens in the real world [47].

One important point to mention is the distinct behaviors observed when the locale where the transmission starts is varied. When the first infected individual arrives in a locale with slow virus spread (like FU 9, FU with lower population density and lower interstate flow), the infection only spreads with power law distribution. Furthermore, considering both distributions, the initial conditions substantially changed the herd immunity levels.
Another point to emphasize is the infection due to the first neighbors: even considering a $p_2$ low influence ($\phi 1.0$), the accumulated number of infected is higher than the usual case in which only the infected individuals present in the same site transmit the pathogen ($\phi = 0.0$). Furthermore, we emphasize as an important observation that, for $p_g = 0.06$ and $\phi = 0.0$, only the power law distribution of individuals generated an active spreading process. Knowing that aerosol particles are a considerable mechanism for spreading the virus in many respiratory diseases, particularly for SARS-CoV-2 spreading [43], our results reinforced that epidemiological modeling should not ignore this mechanism.

Our studies are promising, so we intend to continue using the model to investigate the relationship between population characteristics and the robustness of the infection. In addition, this work is useful to understand spatial heterogeneities’ influence in extended systems in which spatial modeling constitutes a significant ingredient, such as analysis of epidemics of other pathogens [13], urban mobility systems [48] and description of a wide variety of social phenomena [49].

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