**Trends**
in Computational and
Applied Mathematics

# Why Can We Observe a Plateau Even in an Out of Control Epidemic Outbreak? A SEIR Model with the Interaction of $n$ Distinct Populations for COVID-19 in Brazil

M. J. LAZO[1*] and A. DE CEZARO[2]

**ABSTRACT.** This manuscript proposes a model of $n$ distinct populations interaction structured SEIR-compartmental model to describe the spread of COVID-19 pandemic diseases. The proposed model has the flexibility to include geographically separated communities as well as taking into account aging population groups and their interactions. We show that distinct assumptions on the dynamics of the proposed model lead to a plateau-like curve of the infected population, reflecting collected data from large countries like Brazil. Such observations aim to the following conjecture: "COVID-19 diseased diffusion from the capitals to the Brazil interior, as reflected by the proposed model, is responsible for plateau-like reported cases in the country". We present numerical simulations of some scenarios and comparison with reported data from Brazil that corroborate with the aforementioned conclusions.

**Keywords:** COVID-19, plateau, SEIR-model.

## 1 INTRODUCTION

The mathematical modeling of infectious disease has played an important role in the definition of action protocols and public policies to combat diseases aiming at the least social impact. It has been successfully used since the Bernoulli's pioneer work [2] on infectious diseases. An up-to-date example of the importance of mathematical modeling on public policies for epidemic diseases is the recent change in the UK's strategies regards to the COVID-19 pandemic [5, 7]. An extensive review of the mathematical modeling of infectious diseases can be found in [8, 10, 11, 12] and references therein.

COVID-19 is by now known as a rapidly spread contagious diseases, with a first registered outbreak at the end of December 2019 in Wuhan (China) and from there spread rapidly around the

---

*Corresponding author: Matheus Jatkoske Lazo – E-mail: matheuslazo@furg.br

[1]Instituto de Matemática, Estatística e Física, IMEF, Universidade Federal do Rio Grande, Av. Itália, km 8, 96203-900, Rio Grande, RS, Brazil – E-mail: matheuslazo@furg.br https://orcid.org/0000-0001-9741-9411

[2]Instituto de Matemática, Estatística e Física, IMEF, Universidade Federal do Rio Grande, Av. Itália, km 8, 96203-900, Rio Grande, RS, Brazil. – E-mail: adrianocezaro@furg.br https://orcid.org/0000-0001-8431-9120

globe causing mortality without precedents in the recent human history e.g [3, 6, 9, 15, 20, 22, 23] and references therein. Since up-to-day there is no safe vaccine or treatment, the remaining alternative for the public policies to control the outbreak was the social mitigation, tacked in some places to the extreme of severe lock-downs [3, 6, 9, 15, 20, 22]. The main goal of such a strategy was to "flatness the infection curve" such that the public health service could support the eventual high demand for ICU beds [3, 6, 9, 15, 20, 22].

Many countries have successfully implemented control strategies for the COVID-19 pandemic outbreak employing massive testing and isolation allied with social distance and population mitigation [3, 6, 9, 15, 20, 22]. Such social measures can be identified by the emergence of a plateau in the infected cases reported on such countries [1, 20]. Its success can be measure due to the relatively low mortality rate due to COVID-19 and an early secure economy reopening. Although, Brazil started with some kind of social distance measures since the early stages of the epidemic (around the end of March, with the first confirmed case on February 26, 2020). However, from the of May to the beginning of September the reported daily mortality average is around 1000 cases (daily new infected average is around 50.000 cases) configuring a plateau-like shape [4, 14].

Nevertheless, in some countries the public authorities are pointing for a massive economy reopening, in contradiction of the majority of the epidemiological specialist [17, 19].

With one eye on divulged official data, that reveal a plateau-like shape for the reported cases from countries as Brazil [4, 14, 16], for which several mechanisms, like social distance, massive testing and social isolation, were never effectively and seriously implemented, we shall questioning: *"Why can we observe a plateau even in an out of control epidemic outbreak?"*.

In this context, the main objective of the present work is to analyze how a plateau-like in the infected cases can arouse in an out of control epidemic outbreak and to analyze some scenarios for the COVID-19 epidemic in Brazil. Within this purpose, we take into account the two main tools to study the spread of this disease: a simple mathematical model and population interactions. Actually, we propose and analyze an structured (SEIR)-like compartmental epidemic model, where $S$, $E$, $I$ and $R$ represents the proportional of the population that is Susceptible , Exposed, Infected (and Infectious) and Recovered or Removed, respectively. The SEIR model is a generalization of the well-known (SIR) compartmental model [11, 12] that includes the exposed fraction of the population, denote by $E$. The literature on compartmental models and its applications in the COVID-19 outbreak has grown as faster as the pandemic itself, making a complete literature overview almost impossible. Therefore, we shall mention publications that are closely related to this manuscript. Age-structured SEIR models with social mixing were analyzed in [1, 3, 6, 20, 22], where was analyzed the effectiveness of control measures aimed at reducing the social mixing population in different countries as China, Italy, Uk, US, and Brazil. For a comprehensive overview of related works, see [1, 3, 6, 9, 15, 20, 22] and references therein. In special, in [1] the authors propose to include dynamics for asymptomatic and pre-symptomatic individuals in a modified SEIR model to explain the existing plateau in COVID-19 reported cases. However, such dynamics need to be calibrated, and it is possible only if a massive testing program is considered.

Moreover, these approaches can not be applied to explain how a plateau-like phenomenon arises in an out of control epidemic outbreak.

**Main contributions:**   Our main contribution with this manuscript is to provide enough shreds of evidence that a structured SEIR model, where the structure is characterized by $n$ distinct populations in interaction (see (2.1)), could predict a plateau-like shape for infected cases. The distinct populations can represent, for example, geographically separated communities, different groups (such as the elderly or people with co-morbidity ), among others. In the analysis that follows (see Section 3), such plateau is a product of a diffusion-like effect withing distinct populations. Although the derived analysis seems to be simple, it is possible to simulate distinct scenarios, reflecting the COVID-19 infected data ranging from countries where strict vertical isolation was implemented to scenarios with practically no population mitigation was adopted. In particular, we conjecture that the COVID-19 diseased diffusion from the capitals to the Brazil interior, reflected by the proposed model, is responsible for the plateau-like reported cases in the country.

The work is structured as follows. In Section 2, we present the model. We devote Section 3 to share some known facts about the proposed model as well as to analyze the scenarios of the model that predicts a plateau-like shape of reported cases. We also analyze what shall be the real-life scenario that reflects such a situation. The plateau-like shape can be associated with the diffusion of the disease within populations, see Subsection 3.1. In Subsection 3.2, we briefly discuss how the proposed model can be use to predict the scenario for vertical an horizontal social isolation. In Section 4, we present numerical simulations of a diversity of scenarios (see Subsection 4.1), for with an extensive discussion is provided. Moreover, we also show how the proposed model can describe reported Brazilian COVID-19 infected cases in Subsection 4.2. In subsection 4.3, we show how vertical social isolation is illustrated by the proposed model. Finally, Section 5 is dedicated to conclusions.

## 2   THE MODEL

In the forthcoming analysis, we consider a variation of the well-known epidemiological SIR compartmental model proposed by Kermack and Mckendrick [13]. Actually, our model is a generalization of the classical SEIR model [11, 12] where we introduce the interaction of $n$ distinct populations. Let $N_i$ be the number of individuals in population $i$ ($i = 1, 2, ..., n$), and $N_T = N_1 + N_2 + \cdots + N_n$ be the total integrated population. Let $S_i$, $E_i$, $I_i$ and $R_i$ be the fractions, in regard to $N_i$, of population $i$ that are susceptible, exposed, infectiously and recovery, respectively, at time $t$. In the model we consider, the time evolution is given by the following dynamic system for $i = 1, 2, ..., n$:

$$\dot{S}_i = -S_i \sum_{j=1}^{n} \beta_{ij} I_j + \mu_i (1 - S_i)$$

$$\dot{E}_i = S_i \sum_{j=1}^{n} \beta_{ij} I_j - (\alpha_i + \mu_i) E_i \qquad (2.1)$$

$$\dot{I}_i = \alpha_i E_i - (\gamma_i + \mu_i) I_i$$

$$\dot{R}_i = \gamma_i I_i - \mu_i R_i,$$

where $\beta_{ij}$ are the disease transmission rate (proportional to the average contact rate in the population and within the population), $\alpha_i$ is the inverse of the incubation period, $\gamma_i$ is the inverse of the mean infectious period, for $i = 1 \cdots, n$. Furthermore, we assume that mortality rates $\mu_i$ is equal to the birth rates, such that the total population $N_i$ is constant during the diseases. Hence, we have $S_i(t) + E_i(t) + I_i(t) + R_i(t) = 1$.

Moreover, the dynamics (2.1) is considered with the following initial conditions

$$S_i(0) = 1 - I_i(0), E_i(0) = 0, I_i(0), R_i(0) = 0, \qquad (2.2)$$

where $I_i(0)$ is the fraction of the population $i$ infected at the time 0.

## 3   SOME FACTS ABOUT THE MODEL

In this section, for easiness, we consider the model (2.1)-(2.2) with $\mu_i = 0$. Notice first that, from the third equation in (2.1), we get that the variation of $I_i(t)$ is proportional to the variation of $E_i(t)$. In this setting, summing up the second and the third equation in (2.1), we have the well-known SIR model, with $\hat{I}_i(t) = I_i(t) + E_i(t)$. We consider that the properties to be explored are be well understood if some well-known facts about the model (2.1)-(2.2) are revisited. We provide some details for the sake of completeness. The model (2.1)-(2.2) has a unique smooth solution, that depends continuously on the parameters and the initial conditions, e.g. [21]. Then, whenever $S_i(0)$ and $\hat{I}_i(0)$ are strictly positive, results in $S_i(t)$ and $\hat{I}_i(t)$ non negative, for all $i = 1, \cdots, n$. It follows from the first equation in (2.1) that $S_i(t)$ is decreasing. Moreover, adding the first three equations in (2.1), we get the following conservation law

$$S_i(t) + \hat{I}_i(t) + \gamma_i \int_0^t \hat{I}_i(s) ds = S_i(0) + \hat{I}_i(0). \qquad (3.1)$$

From (3.1), we get that $\hat{I}_i(t) < \infty$, for all $t \geq 0$. Furthermore, $\int_0^\infty \hat{I}_i(t) dt \leq \infty$. Since, $S_i(t)$ is decreasing, (3.1) also implies that $S_i^\infty := \lim_{t \to \infty} S_i(t) > 0$. Consequently, (3.1) also imply that $\lim_{t \to \infty} \hat{I}_i(t) = 0$. The *basic reproduction number* of the population $i$ ,$\mathscr{R}_0^i$, is the quantity that express the expected number of cases directly generated by one case in a population and withing the selected population, at the initial phase of the infection, is defined as $\frac{\beta_{ii} S_i(0)}{\gamma_i}$. It is well-known that if $\mathscr{R}_0^i > 1$, $\hat{I}_i(t)$ start increasing and then decreasing, e.g. [10, 11, 12]. Therefore, given the smoothness of $\hat{I}_i(t)$ (as a result of the existence of a solution of (2.1)) and the above mentioned

properties of $\hat{I}_i(t)$, we conclude that it trajectory has a concave hump with extremes in $\hat{I}_i(0)$ and $\hat{I}_i(\infty) = 0$, see Figure 1. Hence, $\hat{I}_i(t)$ attains a maximum at a point $t_p^i$, known as the turning point. Furthermore, is reasonable to assume that $\hat{I}_i(t_p^i) \neq 0$. Adding the second and third equation in (2.1) and the fact that $\dot{\hat{I}}_i(t_p^i) = 0$, implies that

$$S_i(t_p^i) = \frac{\gamma_i}{\beta_{ii}} \left( \frac{1}{1 + \sum\limits_{j \neq i}^{n} \frac{\beta_{ij}}{\beta_{ii}} \frac{\hat{I}_j(t_p^i)}{\hat{I}_i(t_p^i)}} \right), \quad \text{for } i \in \{1, \cdots, n\}. \tag{3.2}$$

Although simple, the analysis of the equation (3.2) revels several scenarios for the dynamics, as pointed below:

1. Assuming that we have $n$ isolated populations, i.e., $\beta_{ij} = 0$ for $j \neq i$, then

$$S_i(t_p^i) = \frac{\gamma_i}{\beta_{ii}},$$

   as in the canonical SIR model. In this particular setting of no-cross contamination between different populations, we have $t_p^i = t_p^j$ and then, we see the pick of the populations as one.

2. It is clear from (3.2) that $S_i(t_p^i)$ is lower and therefore $\hat{I}_i(t_p^i)$ is higher, depending on the infected connection network, since the quantity $\sum\limits_{j \neq i}^{n} \frac{\beta_{ij}}{\beta_{ii}} \frac{\hat{I}_j(t_p^i)}{\hat{I}_i(t_p^i)}$ appears in the quotient. It implies that the infection would be higher as higher is the infected connection network. Consequently, any kind of population isolation shall be tacked horizontally on the populations, in order of the diseases spread mitigation be effective.

3. Let $\mathscr{I}(t) := \sum_{i=1}^{n} \hat{I}_i(t)/n$ and $\mathscr{S}(t) := \sum_{i=1}^{n} S_i(t)/n$ the total proportion of the population infected/exposed and susceptible, respectively. By adding (3.1), we find out that the same behaviour discussed above is true also for $\mathscr{I}(t)$. Indeed, its expected trajectory is a positive concave hump, beginning at $\mathscr{I}(0)$ and ending at $\mathscr{I}(\infty)$. Furthermore, the maximum of $\mathscr{I}(t)$ will occurs at $t_p^{i^*}$ (that is population dependent) related to maximum value of $\sum\limits_{j \neq i}^{n} \frac{\beta_{ij}}{\beta_{ii}} \frac{\hat{I}_j(t_p^{i^*})}{\hat{I}_i(t_p^{i^*})}$).

## 3.1 The emerging plateau-like infected curve: A consequence of diseases diffusion within distinct populations

A more interesting question that we would like to discuss in this approach is the observed plateau-like phenomena as a consequence of the diseases diffusion. Below, we argue how the proposed model (2.1) can be used to describe such phenomena in the exposed/infected dynamics.

It started as follows: Assume that the diseases started at the population $i = 1$, i.e., at time $t = 0$, we have $\hat{I}_1(0) > 0$ and $\hat{I}_i(0) = 0$, for $i > 1$. Hence, the diseases will spread out throughout the population thanks to the population interaction (see the first equation in (2.1)). Therefore, it

would take some time for the diseases spread out to the entirely population. It turns out that, for any turning point $t_p^i$, the quantity $\sum_{j \neq i}^{n} \frac{\beta_{ij}}{\beta_{ii}} \frac{\hat{I}_j(t_p^i)}{\hat{I}_i(t_p^i)}$ will present a sort of equilibrium (as $i$ changes) since for the population $j$, with $j$ relatively far-way form $i$, the infection is starting to growth and them $\hat{I}_j(t_p^i)$ have a relatively small value, (for example, is we are looking for $i$ close to 1 and $j$ close to $n$), or then, the opposite situation holds; the infected proportion of the population already start declining, consequently $\hat{I}_j(t_p^i)$ is relatively small ( for example, is we are looking for $i$ close to $n$ and $j$ close to 1). As far as $\beta_{ij}/\beta_{ii}$ remains proportion throughout the population, the diffusion phenomena withing populations takes $S_i(t_p^i)$ at the same level (see (3.2)) . As a consequence, the picks $\hat{I}_i(t_p^i)$ forms a plateau-like effect observed in the infected/exposed compartment $\mathscr{I}$. By the way, this phenomena is observed for the COVID-19 real data on large territorial counties as US and Brazil. In Section 4.2 we discuss the emergence of a plateau-like in real data from Brazil.

Another consequence of the diffusion phenomena discussed above is that the largest $n$ is longer will take for the diseases starts to decline. Consequently, the plateau-like phenomena is larges (see Figure 2). Moreover, it follows from (3.2) that it takes higher levels as higher are the proportion of $\beta_{ij}/\beta_{ii}$, as expected in largest populated cities or metropolitan regions.

## 3.2    Vertical and horizontal social isolation: How far we can get into this discussion with the SEIR model (2.1)?

Since the COVID-19 pandemic outbreak and the lack of a treatment with efficacy evidences, the social isolation is the unique known measure for the pandemic controlling, e. g. [3,5,6,7,9,15,20, 22, 23] and references therein. Some countries as UK and Sweden pointed or adopted a vertical social isolation strategy (to protect only elderly or co-morbidity proportional of the population), contrarily to the World Health Organization recommendation of a horizontal social isolation. Regardless of economical impacts of the adopted social isolation strategy, in this section we discuss how far the proposed model (2.1) can share light on the best strategy to be adopt to protect the population. It is worth to mention that we do not intend to exhaust the discussion on the subject, but only to make some comments based on the model (2.1).

At this point it is reasonable to assume an age-structured population, where $i = 1$ represents the proportion of elderly and co-morbidity population. Although the vertical isolation seem reasonable (it is equivalent to take $\beta_{11}$ as lower as possible, but of course, it is impossible assume it to be zero), since the mortality for the COVID-19 are concentrated mostly in the elderly/co-morbidity proportion of the population [18], it follows from (3.2) that $\beta_{11}$ lower will get effect on the number of infected at the class $i = 1$, at least on it pick, might be compensate for the interactions with the other ages-classes ($\beta i j \neq 0$) on the day-to-day life. The particular in-housing interaction between many aging people are the reality of many families on lower incoming countries like Brazil [18]. Notice that is sufficient that $\hat{I}_j(t_p^i)$, for one $j \neq 1$ with a high value to take $S_1(t_p^i)$ down (and consequently $\hat{I}_1(t_p^i)$ be large). See the scenario presented in 4.3 for a numerical representation of such situation.

On the other hand, in a horizontal isolation scenario we have $\beta_{ij}$ (consequently, $\hat{I}_j(t)$ for all $t$) closed to zero, for all $i, j \in \{1, \cdots, n\}$. Hence, it follows from (3.2) that quantity $S_i(t_p^i)$ is large resulting in $\hat{I}_i(t_p^i)$ relatively closed to $\hat{I}_i(0)$, meaning that pressure on the health system might be kipped under control.

## 4   NUMERICAL SOLUTIONS

In this section, we present numerical solutions for some particular cases of our model (2.1). We consider, for simplicity, that all the $n$ populations have the same number $N$ of individuals, namely, $N_i = N = 1000000$. We also consider the simplest interaction case where each population interacts with only two neighbour populations, namely, $\beta_{ij} = \overline{\beta} \neq 0$ if $j = i \pm 1$, $\beta_{ij} = 0$ for $|j - i| > 1$. In this case we have a one dimensional chain of populations where $|j - i|$ can be used to define a distance from populations $i$ and $j$. Furthermore, in order to avoid asymmetries in the interactions of the first ($i = 1$) and the last ($i = n$) populations, we also consider $\beta_{1n} = \beta_{n1} = \overline{\beta}$ (this consideration implies that we have a periodic uni-dimensional chain). Finally, we set $\beta_{ii} = \beta$, $\alpha_i = \alpha$, $\gamma_i = \gamma$, $\mu_i = \mu = 0$ (homogeneous populations). All numerical solution are obtained by the traditional backward finite difference method with a time step of $\Delta t = 0.5$ days.

### 4.1   Several distinct populations

We consider in this case $\alpha = 1/5$ (we are supposing that the meantime before an exposed individual becomes infectious is five days), $\gamma = 1$ (the meantime before isolation for infectiously individuals is one day), $\beta = 1.5$ to result in a severe epidemic outbreak, and $\mu = 0$. For the interaction between neighboring populations we consider $\overline{\beta} = 0.02$, that is the contagious rate from individuals outside the population is seventy-five times smaller than from individuals of the same population. We did not calibrate the parameters w.r.t. any reported data. In particular, the parameter choices was adopted only to present simulated scenarios.

Initially, we consider that there is 200 infectious individual in population $i = 1$ and zero in the other populations.

In Figure 1 we show the role of interaction $\overline{\beta}$ in each population for $n = 4$. In Figure 1 (a) we show the time evolution of exposed $E_i$ and infected $I_i$ compartments. The exposed and infected compartments of population $i = 1$ reaches its maximum point first, followed by populations $i = 2$ and $i = 4$. The last population to reach its epidemic peak is $i = 3$. These results are consistent since the epidemic outbreak starts in population $i = 1$, propagating to the first neighbouring populations $i = 2$ and $i = 4$, and finally achieving the most distant population $i = 3$. The total exposed $E = (E_1 + E_2 + E_3 + E_4)/4$ and infected $I = (I_1 + I_2 + I_3 + I_4)/4$ fractions in relation to the total population $N_T = N_1 + N_2 + N_3 + N_4$ are showed in Figure 1 (b).

The difference in the time that each population reach its maximum point have as a consequence the emergency of a plateau when the number $n$ increase. In Figure 2 (a) we show the total exposed $E = \sum_{i=1}^{n} E_i/n$ and infected $I = \sum_{i=1}^{n} I_i/n$ fractions for $n = 1, 10, 20$, the case $n = 4$ was displayed in Figure 1 (b). For $n = 1$ we have the classical SEIR model [11, 12] with a sharp curve for
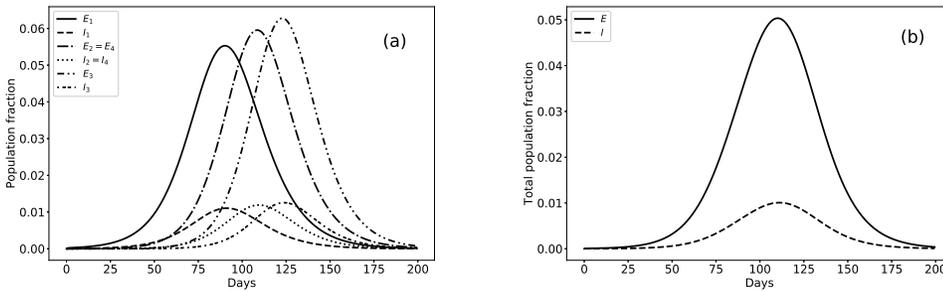
Figure 1: In (a) we display the time evolution of of exposed $E_i$ and infected $I_i$ fractions for each population $i$ with $n = 4$, $\beta = 1.5$, $\overline{\beta} = 0.02$. The total exposed $E = (E_1 + E_2 + E_3 + E_4)/4$ and infected $I = (I_1 + I_2 + I_3 + I_4)/4$ fractions are displayed in (b).

both exposed and infected fractions. For $n = 4$ (see Figure 1 (b)), both curves broaden but still there are not a plateau. By increasing the number of distinct populations to $n = 10$ a well-defined plateau arouses. For $n = 20$ we can see that the plateau extension increases with the growth of $n$. As a consequence of the appearance of the plateau, we have an increase in the duration of the epidemic outbreak, but with a smaller fraction of sick individuals in the population at every moment. However, the accumulated fraction of sick people $(I + R)$ at the end of the outbreak varies little with $n$, as can be seen in Figure 2 (b).

Finally, Figure 3 displays the role of the intensity of interaction $\overline{\beta}$ for the epidemic outbreak dynamics. We consider two scenarios with $n = 20$. For $\overline{\beta} = 0.02$ we have a strong interaction between distinct populations (a population is heavily contaminated by neighboring populations). As a consequence, we observe a plateau that results from small-time distances between the epidemic peaks for each individual population $i$. For a small interaction $\overline{\beta} = 0.001$ (distinct populations are almost isolated) the time-distances between the epidemic maximum points for each individual population $i$ increases, resulting in an oscillatory behavior for exposed and infected fractions (instead of a plateau) and in a long total time duration for the epidemic outbreak.

## 4.2  Comparing with real data from Brazil

It is important to stress that it is not the objective of the present work to describes real data by using realistic values for the model parameters (as realistic values for populations $N_i$ and parameters $\alpha_i$, $\beta_{ij}$, $\gamma_i$ and $\mu_i$). The result displayed here shows that our model has a great potential to describe real epidemic outbreak, but a detailed stud of real data will be done in a future work. Our present objective is only to show that the model has the ingredients to correctly describes the behavior of COVID-19 dynamics found in real data from Brazil, including the appearance of a plateau phenomenon. With $n = 200$ and $N_i = N = 1000000$ we found that our model describes very well the behavior of COVID-19 epidemic outbreak when compared against real data from Brazil (see Figure 4). The real data displayed in Figure 4 is from the ministry of health of Brazil
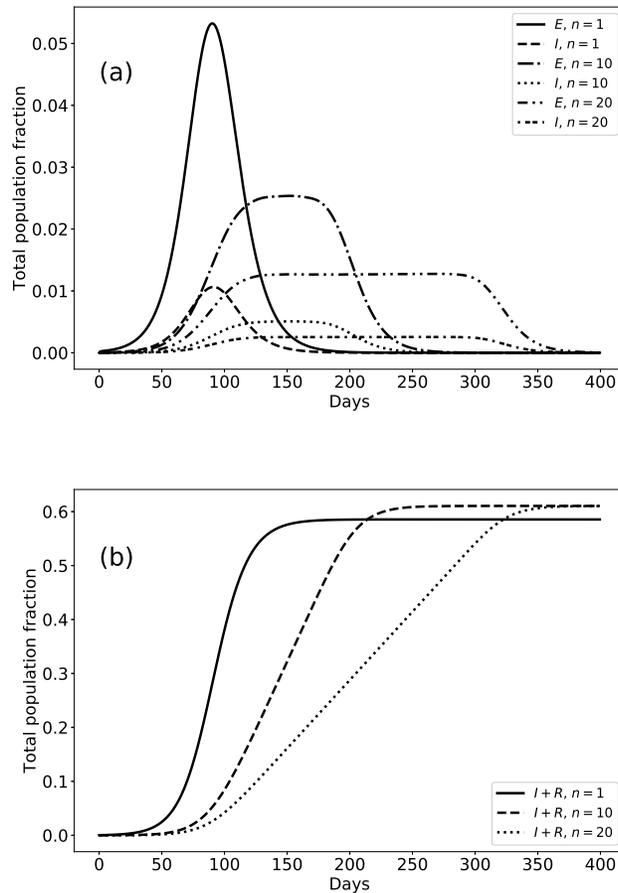
Figure 2: The total exposed $E = \sum_{i=1}^{n} E_i/n$ and infected $I = \sum_{i=1}^{n} I_i/n$ fractions are show in (a) for $n = 1, 10, 20$, $\beta = 1.5$ and $\overline{\beta} = 0.02$. In (b) we display the accumulated fraction $I + R$.

from February 26 up to July 28 of 2020 [16]. The model parameters are set to $\alpha = 1/5$, $\beta = 1.5$, $\overline{\beta} = 0.01$ and $\gamma = 1.004$. Figure 4 (a) shows the diary number of infected individual, and Figure 4 (b) displays the accumulated number of sick people $(I + R)$. The emergence of a plateau in the real data is characterized by an almost constant mean value for new reported daily cases, which results in an almost linear growth for the total accumulated cases. By looking at the real data in Brazil, in Figures 4 (a) and (b), we can stipulate that the COVID-19 epidemic outbreak reaches a plateau in Brazil approximately four months after the first reported case (at February 26). From these figures, we see a good concordance between real data and our model both in the emergence of a plateau and in the general curve shape of the daily and total accumulated cases, respectively. This result indicates that the plateau of the COVID-19 epidemic outbreak in Brazil may be a consequence of the disease's geographic diffusion. This fact motivates further research aiming at
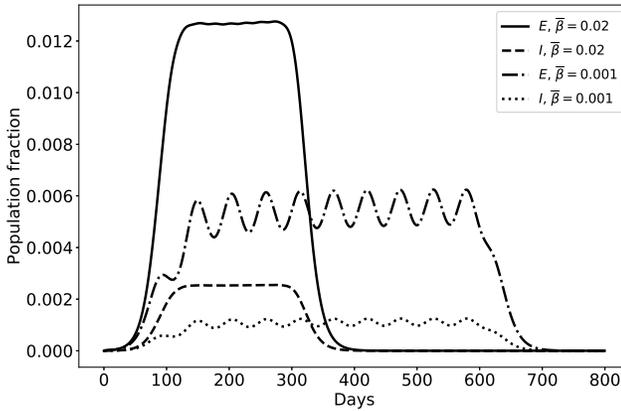
Figure 3: The total exposed $E = \sum_{i=1}^{n} E_i/n$ and infected $I = \sum_{i=1}^{n} I_i/n$ fractions for $\overline{\beta} = 0.02$ and $\overline{\beta} = 0.001$, respectively. In both cases we have $n = 20$ and $\beta = 1.5$.

a more accurate description of the real problem through a more realistic choice for our model's parameters.

### 4.3     Vertical social isolation

Finally, in addition to populations in different geographic regions, our model (2.1) can also be used to describes different partitions of a population in the same geographic location. We consider as an example the problem of vertical social isolation. In this case, a number of $N_1$ individuals in risk groups (such as the elderly or people with co-morbidity) are isolated, while the rest $N_2$ individuals of the population are not confined. Let us assume that isolated individuals are confined alone. In this case, we should have $\beta_{11} = 0$ since isolated persons do not have contact with other isolated individuals. The disease contagion follows from contact with non-confined persons. Let also we set $\beta_{22} = 1.5$ for the disease transmission rate of non-isolated individuals (proportional to the average contact rate in the $i = 2$ population). By supposing a hypothetically simple case where non-confined persons go out from home five times a week, while isolated individuals go out only one time a week, we can set $\beta_{12} = \beta_{21} = \beta_{22}/5 = 0.3$.

For simplicity, let us consider $N_1 = N_2 = 1000000$ and that initially there are 200 infectious individual in the non-confined population and zero in the isolated one. We show the exposed and infected fractions for isolated and non-confined individual in Figure 5 (a). As expected, the epidemic outbreak is more severe for non-confined individuals. However we despite the small disease transmission rate $\beta_{12} = \beta_{21}$, the total fraction of isolated persons that becomes sick is not negligible as can be seen in the accumulated number of sick people $(I_i + R_i)$ in Figure 5 (b).
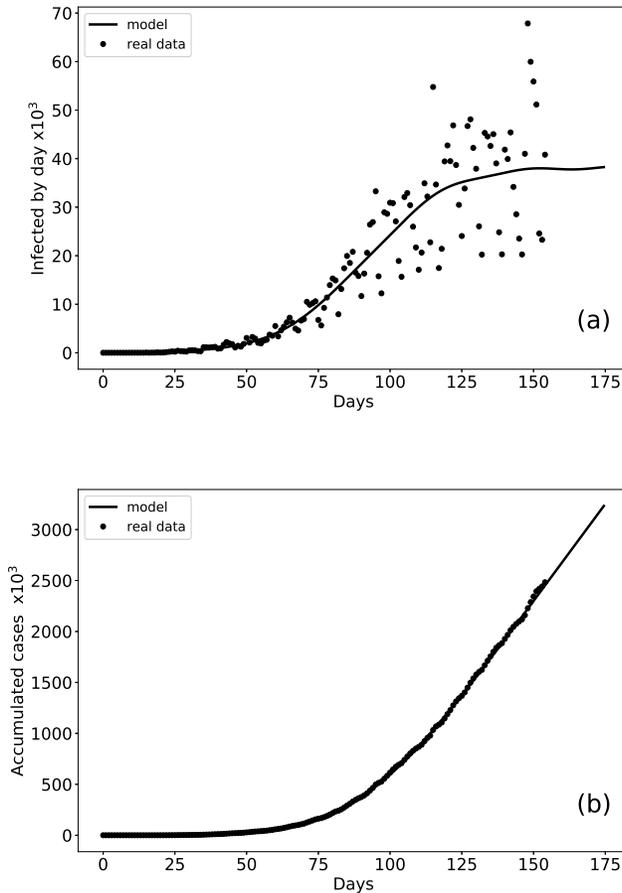
Figure 4: In both figures the dots are real data from the Ministry of Health of Brazil [16], and the solid lines are obtained from our model with $n = 200$, $\beta = 1.5$, $\overline{\beta} = 0.01$, $\gamma = 1.004$ and $\alpha = 1/5$. The daily infected cases are displayed in (a) and the accumulated $I + R$ cases is shown in (b).

## 5  CONCLUSIONS AND FUTURE DIRECTIONS

The proposed model of $n$ distinct populations interaction structured SEIR (2.1) stands as one alternative to describe the spread of COVID-19 pandemic diseases. The proposed model has the flexibility to include geographically separated communities as well as taking into account aging population groups and their interactions. Furthermore, we have shown how some strategies of non-pharmacological intervention as vertical and horizontal social isolation can be discussed using the proposed model. Analyzing some possible scenarios reflected by the proposed model, we show how a plateau-like curve of infected could be a result of a disease's diffusion effect within distinct populations, resembling collected data from large countries as Brazil (see Fig-
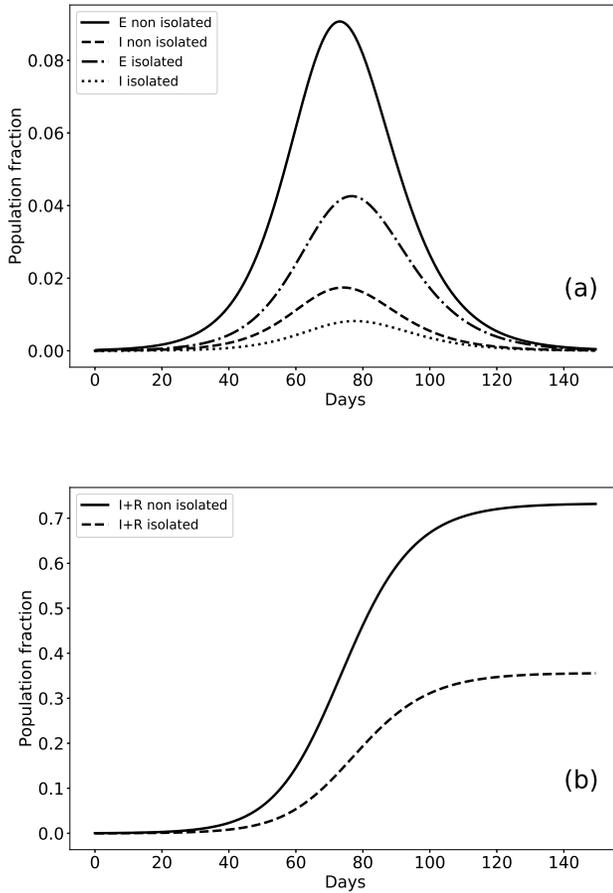
Figure 5: The time evolution of exposed $E_i$ and infected $I_i$ fractions for isolated ($\beta_{11} = 0$) and non isolated ($\beta_{22} = 1.5$) populations is shown in (a) for $\beta_{12} = \beta_{21} = \beta_{22}/5 = 0.3$. The the accumulated $I + R$ cases are displayed in (b).

ure 4). In particular, we conjecture that the COVID-19 diseased diffusion from the capitals to the Brazil interior, as reflected by the proposed model, is responsible for plateau-like reported cases in the country. Collaborating with the analysis, we also present in Section 4 numerical solutions for some scenarios of the model (2.1) showing its applicability, in particular for describing the plateau-like shape of reported infected cases in Brazil.

**Future directions:**    Many open questions in regard to the proposed model (2.1) remains, and shall be explored in the future. Between them, we pointed out the following:

- Investigate more realistic geometries, where a population interacts with more than two neighbors.

- Include more partition in the model, as for example dead and quarantine fractions.

- Explore the complexity of the population interplay network more carefully, including age and distinct population interaction.

- Analyze bifurcations and its consequences.

- Study optimal strategies for vaccination associated with the interacted population dynamics (2.1).

**RESUMO.** Este manuscrito propõem um modelo compartimental estruturado SEIR com *n* populações distintas interagindo para descrever a dissiminação da pandemia de COVID-19. O modelo proposto possui a flexibilidade de incluir comunidades geograficamente sepa- radas, bem como levar em conta grupos populacionais com idades distintas e sua interações. Mostramos que hipóteses distintas sobre a dinâmica do modelo proposto leva a uma es- trutura de platô na curva da população infectada, o que está em correspondência com os dados coletados em países de grandes dimensões como o Brasil. Tais observações sug- erem a formulação da seguinte conjectura: "o efeito da difusão da COVID-19 das grandes cidades para o interior do Brasil, como especulado pelo modelo, é o resposável pela forma de platô dos casos reportados de infecção no país". Apresentamos cenários numéricos e comparações com os dados de casos reportados de infecções por COVID-19 no Brasil que colaboram com as conclusões acima mensionada.

**Palavras-chave:** COVID-19, platô, modelo-SEIR.

## REFERENCES

[1] S. Ansumali & M. Prakash. A Very Flat Peak: Why Standard SEIR Models Miss the Plateau of COVID-19 Infections and How it can be Corrected. *medRxiv*, (2020). doi:10.1101/2020.04. 07.20055772. URL https://www.medrxiv.org/content/early/2020/05/15/2020.04.07. 20055772.

[2] D. Bernoulli. Essai d'une nouvelle analyse de la mortalité causée par la petite vérole, et des avantages de l'inoculation pour la prévenir. *Histoire de l'Acad., Roy. Sci.(Paris) avec Mem*, (1760), 1–45.

[3] C. Castilho, J.A.M. Godim, M. Marchesin & M. Sabeti. Assessing the efficiency of different con- trol strategies for coronavirus (COVID-19) epidemic. *Electronic Journal of Differential Equations*, **2020**(64) (2020), 1–17.

[4] M. Fagundes. WHO Says Brazil's Covid-19 Curve Has Plateaued (2020). URL https://www.bloomberg.com/news/articles/2020-07-17/ who-says-brazil-s-covid-19-curve-has-plateaued.

[5] N. Ferguson *et al.* Report 9: Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand. *Imperial College COVID-19 Response Team*, (2020), 1–20. doi:https://doi.org/10.25561/77482. URL `https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-NPI-modelling-16-03-2020.pdf`.

[6] G. Giordano, F. Blanchini, R. Bruno *et al.* Modelling the COVID-19 epidemic and implementation of population-wide interventions in Italy. *Nat Med*, **26** (2020), 855–860.

[7] J. Govaert. Coronavirus: UK changes course amid death toll fears (2020). URL `https://www.bbc.com/news/health-51915302`.

[8] J.N. Hays. "Epidemics and pandemics: their impacts on human history". Abc-clio (2005).

[9] S. He, Y. Peng & K. Sun. SEIR modeling of the COVID-19 and its dynamics. *Nonlinear Dyn*, (2020), doi.org/10.1007/s11071–020–05743–y.

[10] H.W. Hethcote. Three basic epidemiological models. In "Applied mathematical ecology". Springer (1989), pp. 119–144.

[11] H.W. Hethcote. The mathematics of infectious diseases. *SIAM review*, **42**(4) (2000), 599–653.

[12] M. Keeling & P. Rohani. "Modeling Infectious Diseases in Humans and Animals". Princeton University Press (2007).

[13] W. Kermack & A. Mckendrick. A Contribution to the Mathematical Theory of Epidemics. *Proceedings of the Royal Society of London. Series A, Containing papers of a Mathematical and Physical Character*, **115**(772) (1927), 700–721.

[14] B. Lima & M. Cardim. Covid-19 no Brasil: mortes se estabilizam em platô nas alturas (2020). URL `https://www.correiobraziliense.com.br/app/noticia/brasil/2020/07/12/interna-brasil,871435/covid-19-no-brasil-mortes-se-estabilizam-em-plato-nas-alturas.shtml`.

[15] A. Nande, B. Adlam, J. Sheen, M.Z. Levy & A.L. Hill. Dynamics of COVID-19 under social distancing measures are driven by transmission network structure. *medRxiv*, (2020). doi:10.1101/2020.06.04.20121673.

[16] M. of Health of Brazil. Painel Coronavírus (2020). URL `https://covid.saude.gov.br/`.

[17] C. Oliveira. Reopening in SP is sending "population to a slaughterhouse", warns COVID specialist. *Brasil de Fato, 2020/07/12*, (2020). URL `https://www.brasildefato.com.br/2020/06/12/reopening-in-sp-is-sending-population-to-a-slaughterhouse-warns-covid-specialist`.

[18] W.H. Organization. WHO Coronavirus Disease (COVID-19) Dashboard (2020). URL `https://covid19.who.int`. 2020/7/29.

[19] A. Park. Here's How Scientists and Public-Health Experts Recommend the U.S. Gets Back to 'Normal'. *TIME, 2020/04/30*, (2020). URL `https://time.com/5829387/coronavirus-reopening-science`.

[20] K. Prem *et al.* The effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan, China: a modelling study. *Lancet Public Health*, **5** (2020), e261–70.

[21] J. Sotomayor. "Lições de Equações Diferenciais Ordinárias", volume 11. Instituto de Matemática Pura e Aplicada, CNPq (1979).

[22] A. Teimouri. An SEIR Model with Contact Tracing and Age-Structured Social Mixing for COVID-19 outbreak. *medRxiv*, (2020). doi:10.1101/2020.07.05.20146647.

[23] J. Wu, K. Leung, M. Bushman *et al.* Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. *Nat. Med.*, (2020), https://doi.org/10.1038/s41591–020–0822–7.