

Characteristics and Evolution of COVID-19 Cases in Brazil: Mathematical Modeling and Simulation

Características e Evolução dos Casos COVID-19 no Brasil: Modelagem Matemática e Simulação

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ABSTRACT

The pandemic caused by the coronavirus of severe acute respiratory syndrome 2 (SARS-CoV-2), the etiological agent of the 2019 coronavirus disease (COVID-19), represents a threat of great magnitude not faced in this century. In Brazil, the outbreak triggered many cases of people infected with COVID-19. Analyzing the data of infection cases and their mathematical interpretation are essential for supporting and guiding governmental measures to suppress and mitigate the impact of COVID-19. This means that estimates with mathematical models to assess the development potential of sustained human-human transmission are needed. Since the disease has its own biological characteristics, the models need to be adapted to the variability of the regions characteristics and the decision-making by both the government and the population, in order to be able to deal with real situations. Thus, we analyzed the official data of COVID-19 in Brazil and used the Johnson-Mehl-Avrami-Kolmogorov (JMAK) equation to predict the evolution of the disease. The model indicates that a nucleation rate is of fourth-order, which indicates that Brazilians are crowding with no respect to measures of social distance and disease prevention. This is, our findings suggest that federal and state governments must control events that cause crowds of people, there is a rapid growth of a nucleus and the creation of new clusters that are strongly dependent on the type of social mobility. In our opinion, the political authorities were unable to control the spread of the disease in Brazil, given that social mobility was partially interrupted by the federal and state governments.

Keywords: COVID-19, infectious diseases, mathematical modeling, Avrami equation, epidemiology.

RESUMO

A pandemia causada pelo coronavírus da síndrome respiratória aguda grave 2 (SARS-CoV-2), agente etiológico da doença coronavírus 2019 (COVID-19), representa uma ameaça de grande magnitude não enfrentada neste século. No Brasil, o surto desencadeou muitos casos de pessoas infectadas com COVID-19. A análise dos dados dos casos de infecção e sua interpretação matemática são essenciais para apoiar e orientar as medidas governamentais para suprimir e mitigar o impacto do COVID-19. Isso significa que são necessárias estimativas com modelos matemáticos para avaliar o potencial de desenvolvimento da transmissão humano-humana sustentada. Uma vez que a doença possui características biológicas próprias, os modelos precisam ser adaptados à variabilidade das características das regiões e à tomada de decisões tanto do governo quanto da população, para poderem lidar com situações reais. Assim, analisamos os dados oficiais do COVID-19 no Brasil e usamos a equação de Johnson – Mehl – Avrami – Kolmogorov (JMAK) para prever a evolução da doença. O modelo indica que a taxa de nucleação é de quarta ordem, o que indica que os brasileiros estão se aglomerando sem respeitar medidas de distância social e prevenção de doenças. Ou seja, nossos achados sugerem que os governos federal e estadual devem controlar eventos que causam multidões de pessoas, há um rápido crescimento de um núcleo e a criação de novos clusters que são fortemente dependentes do tipo de mobilidade social. Em nossa opinião, o poder político não conseguiu controlar a disseminação da doença no Brasil, visto que a mobilidade social foi parcialmente interrompida pelos governos federal e estadual.

Palavras-chave: COVID-19, doenças infecciosas, modelagem matemática, Equação de Avrami, epidemiologia.

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1. INTRODUCTION

Given the global scenario of the pandemic caused by the new coronavirus, the severe acute respiratory syndrome-associated coronavirus (SARS-CoV-2), each government has proposed fundamental emergency measures to halt the transmission and spread of the virus and mitigate its impacts. Specifically in Brazil, the outbreak first occurred by importing the pathogen into the São Paulo State (BRASIL, 2020), and then into other regions of the country, which triggered a large number of cases of people infected with the novel coronavirus. Soon after, on 20 March 2020, the Brazilian Ministry of Health declared community-acquired infection (KUCHARSKI et al., 2020). Thus, the federal and state governments have proposed self-protection measures such as wearing a mask and quarantine to restrict the movement of people with the aim of containing virus transmission. Additionally, after more than one year of the pandemic, the battle to control it continues.

Considering there are not enough vaccines for the entire population and drugs proven to be effective for the treatment of coronavirus disease (COVID-19), analyzing data of infection cases and their mathematical interpretation is important to support and guide the government measures for suppressing and mitigating the impacts of COVID-19. This means that making estimates with mathematical models is needed to assess the potential development of sustained human-to-human transmission (BRASIL, 2020). Therefore, the simulation may guide the government on how to reopen the economy safely while the virus is still circulating in the population. This has become a problem of significant concern and importance to elected leaders in Brazil and its states.

Since the disease has its own particular biological characteristics, models must be adapted to each specific case, to the region characteristics, and to decision making by the government and the population for being capable of dealing with real situations (IVORRA et al., 2020; SAVI; SAVI; BORGES, 2020). In other words, this is a new virus that creates a completely new situation. For COVID-19, it is important to estimate those quantities that are being shared, debated, and updated daily, as mentioned by (HILL, 2020).

The dynamics description of coronavirus infection in humans requires the simulation of different scenarios to avoid false estimates. According to Verity et al. (2019), during the exponential growth phase of an epidemic, the time observed between the onset of symptoms and results (recovery or death) is suppressed, and naive estimates of the times

observed provide biased responses of real time. According to these authors, ignoring this effect tends to influence the down estimate in the number of deaths (ibidem).

In literature, some examples of mathematical models related to the dynamics of infectious diseases can be found. The first mathematical model used to describe the epidemic was the compartment model of the type susceptible–infected–recovered (SIR) proposed by Kermack and McKendrick in 1927 (KERMACK; MCKENDRICK, 1991). In summary, in the SIR model the population is divided into the (fixed) population of N in three individual classes: the susceptible group (S) where there are people that may be infected; the infected group (I) are individuals sick and may disseminate the disease; the recovered group (R) are those who were infected and became immune or died. Therefore, the simplified version of the governing equations considers the interaction among all these populations, being expressed by the following set of differential equations,

$$\frac{dS}{dt} = -\beta SI \quad (1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (2)$$

where β describes the effective contact rate of the disease, γ is the mean recovery rate, and $N = S(t) + I(t) + R(t)$. In this model, the number individual S decreases with time t and during the infected I becomes recovered (R). The SIR model describes the change in the population of each of these compartments in terms of two parameters, β and γ .

Based on this model, number of studies have already explored the dynamics of the spread of COVID-19 with various methodologies (HILL, 2020; KERMACK; MCKENDRICK, 1991; CINTRA, 2020) to characterize disease transmission and infection risk in different sceneries and generalization. Alternately, other researchers have reported other models predicting the dates and heights of the peaks in severely affected countries (TSALLIS; TIRNAKLI, 2017; ZHANG, 2021). Some of these studies have intended to help public administrators in action plans and resource allocation to expand the health system, principally, to attend to the fraction of the population more vulnerable. Therefore, the new mathematical methods and the SIR-modified models have also intended this by including

other parameters such as death, hospitalization, critical compartments, and the calculation process for requiring beds and ICU beds, and also to enhance the disease transmission visibility in order to mitigate the coronavirus disease (SINGH; BAJPAI; GUPTA, 2020).

In this context, with data from COVID-19 outbreaks, our research group initiated the outbreak modeling and simulation considering the social distance measures adopted in Brazil (CINTRA, 2020) Our main objective was to predict the cases of the new coronavirus by finding out the transmission characteristics of COVID-19 in Brazil, in specific regions, to assist in the decision-making by government authorities. To this end, we use a crystal growth model to analyze the data obtained and describe the limitations of this methodology.

2. METHODOLOGY

We used the database of the Brazilian Ministry of Health to make the estimate of the infected number. The extracted database contains the epidemiology timelines in Brazil and each state. For analysis, we needed to obtain the approximate size of the population (N) of each state and of Brazil. In this case, we adopted the population estimates for each state calculated by the Brazilian Institute of Geography and Statistics (Instituto Brasileiro de Geografia e Estatística—IBGE) for 2019 [17]. Moreover, we considered the size of the population is constant.

2.1 Description of the cases of COVID-19 with the Johnson–Mehl–Avrami–Kolmogorov model.

Our prediction model is based on the Johnson–Mehl–Avrami–Kolmogorov (JMAK) theory. This theoretical model is briefly described in Nascimento et al. (2020, 2021). For the present paper, uncontaminated people will be the universe to be transformed from the uncontaminated to the contaminated state. Thus, for the application of the JMAK equation in cases of epidemics, we consider that:

- Temperature T represents the degree of people circulating on the streets, in their neighborhoods, and making the pandemic grow at the contaminated border, without long-distance transport to form new nuclei.
- Parameter k describes the expansion rate of COVID-19 cases over time - we considered k to be a constant at first approximation, since T is constant (represents

the number of contaminated people advancing in the uncontaminated neighborhood at a constant rate);

- **f** is the fraction of people infected in a population.
- **n** represents the ability to create new nuclei of contaminated people and is associated to the transport of people in long-range means of transportation, such as by plane, subway, bus, and train.
- The number of people recovered (immunized and killed) were not considered.

In our model, a person infected with COVID-19, when in a region not affected by the disease, can generate a nucleus (cluster 1) of infected people at a certain time, which we consider as the initial time ($t = 0$) of the disease outbreak. In this situation, some people acquire the disease. At a certain moment, a person from that nucleus moves to another region where there is no infection by some form of public transport, and a second nucleus may appear (cluster 2). We consider that the clusters have different sizes because they were created at different times, and the contaminated nucleus grows over time, as shown in Figure 1A, 1B. If no measure to contain the disease outbreak is taken, other people infected with the disease create new nuclei in regions not yet affected by the virus. At a given time $t_x > 0$, we will have other nuclei formed, as shown in Figure 1C.

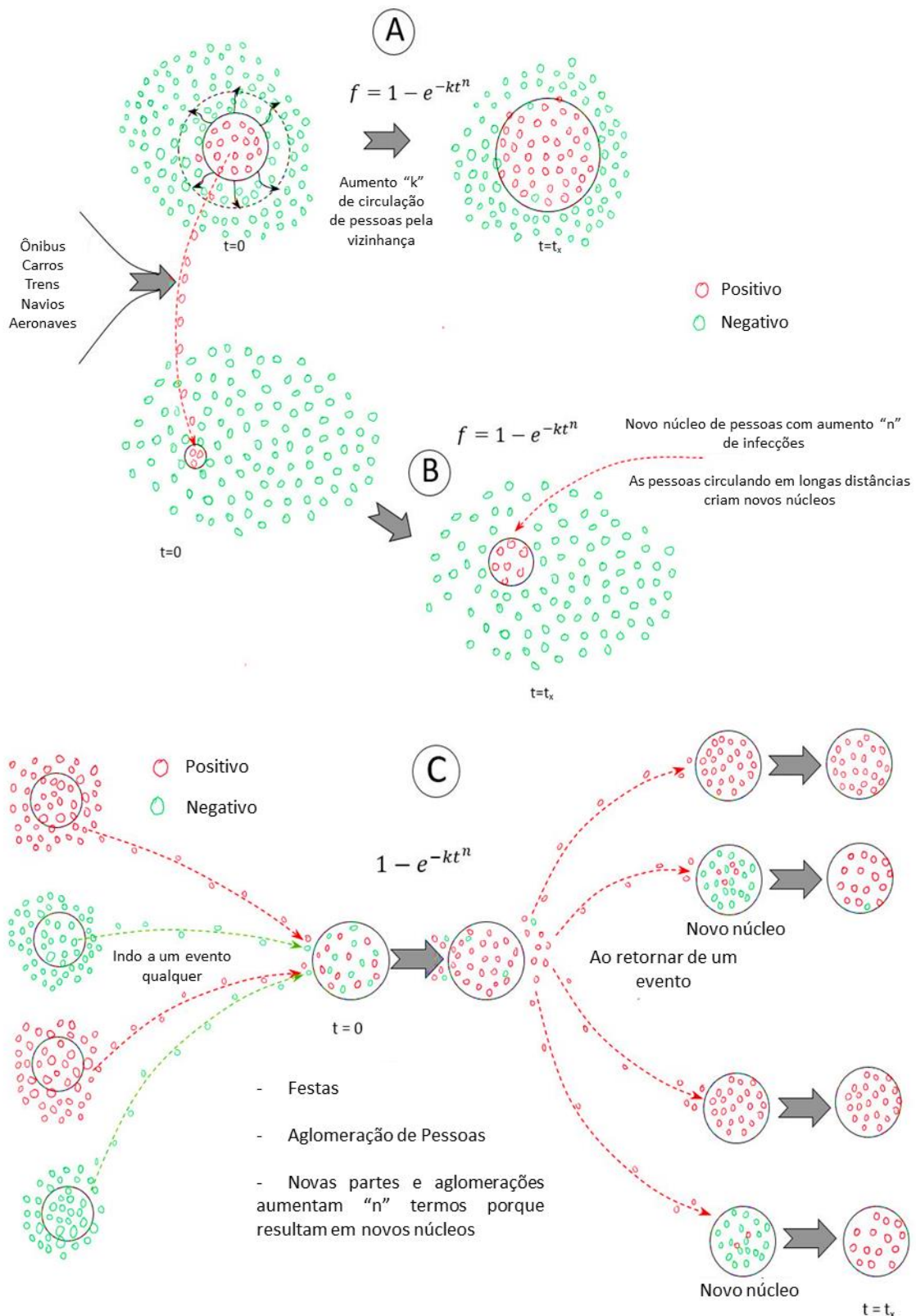


Figure 1. From Nascimento et al. (2021). Nucleation model of people infected by COVID-19. (A) An infected individual travel by public transportation from one region to other and spreads the disease. (B) An infected individual creates a new cluster of novel coronavirus. (C) Infected people create new nuclei in regions not yet affected by the virus in a given time.

Depending on the types of events (parties, concerts, football matches, etc.) that cause crowds of people, there is a rapid growth of a nucleus and the creation of new clusters that are strongly dependent on the type of social mobility (plane, subway, bus, and train). In this description, the model does not allow us to measure the mobility parameter. However, the ease of mobility is related to parameter n of the JMAK function. If the value of n is equal to one, no new nuclei are created; but the higher its value, the more nuclei are generated. For $n > 2$ we had an indication that the disease spread is out of control.

2.2 Determining the Adjustment Parameters

For obtaining the parameters n and k , we linearized Equation (3) for applying natural logarithm both side and we obtain:

$$\ln \{-\ln(1 - f(t))\} = n \ln(t) + \ln(k) \quad (4)$$

Then, we built the graph $\ln \{-\ln(1 - f(t))\}$ versus $n \ln(t)$, as shown in Figure 2.

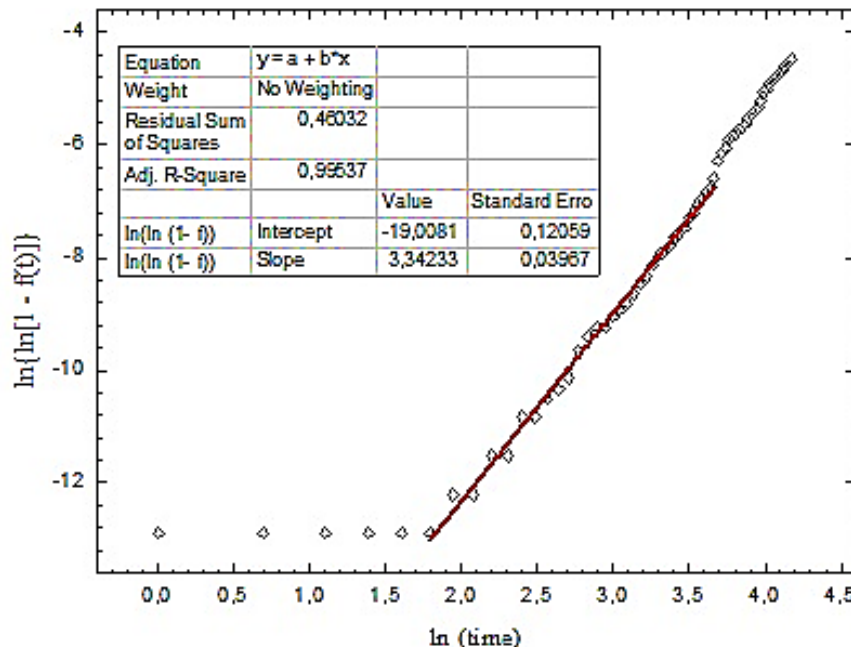


Figure 2. The line was adjusted in the interval between the 6th and the 39th day, with $R^2 = 0.99146$.

We then used these adjustment parameters to find the number of total cases and the daily number of cases. For this purpose, knowing the total population of the analyzed region is needed.

3. RESULTS

Prediction of the number of people infected calculated with the Johnson–Mehl–Avrami–Kolmogorov function

3.1. Estimate with the Percentage of Infected People for Brazil

Countries that have already experienced the peak of the COVID-19 outbreak have different percentages of infected people, as described in Table 1. Thus, our insight is that the disease will affect between 1 and 3% of the Brazilian population.

Table 1. Number of confirmed cases of COVID-19 in some countries. Source: <https://www.worldometers.info/coronavirus/>.

Country	No. of Infected People	Population	<i>p</i> %
Italy	197,641	60,461,826	0.327
Canada	48,489	37,742,154	0.128
South Korea	11,018	56,263,639	0.020
Australia	7019	25,811,863	0.027
United Kingdom	236,711	67,840,351	0.349
Italy	223,885	60,472,892	0.370
United States	1,471,967	330,753,490	0.445
Spain	274,367	46,752,506	0.587
Brazil	241,080	212,376,810	0.114
Espírito Santo State	5013	4,018,650	0.125

The results of simulations are shown in Figure 3.

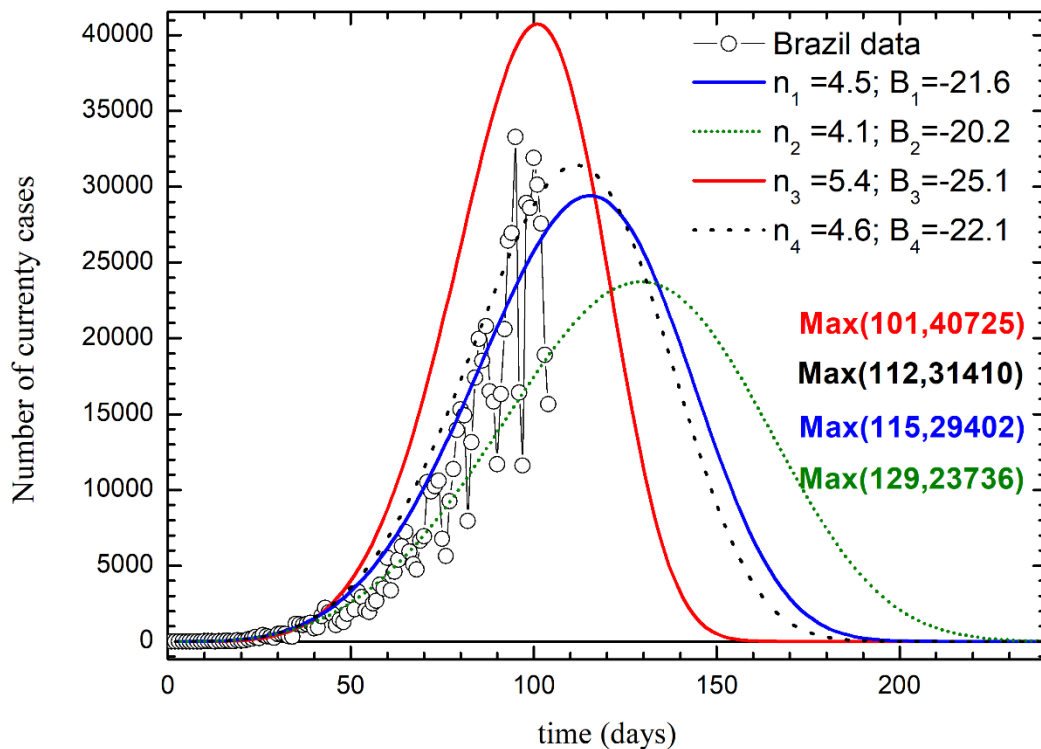


Figure 3. Estimate of people infected with COVID-19 considering 1% of the infected Brazilian population.

Our estimate indicates that the peak of the disease will occur on June 29th and will affect 29,402 infected people on that day. In addition, the disease's nucleation rate was 4.5, which indicates that the disease is expanding very rapidly in Brazil.

3.2. Prediction for Espírito Santo State

COVID-19 was first detected in Brazil in the eighth epidemiological week, with nine confirmed cases. Since the first one, health authorities have not carried out mass testing, suggesting the underreporting of the disease cases. The Brazilian Ministry of Health detected a 705% increase in admissions for severe acute respiratory syndrome (SARS) up to the 21st epidemiological week of 2020, compared to the same period in 2019. We obtained this information on June 4th, on the Brazilian Ministry of Health website.

Regarding such data, Cintra and Nunes [12] noted that, the number of hospitalizations for SARS-CoV-2 in Brazil was 12,260 in the 13th epidemiological week, whereas the number was 1123 in 2019. Given the average history between 2017 and 2019, 90% of hospitalizations are excessive cases that the researchers associated to COVID-19. Likewise, Bastos et al. [17] observed a significant increase in hospitalizations for SARS when analyzing the historical average between the 9th and 12th epidemiological

weeks of the decade of 2010. This reinforces our hypothesis that the Brazilian health system underreports COVID-19 cases.

To estimate the underreporting factor, we analyzed the data on deaths from COVID-19. The COVID Registral Panel website [18] reports that there are six deaths from SARS in 2019 versus 62 deaths in 2020, an increase of approximately 1000%. Then, we can define factor 10 as an underreporting correction. Therefore, if we corrected the COVID-19 data by factor 10, we had the following evolutions in the number of cases, which can be seen in Figure 4A.

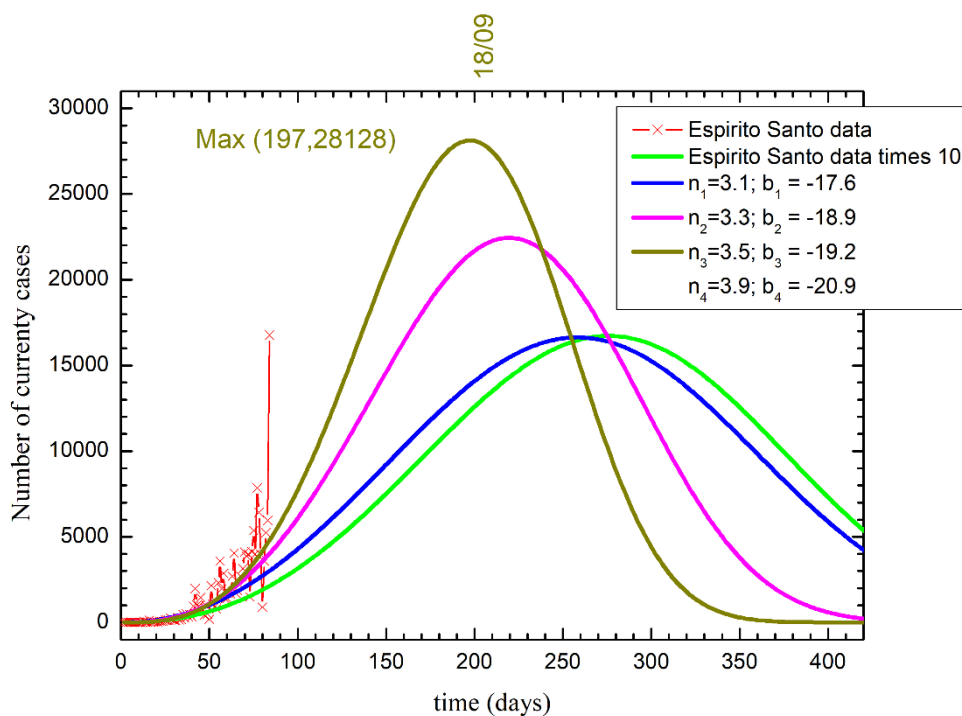


Figure 4. (A) Official data on COVID-19 corrected by the factor 10x. The closed square symbol represents the official data, and the cross symbol, the official data multiplied by 10.

As seen in the expansion (see Figure 4B), in the dark yellow curve ($n_4; b_4$), we will have the peak on day 197 (September 18th), with 28,128 people infected. In this epidemiological scenario, there will be 4.019 million people infected, which is a very bad estimate, because the total number of infected people is close to the total population of the Espírito Santo State.

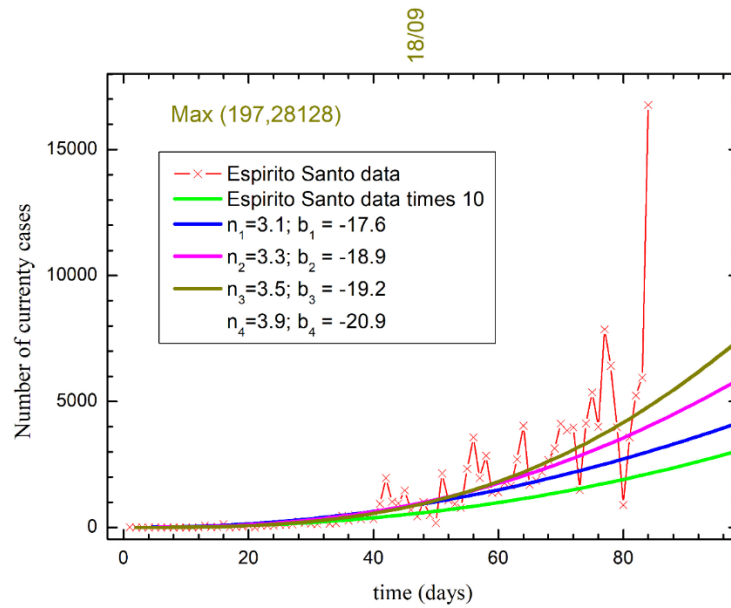


Figure 4. (B) Expansion of adjustments with the JMAK function.

Considering 1% of the population infected by COVID-19 in the Espírito Santo State, the adjustment parameters were $n = 5.3$ and $b = 24.8$, as shown in Figure 5.

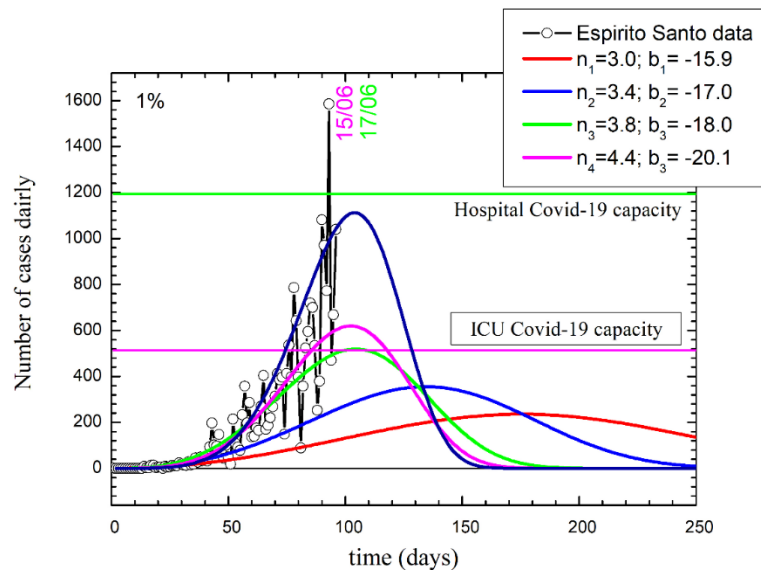


Figure 5. Estimate of people infected with COVID-19 considering 1% of the infected population of Espírito Santo State.

However, in the last epidemiological week, there was a big data variation, which can be explained by the number of people circulating during the week, compared to the weekend. It is important to mention that in the state of Espírito Santo there were only buses as the only option for public transport. This is an important factor for COVID-19

spread in the metropolitan regions in the state. Thus, in our opinion, the parameter n should be less than 3.

The peak of infection was estimated to occur on day 105 (19 June 2020), with 519 people infected on this day. According to the COVID-19 Panel on the Espírito Santo State, there are 490 beds in the intensive care unit (ICU) dedicated to COVID-19, of which 473 (60.03%) are occupied (see Table 2).

Table 2. Beds in hospitals in Espírito Santo State. Update of beds in intensive care units (ICU) on 25 May 2020.

	Total Beds	Occupied Beds	Occupancy Rate
ICU	490	380	77.55%
Nursery	575	301	52.35%
Total beds COVID-19	1065	681	63.94%

In this epidemiological scenario, the state's health system will not support the demand for beds.

3.3. Prediction for the Pára State

Figure 6 shows the evolution and simulations for the Para State. Considering that 1% of the population is infected with COVID-19, the adjustment parameters that describe the evolution of daily cases are $n = 5.7$ and $b = 24.9$. Despite daily variations, the difference between official and simulated data is in good agreement.

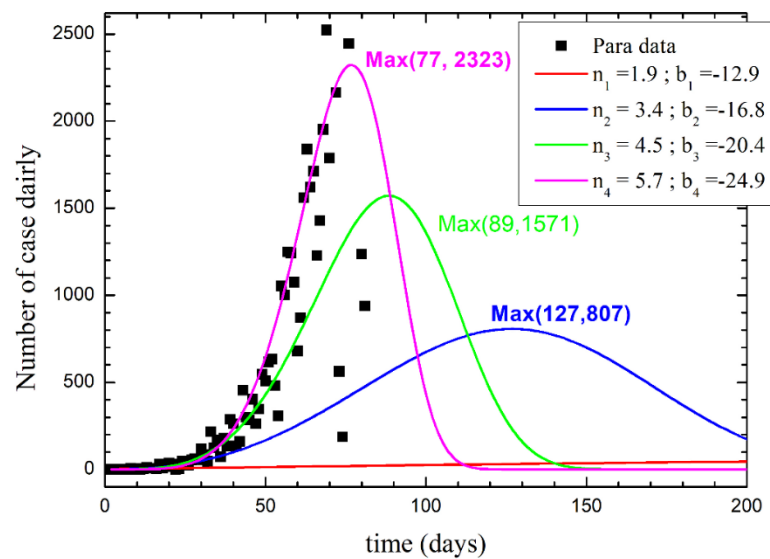


Figure 6. Estimate of people infected with COVID-19 considering 1% of the infected population of the Pará State.

Parameter n found for the Pará State is highlighted for having a higher value than that determined for Brazil (4.5). The first case registered in the state was on March 19th, and the state government implemented measures of social isolation. In Belem City, the city hall decreed a lockdown on May 5th for 20 days. However, there was a strong growth of the disease when compared to the rest of the country. Our result suggests that the mobility restriction measures did not work in the Pará State.

4. CONCLUSIONS

In the present study, we analyzed the official data of COVID-19 in Brazil and used the JMAK function to predict the disease evolution. For our analysis, we considered close contact events that are social events and scenarios such as living together, dining together, traveling together, and working together are responsible for the dissemination of the disease. The model indicated that the nucleation rate is in the order of four, which suggests that Brazilians are gathering without respecting measures of social distance and disease prevention. In our opinion, the political authorities were unable to control the spread of the disease in Brazil, considering that social mobility was partially interrupted by the federal and state governments. Therefore, the series of non-pharmaceutical interventions and the public compliance that took place in Brazil are an important role to break the spread of COVID-19. Summarizing the results, we estimated that 1% of the Brazilian population is infected:

- Peak estimated to occur on June 29th;

- Total number of infected people = 2.1 million.
- As to the Espírito Santo State, the estimate says that 1% of the state's population is infected:
- Peak estimated to occur on June 19th;
- Total number of infected people = 40,186.
- Estimating a scenario for the Pará State, 1% of the population is infected:
- Peak estimated to occur on June 3rd;
- Total number of infected people = 86,029.

Given these scenarios, free movement of people is not recommended. In our opinion, the only possible alternative now is to keep social distancing measures, avoid gathering, and restrain access of people to public transportation.

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