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A Logistic Fractional Model with Control Measures for Cumulative Cases of COVID-19

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ABSTRACT. The curve of cumulative cases of individuals infected by COVID-19 shows similar growth to the logistic curve in the period referring to each epidemic "wave", as each peak of active cases is called. Considering that in pandemic scenarios it is common to seek control measures based on previous experiences, in this paper we model the curve of cumulative cases through a logistic model with infected removal to include the control measures in the dynamics. This model is based on fractional differential equations to also include the memory effect. We study the scenario of the first two "waves" in the analyzed countries: Brazil, China, Italy, and Switzerland. Scenarios with and without control measures are compared, proving the importance of control measures such as isolation. Moreover, this model makes it possible to determine the portion of the population that did not participate in the dynamics of the spread of the disease, as well as to analyze how the number of infected people reduced in each country.

Keywords: logistic model with removal, fractional differential equations, social isolation.

1 INTRODUCTION

In December 2019, an outbreak of pneumonia began, which later, in February 2020, was detected as a COVID-19 pandemic [9, 16]. This disease is caused by the coronavirus, which are known to cause respiratory infection [16].

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There are still uncertain questions about the behavior of this virus and its variants, but it is believed that the spread occurs mainly by respiratory droplets, similar to what happens with influenza. The virus is released in respiratory secretions when an infected person coughs, sneezes, or talks. Through droplet transmission, the individual is infected by coming into direct contact with the mucous membranes. The droplets normally do not reach more than two meters and apparently do not remain in the air [15].

The data indicate that transmission is more likely in the early stage of infection, as viral ribonucleic acid (RNA) levels appear to be highest soon after the onset of disease symptoms [20]. Preliminary evidence suggests that some antibodies induced in those who have been infected are protective. However, when in fact the previously infected person presents a protective immune response, as occurs with the vaccinated individual, the duration of this immunity is not known [4].

To reduce the risk of transmission in the community, social distancing is recommended. In addition, individuals should diligently wash their hands or use hand sanitizer, practice respiratory hygiene (for example, cover their cough and wear protective masks), avoid crowds, and close contact with sick individuals [17].

Applied mathematics allows us to study quantitative aspects of a disease, such as the speed at which it spreads and important parameters that facilitate public decision-making so that an epidemic or pandemic does not occur. It is common to find mathematical models proposed through ordinary differential equations. Currently, fractional differential equations are also used, which allow considering the memory effect in the dynamics of the model since the fractional operators are non-local. As the memory effect is present in epidemic situations, mainly with the aim of taking advantage of previous experiences to contain the spread of the disease, it is important to consider this effect in the dynamics of the model [1,2,5,13,19].

Among the existing fractional derivatives, the most common are those of Caputo and Riemann-Liouville. In mathematical modeling, the most used is that of Caputo, due to its unusual property among fractional derivatives: the derivative of a constant is zero, that is, it follows the intuitive idea of classical derivatives for intervals neither increasing nor decreasing. Another advantage of the Caputo derivative is that it allows considering classical initial conditions in the model system [1,3,5,11,14]. It is possible to see in [5] that the Caputo derivative at an instant t considers the entire history of the dynamics, since it is proportional to the average of the variations (classical derivatives) at all previous instants.

In addition to epidemiological and applied mathematics in general, fractional calculus has been highlighted in several applications of physics, chemistry, biology, engineering and other areas. Moreover, an attractive feature of fractional models is the better ability to fit data than classical models [1,2,5].

This article is structured as follows: in Section 2 we present, analyze and justify the model proposed in this paper. In Section 3 we present the method used and discuss the results obtained. Finally, in section 4 we present the conclusion.

2 MATHEMATICAL MODELING

In this section, we present the model proposed in this paper to describe the evolution of the pandemic caused by the coronavirus. Thus, only the evolution of individuals confirmed infected by the disease is analyzed, through the curve of cumulative cases. It is important to note that it is through the curve of active cases of the disease that the so-called "waves" can be observed. On the other hand, analyzing the cumulative cases (which only increases in quantity) in the period referring to each "wave", it can be concluded that initially the number of cases grows exponentially and, from the peak of the "wave" (where active cases start to decrease), the number of cumulative cases starts to grow more slowly, where there is an inflection point. When the number of active cases stops growing (end of the first "wave", before starting the next one) the number of cumulative cases tends to stabilize. Then, a similar behaviour to the logistic growth can be seen in the curve of cumulative cases [8] in the period referring to each "wave" of active cases.

Thus, in our model, we use logistic growth to model the curve of cumulative cases of COVID-19. Moreover, we consider fractional differential equations via Caputo derivative, since they provide the modeling of memory effect in dynamics [5,12]. It is important to consider the memory effect in pandemic situations, since over time people take preventive measures to control the disease and, for that, they consider previous experiences. In addition, we have included an infected removal term. This term represents the measures to control the epidemic [10]. Thus, the model is described by the following initial value problem:

$$\begin{cases} {}^{\mathrm{C}}\mathscr{D}_t^{\alpha} I = r^{\alpha} I \left(1 - \frac{I}{K}\right) - p^{\alpha} I \\ I(0) = I_0 \end{cases}, \tag{2.1}$$

where $I(t)$ is the number of confirmed cases of coronavirus infection in time t, given in days, $r \in [0,1]$ is the rate of contagion with free mobility of people, $K > 0$ is the carrying capacity, $p \in [0,1)$ is the portion of individuals removed from the dynamic, due to social isolation or other control measures, and $\alpha \in (0,1)$ is the fractional order of the Caputo derivative. Note that in (2.1) the parameters r and p must be raised to α due to the need to correct the dimensions. Further details of this dimensional analysis can be found at [6].

Another way to do dimension correction in a fractional model is to perform the product between $\frac{1}{\tau^{1-\alpha}}$ and the operators on the left side of (2.1), where τ is any constant with dimension $(\text{time})^1$. Thus, the term $\frac{1}{\tau^{1-\alpha}} {}^{\mathrm{C}}\mathscr{D}_t^{\alpha}$ has dimension $(\text{time})^{-1}$. In this way, if we take $\bar{r} = \tau^{1-\alpha} r$ and $\bar{p} = \tau^{1-\alpha} p$, we can rewrite (2.1) so that the parameters $\bar{r}$ and $\bar{p}$ appear in place of r and p, which are not raised to the power α. It is easy to prove this form of dimension correction through the equation (2.2), found in [5],

$${}^{\mathrm{C}}\mathscr{D}_t^{\alpha} f(t) = \frac{t^{1-\alpha}}{\Gamma(2-\alpha)} E\left[f'(tW)\right] \Rightarrow t^{\alpha-1} {}^{\mathrm{C}}\mathscr{D}_t^{\alpha} f(t) = \frac{E\left[f'(tW)\right]}{\Gamma(2-\alpha)}, \tag{2.2}$$

where for $\alpha \in (0,1)$, ${}^{\mathrm{C}}\mathscr{D}_t^{\alpha}$ and $f'(t)$ are the Caputo derivative and the classical derivative of f at time t, respectively, and W is a random variables with beta distribution, $W \sim B(1, 1-\alpha)$.

Note that $E\left[f'(tW)\right]$ is a weighted average of $f'(s)$ that has dimension: population × (time)$^{-1}$. Therefore, both sides have dimension population × (time)$^{-1}$. We chose the first form of dimension correction (generating the model (2.1)) as this makes it easier to get the parameters of the original model.

2.1 Model analysis

In the classic logistic model with removal ($\alpha = 1$), an asymptotically stable equilibrium occurs at $\bar{I} = \left(\frac{r-p}{r}\right)K$, if $p \neq 0$, and at $\bar{I} = K$, if $p = 0$ (without removal) [8]. Thus, p can be seen as an epidemic control measure.

We can rewrite the differential equation (2.1) as follows:

$$ {}^{\mathrm{C}}\mathscr{D}_t^{\alpha} I = (r^{\alpha} - p^{\alpha}) I \left(1 - \frac{I}{\left(\frac{r^{\alpha}-p^{\alpha}}{r^{\alpha}}\right)K}\right), \tag{2.3}$$

where the carrying capacity can be better identified:

$$\bar{K} = \left(\frac{r^{\alpha} - p^{\alpha}}{r^{\alpha}}\right)K.$$

According [5], for $\alpha \in (0,1)$,

$$ {}^{\mathrm{C}}\mathscr{D}_t^{\alpha} I = \frac{t^{1-\alpha}}{\Gamma(2-\alpha)} E\left[I'(tW)\right],$$

where W is a random variable with beta distribution of parameters 1 and $1-\alpha$, that is, $W \sim B(1, 1-\alpha)$. Thus, ${}^{\mathrm{C}}\mathscr{D}_t^{\alpha} I$ is proportional to the mathematical expectation of $I'(s)$, $0 \leq s \leq t$. In the case studied here, $I(s)$ represents cumulative cases, so that $I'(s) \geq 0$ and, therefore, ${}^{\mathrm{C}}\mathscr{D}_t^{\alpha} I \geq 0$. This fact implies $r^{\alpha} \geq p^{\alpha} (r \geq p)$, that is, the contagion rate (r) is always higher than the rate of removal of the individual from the dynamics (p).

Thus, as $I'(t) \geq 0$, the equilibrium is characterized by a constant value where $I(t)$ approaches it asymptotically. Furthermore, ${}^{\mathrm{C}}\mathscr{D}_t^{\alpha} I = 0 \Leftrightarrow E[I'(s)] = 0$, where $I'(s) = 0$, for all $0 \leq s \leq t$. Thus, according to (2.3), the equilibrium value is given by $\bar{K} = \left(\dfrac{r^{\alpha} - p^{\alpha}}{r^{\alpha}}\right)K$. That is, when $t \to \infty$, we have

$$I(t) \to \left(\frac{r^{\alpha} - p^{\alpha}}{r^{\alpha}}\right)K.$$

Thereby, if $p = 0$, $I(t) \to K$. On the other hand, if $p \neq 0$, then $\left(\frac{r^{\alpha}-p^{\alpha}}{r^{\alpha}}\right)K < K$. That is, the new carrying capacity (of the scenario with control) is less than the capacity of the scenario without control ($p = 0$). Moreover, the curve $I(t)$ tends to stabilize at a value ($\bar{K}$), which is smaller and smaller as p increases.

3 AN APPLICATION TO CUMULATIVE CASES OF COVID-19

In this section, we use cumulative case data of COVID-19 available in [18] to evaluate the model (2.3) analyzing the spread of the disease in the first two “waves” of China, Italy Switzerland, and Brazil. We divided the data into two parts: the first part refers to the period of the first “wave” and the second part refers to the period of the second “wave”. Then, the model proposed here is used in each part of the data separately. The only exception occurs with China, because the country presented only one ”wave”, with no need to separate the data. We emphasize that although the data used represent the curve of cumulative cases, it is through the curve of active cases that the respective periods of occurrence of the “waves” are analyzed.

In each part of the data, a data fitting is performed using the least squares method. With this, it is possible to determine the four parameters of the model: the order of the derivative (α), the contagion rate (r), the infected removal parameter (p), and the constant K that compose the new carrying capacity of the model: $\bar{K} = \left(\frac{r^\alpha - p^\alpha}{r^\alpha}\right) K$.

For the fitting process, we consider the period of the first “wave” as starting on the day the first case occurred, while the period of the second “wave” starting from the moment the number of cases increased considerably again, characterizing the exponential curve of the first phase of logistic growth. We consider both “waves” ending on the day when the number of cases was the lowest in the stability period between both “waves”. Such stability period is disregarded in the fitting process, but the data from this period are plotted together with the others.

The least squares method is applied numerically through the Nelder-Mead optimization algorithm. To determine the numerical solution of the fractional differential equation, the Predictor-Corrector approach is used [1, 7].

The smaller is the number of parameters to be numerically determined, the better is the effectiveness in the response given by the program. Therefore, in the period referring to the second “wave” we fixed the value of r found in the first one. This is not a problem since the contagion can be described by the expression $r^\alpha - p^\alpha$, so it is reasonable to assume that from one “wave” to another what changes is the control, characterized by the parameter p.

The value $p = 0$ means that no control measure is adopted. Thus, it is possible to project the pandemic scenario if no control measures had been adopted. It is worth remembering that, in this scenario without control, the carrying capacity of the curve is K.

Below we can see the results obtained in the analysis of each country. First, the scenario of China is studied, since in this country only one “wave” occurred and, then, it is possible to observe more clearly the applicability of the model proposed here. This is because, in this case, the model can be used without the need to separate the data into two parts. For the other countries, we study the first two “waves” to show that the model can be applied to analyze more than one “wave”, provided that this is done for each one separately. Moreover, we show how the behavior of the curve of the cumulative case would be if the second and/or third “wave” did not appear in

Italy, Switzerland, and Brazil. Also, we compared the scenario with and without isolation in all countries.

3.1 China

When analyzing the scenario in China, we obtain the following values for the parameters: $\alpha = 0.849, r = 0.640, K = 163.913 \times 10^3$ and $p = 0.276$.

As α is closer to 1 (classic case, without memory) than to 0, we can conclude that in this period there was little memory effect and that the convergence to the carrying capacity is faster [5].

Control measures are characterized by the parameter $p = 0.276$, indicating that approximately 27.6% of the population did not participate in the infection dynamics.

Furthermore, it is possible to compare the carrying capacity of the scenario with control with that of the scenario without control. They are, respectively,

$$\bar{K} = 83.605 \times 10^3 \qquad \text{and} \qquad K = 163.913 \times 10^3.$$

Thus, the control measures adopted in that country were enough to practically reduce by half (1.96 time) the total number of people affected by COVID-19.

In Figure 1, the blue dots curve represents the real data, and the green dashed curve represents the solution of the model (2.3) in the scenario that occurred, with isolation. We can see that the fractional model presents an excellent fit to the data.

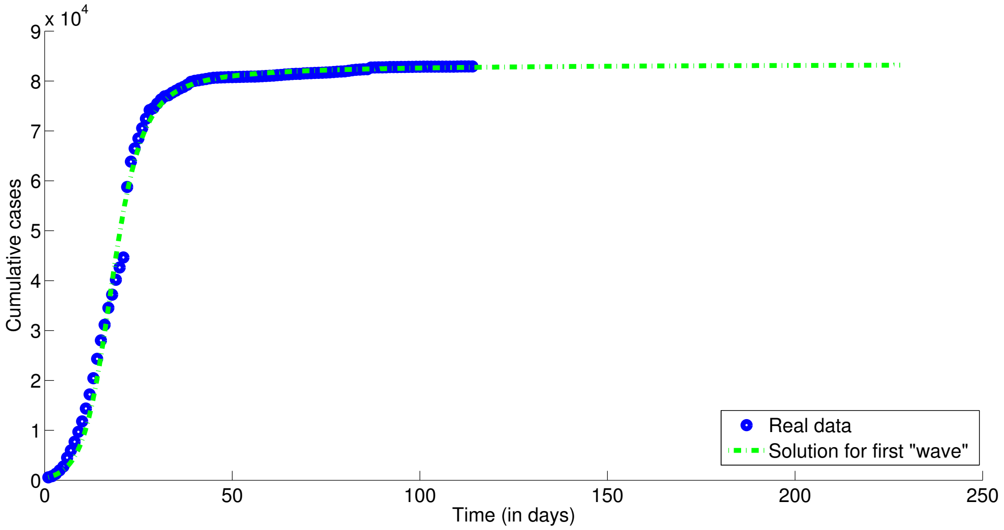

Figure 1: Solution of the model (2.3) in the scenario with isolation of China, compared to the real data. For this scenario, $\alpha = 0.849, r = 0.640$, $K = 163.913 \times 10^3$ and $p = 0.276$.

Note that the solution curve indeed tends to the carrying capacity $\bar{K}$ found in the previous analysis as being the asymptotically stable equilibrium of the model. This value refers to the scenario with isolation, that is, for $p \neq 0$. Thus, taking $p = 0$, we can see in Figure 2 a projection of the scenario without isolation, characterized by the red dotted curve, which converges to K.

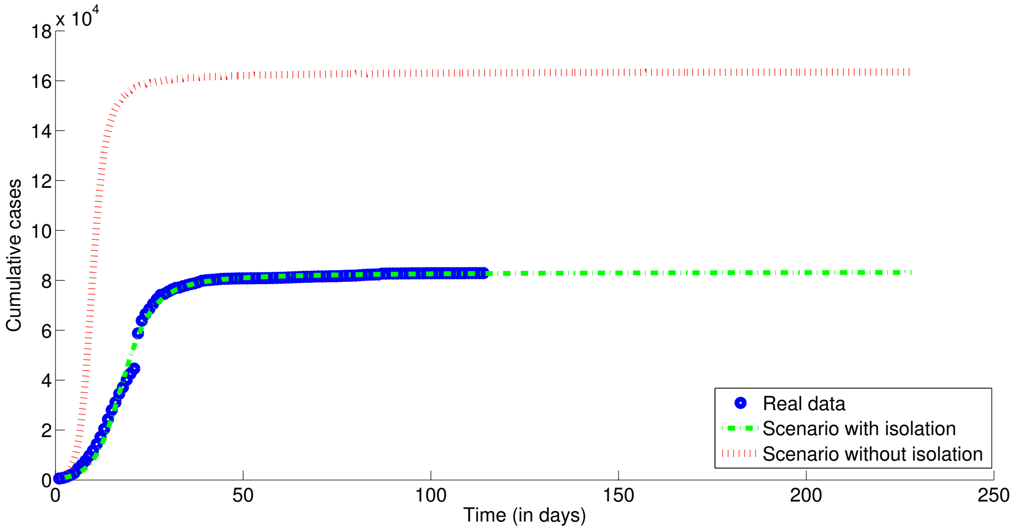

Figure 2: Solution of (2.3) in scenarios with and without (projection) isolation in China, compared to real data.

In the case of China, since there is only one "wave", we see that the model describes well the curve of cumulative cases of COVID-19, without the need to separate the data, showing the time and the value in which the curve stabilized. Furthermore, we see that indeed the real data curve presents a logistic behavior.

3.2 Italy

3.2.1 First "wave"

In the period referring to the first "wave" in Italy, the values obtained for the parameters are: $\alpha = 0.323, r = 0.871, K = 506.869 \times 10^3$ and $p = 0.026$.

The fact that α is closer to 0 than to 1 allows us to conclude that, in this period, there was a large memory effect and that convergence to the carrying capacity is slower [5].

Control measures are characterized by the parameter $p = 0.026$, indicating that approximately 2.6% of the population did not participate in the infection dynamics during this period.

Furthermore, it is possible to analyze the carrying capacity of the scenario with control, which is

$$\bar{K} = 343.779 \times 10^3.$$

Compared to the estimated value for the carrying capacity of the scenario without isolation (K), the control measures adopted were sufficient to reduce the total number of people affected by COVID-19 by approximately 1.47 time.

In Figure 3, the blue dot curve represents the real data and the green dashed one represents the solution of the model (2.3) in the scenario that occurred in the first "wave", which is with isolation. The red dotted curve represents a projection ($p = 0$) of the first "wave" if there was no isolation. We can see, again, the optimal data fit provided by the fractional model.

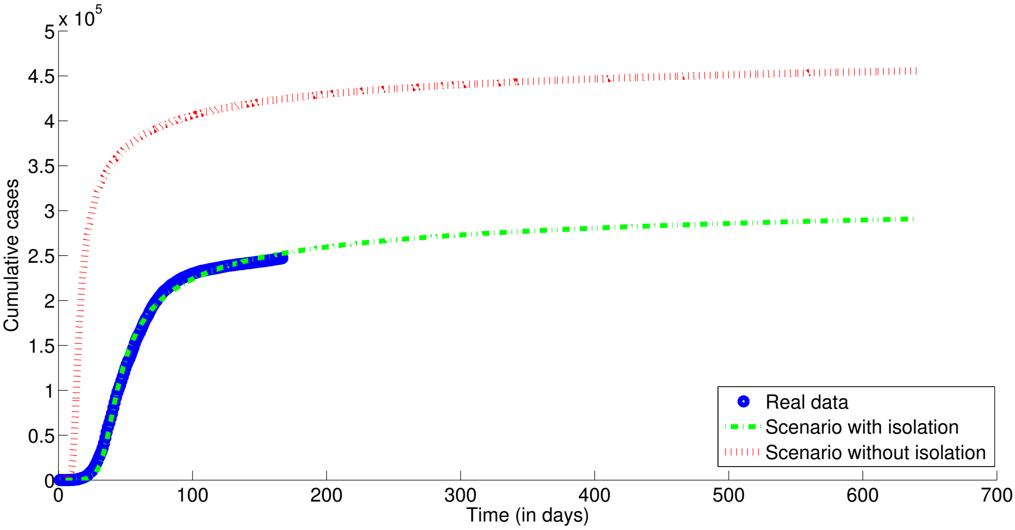

Figure 3: Solutions of the model (2.3) in the scenarios with and without isolation for the first "wave" in Italy, compared to the real data. For this scenario, $\alpha = 0.323$, $r = 0.871$, $K = 506.869 \times 10^3$ and $p = 0.026$.

3.2.2 Second "wave"

To illustrate the model (2.3) in more than one "wave", we now analyze the second "wave" scenario. The values obtained for the parameters are: $\alpha = 0.445$, $r = 0.871, K = 44.801 \times 10^6$ and $p = 0.552$.

As α is closer to 0 than to 1, we conclude that during the second "wave" the memory effect is strongly present and convergence to carrying capacity is slower [5]. Moreover, compared to the first "wave" scenario we see that the memory effect has reduced.

The parameter p indicates that there is more control in this period than in the first "wave", and suggests that approximately 55.2% of the population did not participate in the infection dynamics.

The carrying capacity of this new scenario, with control, is

$$\bar{K} = 8.227 \times 10^6.$$

Compared to the estimated value for the carrying capacity of the scenario without isolation (K), the control measures adopted would reduce the number of infected by approximately 5.45 times.

In Figure 4, the blue dot curve represents the real data and the dashed curves represent the solution of the model (2.3) in the scenarios that occurred (with isolation) being the green curve for the first “wave” and the pink curve for the second “wave”.

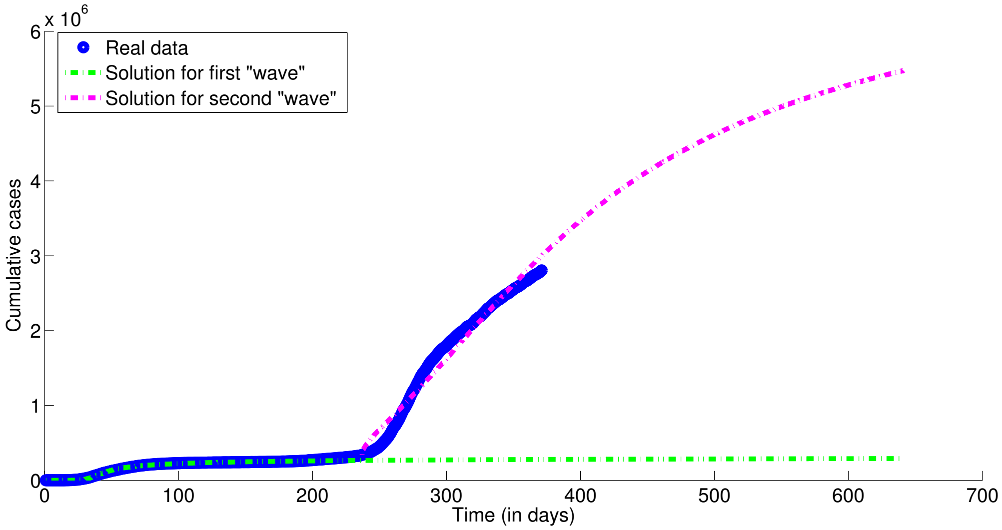

Figure 4: Solutions of the model (2.3) in the scenario with isolation for the first and second “wave” in Italy, compared to the real data. For this scenario, $\alpha = 0.445$, $r = 0.871, K = 44.801 \times 10^6$ and $p = 0.552$.

It can be seen, again, that the fractional model presents an excellent fit to the data. Furthermore, it is possible to see that in the curve of cumulative cases (real data) there is an inflection point when the new “wave” of active cases starts, which is marked by the beginning of the pink curve. If there were no new “wave”, the model (2.3) indicates that the trend would be for the number of cumulative cases to grow to approximately 8 million people and then stabilize.

3.3 Switzerland

3.3.1 First “wave”

In the period referring to the first “wave” in Switzerland, the values obtained for the parameters are: $\alpha = 0.466, r = 0.846, K = 57.799 \times 10^3$ and $p = 0.091$.

The fact that α is closer to 0 than to 1 allows us to conclude that, in this period, there was a reasonably large memory effect [5]. This case contemplates this effect more than the case of China, but less than the case of Italy. Furthermore, we can conclude that convergence to carrying capacity is given relatively slower.

Control measures are characterized by the parameter $p = 0.091$, indicating that approximately 9.1% of the population did not participate in the infection dynamics during this period.

Furthermore, it is possible to analyze the carrying capacity of the scenario with control, which is

$$\bar{K} = 37.344 \times 10^3.$$

Compared to the estimated value for the carrying capacity of the scenario without isolation (K), the control measures adopted were sufficient to reduce the total number of people affected by COVID-19 by approximately 1.55 time.

In Figure 5, the blue dot curve represents the real data and the green dashed one represents the solution of the model (2.3) in the scenario that occurred in the first "wave", which is with isolation. The red dotted curve represents a projection ($p = 0$) of the first "wave" if there was no isolation. We can see, again, the optimal data fitting provided by the fractional model.

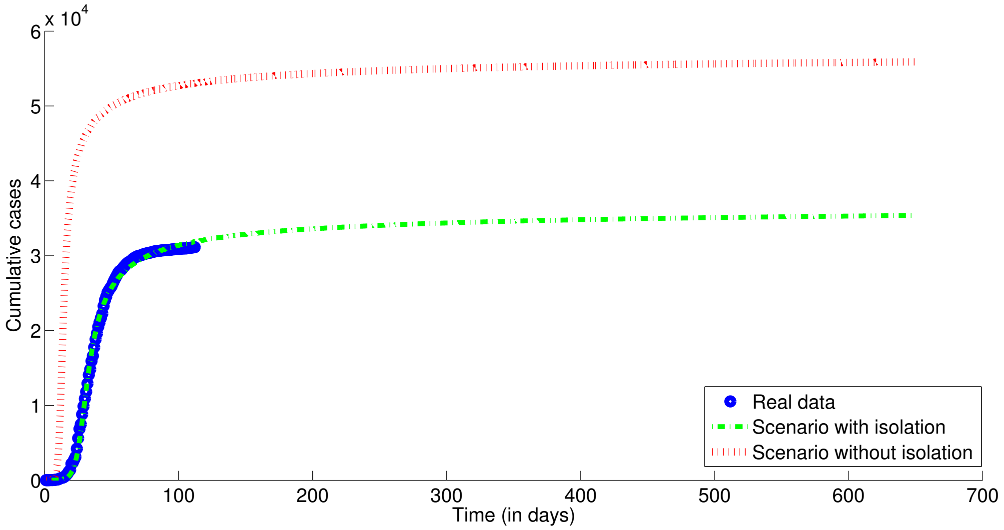

Figure 5: Solutions of the model (2.3) in the scenarios with and without isolation for the first "wave" in Switzerland, compared to the real data. For this scenario, $\alpha = 0.466, r = 0.846, K = 57.799 \times 10^3$ and $p = 0.091$.

3.3.2 Second “wave”

To illustrate the model (2.3) in more than one “wave”, we now analyze the second “wave” scenario. The values obtained for the parameters are: $\alpha = 0.729$, $r = 0.846, K = 5.573 \times 10^6$ and $p = 0.714$.

As α is closer to 1 than to 0, we conclude that in the second “wave” the memory effect is little present and convergence to carrying capacity is faster [5]. Moreover, compared to the first “wave” scenario we see that the memory effect has reduced.

The parameter p indicates that there is more control in this period than in the first “wave”, and suggests that approximately 71.4% of the population did not participate in the infection dynamics. The support capacity of this new scenario, with control, is

$$\bar{K} = 649.674 \times 10^3.$$

Compared to the estimated value for the carrying capacity of the scenario without isolation (K), the control measures adopted would reduce the number of infected by approximately 8.58 times.

In Figure 6, the blue dot curve represents the real data and the dashed curves the solution of the model (2.3) in the scenarios that occurred (with isolation) being the green curve for the first “wave” and the pink curve for the second “wave”.

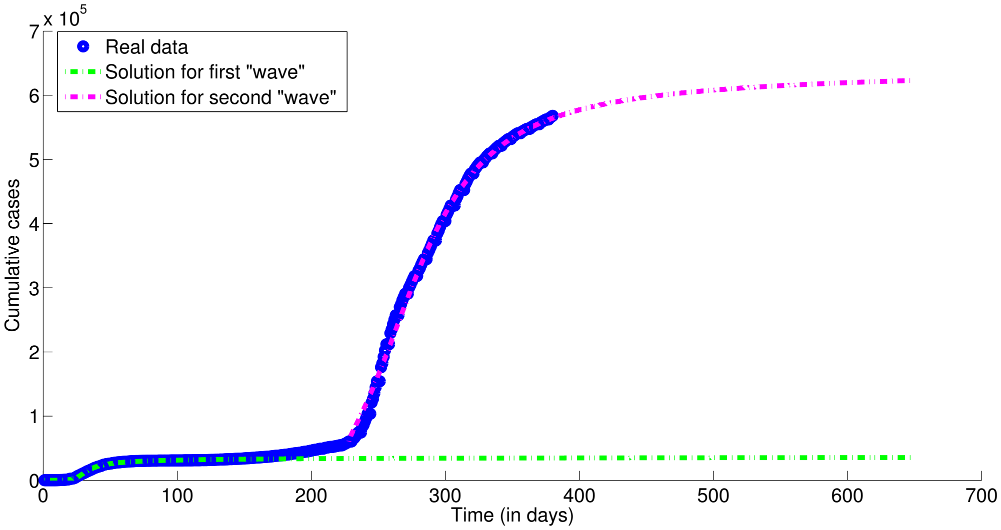

Figure 6: Solutions of the model (2.3) in the scenario with isolation for the first and second “wave” in Switzerland, compared to the real data. For this scenario, $\alpha = 0.729, r = 0.846, K = 5.573 \times 10^6$ and $p = 0.714$.

It can be seen, again, that the fractional model presents an excellent fit to the data. Furthermore, it is possible to see that in the curve of cumulative cases (real data) there is an inflection point when the new "wave" of active cases starts, which is marked by the beginning of the pink curve. If there were no new "wave", the model (2.3) indicates that the trend would be for the number of cumulative cases to grow to approximately 650 thousand people and then stabilize.

3.4 Brazil

3.4.1 First "wave"

In the period referring to the first "wave" in Brazil, the values obtained for the parameters are: $\alpha = 0.277, r = 0.276, K = 12.068 \times 10^6$ and $p = 0.001$.

The fact that α is closer to 0 than to 1 allows us to conclude that, in this period, there was a large memory effect and that convergence to the carrying capacity is slower [5].

Control measures are characterized by the parameter $p = 0.001$, indicating that approximately 0.1% of the population did not participate in the infection dynamics during this period.

Furthermore, it is possible to analyze the carrying capacity of the scenario with control, which is

$$\bar{K} = 9.253 \times 10^6.$$

Compared to the estimated value for the carrying capacity of the scenario without isolation (K), the control measures adopted were sufficient to reduce the total number of people affected by COVID-19 by approximately 1.3 time.

In Figure 7, the blue dot curve represents the real data and the green dashed one represents the solution of the model (2.3) in the scenario that occurred in the first "wave", which is with isolation. The red dotted curve represents a projection ($p = 0$) of the first "wave" if there was no isolation. We can see, again, the optimal data fitting provided by the fractional model.

3.4.2 Second "wave"

To illustrate the model (2.3) in more than one "wave", we now analyze the second "wave" scenario. The values obtained for the parameters are: $\alpha = 1$, $r = 0.276$, $K = 705.677 \times 10^6$ and $p = 0.267$.

As $\alpha = 1$, coinciding with the classic case, we conclude that during the second "wave" the memory effect is not present and the convergence to carrying capacity is faster [5]. Moreover, compared to the first "wave" scenario we see that the memory effect has reduced.

The parameter p indicates that there is more control in this period than in the first "wave", and suggests that approximately 26.7% of the population did not participate in the infection dynamics.

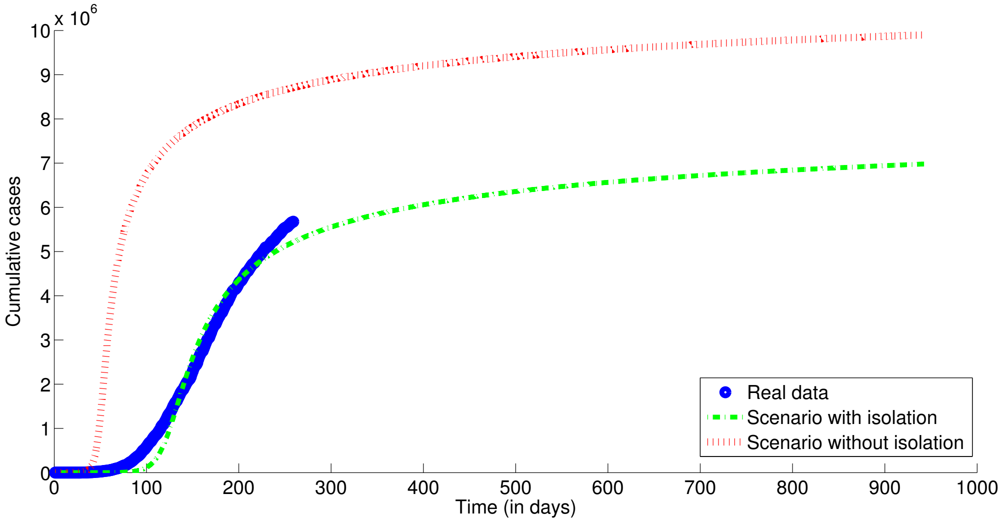

Figure 7: Solutions of the model (2.3) in the scenarios with and without isolation for the first "wave" in Brazil, compared to the real data. For this scenario, $\alpha = 0.277, r = 0.276, K = 12.068 \times 10^6$ and $p = 0.001$.

The support capacity of this new scenario, with control, is

$$\bar{K} = 24.417 \times 10^6.$$

Compared to the estimated value for the carrying capacity of the scenario without isolation (K), the control measures adopted would reduce the number of infected by approximately 28.9 time.

In Figure 8, the blue dot curve represents the real data and the dashed curves represent the solution of the model (2.3) in the scenarios that occurred (with isolation) being the green curve for the first "wave" and the pink curve for the second "wave".

It can be seen, again, that the fractional model presents an excellent fit to the data. Furthermore, it is possible to see that in the curve of cumulative cases (real data) there is an inflection point when the new "wave" of active cases starts, which is marked by the beginning of the pink curve. If there were no new "wave", the model (2.3) indicates that the trend would be for the number of cumulative cases to grow to approximately 24 million people and then stabilize.

3.5 Comparison between countries

In this subsection, Table 1 presents the values of the parameters obtained in the analysis of each country, in order to facilitate the comparison between them.

About the first "wave" it is possible to conclude that the country with the highest rate of contagion (r) is Italy, followed by Switzerland, China, and then Brazil. On the other hand, the country that

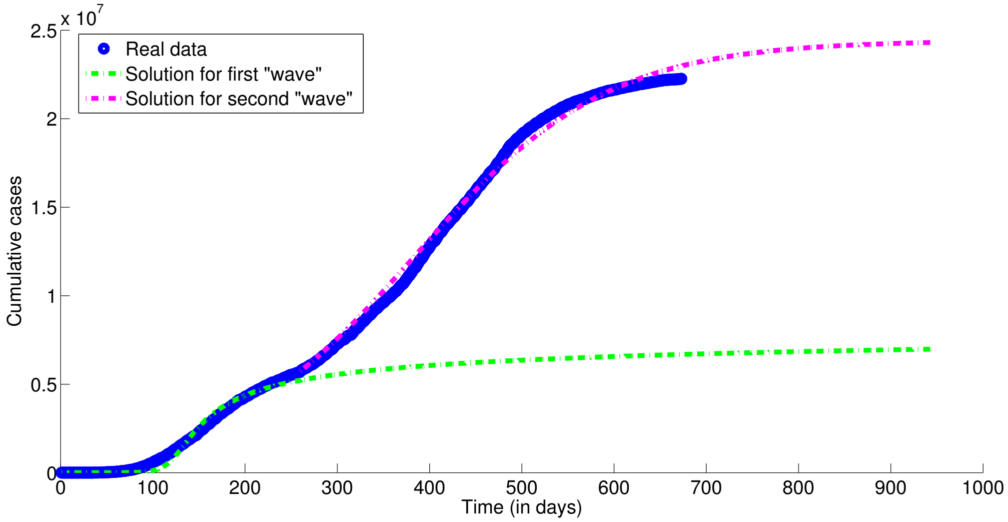

Figure 8: Solutions of the model (2.3) in the scenario with isolation for the first and second "wave" in Brazil, compared to the real data. For this scenario, $\alpha = 1$, $r = 0.276, K = 705.677 \times 10^6$ and $p = 0.267$.

Table 1: Parameters obtained for each country in the respective "waves".

		China	Italy	Switzerland	Brazil
First "wave"	α	0.849	0.323	0.466	0.277
	r	0.640	0.871	0.846	0.276
	K	163.913×10^3	506.869×10^3	57.799×10^3	12.068×10^6
	$\bar{K}$	83.605×10^3	343.779×10^3	37.344×10^3	9.253×10^6
	p	0.276	0.026	0.091	0.001
Second "wave"	α	-	0.445	0.729	1.000
	r	-	0.871	0.846	0.276
	K	-	44.801×10^6	5.573×10^6	705.677×10^6
	$\bar{K}$	-	8.227×10^6	649.674×10^3	24.417×10^6
	p	-	0.552	0.714	0.267

managed to obtain greater control (highest value of p) over the spread of the coronavirus is China, followed by Switzerland, Italy, and finally, Brazil, which showed very little control. In fact, through the projection made in this paper, it is noted that China is the country that showed the greatest decrease in the carrying capacity from K (from the scenario without isolation) to $\bar{K}$ (from the scenario with isolation), having decreased almost 2 times. That is, China is the country that has best managed to reduce the number of infected people through control measures. Switzerland, Italy, and Brazil showed a decrease in carrying capacity of 1.55, 1.47, and 1.30

times, respectively. Finally, it can be seen that in China there was the smallest memory effect, which makes sense since it was the first country to deal with coronavirus and therefore nothing was known about it at the time.

For the second “wave”, among the countries where it occurred, the order of greater control of the spread of the disease is the same as in the first “wave”: Switzerland, Italy and, again lastly, Brazil. In addition to the little control, it is worth noting that in Brazil the memory effect is non-existent in this “wave”. On the other hand, the country that showed the greatest reduction in carrying capacity is Brazil, having decreased approximately 29 times. In this country, indeed the increase in the control parameter in the second “wave” was very large (267 times). Switzerland and Italy showed a decrease in carrying capacity of 8.58 and 5.45 times, respectively.

It is worth noting that in these three countries with the second “wave”, there was an increase in control simultaneously with a reduction in the memory effect. This means that the individuals failed to act as indicated according to previous experience (ignoring memory), but learned/accustomed to following these measures mechanically.

4 CONCLUSION

The logistic fractional model proposed in this paper includes memory effect and control measures. It shows good results in representing the curve of cumulative cases of COVID-19 for each period referring to a “wave” of active cases. To illustrate this, we studied the unique “wave” from China and the first two “waves” from Italy, Switzerland and Brazil. Then, we observed a great data fit, showing that the model is useful to determine important parameters related to the COVID-19 pandemic and to investigate what the curve of accumulated cases would be like if no new “waves” appeared after the “wave’ ” under analysis. With this, we can analyze the number of cases that would be reached when the curve stabilized.

In addition, the model allows the projection of a scenario without control measures, comparing it with the scenario that occurred (with control measures). Moreover, we can determine how many times the number of cases was reduced after some control measure was enacted and calculate the portion of the population that did not participate in the dynamics of disease propagation.

The simulations made for China, Italy, Switzerland, and Brazil prove the theory that the greater the control, the better the scenario of the current pandemic, reducing the number of cases of the disease. However, if the current control measures are not maintained, reinforced, or improved, the tendency is to emerge new “waves” and, with that, new inflection points that give rise to several other logistic curves, which are connected to each other for each “wave”, as can be seen from the first two “waves” illustrated in Figures 4, 6 and 8.

The model satisfactorily describes the variation in the carrying capacity of infected people for different values of p, parameter that represents the presence of control measures. Increasing the value of this parameter is crucial to decelerate the growth of the infected curve. This is clear in this work, in which it is evident that the increase in p implies a decrease in carrying capacity, that is, the greater the control measure, the smaller the number of cumulative cases of COVID-19 in each “wave”. Also, the parameter α can indicate the degree of memory effect on the studied “wave” and, with that, indicate whether the curve grows slower or faster.

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