



Adaptive SIR model for propagation of SARS-CoV-2 in Brazil

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ABSTRACT

We study the spreading of SARS-CoV-2 in Brazil based on official data available since March 22, 2020. Calculations are done via an adaptive susceptible–infected–removed (SIR) model featuring dynamical recuperation and propagation rates. We are able to reproduce the number of confirmed cases over time with less than 5% error and also provide with short- and long-term predictions. The model can also be used to account for the epidemic dynamics in other countries with great accuracy.

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1. Introduction

At the end of December 2019, the World Health Organization (WHO) became aware of several cases of pneumonia in Wuhan City, Hubei Province of China. Soon after that, a novel coronavirus outbreak was reported and tagged as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1–3], possibly originated from bats [4]. A few days after the virus had been identified in China, an exponentially fast growing of patients was observed, leading Chinese authorities to take immediate actions so as to contain the spreading of the disease. These involved social distancing, contact tracing, large-scale testing, and serious quarantine of those who had contact with infected people [5].

On March 11, 2020, such outbreak reached the status of global pandemic. Worldwide, the number of SARS-CoV-2 cases continues to increase, with many countries facing a serious second contagious wave, amounting to over 85 million confirmed cases and 1 million and 800 thousand deaths, as of January 3 [6].

The transmission process of SARS-CoV-2 is still under scrutiny. According to the US Centers for Disease Control and Prevention (CDC), the virus propagation can occur either through direct or indirect contact, droplets and aerosol in short- and long-ranged transmissions, respectively [2,7]. A common figure used to estimate how fast the virus is propagating, in a given context, is the basic reproduction number R_0 , such that $R_0 > 1$ implies exponential growth and, generally, a number of confirmed cases of the same order as of the size of the population, leading to harsh consequences to healthcare systems. For instance, a number of works [1,8–11] estimated R_0 values above 2 for China and Europe in the first few months on the pandemic, which is quite high. In a case study for the city of Wanzhou, China [5] the authors reported a reduction of this parameter from 1.64 to 0.31–0.39 as a consequence of rigorous propagation control measures.

In [12] the R_0 value for Brazil was estimated at 3.1 and according to data available at the COVID-19 Data Repository by the Center for Systems Science and Engineering at Johns Hopkins University [13], it had stayed below 1 for a couple of months until the end of October. A second contagious wave in Brazil has now become evident due to the increasing number of daily new cases as well as of hospitalizations. Records suggest that it has been uprising since early November – about fifteen days prior to Municipal Elections – and reached $R_0 \approx 1.19$ as of December 4 [13].

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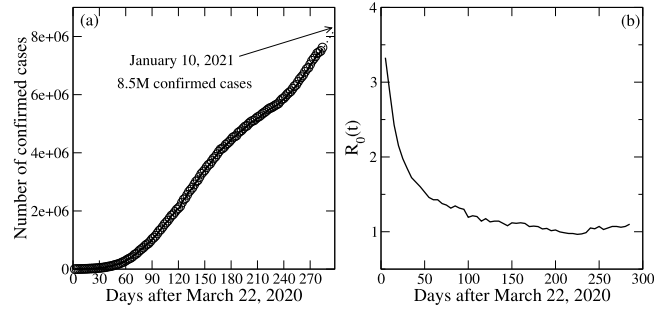


Fig. 1. (a) Number of confirmed cases (accumulated) of SARS-CoV-2 in Brazil. Symbols stand for official data and the solid line represents the results obtained via the SIR model. They both agree quite well, with an error of less than 5%. Dashed line is the prediction for the following ten days, terminating on January 10, 2021. (b) Basic reproduction number $R_0(t) = S(t)\beta(t)/\gamma(t)$ versus time. Each point is the outcome of a 5-day average. Estimated R_0 currently approaches 1.10 based on data retrieved for the last days of December.

In this work we further investigate the dynamics of the SARS-CoV-2 epidemic within the Brazilian territory from March to December, covering the second wave as well. To achieve this task, we resort to an adaptive susceptible–infected–removed (SIR) model [14–21], which also allows us to predict epidemic evolution within 10–20 days ahead. The calculations employ dynamic recuperation and propagation rates (namely γ and β parameters in the SIR model) and we are able to reproduce the time series of the number of confirmed cases with less than 5% error. Our model estimates $R_0 \approx 1.10$ as of the end of December, 2020. We also reproduce epidemic dynamics for UK, Germany, Italy, and France, thereby confirming the versatility and accuracy of the model.

2. Model

In the present work we apply a SIR model to study the dynamics of the SARS-CoV-2 in Brazil. In such description, population is divided into those susceptible to the virus (S), infected (I), and removed (R), the latter accounting for the cases which had an outcome, including recovered and deceased people. The model encompasses the following three equations:

$$\frac{dS}{dt} = -\beta(t)IS, \quad (1)$$

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

$$\frac{dR}{dt} = \gamma(t)I, \quad (3)$$

where $\beta(t)$ is the infection rate and $\gamma(t)$ is the recovered rate, with $R_0(t) \equiv S(t)\beta(t)/\gamma(t)$. In our investigation we modify the SIR equations so as to have dynamic updates of $\gamma(t)$ and $\beta(t)$ during time evolution. The proper time series is obtained from official data available in the repository of Ref. [13] from March 22 on for gauging purposes.

The equations above are solved for a wide range of γ and β values and the ones corresponding to those solutions closest to real data are kept. Throughout the simulations, we run γ within interval [0.07, 0.13] and β within [0.05, 0.6]. These parameter windows are roughly the same as the ones used in previous application of SIR models for epidemic simulation, including that of SARS-CoV-2 [22,23].

3. Results

Initial parameters are set to $R(t = 0) = 0$, $S(t = 0) = 1 - I(t = 0)$, meaning that all uncontaminated Brazilians are susceptible to infection, and $I(t = 0) = 1450/(2.1 \times 10^8)$, with 1450 being the number of confirmed cases as of March 22, 2020, and 2.1×10^8 representing the size of the Brazilian population. Note that it is reasonable to assume $R = 0$ at the beginning of the epidemic as the number of recovered and deceased people as of March 22 should be, at most, of the same order as the number of infected people, which is negligible in respect to the total population.

In Fig. 1(a) we plot the number of accumulated cases versus time (that is the number of elapsed days after March 22). It is immediate to see that the results obtained via the SIR model agree remarkably well with the official data over SARS-CoV-2 epidemic behavior in Brazil, the relative error being less than 5%. Using γ and β values as of December 31, we are able to predict the evolution of the epidemic 10 days ahead [see dotted line in Fig. 1(a)] This is obtained performing a 5-day average from December 27 to 31, resulting in $\gamma = 0.079(1)$ and $\beta = 0.136(1)$. Our prediction gives about 8.5×10^6 cases on January 10, 2021.

Fig. 1(b) depicts $R_0(t) = S(t)\beta(t)/\gamma(t)$ versus time. According to our outcomes, the current value of $R_0 \approx 1.10$ what indeed indicates a second contagious wave that possibly begun around early November, as corroborated by data obtained

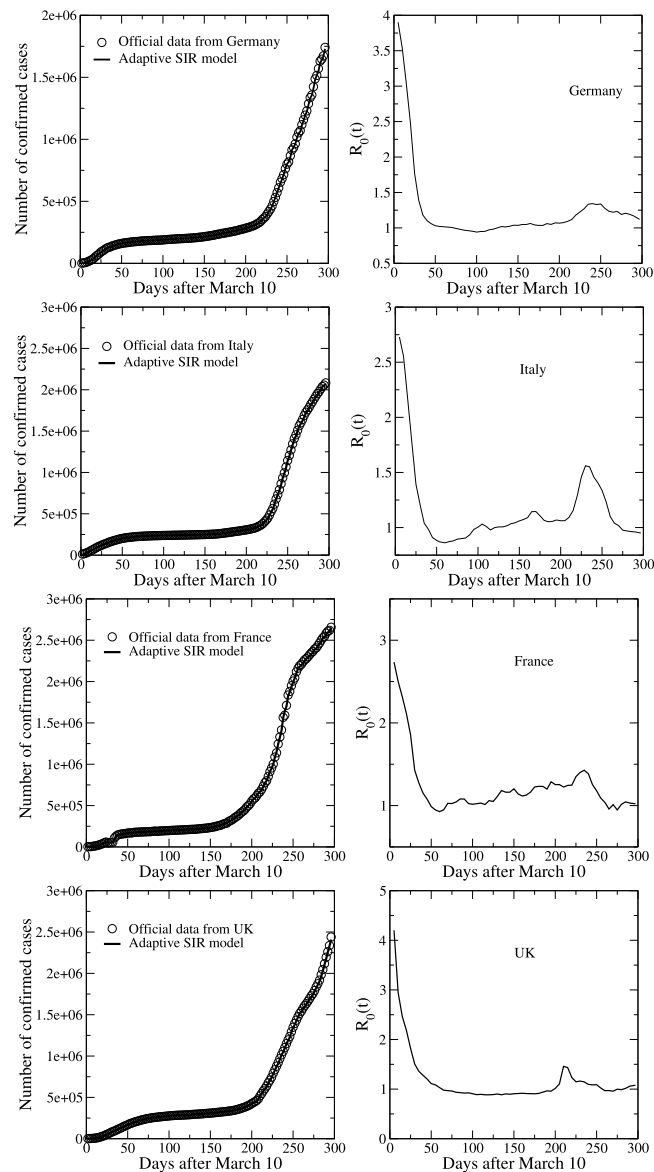


Fig. 2. (Left) Accumulated number of confirmed cases and (right) basic reproduction number R_0 for Germany, Italy, France, and UK. Official data is represented by circles and results from the adaptive SIR model are denoted by the solid lines.

elsewhere [13]. This uprising on the number of SARS-CoV-2 infections in Brazil, however, not as sharp as in many countries in Europe, for instance (see Fig. 2). Possible reasons are that the former has not taken harsh lockdown measures and due to its continental size alongside basic sanitation problems.

For comparison and also to assess the versatility of the SIR model employed here, we now reproduce the epidemic dynamics for Germany, Italy, France, and UK. The procedure is the very same as done previously. Data for those countries was extracted from Refs. [13] after March 10 on in order to estimate $\gamma(t)$ and $\beta(t)$. Our results are summarized in Fig. 2. Simulation outcomes (solid lines) for those countries are also in excellent agreement with official data (symbols), again up to an error below 5%. Therein we see a sharp onset of the second contagious wave taking place at the end of September as told by the sudden increase on the number of confirmed cases as well on the R_0 value. At this point, it is useful to compare the behavior of R_0 displayed by those countries with that of Brazil [Fig. 1(b)] which displays a smoother profile. Out of those places, only Italy featured $R_0 < 1$ based on calculations carried out for the last few days of our simulation window (that is the end of December). Of course that it does not necessarily mean that the virus spreading is decelerating for the R_0 parameter is too simplistic to account for the real dynamics of an epidemic. Yet, its time series may provide with relevant information overall. The above outcomes prove that the SIR model works quite well in estimating epidemiological parameters as well as reproducing the spreading of SARS-CoV-2 elsewhere.

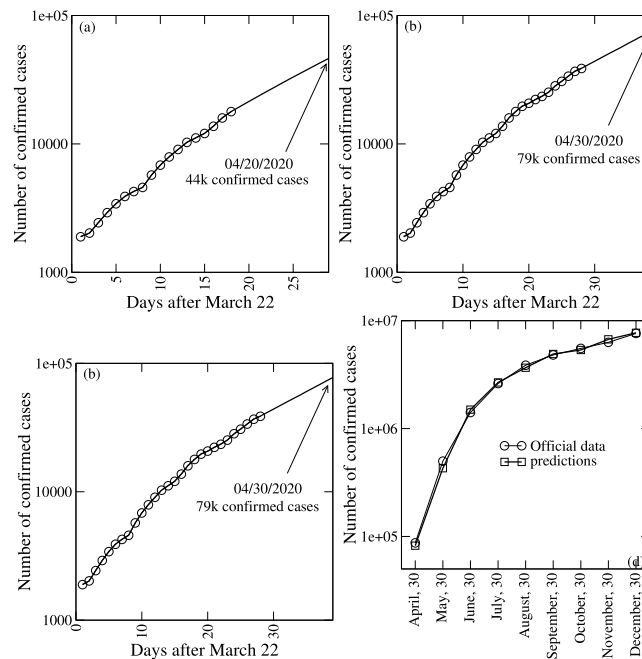


Fig. 3. (a–c) 10-day predictions realized on end dates April 10, 20, and 30, respectively, for Brazil. (d) Comparison between official data and predicted outcomes at specific days.

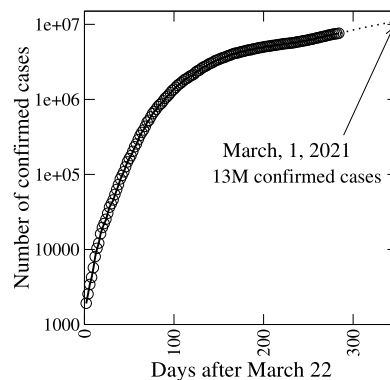


Fig. 4. Number of accumulated cases evaluated via the SIR model considering the evolution trend of R_0 as shown in Fig. 1(b). Dotted line is the prediction for times $t > 286$.

To take another glimpse over the effectiveness of the SIR model, it is convenient to provide with predictions made at earlier times to see whether these went as expected. In Figs. 3(a), 3(b), and 3(c) we show simulations based on official data retrieved until the closing dates April 10, 20, and 30, respectively, alongside predictions for 10 days ahead for Brazil. Fig. 3(d) compares these predictions with the (now obtained) official data therein showing excellent agreement.

Last, we want to show that it is also possible to carry out long-term predictions using the SIR model, say, 60 days ahead. We emphasize that this level of prediction must always be interpreted with caution, especially given the complex nature of such pandemic. Still, we are able to estimate the order of magnitude of the number of cases if we assume that $R_0(t)$ maintains its trend as showed in Fig. 1(b). We projected it by taking into account the last 15 points between $t = 271$ and $t = 286$. As a result, Fig. 4 shows our estimation for the number of cases at times $t > 286$. Simulations reveal that we may reach about 13 million cases on the first day of March.

4. Conclusions and outlook

The adaptive SIR model worked quite well in reproducing the dynamics of SARS-CoV-2 in Brazil as well as in other countries, when compared to official data retrieved from March on, by virtue of dynamical updating of parameters γ and β . Here we focused on the evolution of the basic reproduction number R_0 as well as the number of confirmed cases.

We were able to carry out both short- and long-term predictions for the epidemic evolution of 10 and 60 days ahead, respectively. The number of confirmed cases of SARS-CoV-2 is expected to reach 8.5 million cases at on January 10 and about 13 million cases on March 1st.

We stress that predictions over 10–20 days in advance crucially depends on the choice of γ and β . While the procedure works accurately for short-term predictions, it must be treated with caution in the long run, as one should do for any other model used to predict the SARS-CoV-2 pandemic. Long-term analysis calls for further assumptions over β as generally γ (related to the recuperation rate) is almost a constant of about 0.080(1), which corresponds to 15 days on average. And the infection rate parameter β depends on various factors such as social distancing policies.

One of the perks of the model used here is the easiness to estimate R_0 on a daily basis and also to reproduce the historical series of the total number of confirmed cases up to an error of less than 5%, all that in just a few computational minutes. Henceforth, it is a convenient tool for assessing some important underlying dynamical parameters in epidemic evolution.

CRediT authorship contribution statement

I.F.F. dos Santos: Conceptualization, Methodology, Numerical calculations of figs. 1, 2. **G.M.A. Almeida:** Software, Validation, Writing - original draft. **F.A.B.F. de Moura:** Conceptualization, Methodology, Software, Numerical calculations of figs. 3, 4, Writing - original draft.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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