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

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We study the spreading of SARS-CoV-2 in Brazil based on official data available since March 22, 2020. The calculations are based on an adaptive susceptible-infected-removed (SIR) model featuring dynamical recuperation and propagation rates and can reproduce the number of confirmed cases over time with less than 5% error. Furthermore, it is possible to predict the epidemic progression in the near future and we go on to estimate the time required to stabilize the virus propagation. The model is also proved to be accurate for analyzing the epidemic dynamics in other countries.

I. 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]. Some studies argues about the likelihood that the virus had originated from bats [4]. Few days after the virus had been identified in China, a exponentially fast growing of patients was observed, leading Chinese authorities to take immediate actions so as to contain the spreading of the disease. On March 11, 2020, such outbreak reached the status of global pandemic. Worldwide, the number of SARS-CoV-2 cases continues to increase with the total number of registered cases and deaths reaching over 7 million and 400 thousand, respectively (as of June 12).

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, 5]. A number of works [1, 6–9] has reported on the basic reproduction number, R_0 , for China and Europe and the obtained values range from 2.2 to 3.7. We emphasize that $R_0 > 1$ implies exponential growing and, generally, a number of confirmed cases of the same order as of the size of the population. This scenario leads to harsh consequences to healthcare systems.

In this work we investigate the dynamics of the SARS-CoV-2 epidemic within the Brazilian territory from March to June. To achieve this task, we resort to an adaptive susceptible-infected-removed (SIR) model [10, 11], which also allows us to predict epidemic evolution within 10-20 days. The calculations employ dynamical choice of recuperation and propagations 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. At the end we provide with an estimation of the time needed to break the epidemic.

II. 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 those removed (R). The latter stands for cases which had an outcome and includes 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 β is the infection rate and γ is the recovered rate, with $R_0 \equiv \beta/\gamma$. In our investigation we modify the SIR equations so as to have dynamical updates of γ and β during time evolution. In order to obtain the proper time series for $\beta(t)$ and $\gamma(t)$ we use official data provided by Brazilian Government for gauging purposes. Data is retrieved using Ref. [12] from March 22 on.

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 [13, 14].

III. RESULTS

Initial parameters are set to $R(t=0) = 0$, $S(t=0) = 1$, meaning that all Brazilians are susceptible to infection, and $I(t=0) = 1450/(2.2 \times 10^8)$, with 1450 being the number of confirmed cases as of March 22 and 2.2×10^8 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

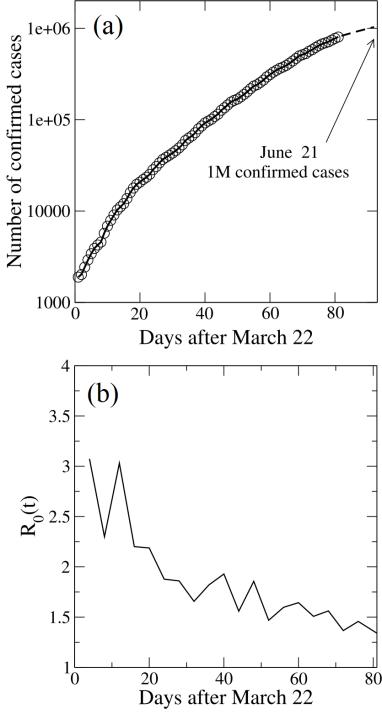


FIG. 1. (a) Number of confirmed cases (accumulated) of SARS-CoV-2 in Brazil. Symbols stand for official Government data and the solid line represents the results obtained via the SIR model. They both agree quite well, with an error of less than 5%. Dashed line is the prediction for the following ten days, terminating on June 08. (b) Basic reproduction number $R_0(t) = \beta(t)/\gamma(t)$ versus time. Each point is the outcome of a 5-day average. Estimated R_0 currently approaches 1.35(5).

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%. Figure 1(b) depicts $R_0(t) = \beta(t)/\gamma(t)$ versus time. According to our outcomes, the current value of R_0 approaches 1.35(5) as also obtained elsewhere [15]. Using γ and β values as of early June, we are able to predict the evolution of the epidemic into about ten days ahead [see dashed line in Fig. 1(a)] This is obtained performing a 5-day average from June 6 to 11, resulting in $\gamma = 0.09$ and $\beta = 0.122$. Our predictions estimate about 10^6 cases on June 21.

We are now to reproduce the epidemic dynamics for Germany and Italy in order to test the model accuracy as well as to evaluate the behavior of R_0 . The procedure is the very same as done for Fig. 1 Data for both countries is extracted from Refs. [16, 17], after March 10, in order to estimate $\gamma(t)$ and $\beta(t)$. Our results are summarized

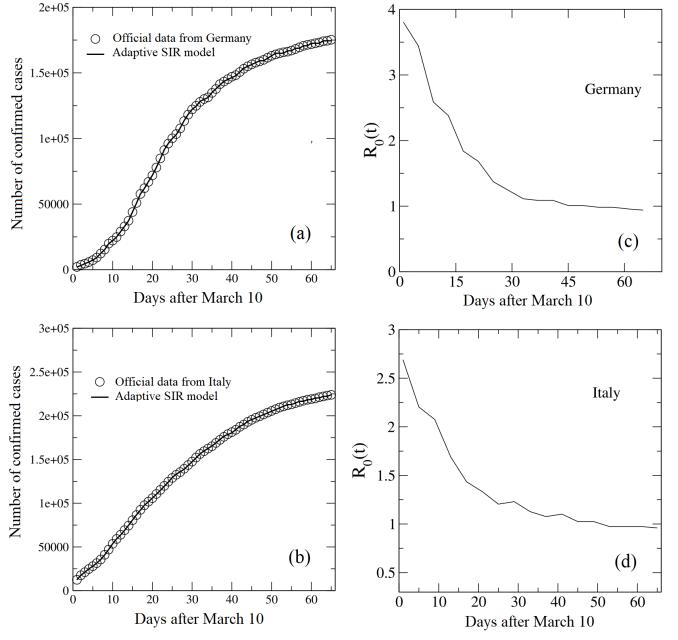


FIG. 2. (a,b) Number of confirmed cases accumulated after March 10 in Germany and Italy, respectively. Official data is represented by circles and results from the adaptive SIR model are denoted by the solid lines. (c,d) Corresponding evolution of the basic reproduction number R_0 .

in Figs. 2(a) through 2(d). Simulation outcomes (solid lines) for Germany and Italy are also in excellent agreement with official data (symbols), again up to an error below 5%. As for the results for the basic reproduction number $R_0(t)$ [see Figs. 2(c) and 2(d)], we see that it corroborates with those found in the literature (see e.g. [6] and references within). Our approach thereby proves to work quite well in estimating epidemiological parameters as well as reproducing spreading of SARS-CoV-2 elsewhere.

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 end dates April 10, 20, and 30, respectively, alongside predictions for 10 days ahead for Brazil. Figure 3(d) compares these and other predictions with (now obtained) official data therein showing excellent agreement.

We are now to address one the most important matters in respect to the dynamical evolution of the virus which is when its propagation happens to be contained. Let us first emphasize that long-term predictions, say, over 20 days into the future may not be accurate. Yet, we are able to estimate the order of magnitude of the number of cases. To begin with, we shall assume that $R_0(t)$ maintains the same decreasing rate as showed in Fig.1(b) between $t = 20$ and $t = 81$. Therefore, we consider that $R_0(t > 81)$ (i.e. days after June 11) is de-

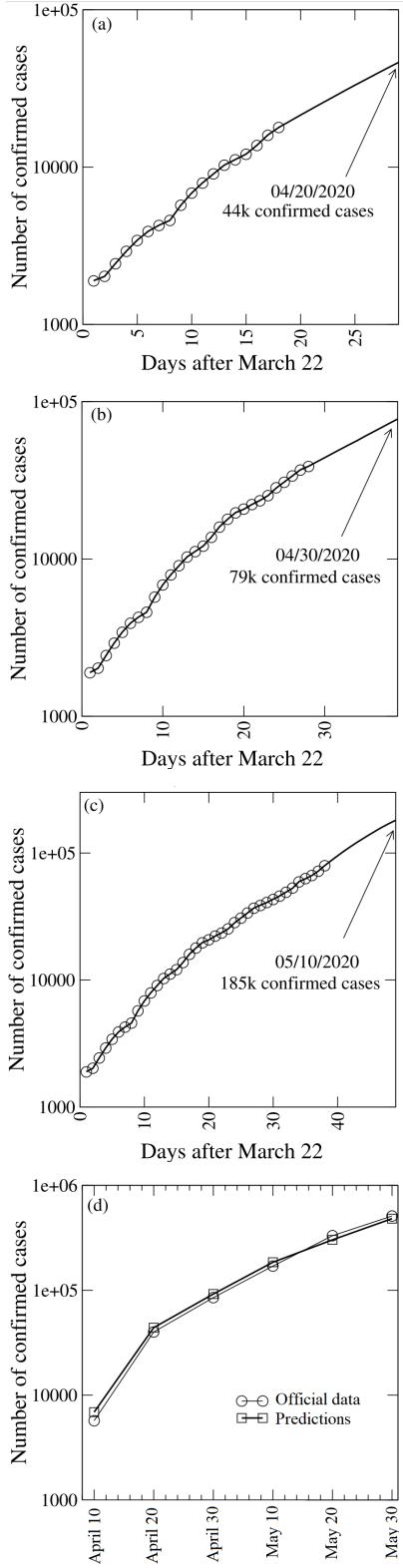


FIG. 3. (a-c) 10-day predictions realized on end dates April 10, 20, and 30, respectively, for Brazil. (d) Comparison between official data and predicted outcomes at specific days.

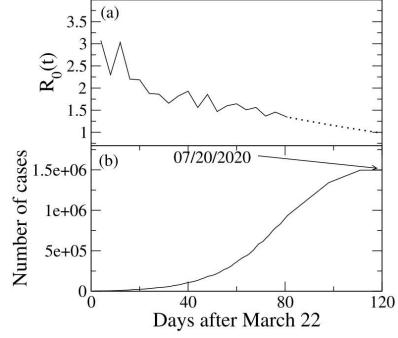


FIG. 4. (a) Basic reproduction number $R_0(t)$ versus time as simulated for Brazil. We mention that for $0 < t < 81$ calculations are based upon official data. For $t > 81$, we extrapolate the trend of R_0 based on its behavior within $20 < t < 81$. (b) Number of accumulated cases predicted by the SIR model considering the time evolution of R_0 as shown in panel (a).

creasing following the dotted line showed in Fig. 4(a). Using this series for $R_0(t)$ we estimate the number of cases for times $t \gg 81$ (see Fig. 4(b)). Simulations reveal that for $t = 120$ (on July 20) there is a possibility that the epidemic is contained in Brazil, with the accumulated number of confirmed cases being of the order of 1.5×10^6 .

IV. CONCLUSIONS AND OUTLOOK

The adaptive SIR model employed here works satisfactorily to reproduce 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 $R_0 = \beta/\gamma$ as well as the number of confirmed cases.

We were able to carry out a 10-day prediction for the epidemic evolution. The number of confirmed cases of SARS-CoV-2 is expected to reach a million cases at the beginning of June 21. According to the simulations, we also estimate that contention of the epidemic in Brazil will take place at the end of July (close to the 20th). At this point, the total number of cases will be approximately 1.5×10^6 and, considering the current mortality rate, about 100k deaths is expected, falling within the figure projected by the Institute for Health Metrics and Evaluation (IHME) in the U.S. [18] (that is 106,357 in July 20, as accessed in June 12).

We stress that predictions over 10 to 20 days in advance crucially depends on the choice of γ and β . While the procedure may work for short-term predictions, it is not appropriate in the long run. Because of that, long-term analysis calls for further assumptions over β as generally γ (related to the recuperation rate) is almost a constant

of about $0.085(5)$, which corresponds to 12 days on average. The infection rate parameter β depends on various factors such as of social distancing rules. In our simulations, based on the trend observed for β , it is reasonable to assume it is decreasing (and so is R_0). We can only hope that, given social distancing levels are still in place, that trend is a reality. We emphasize, though, that such decreasing is a slow one, thereby requiring about 30 to 60 days to control the epidemic.

One of the perks of the model worked out 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.

ACKNOWLEDGEMENTS

The authors declare that there is no conflict of interest.

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Figures

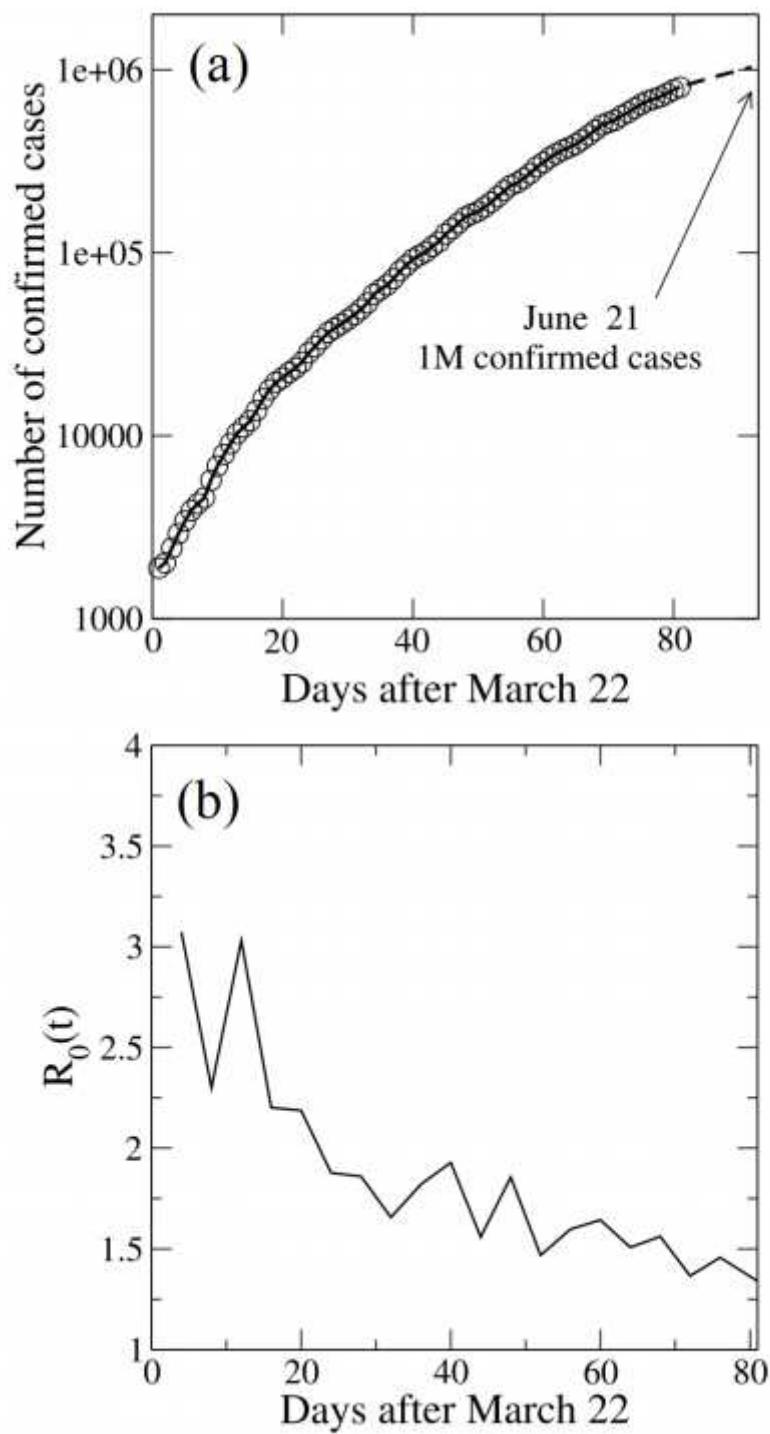


Figure 1

(a) Number of confirmed cases (accumulated) of SARS-CoV-2 in Brazil. Symbols stand for official Government 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,

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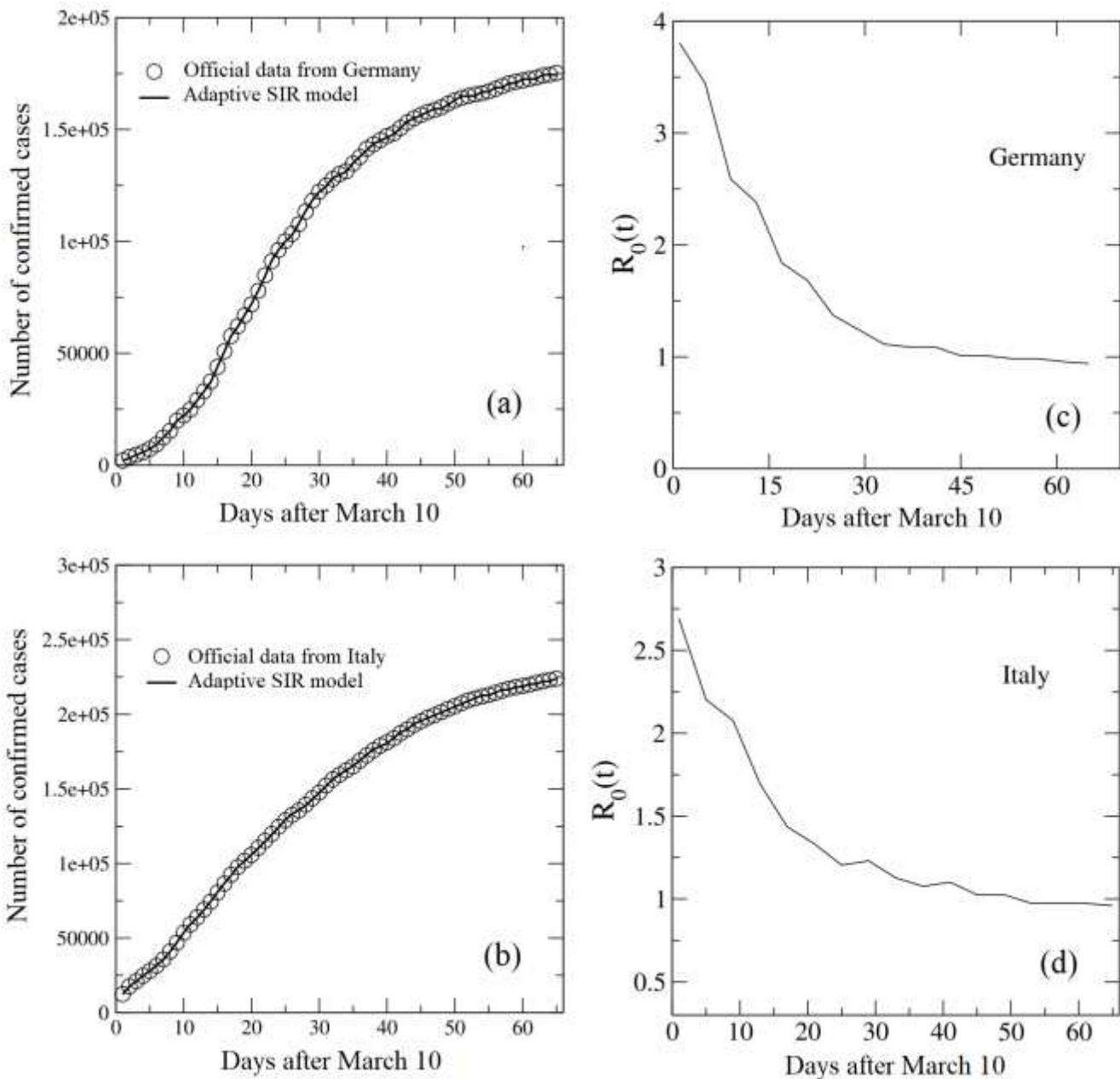


Figure 2

(a,b) Number of confirmed cases accumulated after March 10 in Germany and Italy, respectively. Official data is represented by circles and results from the adaptive SIR model are denoted by the solid lines. (c,d) Corresponding evolution of the basic reproduction number R_0 .

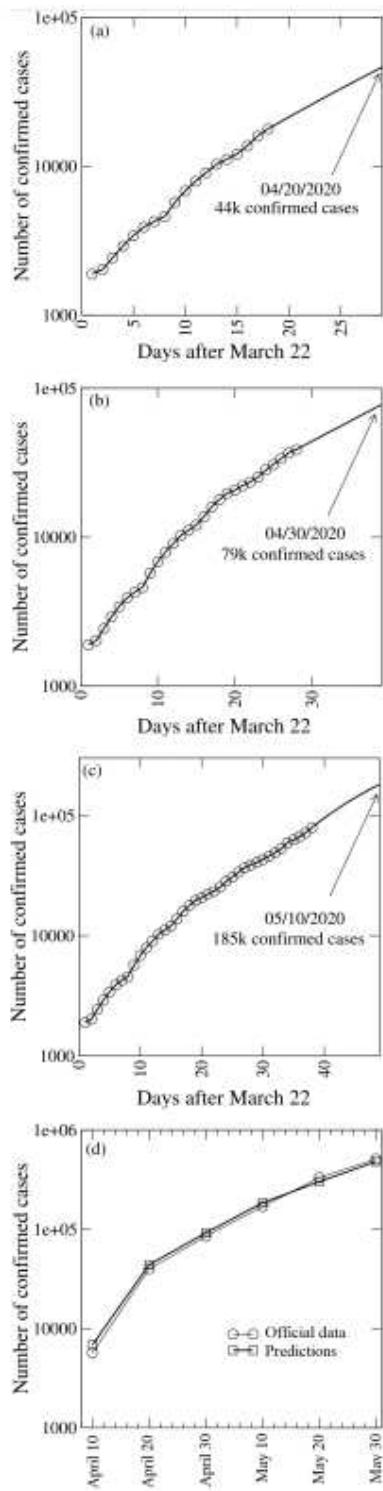


Figure 3

(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.

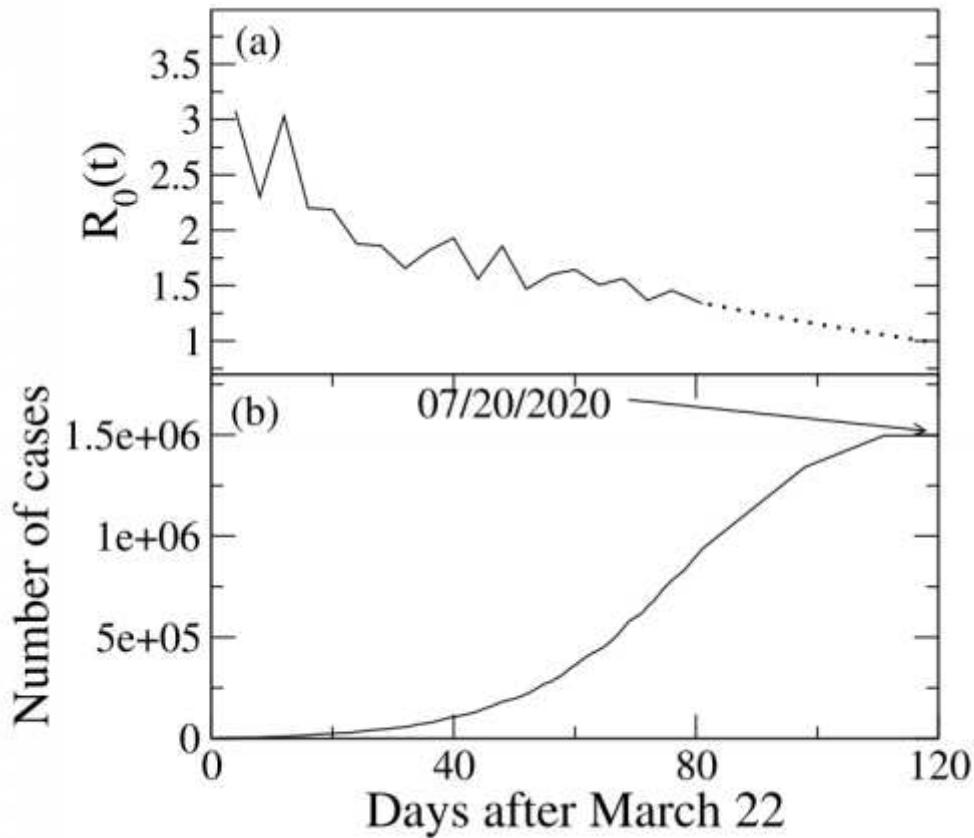


Figure 4

(a) Basic reproduction number $R_0(t)$ versus time as simulated for Brazil. We mention that for $0 < t < 81$ calculations are based upon official data. For $t > 81$, we extrapolate the trend of R_0 based on its behavior within $20 < t < 81$. (b) Number of accumulated cases predicted by the SIR model considering the time evolution of R_0 as shown in panel (a).

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