

Evolution of SARS-CoV-2 in the state of Alagoas-Brazil via an adaptive SIR model

I. F. F. Dos Santos, G. M. A. Almeida and F. A. B. F. De Moura*

*Instituto de Física, Universidade Federal de Alagoas
Maceió, AL, 57072-970, Brazil
fidelis@fis.ufal.br

Received 16 July 2020
Accepted 13 November 2020
Published 10 December 2020

We investigate the spreading of SARS-CoV-2 in the state of Alagoas, northeast of Brazil, via an adaptive susceptible-infected-removed (SIR) model featuring dynamic recuperation and propagation rates. Input parameters are defined based on data made available by Alagoas Secretary of Health from April 19, 2020 on. We provide with the evolution of the basic reproduction number R_0 and reproduce the historical series of the number of confirmed cases with less than 10% error. We offer predictions, from November 16 forward, over the epidemic situation in the near future and show that it will keep decelerating. Furthermore, the same model can be used to study the epidemic dynamics in other countries with great easiness and accuracy.

Keywords: SARS-CoV-2; SIR model; epidemic dynamics.

1. Introduction

Since the outbreak of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)¹⁻³ had reached the status of worldwide pandemic on March 11, 2020, several countries set about to take serious measures so as to contain the spreading of the virus and avoid the collapse of their healthcare system.

Not long after the coronavirus had been first reported in Wuhan City at the Hubei Province of China, an exponentially fast growing of infected people was observed, immediately suggesting the epidemic would feature a high basic reproduction number R_0 , which is the expected number of cases spawned by one infected person in a location where all individuals are prone to infection. Such parameter is a very important figure when accessing epidemic dynamics via mathematical models. In reality, it depends on several factors including the nature of the virus itself, number of susceptible people, and degree of social contact. When $R_0 > 1$, it indicates exponential growth and possibly a number of confirmed cases of the same order as of the population size, which is when the healthcare system situation may

*Corresponding author.

get critical. Various works has estimated the basic reproduction number R_0 for many countries ^{1,4-7}.

The number of SARS-CoV-2 cases continues to increase worldwide, the total number of registered cases and deaths reaching over 43 million and 1.1 million, respectively (as of November 16) ⁸, with many countries facing a second wave of the disease. According to official data, Brazil holds the third position in terms of registered cases, standing behind the United States and India. On the other hand, it holds the 6th position in both total cases and deaths per million of population, which is a interesting fact. The virus spread in Brazil have been decelerating since August⁸ and measures to put the economy back on track have been pushed nationwide. Still, those must take the imminent risk of a second contagious wave into account⁹.

Recently, we have investigated the dynamics of the SARS-CoV-2 epidemic within the Brazilian territory¹⁰ using an adaptive susceptible-infected-removed (SIR) model^{11,12}, which allowed us to predict epidemic evolution within 10-20 days ahead with fair accuracy. Therein, we estimated that R_0 would be approaching 1 at the end of July. In this work, we carry out a more local investigation addressing the state of Alagoas, northeast region of Brazil. By employing dynamic updating of the recuperation and propagation rates, namely γ and β , we reproduce the daily evolution of the number of confirmed cases up to November 16 with less than 10% error. We also estimate the evolution of the basic reproduction number and show that the virus spread will keep slowing down for the next 45 days.

2. Model

We use an adaptive SIR model to investigate the spreading of SARS-CoV-2 in the state of Alagoas. The model basically comprises a set of coupled differential equations involving the following population variables: those susceptible to the virus (S), infected individuals (I), and those who had an outcome (R), that including recovered and deceased people. The equations read

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

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

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

where β and γ are, respectively, the infection and recovery rates, with the basic reproduction number $R_0 \equiv \beta/\gamma$. Note that $\beta = \beta(t)$ and $\gamma = \gamma(t)$ and we set the time series to follow official data provided by Alagoas Secretary of Health¹³. The above equations are then solved for several $\{\gamma(t), \beta(t)\}$ and those that yield outcomes closest to reality are kept. Throughout the simulations, we run $\gamma \in [0.06, 0.13]$ and $\beta \in [0.05, 0.6]$. We mention that those ranges have been used in SARS-CoV-2 epidemic simulations via SIR models elsewhere.^{14,15}

Evolution of SARS-CoV-2 in the state of Alagoas-Brazil via an adaptive SIR model

3. Results

To warm up, let us first access the accuracy of the model by reproducing the epidemic dynamics and the corresponding $R_0(t)$ for Germany and Italy, based on available official data taken from Refs. 16, 17 from March 10 on, over 65 days, so as to estimate $\gamma(t)$ and $\beta(t)$. Results are shown in Figs. 1(a) through 1(d). Simulation for both countries (solid lines) are seen to be in fine accordance with official data (symbols), up to 5% error. The values found for the basic reproduction number $R_0(t)$ [see Figs. 1(c) and 1(d)], corroborates with the existing literature (see, e.g.,⁴). The adaptive SIR model thereby seems to account for epidemiological parameters of

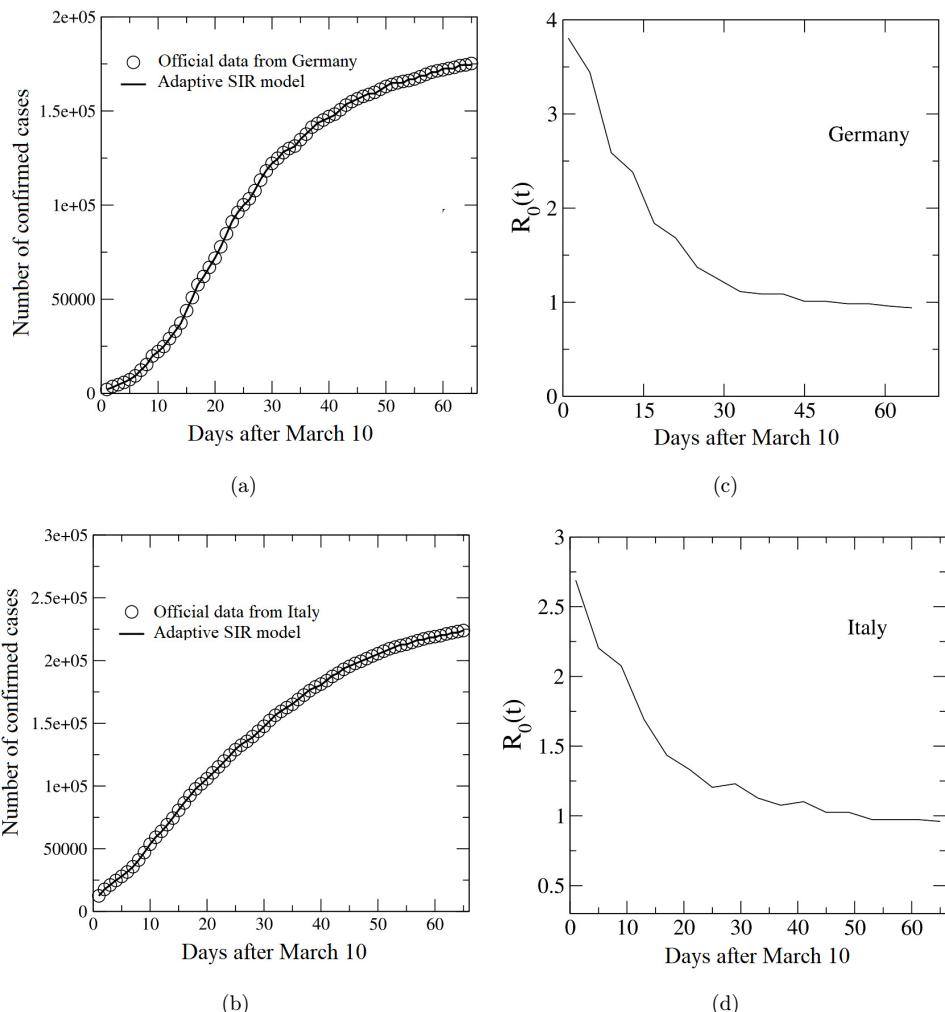


Fig. 1. ((a),(b)) Accumulated number of confirmed cases from March 10 on for Germany and Italy, respectively. Official data is given by circles and simulations via the adaptive SIR model are expressed by the solid lines. ((c),(d)) Daily evolution of the basic reproduction number R_0 .

I. F. F. Dos Santos, G. M. A. Almeida & F. A. B. F. De Moura

SARS-CoV-2 pretty well. It is important to notice that this behavior took place in the early stages of the pandemic, for now (as of November, 2020) both countries are facing the so-feared second wave of contagion, as many other countries in Europe⁸.

Let us move on to the state of Alagoas, in Brazil. We shall set initial parameters as $R(t=0) = 0$, $S(t=0) = 1 - I(t=0)$, meaning that all citizens are prone to infection, and $I(t=0) = 160/N_P$, with 160 being the number of confirmed cases as of

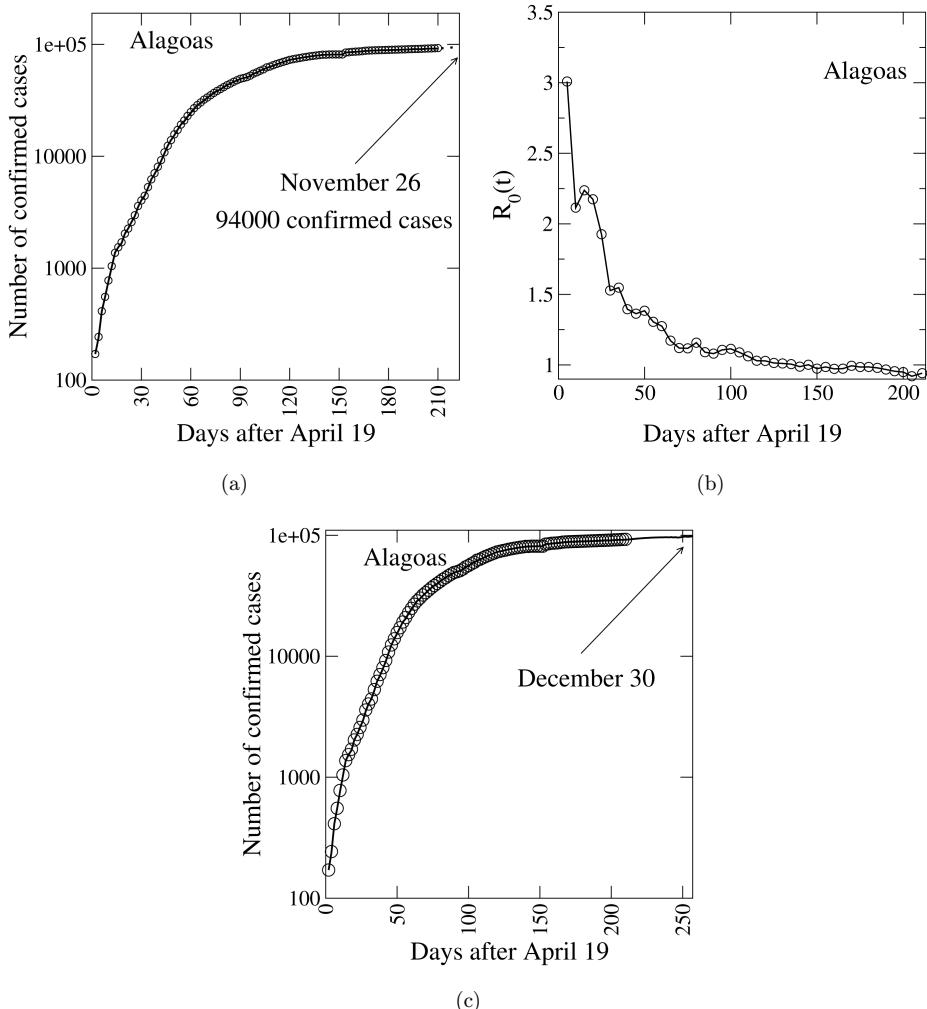


Fig. 2. (a) Number of confirmed cases (accumulated) of SARS-CoV-2 in the state of Alagoas, Brazil. Symbols represent official data and the solid line the results obtained via the SIR model. They both agree well, with an error of less than 10%. Dotted line gives off the prediction for the following ten days, terminating on November 26. (b) Basic reproduction number $R_0(t) = S(t)\beta(t)/\gamma(t)$ against time. Each point is the outcome of a 5-day average. Estimated R_0 currently approaches 0.95(2). (c) Long-term prediction for the epidemic evolution. It suggests that the virus spread will keep decelerating and one may expect roughly 50-80 new cases daily for the next 30 to 45 days.

April 19 and $N_P = 3.3 \times 10^6$ the state's population size. We stress that it is fair to bypass the number of recovered and deceased individuals ($R = 0$) at the early stages of the epidemic since it turns out to be negligible in respect to the total population. In Fig. 2(a) we display the accumulated number of registered cases versus time starting from the April 19. Once again, simulations outcomes agree well with official data, with the relative error being less than 10%. Figure 2(b) shows the evolution of $R_0(t) = S(t)\beta(t)/\gamma(t)$ against time and we point out that its current value approaches 0.95(2), following the tendency observed for Brazil according to results reported in Ref. 10. Using γ and β values as of November 16 — a 5-day average from November 11 to 16 is performed yielding $\gamma = 0.08$ and $\beta = 0.116$ — we predict the evolution of the epidemic ten days in advance [see dashed line in Fig. 2(a)]. It gives off about 94000 confirmed cases for November 26.

By following the behavior of R_0 we observe that the reproduction factor has been marginally close to 1 during the last couple of months [the average being 1.00(2)]. Based on this trend we perform numerical simulations for 45 days in advance, up to December 30 (see Fig. 2(c)). Our calculations suggest that the number of cases will continue to increase with slower speed. It is not possible, however, say much about what the situation will be after that. R_0 may become much less than 1, an optimistic guess, but long-term predictions of that nature cannot be accounted by the model.

4. Conclusions and Outlook

The adaptive SIR model used in this work faithfully describes the SARS-CoV-2 epidemic evolution in the state of Alagoas, Brazil, as well as other places around the world, according to robust, official Covid-19 data available on the web^{8,13}. This information has also been used to perform dynamical updating of the parameters γ and β , giving off the basic reproduction number $R_0(t) \equiv S(t)\beta(t)/\gamma(t)$. Our simulations show that its current value approaches 0.95(2), what corroborates with seemingly deceleration of the disease in Brazil.

The accumulated number of confirmed cases is projected to reach about 94000 cases on November 26. In addition to make reasonable short-term predictions, the adaptive SIR model could reproduce the historic series of the number of accumulated cases with less than 10% error. By extrapolating the behavior of R_0 45 days ahead we also found that the number of confirmed cases will continue to increase, but at a slower pace.

Finally, we stress that long-term predictions for epidemic dynamics, regardless of the model being used, should be interpreted with great caution as there are many variables involved, such as the state of social distancing protocols, testing programs, and so forth.

Acknowledgements

This work is supported by CNPq, CAPES, and FINEP (Federal Brazilian Agencies), CNPq-Rede Nanobioestruturas, and FAPEAL (Alagoas State Agency).

References

1. T. Chen *et al.*, *Infect. Dis. Poverty* **9**, 24 (2020).
2. <https://www.who.int/health-topics/coronavirus>.
3. Q. Li *et al.*, *N. Engl. J. Med.* **382**, 1199 (2020).
4. J. Dehning *et al.*, *Science* **369** eabb9789 (2020).
5. J. T. Wu, K. Leung and G. M. Leung, *Lancet* **395**, 689 (2020).
6. S. Zhao *et al.*, *Int. J. Infect Dis.* **92**, 214 (2020).
7. G. Giordano, F. Blanchini, R. Bruno, P. Colaneri, A. Di Filippo, A. Di Matteo and M. Colaneri, *Modelling the COVID-19 Epidemic and Implementation of Population-Wide Interventions in Italy*. Nature Medicine (2020).
8. <https://www.worldometers.info/coronavirus/>.
9. L. López and X. Rodó, *The End of Social Confinement and COVID-19 Re-emergence Risk*. Nature Human Behavior (2020).
10. I. F. F. dos Santos, G. M. A. Almeida and F. A. B. F. de Moura, *Adaptive SIR model for propagation of SARS-CoV-2 in Brazil*. Pre-print: Research Square rs-40116 (2020).
11. W. O. Kermack and A. G. McKendrick, *Proc. Roy. Soc. Lond. A* **115**, 700 (1927).
12. R. M. Anderson and R. M. May, *Nature* **280**, 361 (1979).
13. <https://www.saude.al.gov.br/>.
14. H. Jo, H. Son, S. Y. Jung and H. J. Hwang, medRxiv 2020.04.13.20063412 (2020).
15. J. Arino and S. Porteta, *Infectious Disease Modelling* **5**, 309 (2020).
16. <https://www.worldometers.info/coronavirus/country/germany/>.
17. <https://www.worldometers.info/coronavirus/country/italy/>.