Data analysis and modeling of the evolution of COVID-19 in Brazil

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(Dated: March 30, 2020)

The world evolution of the Severe acute respiratory syndrome coronavirus 2 (SARS-Cov2 or simply COVID-19) lead the World Health Organization to declare it a pandemic. The disease appeared in China in December 2019, and it spread fast around the world, specially in european countries like Italy and Spain. The first reported case in Brazil was recorded in February 26, and after that the number of cases growed fast. In order to slow down the initial grow of the disease through the country, confirmed positive cases were isolated to not transmit the disease. To better understand the evolution of COVID-19 in Brazil, we apply a Susceptible-Infectious-Quarantined-Recovered (SIQR) model to the analysis of data from the Brazilian Department of Health. Based on analytical and numerical results, as well on the data, the basic reproduction number is estimated to $R_0 = 5.25$. In addition, we estimate that the ratio unidentified infectious individuals and confirmed cases is about 10, in agreement with previous studies. We also estimated the epidemic doubling time to be 2.72 days.

Keywords: Dynamics of social systems, Collective phenomena, Data Analysis

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I. INTRODUCTION

The evolution of epidemics is one of the most dangerous problems for a society. The humanity faced severe pandemics during its evolution, like the Spanish flu in 1917, the Honk Kong flu (H3N2) of 1968 and the swine flu (H1N1) in 2009. Several efforts were done since 70’s in order to understand the mathematical evolution and spreading of diseases [1, 2].

Recently, in December, 2019, Wuhan city, the capital of Hubei province in China, became the centre of an outbreak of pneumonia of unknown cause. By January 7, 2020, Chinese scientists had isolated a novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), from these patients with virus-infected pneumonia [3, 4], which was later designated coronavirus disease 2019 (COVID-19) in February, 2020, by World Health Organization.

In order to better understand such new disease, a lot of papers and preprints were published in the last months [5–24], analyzing various properties of the COVID-19, as well as modeling its evolution in many countries. Our target in this work is to perform a data analysis of the evolution of COVID-19 in Brazil. We collected data from the Brazilian Department of Health, and apply a Susceptible-Infectious-Quarantined-Recovered (SIQR) model to analyze the COVID-19 dynamics.

This work is organized as follows. In Section II we present the SIQR model, and define its parameters. In Section 3 we perform the data analysis and present analytical and numerical results based on the SIQR model. Finally, we present a discussion in Section IV. Some numerical details are presented in an Appendix.

II. MODEL

The model considered in this work is a variant of the Susceptible-Infected-Recovered (SIR) model [1, 2]. In addition to the usual compartments Susceptible (S), Infected (I) and Recovered (R), an extra compartment is considered, namely Quarantined (Q) [7, 8, 25]. \( N \) is the total number of individuals in the population, assumed constant since we are studying the early phase of the epidemic. In this case, we have the normalization condition at each time step, i.e., \( N(t) = S(t) + I(t) + Q(t) + R(t) \).

Notice that both I and Q individuals are infected, but as discussed in [7] this separation is
convenient because it models the fact that many governments (including the Brazilian one) are forcing individuals tested positive (confirmed cases) to self-isolate from the community, and also because it distinguishes between the infectious people who do self-isolate, and/or those who do not (mostly likely because they have not developed the symptoms of the disease and are not aware of actually being infectious). Thus, the SIQR model may be described by the following rate equations:

\[
\begin{align*}
\frac{dS}{dt} &= -\beta \frac{SI}{N} \\
\frac{dI}{dt} &= \beta \frac{SI}{N} - (\alpha + \eta) I \\
\frac{dQ}{dt} &= \eta I - \gamma Q \\
\frac{dR}{dt} &= \gamma Q + \alpha I
\end{align*}
\]

In the above equations, \( \beta \) denotes the infection rate, \( \alpha \) is a rate that quantifies the recovering of asymptomatic individuals, \( \eta \) is the rate of detection of new cases. Finally, \( \gamma \) stands for the recovering of quarantined individuals.

### III. RESULTS

Looking at the data, the first case in Brazil was reported in February 26. Thus, so far a relatively small fraction of the Brazilian population has been found positive for COVID-19, which means we are still in the early phase of the epidemic where we have \( S/N \approx 1 \). In this case Eq. (2) can be approximated to

\[
\frac{dI}{dt} = [\beta - (\alpha + \eta)] I ,
\]

that can be directed integrated to obtain

\[
I(t) = I_0 e^{[\beta - (\alpha + \eta)] t} ,
\]

where \( I_0 \) is the number of infectious individuals at the beginning of the outbreak. Eq. (6) can be rewritten as \( I(t) = I_0 e^{(\alpha+\eta)(R_0-1) t} \), and one can obtain the expression for the basic reproduction number \( R_0 \),

\[
R_0 = \frac{\beta}{\alpha + \eta} .
\]

1 In this case, an infected individual is positive tested and becomes a confirmed case. This individual is isolated (quarantined).
As it is well known, the basic reproduction number $R_0$ is an indicator of the occurrence of an outbreak (if $R_0 > 1$). We will see in the following that one can estimate its value from the data.

As discussed in [8], the number of individuals that have been confirmed positive for COVID-19 and put in isolation does not correspond to $I$ but to $Q + R$. One can found a relevant analytical expression summing Eqs. (3) and (4),

$$
\frac{d}{dt} [Q + R](t) = (\alpha + \eta) I(t) .
$$

(8)

Substituting the result (6) in Eq. (8) and integrating over $t$, one obtains

$$
[Q + R](t) = \frac{\alpha + \eta}{\beta - (\alpha + \eta)} I_0 \left(e^{[\beta-(\alpha+\eta)]t} - 1\right) .
$$

(9)

We fitted Eq. (9) to the Brazilian COVID-19 data [26] from February 26, 2020 through March 25, 2020. The estimated values were $(\alpha + \eta) I_0 = 0.482$ and $\beta - (\alpha + \eta) = 0.255$ (see details in the Appendix). Based on data, we take $I_0 = 8$ (see Appendix), which gives us $\alpha + \eta = 0.06$ and $\beta = 0.315$. Considering those estimates, we plot in Fig. 1 the temporal evolution of the number of cases together with Eq. (9).
FIG. 2. (Color online) Time evolution of the number of Infected (I), Quarantined (Q) and total confirmed cases (Q+R), obtained by the numerical integration of the Eqs. (1) to (4). Data of confirmed cases are exhibited as well (squares). The parameters are $I_0 = 8$, $\beta = 0.315$, $\eta = \alpha = 0.03$ and $\gamma = 0.04$.

Based on the above-mentioned fitted values, one can estimate from Eq. (7) $R_0 = 5.25$, which is in line with previous estimates of $R_0$ falling between 1.4 and 6.5 [5, 8, 11, 16, 18].

In addition, one can estimate the epidemic doubling time, that characterize the sequence of intervals at which the cumulative incidence doubles. From the above result $I(t) = I_0 e^{(\alpha+\eta)(R_0-1)t}$ one can obtain the doubling time as $\tau = \ln 2 / [(\alpha+\eta)(R_0-1)]$. Based on the above estimated parameters, we have $\tau = 2.72$ days, which falls in the range $1.4 < \tau < 3.0$ estimated in China [19].

As discussed in the Appendix, we estimate $\eta = 0.03$, $\alpha = 0.03$ and $\gamma = 0.04$. Considering those values, as well as the previous estimated values of $\beta$ and $I_0$, we plot in Fig. 2 the time evolution of the number of Infected (I), Quarantined (Q) and total confirmed cases (Q+R), obtained by the numerical integration of the Eqs. (1) to (4). For these curves, we considered $N$ as the total brazilian population, $N = 2.17 \times 10^8$. One can see that the number of infected and nonconfirmed cases $I$ grows faster than the number of confirmed and isolated individuals Q. This unbalance is observed in all the world, since there is a huge number of undocumented infection cases for the COVID-19, as discussed in a recent work [5].
For better quantify the unbalance among unidentified infectious individuals and confirmed and isolated cases, one can discuss about the ratio \( I/Q \). Taking the ratio of Eqs. (3) and (2), and considering the approximated result for short times, Eq. (5), one can obtain

\[
\frac{I}{Q} = \frac{\gamma + \beta - (\alpha + \eta)}{\eta}.
\]

(10)

Based on the estimated values of the parameters, Eq. (10) gives us \( I/Q \approx 9.83 \), i.e., for each patient in quarantine approximately \textit{nine/ten} infectious individuals are present in the population\(^2\). This is in agreement with a recent work that states that 86\% of all infections were undocumented in China\(^5\). Thus, there are still many unidentified cases that do not appear in the official statistics.

IV. DISCUSSION

The number of confirmed cases of COVID-19 in Brazil are growing exponentially fast. Based on the data, we considered a Susceptible-Infectious-Quarantined-Recovered (SIQR) on a fully-connected population. Despite the simplicity of the model, we can made estimates of the infection rate, the rate which individuals are isolated from the population and some others, as well as the basic reproduction number and the doubling time of the epidemics, based on fitting data available at the site of the Brazilian Department of Health.

For the considered parameters, we observed that the number of quarantined individuals grows fast (exponentially), stabilizes and after it decays to zero, as it is standard in compartmental models. Based on the data, we can see that the number of such isolated individuals grows until Day 90 from the beginning of the diseases spreading (February 26, 2020). Thus, the model predicts that the maximum number of isolated individuals will occur about May 25, 2020. This is in line with a recent estimate\(^{15}\). These peak is associated with the isolation of about 20\% of the brazilian population.

This pessimistic estimate can be modified if the government imposes limitations for the population, as was done in some countries like Italy, Spain and India. In order to reduce the growing of the number of cases, social isolation was suggested in some brazilian states, but it was only a suggestion by the local governements, i.e., there is no mandatory quarantine. In a

\(^2\) This number of course depends on a precise estimate of the value of \( \gamma \), but usually the recovered rates are small, in the range \(0.01 < \gamma < 0.05\), which give us \(8.83 < (I/Q) < 10.16\).
recent work [15], the authors analyzed the potential role of non-pharmaceutical interventions in UK and USA. They conclude that the effectiveness of any one intervention in isolation is likely to be limited, requiring multiple interventions to be combined to have a substantial impact on transmission.

Other recent work [12] studied the role of people mobility in the diffusion of the COVID-19 in China. They show that travel restrictions are useful in the early stage of an outbreak when it is confined to a certain area that acts as a major source. In the case of Brazil, the major sources are the cities of Sao Paulo and Rio de Janeiro, and immediate actions of restrictions in mobility need to be adopted to control the spread of COVID-19 [27].

Appendix

In this appendix we discuss about the estimates of the model’s parameters. Considering Eq. (9), we did a least squares fitting of the data considering a function $f(t) = (a/b) (e^{bt} - 1)$. In comparison with Eq. (9), we have the identification $a = (\alpha + \eta) I_0$ and $b = \beta - (\alpha + \eta)$. The fitting procedure gives us $a = 0.428 \pm 0.137$ and $b = 0.255 \pm 0.012$. Thus, we have $(\alpha + \eta) I_0 = 0.428$ and $\beta - (\alpha + \eta) = 0.255$.

The time in our graphics were counted after the first confirmed case in Brazil, i.e., Day 1 was February 26, 2020. The number of confirmed cases kept almost constant for some days, and start to grow faster since day 9 (March 5, 2020), where 8 cases were confirmed. In this case, we take the number of initial cases as $I_0 = 8$ for the model’s purposes. Thus, from $(\alpha+\eta) I_0 = 0.428$ we obtained $(\alpha+\eta) = 0.06$. Considering this result, from $\beta-(\alpha+\eta) = 0.255$ we obtained $\beta = 0.315$.

As discussed in [8], the parameter $\eta$ is related to the time until patients are tested positive and isolated, but also to the fraction of all infectious individuals that are tested positive. These are mostly symptomatic patients, which we assume are isolated soon after the incubation time is over and first symptoms appear. The incubation time means the time between catching the virus and beginning to have symptoms of the disease. Most estimates of the incubation period for COVID-19 range from 1-14 days, most commonly around $\approx 5$ days [28]. Letting $\delta$ denote the fraction of infectious individuals entering $Q$, we obtain $\eta = \delta \times 0.2$.

It was reported that $\approx 50\%$ of the population is asymptomatic [29], but some milder
cases may also go unnoticed and not end in isolation. Considering the very small quantity of tests made in brazilians, we assume that $\delta = 15\%$ of infectious individuals are tested after an average of 5 days. We thus set $\eta = 0.15 \times 0.2 = 0.03$. From the above obtained relation, $(\alpha + \eta) = 0.06$, we have $\alpha = 0.03$.

Finally, until the present date the number of recovered individuals in Brazil is so small, and it is hard to obtain an estimate of $\gamma$. In this case, for most results we considered $\gamma = 0.04$, in line with [8]. Notice that the main result of the model, the total number of confirmed cases $Q + R$ do not depend on $\gamma$, as we can see in Eq. (9).

ACKNOWLEDGMENTS

The author acknowledges financial support from the Brazilian scientific funding agencies Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ).

[1] R. M. Anderson, R. M. May, Infectious Diseases of Humans: Dynamics and Control (Oxford University Press, Oxford, 1991).

[2] N. T. J. Bailey, The Mathematical Theory of Infectious Diseases and its Application (Hafner Press, New York, 1975).

[3] A. L. Phelan, R. Katz, L. O. Gostin, The Novel Coronavirus Originating in Wuhan, China: Challenges for Global Health Governance, JAMA 2020, DOI:10.1001/jama.2020.1097.

[4] A. L. Gorbalenya et. al., Severe acute respiratory syndrome-related coronavirus: The species and its viruses a statement of the Coronavirus Study Group, bioRxiv 2020, DOI : 10.1101/2020.02.07.937862.

[5] R. Li. et. al., Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2), Science 10.1126/science.abb3221 (2020).

[6] K. Biswas, A. Khaleque, P. Sen, Covid-19 spread: Reproduction of data and prediction using a SIR model on Euclidean network, arXiv:2003.07063 (2020).

[7] M. Bin, P. Cheung, E. Crisostomi, P. Ferraro, C. Myant, T. Parisini, R. Shorten, On Fast Multi-Shot Epidemic Interventions for Post Lock-Down Mitigation:Implications for Simple
Covid-19 Models, arXiv:2003.09930 (2020).

[8] M. G. Pedersen, M. Meneghini, Quantifying undetected COVID-19 cases and effects of containment measures in Italy, preprint 2020, available on-line at https://www.researchgate.net/publication/339915690_Quantifying_undetected_COVID_19_cases_and_effects_of_containment_measures_in_Italy, DOI:10.13140/RG.2.2.11753.85600

[9] F. Zhou et. al., Clinical course and risk factors for mortality of adult inpatients with COVID-19 in Wuhan, China: a retrospective cohort study, The Lancet online first 2020, DOI:10.1016/S0140-6736(20)30566-3

[10] A. E. Botha, W. Dednam, A simple iterative map forecast of the COVID-19 pandemic, arXiv:2003.10532 (2020).

[11] T. Zhou et. al., Preliminary prediction of the basic reproduction number of the Wuhan novel coronavirus 2019-nCoV, Journal of Evidence-based Medicine 13, 3-7 (2020).

[12] M. U. G. Kraemer et. al., The effect of human mobility and control measures on the COVID-19 epidemic in China, Science 10.1126/science.abb4218 (2020).

[13] F. Zullo, Some numerical observations about the COVID-19 epidemic in Italy, arXiv:2003.11363 (2020).

[14] A. Radulescu, K. Cavanagh, Management strategies in a SEIR model of COVID 19 community spread, arXiv:2003.11150 (2020).

[15] N. M. Ferguson et. al., Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand, Imperial College COVID-19 Response Team, 16 March 2020, DOI:10.25561/77482.

[16] A. Lai et. al., Early phylogenetic estimate of the effective reproduction number of SARS-CoV2, Journal of Medical Virology, 25 February 2020, https://doi.org/10.1002/jmv.25723.

[17] S. Zhao et. al., Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak, International Journal of Infectious Diseases 92, P214-217 (2020), https://doi.org/10.1016/j.ijid.2020.01.050.

[18] Y. Liu, A. A. Gayle, A Wilder-Smith, J. Rocklov, The reproductive number of COVID-19 is higher compared to SARS coronavirus, Journal of Travel Medicine 27, Issue 2, March 2020, taaa021, https://doi.org/10.1093/jtm/taaa021.
[19] K. Muniz-Rodriguez et. al., *Epidemic doubling time of the COVID-19 epidemic by Chinese province*, medRxiv 2020, DOI: https://doi.org/10.1101/2020.02.05.20020750.

[20] C. Yin, *Genotyping coronavirus SARS-CoV-2: methods and implications*, arXiv:2003.10965 (2020).

[21] R. I. Gonzalez, F. Munoz, P. Sí Moya, M. Kiwi, *Genotyping coronavirus SARS-CoV-2: methods and implications*, arXiv:2003.10879 (2020).

[22] L. Roques, E. Klein, J. Papaix, S. Soubeyrand, *Mechanistic-statistical SIR modelling for early estimation of the actual number of cases and mortality rate from COVID-19*, arXiv:2003.10720 (2020).

[23] S. L. Chang et. al., *Modelling transmission and control of the COVID-19 pandemic in Australia*, arXiv:2003.10218 (2020).

[24] M. Faggian, M. Urbani, L. Zanotto, *Proximity: a recipe to break the outbreak*, arXiv:2003.10222 (2020).

[25] H. Hethcote, M. Zhien, L. Shengbing, *Effects of quarantine in six endemic models for infectious diseases*, Mathematical Biosciences 180, 141160 (2002).

[26] Brazilian Department of Health, [http://plataforma.saude.gov.br/novocoronavirus/](http://plataforma.saude.gov.br/novocoronavirus/)

[27] Tecnial Note from Brazilian researchers, March 25, 2020, [https://ufrj.br/sites/default/files/img−noticia/2020/03/notatecnica25032020.pdf](https://ufrj.br/sites/default/files/img−noticia/2020/03/notatecnica25032020.pdf)

[28] [https://www.who.int/news−room/q−a−detail/q−a−coronaviruses](https://www.who.int/news−room/q−a−detail/q−a−coronaviruses)

[29] Japanese National Institute of Infectious Diseases, [https://www.niid.go.jp/niid/en/2019−ncov−e/9417−covid−dp−fe−02.html](https://www.niid.go.jp/niid/en/2019−ncov−e/9417−covid−dp−fe−02.html)