Modeling and forecasting the Covid-19 pandemic in Brazil

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Preliminary and evolving
Comments are welcome

Abstract

We model and forecast the evolution of the COVID-19 pandemic in Brazil using Brazilian recent data from February, 25, 2020 to March, 28, 2020. We use two variations of the SIR model and we include a parameter in this model that accounts for the effects of confinement measures. We do not calibrate our models parameters, but we estimate all of them based on a clear hierarchical procedure of squared error minimization. The estimated parameters of the ratio between symptomatic and asymptomatic individuals, the proportion of infected individuals that die and the usual epidemiological parameters have a great match with the ones provided by the literature. Our final models provide precise forecasts of the number of infected individuals. We use these models to discuss different scenarios of public policies. Long terms forecasts show that the confinement policy imposed by the government is able to flatten the pattern of infection of the COVID-19 and we are able to find the optimal date to end the policy. However, our results show that if this policy does not last enough time, it is only able to shift the peak of infection into the future keeping the value of the peak in almost the same value.

1 Introduction

The world has seen an ongoing pandemic of COVID-19 (coronavirus 2) caused by severe acute respiratory syndrome SARS-CoV-2. According to the World Health Organization (WHO), although most people infected with the coronavirus will feel mild respiratory illness or no symptoms and recover without requiring any kind of special treatment, older people, and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease, or cancer may develop serious illness. While the COVID-19 outbreak was first identified in Wuhan, Hubei, China, in December 2019, we could only confirm the first case in Brazil on February, 25, 2020. The first patient in Brasil was a 61-year-old man from São Paulo who had returned from Lombardy (Italy) and tested positive for the virus. Since then, we may confirm 3904 cases (28 March 2020) in roughly the entire Brazilian territory. The public response to the pandemic has been the introduction of measures to ensure quarantine social distancing, such as closing schools, restricting commerce and home office.

We use the Brazilian recent data from February, 25, 2020 to March, 28, 2020 to model and forecast the evolution of the COVID-19 pandemic in Brazil using two versions of the Susceptible-Infected-Recovered (SIR) model (Kermack and McKendrick, 1927). We modify them in order

to account for the effects of confinement measures in the evolution of the disease. Our models provide a good prediction of the short-term Brazilian time series of infected individuals in Brazil. We use them to simulate long-term scenarios of the pandemics that depend on the level of engagement of the Brazilian confinement policy. Long terms forecasts show that the confinement policy imposed by the government is able to flatten the pattern of contamination provided by the COVID-19 and we are able to find the optimal date to end the policy. However, our results show that a short-term policy is only able to shift the peak of infection into the future keeping the value of the peak in almost the same value.

It is worth mentioning that this is a preliminary work based on a limited amount of Brazilian data. Although the authors have been working for a long time with applied dynamical systems and empirical statistics, the authors do not belong to the health field. Furthermore, this work does not consider the economic side effects of pandemic control such as Eichenbaum et al. (2020) and Gormsen and Koijen (2020) or personal views about the Brazilian public policies. Based on Brazilian data, this work intends only to provide some technical material about the evolution of COVID-19, namely estimations and models that may help decision makers to base their decisions. However, this work should never be used as the only source of information.

Our paper relates to the recent interesting contributions of Kucharski et al. (2020), Berger et al. (2020), Read et al. (2020) and Walker et al. (2020) in the sense that all these works try to model the spread of the COVID-19 and to evaluate the countermeasures against this virus. Our paper differs from these works in the following dimensions: (1) Data: While Kucharski et al. (2020) works with data about cases in Wuhan and internationally exported cases from Wuhan, Read et al. (2020) works with early data from Wuhan, Berger et al. (2020) works with the spread of COVID-19 in the USA and Walker et al. (2020) provides a world wide view of the spread of the virus, our focus is on the Brazilian data. This is an important characteristic since different countries may present different demographies and we know that the COVID-19 is riskier for older populations that appear with higher proportion in developed countries. Furthermore, the level of nutrition of the population of the country may affect the probability of contracting and developing the disease. The quality of data may vary from developed countries to underdeveloped ones and, in our paper, we do not use data from other countries to calibrate our models. (2) Models: While we make a minor modification in variations of the deterministic SIR model, Kucharski et al. (2020), Berger et al. (2020), and Walker et al. (2020) base their conclusions on variations of the stochastic SEIR model and Read et al. (2020) estimates the deterministic SEIR model. In fact, since we have a limited database, we use the simplest models that could help us to meet our objectives. The simplicity of this model may also act as regularization scheme that may reduce the difference between the quality of the model when applied in-sample and out-of-sample (Abu-Mostafa and Magdon-Ismail, 2012); (3) Estimation and Calibration: While, our paper estimates all the parameters based on a clear hierarchical procedure based on squared error minimization, Read et al. (2020) estimates all the parameters of a deterministic SEIR model, Berger et al. (2020) calibrates all the parameters, Walker et al. (2020) calibrates a fraction of the parameters and Kucharski et al. (2020) estimates all the parameters of a stochastic SEIR model.

The rest of the work is organized as follows: In Section 2, we introduce the SIR models used in this work and the modification we make in order to estimate the degree of engagement of the population in relation to governmental containment policies. In Section 3, we present the approach used to estimate the parameters of the models. Section 4 presents the short and long term forecasts with the estimated models and the effects of public choices used to fight the disease. Finally, Section 5 presents the main conclusions of the work.

2 Models

The SIR model describes the spread of a disease in a population split into three nonintersecting classes:

(S) Susceptible: the class of individuals who are healthy but can contract the disease;

(I) Infected: the class of individuals who are sick;

(R) Recovered: the class of individuals who are recovered from the disease.

Due to the evolution of the disease, the size of each of these classes change over time and the total population size N is the sum of these classes

$$N(t) = S(t) + I(t) + R(t). \tag{1}$$

Let β be the average number of contacts that are sufficient for transmission of a person per unit of time t. Then $\beta I/N$ is the average number of contacts that are sufficient for transmission with infective individuals per unit of time of one susceptible and $(\beta I/N)S$ is the number of new cases per unit of time due to the S susceptible individuals. Furthermore, let γ be the recovery rate, which is the rate that infected individuals recover or die, leaving the infected class, at constant per capita probability per unit of time.

Based on these definitions, we can write the SIR model as

$$\begin{array}{rcl} \frac{dS}{dt} & = & -\frac{\beta IS}{N} \\ \frac{dI}{dt} & = & \frac{\beta IS}{N} - \gamma I \end{array}. \tag{2}$$

The number of recovered individuals can be evaluated from Eq. (1), since in this version of the SIR model [Eq. (2)] the populations is constant. This is equivalent to add the equation $\frac{dR}{dt} = \gamma I$ to the system above. Actually, since we are modeling a short term pandemic, we do not consider the demographic effects in the population.

If we want to forecast the number of people that die from the disease, then we include a probability ρ of an individual in the class I dying from infection before recovering (Keeling and Rohani, 2011). In this case, we get the following set of equations

$$\begin{array}{rcll} \frac{dS}{dt} & = & -\frac{\beta IS}{N} & \\ \frac{dI}{dt} & = & \frac{\beta IS}{N} - \gamma I - \frac{\rho}{1-\rho}\gamma I = \frac{\beta IS}{N} - \frac{\gamma I}{1-\rho} & \textbf{[SIR]} \\ \frac{dD}{dt} & = & \frac{\rho}{1-\rho}\gamma I & \end{array} \tag{3}$$

where $\frac{\rho}{1-\rho}\gamma I$ is the number of people in the population that die due to the disease per unity of time and D is the number of people that die due to the disease. Note that in this case the number of individuals in the population reduces due to the infection and if one wants to evaluate R, one may integrate $\frac{dR}{dt} = \gamma I$. For the ease of reference, we call this model "**SIR**" model.

Since, in the case of the COVID-19, there is a relevant percentage of the infected individuals that are asymptomatic, we split the class of infected individuals in symptomatic and asymptomatic such as in Robinson and Stilianakis (2013), Arino et al. (2008) and Longini-Jr. et al. (2004):

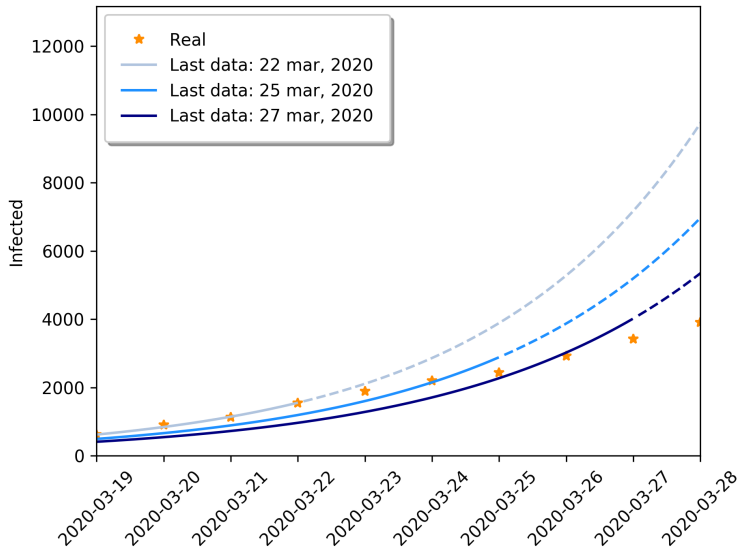

Figure 1: Estimations of the SIR model for different final date points. The solid line corresponds to the last date which the model was estimated, and the dashed line are model predictions. We represent the real data as points.

$$\begin{aligned}
\frac{dS}{dt} &= -(\beta_A I_A + \beta_S I_S)\frac{S}{N} \\
\frac{dI_A}{dt} &= (1-p)(\beta_A I_A + \beta_S I_S)\frac{S}{N} - (\gamma_A) I_A \\
\frac{dI_S}{dt} &= p(\beta_A I_A + \beta_S I_S)\frac{S}{N} - \gamma_S I_S - \frac{\rho}{1-\rho}\gamma_S I_S = p(\beta_A I_A + \beta_S I_S)\frac{S}{N} - \frac{\gamma_S I_S}{1-\rho} \qquad \textbf{[SIAS]} \\
\frac{dD}{dt} &= \frac{\rho}{1-\rho}\gamma_S I_S
\end{aligned} \tag{4}$$

where I_A is the number of asymptomatic individuals, I_S is the number of symptomatic individuals and p is the proportion of individuals who develop symptoms. For ease of reference, we call this model "**SIAS**" (Susceptible-Infected-Asymptomatic-Symptomatic) model. Notice that condition of Eq. (1) being constant does not hold anymore, since $\frac{dN}{dt} = -\frac{\rho}{1-\rho}\gamma_S I_S$.

In order to consider the effect of the confinement policy, we modify the transmission factors of Eqs. (3) and (4) by multiplying them by a parameter $\psi \in [0, 1]$ if within the implementation of government policy, and 1 otherwise. To be precise, we replace β in Eq. (3) by $\psi\beta$, β_A in Eq. (4) by $\psi\beta_A$ and β_S in Eq. (4) by $\psi\beta_S$. Note that doing this procedure we avoid the introduction and estimations of new "βs" and we may use ψ to evaluate the effectiveness of confinement policy. In the end, we may measure the social distance as $1 - \psi$.

3 Estimation procedure

We use the real data provided by the Ministry of Health of Brazil from February, 25, 2020 to March, 27, 2020 to estimate the epidemiological parameters of Eqs. (3) and (4). We estimate all parameters of our model by minimizing the squared error of integrated variables and their real values (Bard, 1974; Brauer et al., 2019). We proceed in a hierarchical procedure. First, we estimate the parameters of the SIR model, namely β, γ and ρ by minimizing the squared error

$$\min_{\beta,\gamma,\rho} \quad \frac{1}{2}\left(\sum_t (I_t - \hat{I}_t)^2 + (D_t - \hat{D}_t)^2\right), \tag{5}$$

	SIR	SIAS
Date	ψ	ψ
03-23-2020	0.760	0.743
03-24-2020	0.716	0.704
03-25-2020	0.671	0.660
03-26-2020	0.670	0.660
03-27-2020	0.670	0.661

Table 1: Estimated values of ψ for the SIR and SIAS models.

where I_t and D_t are the real data provided by the Ministry of Health of Brazil and $\hat{I}_t$ and $\hat{D}_t$ are their estimated values. Second, we estimate the SIAS model. Note that in our data, we lack clear information about the asymptomatic individuals, since the clear recommendation of the Ministry of Health is that to test for the virus only if you have strong symptoms. Otherwise, "stay at home". Furthermore, the mortality rate is evaluated mostly over the symptomatic ones, since the asymptomatic are in many cases not tested. Therefore, we suppose that $\beta_S = \beta$, $\gamma_S = \gamma$ and we keep the value of ρ. Using these parameters, we estimate the parameters β_A, γ_A and p in order to minimize the squared error

$$\min_{\beta_A,\gamma_A,p} \quad \frac{1}{2}\left(\sum_t (I_t - \hat{I}_{S,t})^2 + (D_t - \hat{D}_t)^2\right) , \tag{6}$$

where I_t and D_t are the real data provided by the Ministry of Health of Brazil and $\hat{I}_{S,t}$ and $\hat{D}_t$ are their estimated values. Table 2 presents the epidemiological parameters of our model and some reference values. Some of the lines of this table deserve remarks. First, the basic reproductive number R_0 in both models are comparable to the values for China and Italy. Second, the death rate ρ and the proportion of symptomatic individuals p are very close to the values disclosed by the media. However, we estimate the death rate using data that assumes there are places in hospitals to treat patients with severe infections. Depending on the government policy, we do not know whether this is true or not at the peak of infection.

By changing the final date of the period of estimation of the epidemiological parameters of the model, we note that there is a structural change in the data suggesting the effectiveness of the confinement policy. It is worth mentioning that it is hard to know exactly when social distance measures took effect, mostly because there is a variable incubation period of the virus ((WHO, 2020) indicate a range from 2 to 10 days) and some initiatives of social distance measures (such as home office) started even before the official quarentine period. In fact, after March, 22, 2020, we are able to see in the data two consecutive reductions in the taxes of transmission, depending on the final date that is used for the estimation of the SIR model as shown in Figure 1. So, we define March, 23, 2020, as the initial date that we use to estimate the parameter ψ. In order to estimate the parameter ψ, we keep all model parameters as previously estimated and we also minimize the mean squared error. Furthermore, in order to evaluate the effectiveness of the confinement, we estimate a new value of ψ for each new point of the time series as shown in Table 1, where the left column shows the SIR model factor related to the effectiveness of confinement policy ψ estimations and the right column shows the similar estimations for the SIAS model. Although there is a gap between the factor values ψ of the SIR and SIAS models, both columns suggest that the social distance factor ψ get stabilized after March, 25, 2020. According to the models, the transmission rate (the related to how fast a susceptible person becomes infected) is reduced to approximately 66% of its original value.

4 Forecasts

Figures 2 and 3 present respectively the short-term forcasts of the SIR and the SIAS models, where the models incorporate the ψ factor in order to rescale the transmission factors (β, β_A

Model	Parameter	Value	Other sources
SIR	β	0.449	—
SIR	γ	0.139	1/10 to 1/2 released by (WHO, 2020)
SIR	ρ	0.030	0.011 (Mizumoto et al., 2020), 0.038 released by WHO, 0.028 in 2020-03-27 released by Brazilian Ministry of Health and 0.032 in 2020-03-29 released by Brazilian Ministry of Health
SIR	R_0	3.136	2.5 and 3.8 in early stages of the disease in China according to respectively Anderson et al. (2020) and Read et al. (2020). 2.76 to 3.25 in Italy (Remuzzi and Remuzzi, 2020).
SIAS	β_S	0.449	—
SIAS	γ_S	0.139	—
SIAS	R_S	2.806	—
SIAS	β_A	0.449	—
SIAS	γ_A	0.114	—
SIAS	R_A	0.412	—
SIAS	R_0	3.219	The same as above.
SIAS	ρ	0.030	The same as above.
SIAS	p	0.895	0.820 in (Mizumoto et al., 2020)

In the SIR model, $R_0 = \beta(1-\rho)/\gamma$. In the SIAS model, $R_A = \beta_A(1-\rho)/\gamma_A$ and $R_S = \beta_S(1-\rho)/\gamma_S$ and $R_0 = R_A + R_S$.

Table 2: Estimated values of the epidemiological parameters.

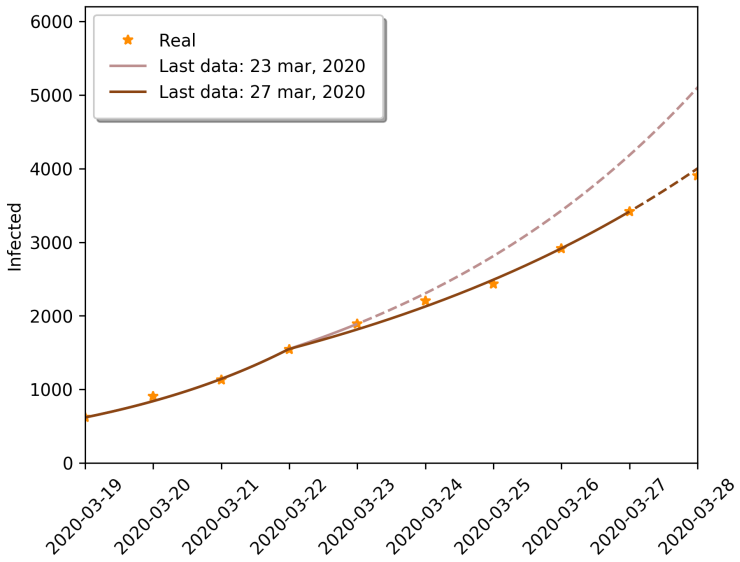

Figure 2: Short term forecast of the SIAS model. The solid line corresponds to the last date which the model was estimated, and the dashed line are model predictions. We represent the real data as points.

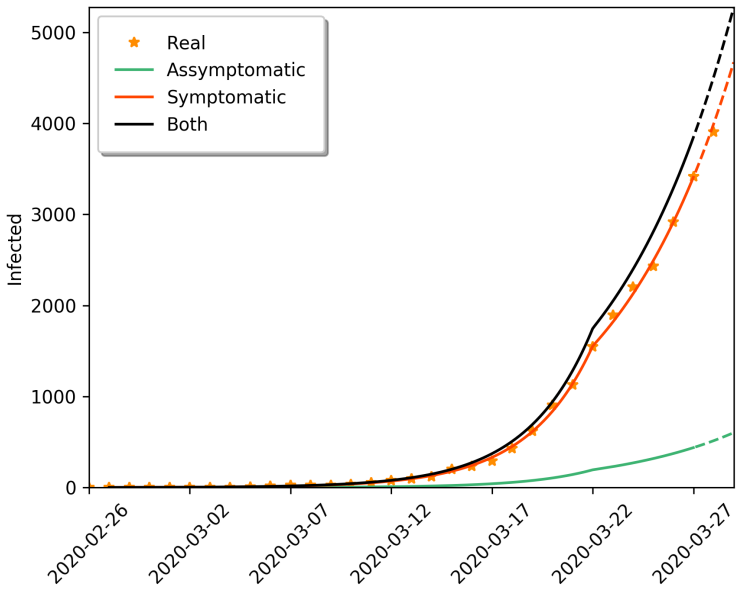

Figure 3: Short term forecast of the SIAS model. The solid line corresponds to the last date which the model was estimated, and the dashed line are model predictions. We represent the real data as points.

and β_S) in a different cenario, one with confinement imposed by the government. Note that Figure 3 explicitly shows the proportion of unknown asymptomatic individuals that when added to the symptomatic individuals skew the total value of infected individuals upwards.

We also use the SIR and SIAS models to provide long term forecasts of the evolution of the COVID-19 pandemic in Brazil depending on quarantine policy considered. While Fig. 4 shows the forecasts for the SIR model, Fig. 5 shows the forecasts for the SIAS model. In particular, we may note that while the SIAS model predicts that the number of infected is higher than the estimates of the SIR model, it also predicts a lower peak for the infected with symptoms, which are the ones that could require medical attention.

We explore four cenarios: (I) no measures of confinement policy (black line); (II) current confinement policy imposed by the government for an indefinite time (blue line); (III) 2-month confinement policy imposed by the government (yellow line); and (IV) optimum limited time confinement policy imposed by the government, so that the second infection peak is not greater

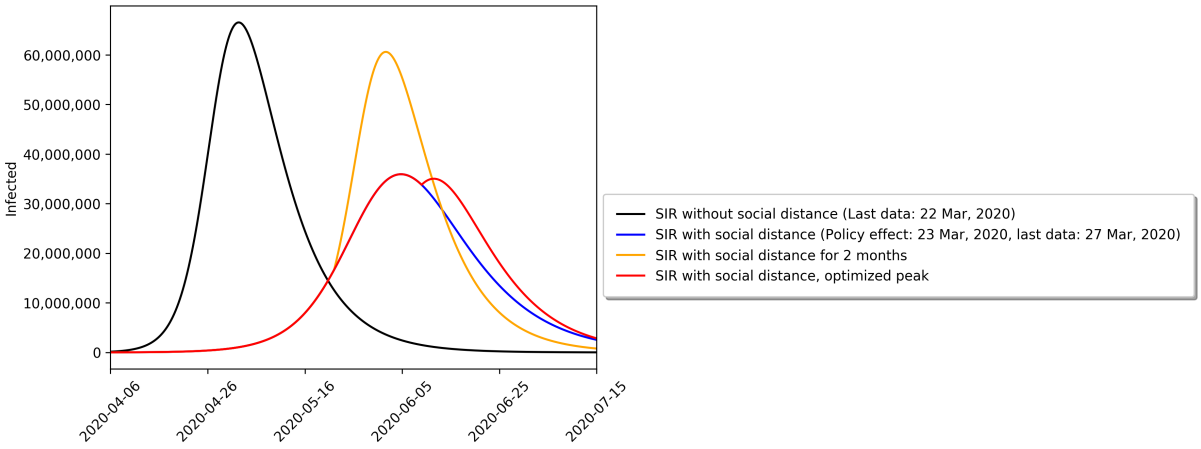

Figure 4: Long term forecasts of number of infected depending on the degree of social distance.

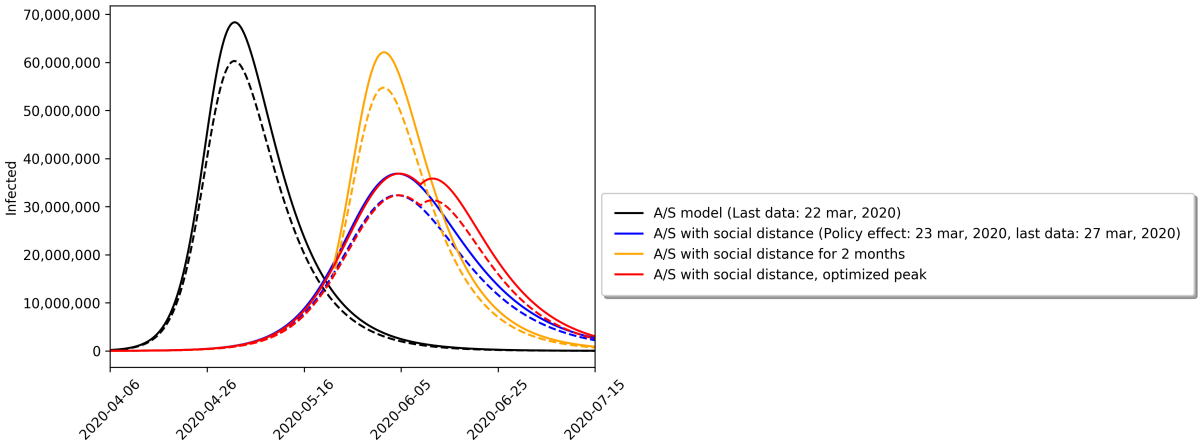

Figure 5: Long term forecasts of number of infected depending on the degree of social distance. Solid lines: number of infecteds. Dashed lines: number of symptomatic.

	SIR		**SIAS**			
	Infected (I)		Infected ($I_A + I_S$)		Symptomatic (I_S)	
Cenario	**Peak (%)**	**Date**	**Peak (%)**	**Date**	**Peak (%)**	**Date**
I	31.6	May, 5	32.5	May, 2	28.6	May, 2
II	17.1	June, 5	17.5	June, 4	15.4	June, 4
III	28.8	June, 2	29.5	June, 2	26.0	June, 1
IV	17.1	June, 5	17.5	June, 5	15.4	June, 5

Table 3: Peaks in each scenario and the dates of occurrence.

than cenario II (red line). In particular, if the last day of the confinement policy is June, 8, 2020, then the largest peak happens in June, 11, 2020 with value equal to 17.4. On the other hand, if the last day of the confinement policy is June, 9, 2020, then the largest peak happens in June, 5, 2020 with value equal to 17.1, that is the same peak of scenario (II). Furthermore, these figures suggest that policies based on short-term confinement are not enough to constrain the evolution of the pandemic, that is, if confinement measurements are released before the optimum, a second peak should be experienced. The peaks and dates in which they occur are detailed in Table 3.

In addition to Figure 5, we also present the evolution of the proportion of asymptomatic and symptomatic in Figure 6. Note that the proportion of individuals who develop symptoms, p in Eq. (4), alters the transmission rate, so it also affects the evolution of asymptomatic and symptomatic quantities over time. So this graph estimates the evolution of this proportion. Researchers estimate that the proportion of assymptomatic could be from 10% [1] to 30% [2], but Mizumoto et al. (2020) noticed the temporal dependence of the proportion. Our estimates suggest that the proportion of assymptomatic is approximately 11% till the peak happens.

Finally, it is worth considering that the SIAS differential equations, presented in Eq. (4), need an initial condition for the number of asymptomatic individuals. If we find the parameters values (β_A, γ_A, p) by solving the optimization problem of Eq. (6) using different conditions, we get different results, that is, different peak values for the symptomatic individuals. If the proportion of asymptomatic individuals is larger, then this may be good news since it may represent less pressure for the health care system. But since we do not have enough tests to map the whole population, we need to work with hypotheses. Our previous simulations supposed that the initial condition for the number of asymptomatic individuals is roughly zero. Figure 7

[1] `https://www.medicalnewstoday.com/articles/covid-19-study-estimates-rate-of-silent-transmission`
[2] `https://www.dw.com/en/up-to-30-of-coronavirus-cases-asymptomatic/a-52900988`

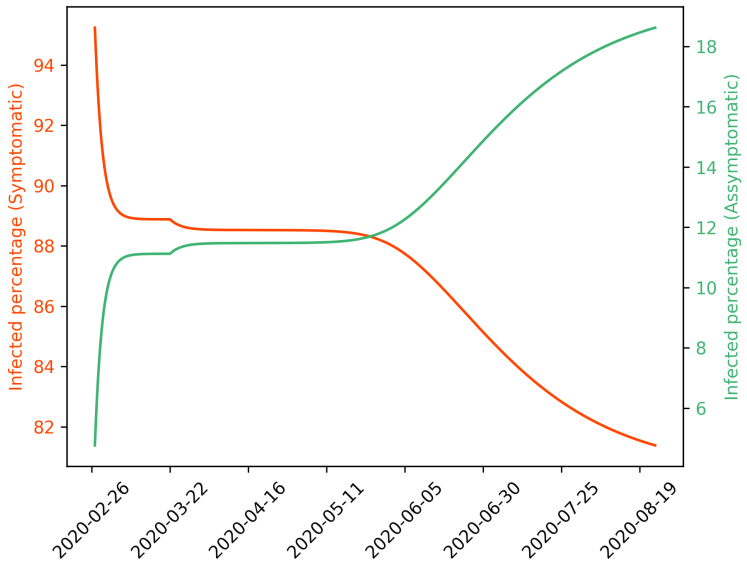

Figure 6: Proportions of assymptomatic and symptomatic. Approximately 6.7% are assymptomatic in March, 30, 2020.

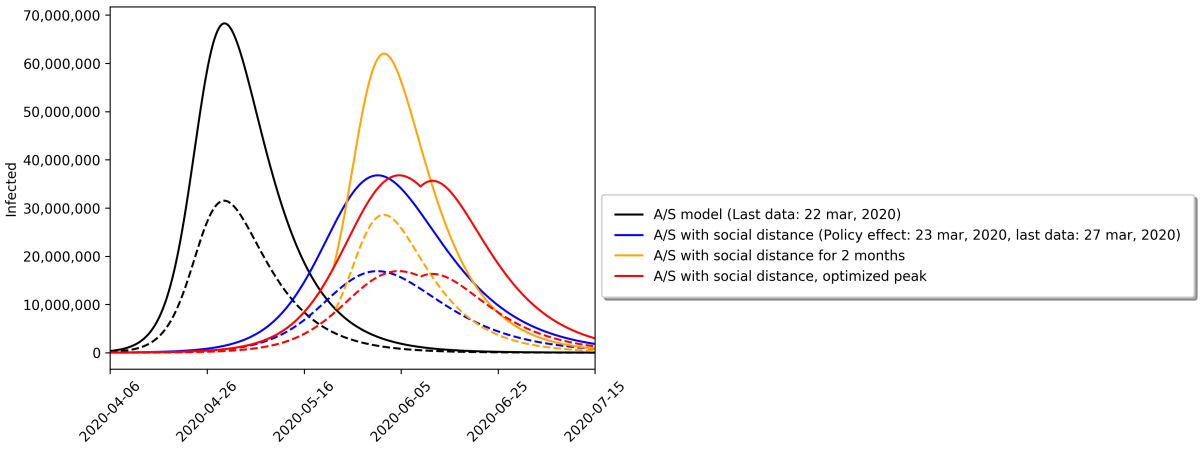

Figure 7: Long term forecasts of number of infected depending on the degree of social distance. Solid lines: number of infecteds. Dashed lines: number of symptomatic. We consider one symptomatic and one assymptomatic in the initial condition.

shows the same SIAS forecast, but with a different initial condition. We suppose now that when the first individual was infected and presented symptoms, there was another asymptomatic as well. So we consider one symptomatic and one assymptomatic as the initial condition. This results in more favorable peaks of 14.9, 8.0, 13.6, and 8.0 for cenarios I to IV, respectively.

5 Conclusions

We use the Brazilian recent data from February, 25, 2020 to March, 28, 2020 to model and forecast the evolution of the COVID-19 pandemic in Brazil.

We estimate two variations of the SIR model using historical data and we find parameters that are in accordance with the literature. We also introduce a factor ψ to account for the effect of the government confinement measures. Our methodology is also able to estimate the asymptomatic individuals, that may not be entirely present in data. Since the Brazilian government does not have enough tests for mass testing, this measure may provide some additional information.

While our short-term forecasts are in great accordance with the data, our long-term forecasts may help us to discuss different types of confinement policies. We also show that the confinement policy imposed by the government is able to flatten the pattern of contamination provided by the COVID-19, but short-term policies is only able to shift the peak of infection into the future keeping the value of the peak in almost the same value. Furthermore, we provide an estimate of the optimal date to end the confinement policy.

Finally, an important discussion is about the effectiveness of vertical containment policies, where only people at risk are placed in confinement. In these policies, as the proportion of the population in confinement is small, the number of confined and infected in this situation behaves similarly to the case we present with control, but with a higher death rate. The opposite happens for people without confinement, that is, a larger proportion of the population behaves as we presented without control, but with a smaller death rate. In fact, the policy's effectiveness is not in reducing the number of infected, but in reducing the number of deaths by confining individuals at risk. We may extend our model to explore these type of scenarios and we leave for future work.

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