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Is the SARS-COV2 mortality rate coefficient decreasing over time?

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Abstract

The outbreak of novel SARS-COV2, which started in China late 2019, rapidly gained the pandemic status. Mathematical models are required to have good accuracy in predicting the oubreak evolution, to allow governments and local authorities to take actions aiming at minimizing the damage for the public health. In the current context there are many uncertainties concerning the parameters entering the SIR model. Here we analyse the evolution of the death rate coefficient in Italy, USA and Brazil. Experimental data supports the conclusion that it is decreasing over time.

Keywords: SARS-COV2, SIR model, death rate coefficient

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The epidemic outbreak leading to the so-called COVID-19 disease, caused by the novel coronavirus SARS-COV2, had started in the late 2019, in the province of Hubei, China. The exact date and location of patient zero is still uncertain, but given the high contagon rate it quickly disseminated throughout the world, being declared pandemic by the World Health Organization (WHO) in March 2020. Within this scenario, mathematical models are crucial in making predictons allowing governments and local authorities to take safety measures aiming at minimizing the potential damaged that can be caused to the population and the health systems [1]. These models are based on the so-called susceptible-infected-recovered (SIR) model and its variants [2–5], but key parameters entering it, such as infection and mortality rate coefficients, suffered from enormous uncertainties at the very beginning, rendering predictions which missed the target by far. The Imperial College London model predicted in early March 2020 more than 500 thosands of deaths in the UK and more than 2 millions in the USA [6, 7]. Therefore, it takes time, while the epidemic unfolds, for a reliable amount of experimental evidence to be collected, allowing the model parameters to be known with less uncertainty. It must be emphasized that there are still many doubts about the correct model to be used in describing the time evolution of SARS-COV2 epidemic process, but it is relatively safe to assume that an infected person which recovered become immune, at least in the time window being considered.

In the present paper we will analyse the evolution of the death rate coefficient μ in Italy, USA and Brazil. Current data supports the conclusion that it is decreasing over time, obeying an exponential law for sufficiently large time scales. The causes for that behavior, to the best of our knowledge, are unknown.

For the sake of simplicity we will take as the starting point the SIRD model, whose equations are written below:

$$\frac{dS}{dt} = -\alpha SI \ , \tag{1}$$

$$\frac{dI}{dt} = \alpha SI - \frac{1}{\tau} I - \mu I \ , \tag{2}$$

$$\frac{dR}{dt} = \frac{1}{\tau} I \ , \tag{3}$$

$$\frac{dD}{dt} = \mu I \ , \tag{4}$$

where $S(t)$, $I(t)$, $R(t)$ and $D(t)$ correspond to the susceptible, actively infected, recovered and dead populations, respectively. For a time scale smaller than 2 years we can neglect

the populational growth for our purposes here. This way, the total population P_0 at $t = 0$ is susceptible, but for time t the constancy of $P_0 = S(t) + I(t) + R(t) + D(t)$ holds. The model parameters are the transmission rate coefficient α, the average recovery time τ and the mortality rate coefficient μ. These input parameters can be time-dependent. The set of equations can be renormalized by P_0, yielding relative values. This way, the transmission rate coefficient must be renormalized to $\alpha' = \alpha P_0$.

From equation (4) we obtain:

$$\mu(t) = \frac{dD(t)/dt}{I(t)} \ , \tag{5}$$

where $dD(t)/dt$ it the daily death rate while $I(t)$ it the actively infected population. Data is taken from the website Worldometer [8], which aggregates information on the coronavirus pandemic worldwide, until July 18th 2020. The moving averages for a 7-day period are being considered, which remove the fast variations that seem to come mainly from the lag in numbers accumulated during the weekends and released latter.

The time evolution of the SARS-COV2 outbreak in the USA is displayed in Figure 1. The time $t = 0$ corresponds to the day when the total number of active cases surpassed 100. Looking at Figure 1-(a) one can see a plateau forming in the interval $80 < t < 100$ days, the a rapid growing in the active cases is observed. However, the daily deaths, measured by the death rate dD/dt did not increased proportionally, as illustrated in Figure 1-(b). As a matter of fact, it has been decreasing since $t = 50$ days. The mortality rate coefficient calculated with the known data is decreasing exponentially and can be well fitted for sufficiently long time ($t > 30$ days) by an exponential funcion of the form $\mu(t) = 10^{-4} + 1.5 \times 10^{-2} e^{-t/30}$. Assuming the uncertainty in total number of deaths is far lower than in the real active cases, since there are a large number of asymptomatic of mildly affected patients which go under the radar of official data, the absolute value of $\mu(t)$ suffers from an uncertainty of one or two orders of magnitude. It has been estimated that the real number of active cases can be 10 to 100 times the registered cases worldwide.

Similar conclusions can be drawn using data from Brazil and Italy, shown in Figures 2 and 3, also displaying an exponential decay behavior for $\mu(t)$ at large time scale. The relaxation time in these cases is around 30 days. USA and Brazil have in common their vast territorial area, much larger than the area of Italy, making it difficult to apply the SIR model neglecting spatial variations for USA and Brazil. From current date, the outbreak

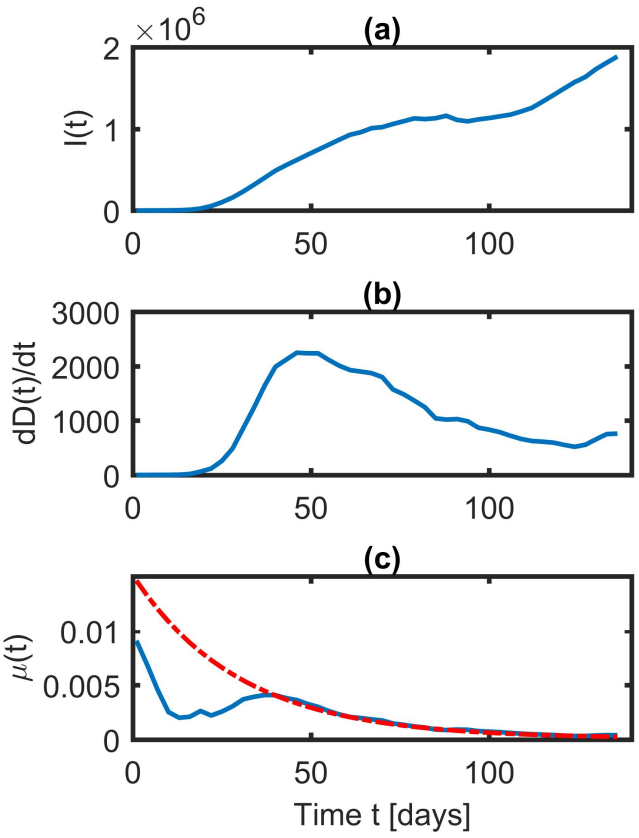

FIG. 1: Evolution of SARS-COV2 outbreak in the USA: (a) Active cases $I(t)$, (b) Death rate $dD(t)/dt$ and (c) Mortality rate coefficient $\mu(t)$. The time $t = 0$ correspondo to the day when the total active cases surpassed 100. The dashed red curve in (c) displays the approximated function $\mu(t) = 10^{-4} + 1.5 \times 10^{-2} e^{-t/30}$.

is near the end in Italy, as can be seen clearly from Figures 3-(a) and 3-(b). Initially, it was thought that $\sim 67\%$ of the population should be infected to obtain herd immunity, but novel models taking into account population heterogeneity significantly lowers that number to $\sim 40\%$ or less [9, 10]. Nonetheless, the general behavior of $\mu(t)$ among the three countries is very similar until now, and the behaviour can be modeled as $\mu(t) = A + Be^{-t/t_0}$.

Going further, we tried to fit the evolution of the outbreak in Italy, using the function $\mu(t) = 10^{-3} + 3 \times 10^{-2} e^{-t/30}$ for the mortality rate coefficient. In equations (1)-(4) we used $\alpha' = 0.14$, adjusted for the fitting, τ is taken to be 14 days, based on publicly available information related to the averaged recovery time. For simulations, we set the normalized

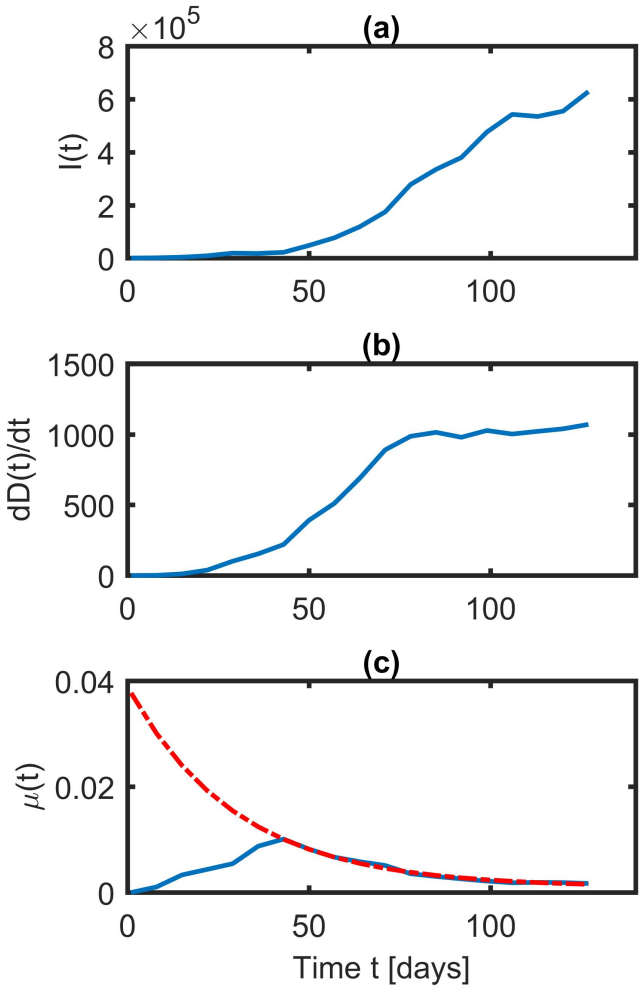

FIG. 2: Evolution of SARS-COV2 outbreak in Brazil: (a) Active cases $I(t)$, (b) Death rate $dD(t)/dt$ and (c) Mortality rate coefficient $\mu(t)$. The time $t = 0$ correspondo to the day when the total active cases surpassed 100. The dashed red curve in (c) displays the approximated function $\mu(t) = 10^{-3} + 3.8 \times 10^{-2} e^{-t/30}$.

initial conditions to $I_0 = 10^{-2}$, $D_0 = 0$, $R_0 = 0$, and a total susceptible population of $P_0 = 5$ millions. A better fitting at the end of the outbreak was aimed. Figures 4-(a) to 4-(c) display the time evolution. The total number of deaths can be calculated integrating (4), leading to the following:

$$D_f = \int_0^{t_f} \mu(t) I(t) dt \ , \tag{6}$$

which yielded a total of 36×10^3 deaths at the end of the outbreak, not far from the real

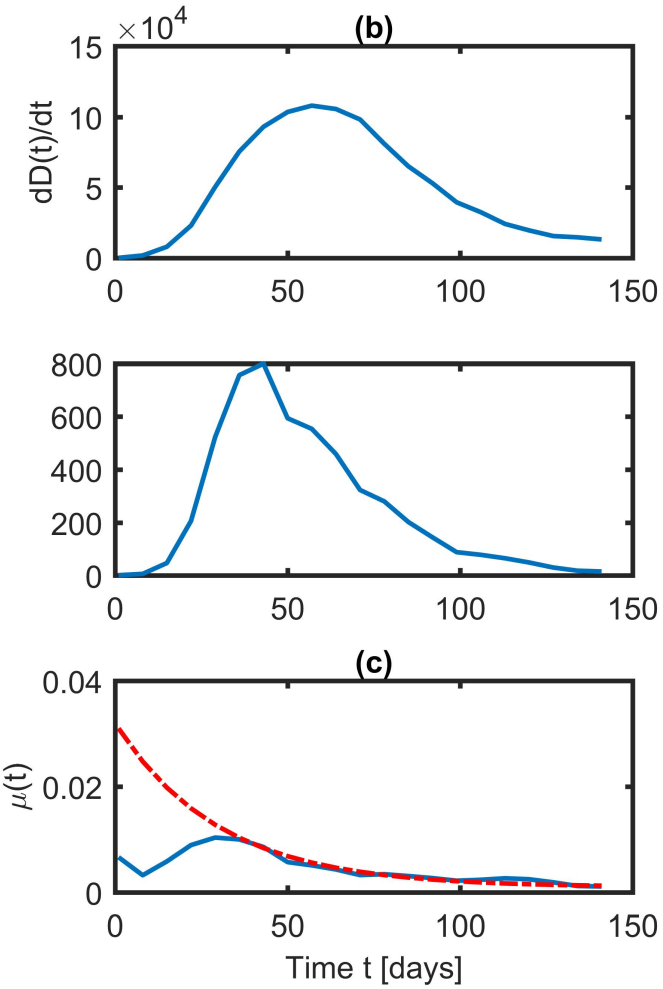

FIG. 3: Evolution of SARS-COV2 outbreak in Italy: (a) Active cases $I(t)$, (b) Death rate $dD(t)/dt$ and (c) Mortality rate coefficient $\mu(t)$. The time $t = 0$ correspondo to the day when the total active cases surpassed 100. The dashed red curve in (c) displays the approximated function $\mu(t) = 10^{-3} + 3 \times 10^{-2} e^{-t/30}$.

value.

The success obtained using a very simple model for the case of Italy encouraged us to simulate the outbreak time evolution for Brazil. Certainly, the obtained results cannot be taken too much seriously, mainly due to country's gigantic territorial extension. Improvements to the model aiming to include geographical aspects could be done quite easily. The results of the SIR model simulations for Brazil are shown in Figures 5-(a) to 5-(c), con-

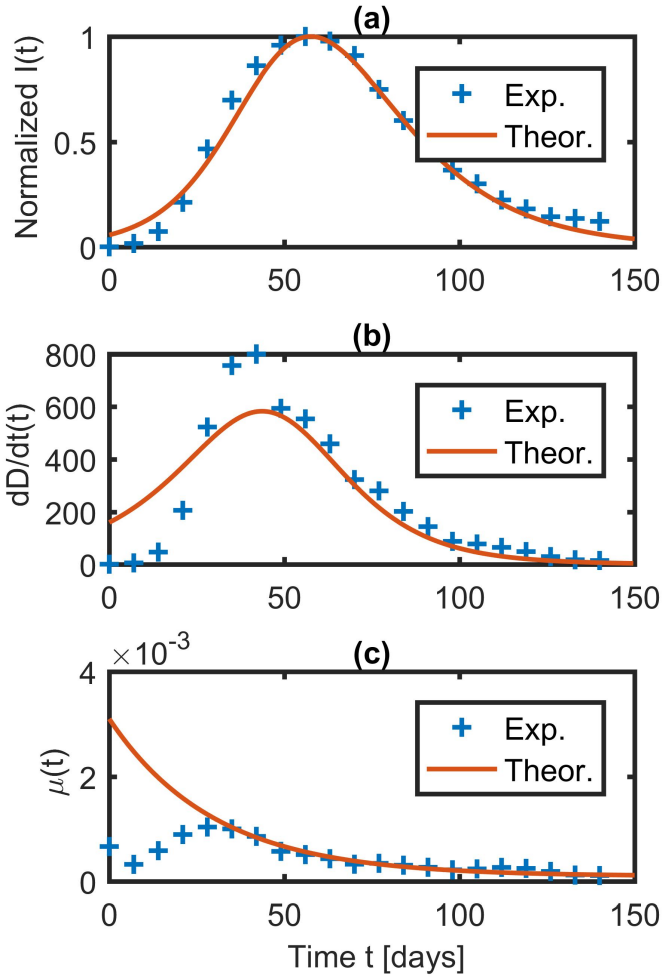

FIG. 4: Simulation of the SARS-COV2 outbreak in Italy using the SIR model: (a) Active cases $I(t)$, (b) Death rate $dD(t)/dt$ and (c) Mortality rate coefficient $\mu(t)$. Simulated values are compared to the publicly available data.

sidering $\alpha' = 0.135$, $\tau = 14$ days, $I_0 = 4 \times 10^{-4}$ and a susceptible population of $P_0 = 50$ millions. This way, the predicted total number of deaths can reach $120,000$ at the end of the outbreak, but it can to be underestimated, given the current scenario in Brazil [11].

In conclusion, taking the current available data on the SARS-COV2 outbreak into consideration, it seems plausible that the mortality rate coefficient is decreasing over time. The real caused for that are unknown, to the best of our knowledge, but a few hypotheses can be put forward, to be known: i) unreliability of the available data, mainly at the beginning

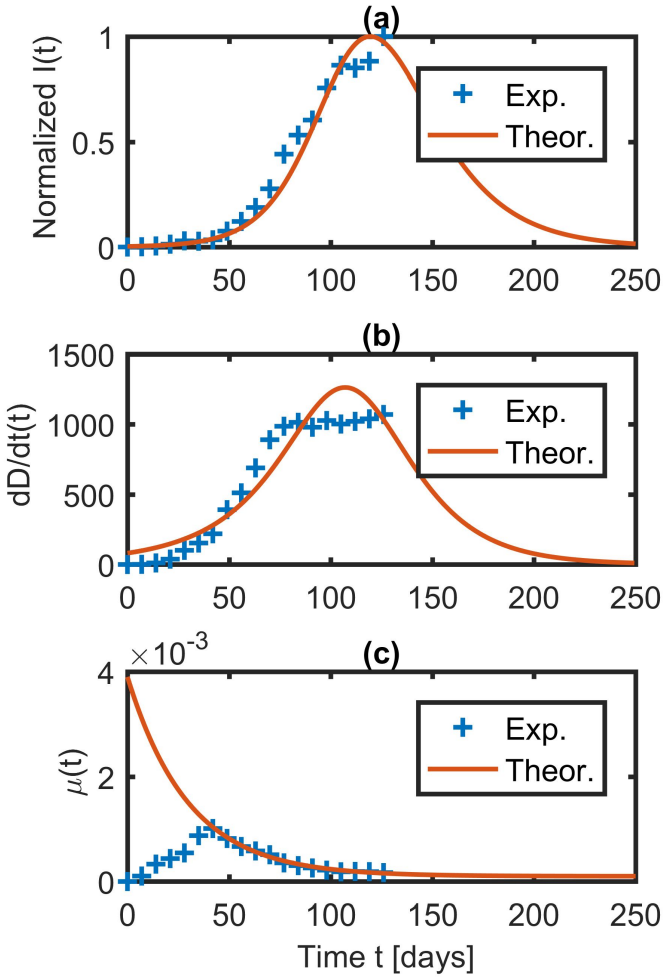

FIG. 5: Simulation of the SARS-COV2 outbreak in Italy using the SIR model: (a) Active cases $I(t)$, (b) Death rate $dD(t)/dt$ and (c) Mortality rate coefficient $\mu(t)$. Simulated values are compared to the publicly available data.

of the outbreak process in the various regions, when the total number of active cases is much more uncertain and can be easily underestimated; ii) natural processes, some of them related to mutations weakening of the virus during transmission.

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The authors declare to have had equal contributions on the paper.
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[1] Bootsma, M. C.; Ferguson, N. M. Proc. Natl Acad. Sci. USA **104**, 7588 (2007).

[2] Shaman, J. et al. Nature Communications **4**, 2837 (2013).

[3] Bjornstad, O. N.; Shea, K. ; Krzywinski, M.; Altman, N. Nature Methods **17**, 557-558 (2020).

[4] Rüdiger, S.; Plietzsch, A.; Sagués, F.; Sokolov, I. M.; Kurths, J.; Scientific Reports **10**, 5919 (2020).

[5] Giordano, G. et al. Nature Medicine **26**, 855 (2020).

[6] Ferguson, N. M. et al. Preprint at Spiral https://doi.org/10.25561/77482 (2020).

[7] Adam, D. , Nature **580**,316 (2020).

[8] Worldometer on Coronavirus, http://worldometers.info/coronavirus/. Last access: July 18th, 2020.

[9] M. G. M. Gomes, R. M. Corder, J. G. King, K. E. Langwig, C. Souto-Maior, J. Carneiro, G. Goncalves, C. Penha-Goncalves, M. U. Ferreira, R. Aguas, Individual variation in susceptibility or exposure to SARS-CoV-2 lowers the herd immunity threshold. medRxiv 10.1101/2020.04.27.20081893 [Preprint]. 21 May 2020;

[10] F. Ball, T. Britton, P. Trapman, Population heterogeneity and consequences for herd immunity to SARS-CoV-2, Version 1, Zenodo (2020); doi:10.5281/zenodo.3899252.

[11] Candido, Darlan S. et al, Science 10.1126/science.abd2161 (2020).