



A Nonlinear Dynamical Map for COVID-19

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Abstract. The new coronavirus disease (COVID-19) has rapidly spread around the world, being considered a pandemic with serious consequences. In this regard, epidemic models became an essential tool to describe and predict epidemic evolution. A classical approach is the compartmental models where different populations are employed to describe the system evolution. Typically, four populations are considered: susceptible, exposed, infected and recovered, giving rise to the SEIR model. This paper proposes a dynamical map to describe Covid-19 epidemic based on the classical SEIR model taking into consideration the effect of vaccination. This novel map describes the evolution of currently infected, cumulative infected and vaccinated population using three coupled nonlinear algebraic equations. Due to the simplicity of the novel model description, useful information to evaluate the epidemic stage can be obtained analytically, allowing the support of decision making. In this regard, the herd immunization and the estimation of the number of deaths should be pointed out. Real epidemic data from Germany, Italy and Brazil are employed in order to verify the model capability to describe the evolution of Covid-19 dynamics.

Keywords: COVID-19, Epidemic Model, Dynamical Map, Nonlinear dynamics, Vaccination

1 Introduction

The novel coronavirus disease (COVID-19) has become a major subject of research from different areas of human knowledge since the World Health Organization characterized it as pandemic in March 11th 2020. Therefore, the development and improvement of new epidemic models are of great importance in order to understand its evolution and to establish proper health strategy plans.

Dynamical perspective is an interesting approach to deal with biomedical systems [1]. Through literature one can find several approaches regarding dynamical epidemic models [2], employed to describe different infectious diseases. An interesting and useful approach is based on population dynamics. These populations are employed to represent the disease, establishing their evolution and interactions. Kermack and McKendrick [3] were one of the pioneers in considering three populations in epidemic models: susceptible, infected and recovered (SIR). They showed the course of an epidemic might not be terminated necessarily by all individuals becoming infected. An evolution of this approach was due to Anderson [4] and May [5] that considered an extra population: exposed (E). Nowadays, a well-established epidemic model is based on the susceptible-exposed-infected-removed (SEIR) framework.

Concerning the COVID-19 pandemic, Lin et al. [6] proposed a conceptual model for COVID-19 evolution in Wuhan, China, considering individual behavior reaction to the outbreak scenario and governmental actions. Ramos et al. [7] developed a novel mathematical model taking into consideration different sanitary and infectiousness conditions of hospitalized people, as well as undetected cases. Chen et al. [8] used an extended SIR model also considering the effect of undetectable persons. Savi et al. [9] applied the SEIR description to investigate the pandemic evolution in Brazil. Results showed the importance of both individual and governmental actions to control the virus spread and to reduce the number of infected. Pacheco et al. [10] improved the model including hospital infrastructure and explicitly splitting removed populations into recovered and deaths. Sujath [11] employed a machine learning method to forecast COVID-19 evolution in India employing linear regression, multilayer perception

and vector auto regression methods.

An alternative to continuous differential models might be established by maps, which are discrete-time and governed by a system of algebraic equations. In this regard, dynamical maps have advantages due to their simplicity. Alonso-Quesada et al. [12] argued the use of discrete-time instead of continuous-time models are preferred since the amount of necessary computation effort can be reduced considerably. Also, since epidemic statistics take place on fixed time intervals, it makes easier to parameterize a discrete-time than a continuous-time epidemic model. Enatsu et al. [13] asserted there are situations that constructing discrete epidemic models are more appropriate to understand disease transmission dynamics and to evaluate eradication policies since they permit arbitrary time-step units, preserving the basic features of corresponding continuous-time models.

This work deals with a novel COVID-19 nonlinear dynamical map that represents the epidemics from the framework of infected, cumulative infected and vaccinated populations. The discrete-time model is developed based on the SEIRV model that considers susceptible-exposed-infected-removed-vaccinated populations, and reduces the six coupled ordinary differential equation into three nonlinear algebraic equations. Good agreement between real data and map simulations was obtained employing COVID-19 data from Germany, Italy and Brazil. Ordinary pandemic scenarios, such as a multi-wave pattern, can be obtained from map simulations. Due to the simplicity of the model, it is possible to obtain analytic expressions regarding the infectious ratio and the herd immunization point. The effect of vaccination is also carried out, which shows its importance to reduce the number of deaths.

2 Mathematical Model

The main objective of this work is to develop a dynamical map to describe COVID-19 epidemics based on the classical SEIR framework. Moreover, an extra population is included considering the effect of vaccination, defining hence an SEIRV model. The populations employed are: susceptible, S ; exposed, E ; active infected, I ; removed, R ; and vaccinated, V . In addition, the cumulative infected population C is incorporated as a useful model information. An essential assumption is that reinfection is neglected and, therefore, each individual can be infected only once. Moreover, once vaccinated, an individual cannot become infected anymore. Another assumption is that the population V accounts only for the vaccinated population, which excludes situations where vaccination occurs after the infection.

On this basis, the SEIRV governing equations are defined as follows.

$$\dot{S} = -\beta SI - v \quad (1a)$$

$$\dot{E} = \beta SI - \sigma E \quad (1b)$$

$$\dot{I} = \sigma E - \gamma I \quad (1c)$$

$$\dot{R} = \gamma I \quad (1d)$$

$$\dot{V} = v \quad (1e)$$

$$\dot{C} = \sigma E \quad (1f)$$

where over dot represents time derivative; β is the transmission rate which is directly associated with social isolation; σ^{-1} is the mean latent period; γ^{-1} is the infectious period; and $v = v(S)$ is the vaccination rate that is considered as a function of the susceptible population. It should be pointed out that dimensionless variables are considered herein and, therefore, $(S, E, I, R, V) \in [0, 1]$ and $S + E + I + R + V = 1$. Since reinfection is neglected and since the average immunity period after vaccination is usually longer than the mean latent period, an exposed individual eventually becomes infected before acquiring immunity. Therefore, the effect of vaccination is herein considered only in Eq. (1a), being characterized by moving susceptible population towards to the vaccinated group.

The map is derived from these differential equations adopting some basic assumptions. By considering each one of the populations, represented by X , its time derivative is treated as $\dot{X} = \lim_{\Delta t \rightarrow 0} (X(t + \Delta t) - X(t))/\Delta t$, which means that $\dot{X} \approx X_{n+1} - X_n$ if $\Delta t = 1$ and n representing the n -th day. Additionally, it is assumed that the ratio E/I in the beginning of the outbreak is kept constant through the whole epidemic period, which means that $E = \Lambda I$ and $\dot{E} = \Lambda \dot{I}$.

Under these assumptions and after algebraic manipulation, the COVID-19 map yields

$$I_{n+1} = \left[1 + \frac{\beta[1 - (C_n + V_n) - (\gamma + \Lambda)I_n] - \gamma}{1 + \Lambda} \right] I_n \quad (2a)$$

$$C_{n+1} = \frac{\{\gamma\Lambda + \beta[1 - V_n - (\gamma + \Lambda)I_n]\}I_n + (1 + \Lambda - \beta I_n)C_n}{1 + \Lambda} \quad (2b)$$

$$V_{n+1} = V_n + v(I_n, C_n, V_n) \quad (2c)$$

with

$$\Lambda = \frac{\gamma - \sigma + \sqrt{(\gamma - \sigma)^2 + 4\beta\sigma}}{2\sigma} \quad (3)$$

and where $\Lambda = E/I$ is a constant estimated by a parametric condition (β, σ, γ) . It is important to highlight that, despite this novel map is employed herein to describe COVID-19 dynamics, it can also be employed to describe the dynamics of any other epidemics.

The vaccination rate in the map is assumed to be a function of the infected, cumulative and vaccinated populations, $v = v(I, C, V)$. Since $0 \leq V \leq 1$, it is imposed the constraint $v(I, C, V) = 0 \forall (I, C, V) \mid C + V = 1$. Vaccination strategy can be implemented by different ways. The simplest case assumes a constant vaccination rate for individuals, $v = \phi$, where ϕ is the vaccination coefficient. A more realistic representation considers that the vaccination rate is proportional to the susceptible population, $v = \phi S$.

The cumulative number of deaths, D , can be estimated based on the total infected population C . Therefore, the total number of deaths is expressed by

$$D_n = \mu C_n \quad (4)$$

where μ is the death rate, which is usually around 2%. It should be pointed out that the current number of deaths can be determined by the difference $D_n - D_{n-1}$.

In epidemic models, the transmission rate β is the critical parameter to characterize the COVID-19 dynamics, being related to social isolation and virus contagious capacity. Virus variants can be represented by changes on this parameter considering that a more contagious variant increases the value of the transmission rate for the same level of social isolation, for example. Nevertheless, virus variants are neglected in this work and, therefore, transmission rate is directly related to social isolation. Since the social isolation is clearly time dependent, it is convenient to define $\beta = \beta(n)$. The time dependence can be established from an adjustment with real data, defining a proper fit. An interesting approach to match real data is the use step functions, defined as follows by Eq. (5) for m steps.

$$\beta(n) = \begin{cases} \beta_1, & \text{if } 0 \leq n \leq T_1 \\ \beta_2, & \text{if } T_1 < n \leq T_2 \\ \dots & \\ \beta_m, & \text{if } n > T_{m-1} \end{cases} \quad (5)$$

The other parameters, σ and γ , usually assumes typical values for COVID-19 dynamics [6, 9]: $\sigma = 1/3$ and $\gamma = 1/5$. These parameters are employed in all simulations. The vaccination coefficient ϕ can also vary through time, which means that vaccination campaigns can be also modeled by step functions. This approach is interesting to describe situations related to lack of vaccines, for example.

2.1 Infectious Rate

A quantity that is often employed in the context of epidemic models is the infectious rate r , defined herein based on the ratio between two subsequent iterations of currently infected population.

$$r_n = \frac{I_{n+1}}{I_n} \quad (6)$$

The infectious increases in a specific time if $r_n > 1$, and decreases otherwise, if $0 < r_n < 1$. The case $r_n = 1$ is the transition between both conditions. By taking the active infected given by Eq. (2a), one can obtain the ratio r_n as a function of I_n and $(C_n + V_n)$, which yields

$$r_n = 1 + \frac{\beta[1 - (C_n + V_n) - (\gamma + \Lambda)I_n] - \gamma}{1 + \Lambda} \quad (7)$$

Consider now the system state space $I-(C + V)$ showing the curves standing for Eq. (7) with $r_n = 1$. This map is a representation of the state space being presented in Fig. 1a for various values of β and constant values of σ and γ . Since the curves are related to $r_n = 1$, the region below each curve is associated with values of $r_n > 1$ while above the curve is related to $r_n < 1$. Hence, the region below the curve is associated with a growth of active cases. The peak of I occurs when the epidemic evolution on the state space crosses the curve for $r_n = 1$. Fig. 1a allows one to obtain the number of total infected plus vaccinated required to prevent the increase in the number of active cases regardless the number of currently infected and considering fixed parametric combination. In other words, when the sum $C + V$ reaches a critical value, the infected population I necessarily decreases. Thus, the herd immunization point, P_h , is defined when this critical situation is achieved and $I = 0$ (see Fig. 1b). In other words, for any given parametric combination, if $C + V \geq P_h$, then $r < 1 \forall I$.

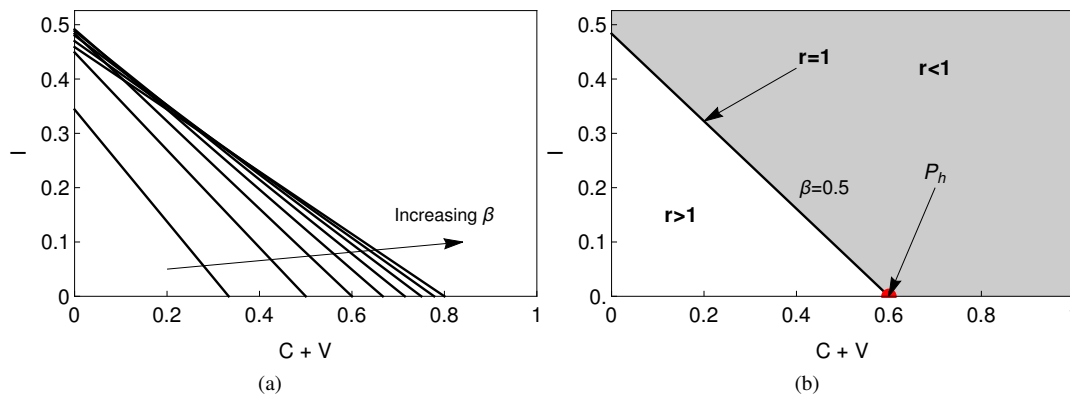


Figure 1. State space $I-(C + V)$ with infectious rate equals to 1 (Eq. (7) with $r = 1$) for $\sigma = 1/3$, $\gamma = 1/5$ and β ranging from 0.2 to 1 with step of 0.1 (a), and the herd immunization point P_h indication for $\beta = 0.5$ (b).

The value of the herd immunization point P_h can be analytically defined as a function of the parameters (β, σ, γ) . By considering $r_n = 1$ and $I_n = 0$ in Eq. (7) and after some algebraic manipulation, one obtains the following expression

$$P_h = 1 - \frac{\gamma}{\beta} \quad (8)$$

One might notice this is a function of the transmission rate β and the infectious period γ^{-1} , being not dependent on the latent period σ^{-1} . Also, it is noticeable an increase of the transmission rate β results in a higher value of P_h . In other words, the higher is the transmission rate, the bigger is the infected-vaccinated population needed to achieve the herd immunization point. Regarding the limit $\beta \rightarrow \infty$, it yields $P_h \rightarrow 1$, as one expected. This means that, in order to have $r_n < 1$, it is necessary that 100% of the population becomes either infected or vaccinated. Finally, making $P_h = 0$, one obtains $\beta = \gamma$, which means that for any $\beta < \gamma$ the number of active cases necessarily decreases regardless the numbers of I or $(C + V)$. Therefore, the higher is the average infectious period, given by γ^{-1} , the lower is the transmission rate coefficient required. In other words, for a larger average time an individual remains infected, the transmission coefficient needs to decrease in order to obtain a negative infectious rate regardless the epidemic stage.

In the sequence, the COVID-19 map is applied to describe the epidemic dynamics using real data from Germany, Italy and Brazil as references.

3 Model Verification

The novel COVID-19 map is now employed to perform a dynamical analysis of the pandemic. Real data from the novel COVID-19 epidemics in Germany, Italy and Brazil are employed as reference considering information from Worldometer website (<https://www.worldometers.info/>). The comparison is established by considering nondimensional values, dividing each population by the total population of the country. In this regard, the following values are adopted to each country: Germany $N_{ger} = 83.03 \times 10^6$; Italy $N_{ita} = 60.36 \times 10^6$; Brazil $N_{bra} = 211 \times 10^6$. The time period ranges from 6th March of 2020 ($n = 0$) to 21st January of 2021. Due to natural seasonality in real data, a 7 day average is then employed, giving rise to a new data set. Both infected I and cumulative C populations are of concern showing a two-wave pattern. Fig. 2 displays the active cases in time for the three countries. For Germany and Italy cases, the first wave peak occurred after April 2020, while the Brazilian case shows a longer first wave, which is actually a plateau pattern. Due to this pattern, the Brazilian

second wave started from a high level value of infected. On the other hand, Germany and Italy present the second wave peak around December 2020 and the number of active cases began to drop at the end period. Based on these observations, COVID-19 is characterized by different patterns. A bell shape behavior is the essential point to be observed, but it is clear the possibility of either multi-wave or plateaus patterns.

Transmission rate is defined by step functions presented in Eq. (9). These functions were obtained employing the Least Square Method to fit real active cases data. Fig. 2 presents the comparison between numerical simulations and real data showing a good agreement for all countries. Based on that, it is possible to conclude that the COVID-19 map captures real data including the multi-wave scenario. The main difficulty is the proper determination of the transmission rate.

$$\beta_{\text{ger}} = \begin{cases} 0.570, & \text{if } 0 \leq n \leq 28 \\ 0.150, & \text{if } 28 < n \leq 143 \\ 0.286, & \text{if } 143 < n \leq 260 \\ 0.220, & \text{if } 260 < n \leq 294 \\ 0.200, & \text{otherwise} \end{cases} ; \quad \beta_{\text{ita}} = \begin{cases} 0.530, & \text{if } 0 \leq n \leq 16 \\ 0.250, & \text{if } 16 < n \leq 45 \\ 0.160, & \text{if } 45 < n \leq 140 \\ 0.257, & \text{if } 140 < n \leq 221 \\ 0.325, & \text{if } 221 < n \leq 260 \\ 0.220, & \text{otherwise} \end{cases} ;$$

$$\beta_{\text{bra}} = \begin{cases} 0.500, & \text{if } 0 \leq n \leq 60 \\ 0.300, & \text{if } 60 < n \leq 95 \\ 0.225, & \text{if } 95 < n \leq 153 \\ 0.200, & \text{if } 153 < n \leq 247 \\ 0.250, & \text{otherwise} \end{cases}$$

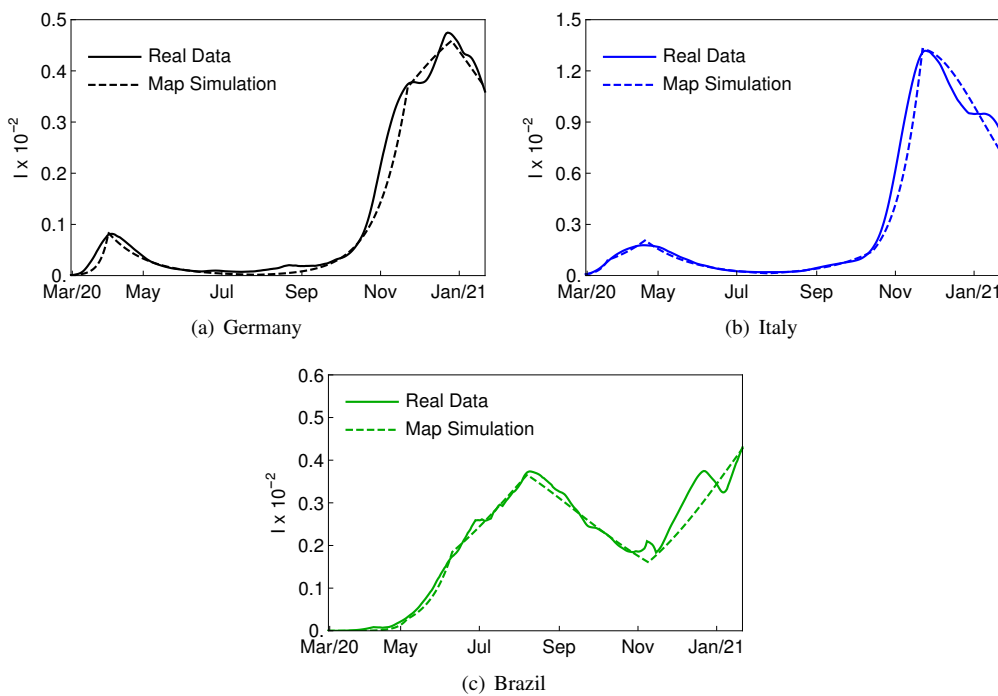


Figure 2. Infected active cases I for Germany (a), Italy (b) and Brazil (c) for the whole period range employed. The continuous line stands for real data and dashed line for the map simulation.

4 Effect of Vaccination

This section investigates the effect of vaccination on the COVID-19 dynamics. It is adopted a situation where the vaccination starts on the last day of the real data period: 21st January 2021. The transmission rate employed in the simulations is the mean value from $\beta(n)$ of the last 90 days of the period range, yielding: $\beta_{\text{ger}} = 0.227$, $\beta_{\text{ita}} = 0.230$ and $\beta_{\text{bra}} = 0.224$. Real data time series is employed to calculate the transmission rate $\beta(n)$ at each time step for each country using Eq. (2a) and employing Newton's method. Moreover, the vaccination model

employed to represent the vaccination approach is $v = \phi$, and three coefficients are adopted: $\phi = 0, 10^{-3}$ and 10^{-2} . The case $\phi = 0$ naturally stands for no vaccination. Fig. 3 presents the effect of vaccination on the evolution of the epidemic for each country, showing that vaccination has a huge impact on the COVID-19 dynamics. The higher the vaccination rate is, the lower is the peak reached by active cases and the lower is the total infected population after the epidemic period. Moreover, it should be noticed that the time required to achieve, for instance, $I = 10^{-4}$ - one infected individual for each ten thousand inhabitants, takes place sooner for higher vaccination rates. As expected, the absence of vaccination results in the worst scenario. These conclusions can be drawn for all the three countries. Hence, vaccination is the only possibility to make P_h increase without increasing C . Finally, since the mean value of transmission rate from last 90 days is employed for each country and not its value at the last real data day, a slope discontinuity might occur in the curves at beginning of simulation time. This outcome, however, does not invalidate simulations predictions since oscillations in real data due to transmission rate oscillations are natural and might lead to such discontinuities.

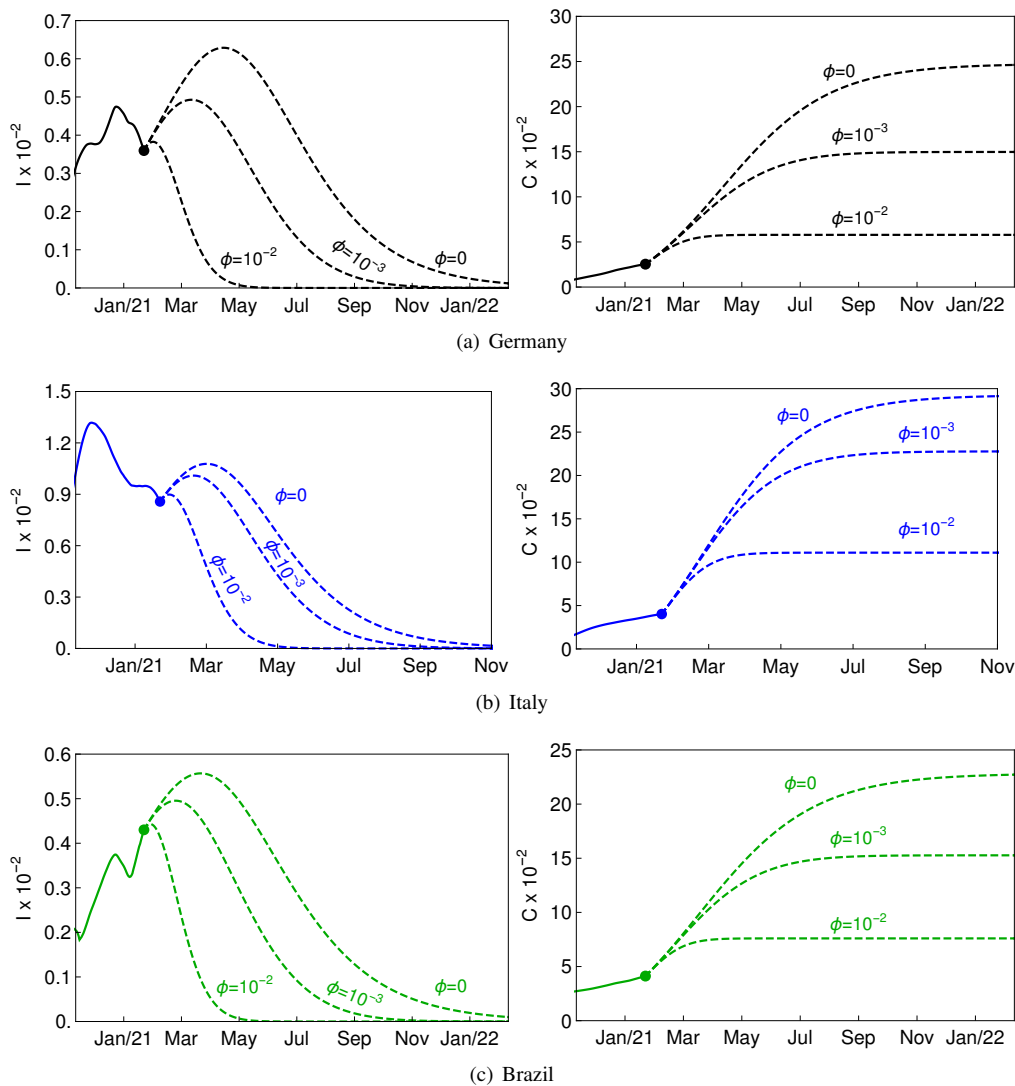


Figure 3. Effect of vaccination in Germany (a), Italy (b) and Brazil (c) countries with $\beta_{ger} = 0.227$, $\beta_{ita} = 0.230$ and $\beta_{bra} = 0.224$, respectively. The continuous lines stand for real data whose final point is marked as a solid point in the each figure. Dashed lines stand for numerical simulations from this point on for three different vaccination coefficients: $\phi = 0, 10^{-3}$ and 10^{-2} .

Regarding the simulation of the number of deaths, the death rate μ is adopted based on the average of the final 90 days of the period: 1.86% for Germany, 3.95% for Italy, and 2.68% for Brazil. Without vaccination, the total infected population reaches 24.75%, 29.27% and 22.83% in Germany, Italy and Brazil, respectively. If the vaccination is implemented with 10^{-2} rate, the number of total deaths can drop to 35%, 67% and 59% in these three countries, respectively.

Additionally, the estimated date to reach $I = 10^{-4}$ for the situations with absence of vaccination is about

February 2022 for Germany and Brazil, and November 2021 for Italy. Nevertheless, considering the vaccination coefficient $\phi = 10^{-2}$ shortens this period in several months, and $I = 10^{-4}$ is reached about April 2021 for all the three countries. Therefore, the vaccination drastically anticipates the end of a huge crisis.

5 Conclusions

This paper proposes a dynamical map to describe COVID-19 epidemics based on the classical SEIRV continuous differential equation. The discrete-time model is advantageous since it requires less computation efforts, avoiding differential equation solution, being easier to determine parameters and allowing the determination of critical scenarios from analytic tools. The infectious ratio and the herd immunization point are some useful examples, where the latter is shown to be a function of the transmission rate and the infectious average period, being independent of the mean latent period. Real data from Germany, Italy and Brazil are employed to verify the map capability to describe the COVID-19 epidemics multi-pattern, showing a good agreement. The effect of vaccination is investigated and results showed that a proper vaccination rate can dramatically reduce the total infected population and deaths. Also, for a higher vaccination coefficient, the end of the epidemics can be anticipated in several months, avoiding thus a possible huge crisis. Based on these results, it is clear that the novel map is useful for COVID-19 scenario evaluation, being an easy alternative to be employed.

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