Dynamical Evolution of COVID-19 in Italy With an Evaluation of the Size of the Asymptomatic Infective Population

Paolo Di Giamberardino, *Member, IEEE*, Daniela Iacoviello, *Member, IEEE*, Federico Papa, and Carmela Sinisgalli

***Abstract*—The present work deals with an Ordinary Differential Equation (ODE) model specifically designed to describe the COVID-19 evolution in Italy. The model is particularised on the basis of National data about the infection status of the Italian population to obtain numerical solutions that effectively reproduce the real data. Our epidemic model is a classical SEIR model that incorporates two compartments of infected subpopulations, representing diagnosed and undiagnosed individuals respectively, and an additional quarantine compartment. Possible control actions representing social, political, and medical interventions are also included. The numerical results of the proposed model identification by least square fitting are analysed and commented with special emphasis on the estimation of the number of asymptomatic infective individuals. Our fitting results are in good agreement with the epidemiological data. Short and long-term predictions on the evolution of the disease are also given.**

***Index Terms*—COVID-19, epidemic ODE model, coronavirus, epidemic spread in Italy, system control and identification.**

I. Introduction

IN January 2020, China announced the outbreak of a novel virus, now known as SARS-CoV-2, in the Wuhan region; after about two months, the whole World is still facing the problem of the fast epidemic spread, often characterised by severe health consequences and high number of deaths.

The dynamics of the contagious and of the spread from China to all the other Countries is studied introducing suitable mathematical models which are able to describe the present evolution as well as to provide possible predictions.

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The basic characteristics of the epidemic spreads can be analysed making use of simple and well known model structures already adopted for different virus diseases. From the SIR (Susceptible-Infected-Recovered classes) model [1], the specificity of the different epidemic spreads has required the introduction of additional compartments, as in the SEIR model [2], [3], with the Exposed class modelling the individuals infected but not yet infectious, or the SIRC one [4], with the Cross–immune individuals that can loose immunity and can be re–infected.

In more recent cases, further refinements in the mathematical models have been introduced to catch the specificities of each epidemic. This has been done for the measles disease [5]–[7] where, despite a vaccine does exist, the presence of immuno–depressed individuals required more specific mathematical models to include them [8]. Another relevant example is represented by the HIV/AIDS disease, where different classes in the population are required to model the social behaviours and the different stages of the disease evolution [9]–[14].

At present, the COVID-19 case represents, from a modelling point of view, a new challenge for a mathematical approach. In fact, while the known simple models are able to describe the epidemic dynamics and to give a reasonable prediction with a short time forecast, a greater effort must be devoted to determine more specific mathematical models able to describe all the classes in which the populations can be divided according to the epidemic diffusion, contagion, presence of symptoms and their level, severity of the produced illness, extent of therapies required. Examples are given in [15]–[17]. Moreover, an important issue is the inclusion in the model of all the possible intervention actions for prevention and containment of the epidemic spread, as well as the medical requirements and therapies as done in [18]. We note that the inclusion of the possible controls in the mathematical description of the initial COVID-19 outbreak is particularly important in the present case, even before the design of specific control strategies, because some social, political and medical actions are activated after the first notifications, so influencing the available epidemiological data. For this reason, the inclusion of the control actions in the epidemic model is mandatory for an effective infection dynamics modelling and for a reliable identification procedure.

In the present work, the COVID-19 outbreak in Italy is analysed and discussed by means of an ODE (Ordinary

Differential Equation) model previously introduced in [18], here adapted to the Italian case and described in Section II. In Section III, the parameter identification is performed to fit the epidemiological data of the Italian spread, provided by the National Institute of Health of Italy (ISS) [19]. The role played by some crucial factors on the numerical results is deeply analysed, with particular emphasis on one of the most uncertain term subject to several opinions, i.e. the number of asymptomatic individuals. The potential negative effects of this term on the long-term disease evolution are shown in Section III-B. Section IV is devoted to the use of the model, tuned on the Italian situation, to provide possible predictions on short and long-term evolutions. In Section V, some conclusions and future work are outlined.

II. The Epidemic Model

The proposed mathematical model is a suitable extension of the classical SEIR model describing the dynamics of an epidemic disease characterized by the presence of a not negligible incubation period (E-phase), when the individuals are infected but not yet infectious [20]. Since the present study aims to evaluate the impact of the asymptomatic infected population on the Italian epidemic spread, the model accounts for the following significant aspects: A) the presence of a quarantined population, containing people spending a precautionary period of total isolation or waiting for test, B) the distinction in the infected population between diagnosed and undiagnosed patients, and C) the presence, among the latter population, of a fraction of asymptomatic infective individuals. The assumed structure appears to be appropriate to mimic the Italian government actions related to test policy and mandatory quarantine. The included compartments also allow us to provide an explicit evaluation the size of asymptomatic undiagnosed infectives. More in details, the models includes six state variables representing the following quantities at time t:

- $S(t)$: number of susceptible individuals;
- $E(t)$: number of exposed individuals, i.e. infected that, having low viral load, are assumed unable to transmit the infection;
- $I_u(t)$: number of undiagnosed infective patients including: (i) the ones that will be always asymptomatic, or feebly symptomatic, during their whole infection period; (ii) the ones that will develop recognisable symptoms. So, in the absence of evident symptoms, they can be diagnosed only by performing a swab test;
- $I_d(t)$: number of diagnosed infective patients who are receiving medical treatments (to cure the infection or its complications). Although infective, we assume that they cannot transmit the virus since their contacts occur only with operators equipped with personal protective devices, making their contagiousness almost zero;
- $Q(t)$: number of people suspected of being infected. They are temporarily isolated and tested for positivity or simply quarantined for precautionary reasons;
- $R(t)$: number of recovered patients, healed spontaneously or after therapy.

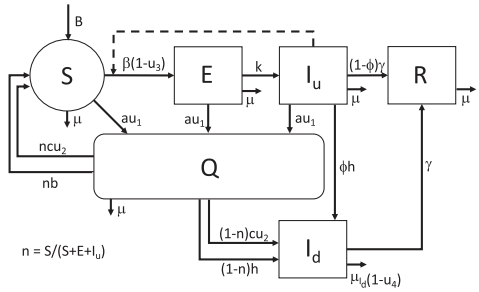

Fig. 1. Block diagram of model (1).

Accounting for the mentioned subpopulations, we describe the spread of COVID-19 in Italy by means of the following time-varying ODE system (see also the block diagram reported in Fig. 1):

$$\begin{aligned}
\dot{S}(t) &= B - \beta(1-u_3(t))S(t)I_u(t) + bnQ(t) \\
&\quad + u_2(t)cnQ(t) - au_1(t)S(t) - \mu S(t), \\
\dot{E}(t) &= \beta(1-u_3(t))S(t)I_u(t) - au_1(t)E(t) \\
&\quad - kE(t) - \mu E(t), \\
\dot{I}_u(t) &= kE(t) - au_1(t)I_u(t) - h\phi I_u(t) \\
&\quad - \gamma(1-\phi)I_u(t) - \mu I_u(t), \\
\dot{I}_d(t) &= h\phi I_u(t) + h\phi(1-n)Q(t) - \gamma I_d(t) \\
&\quad + u_2(t)c(1-n)Q(t) - \mu_{I_d}(1-u_4(t))I_d(t), \\
\dot{Q}(t) &= au_1(t)(S(t)+E(t)+I_u(t)) - bnQ(t) \\
&\quad - h\phi(1-n)Q(t) - u_2(t)cQ(t) - \mu Q(t), \\
\dot{R}(t) &= \gamma(1-\phi)I_u(t) + \gamma I_d(t) - \mu R(t),
\end{aligned} \tag{1}$$

where

$$n = \frac{S(t)}{S(t)+E(t)+I_u(t)}. \tag{2}$$

In system (1), B is the net input rate in compartment S and it accounts for newborn susceptible individuals (but also for the balance between immigration and emigration); μ is the per capita death rate owing to causes not related to the infection (natural death of the population) and it represents the loss rate from any compartment of the model except for I_d; μ_{I_d} is the per capita death rate of diagnosed patients I_d (and obviously it is $\mu_{I_d} > \mu$ because of the disease complications); β is the relative infectivity of individuals in compartment I_u and accounts for two main factors, i.e. the probability of a contagion from one infected-susceptible contact (related to the aggressiveness of the virus) and the frequency of contacts; ϕ represents the fraction of the infective population I_u that shows recognisable symptoms and, then, goes to a medical structure for isolation and therapies; k, h and γ are the per capita transition rates throughout the observed phases of the intra-host disease progression, reported in Fig. 2. In particular, (i) k describes the transition from the infected, E, to the infective phase, I_u, and it is $k = 1/\tau_i$, where τ_i is the mean

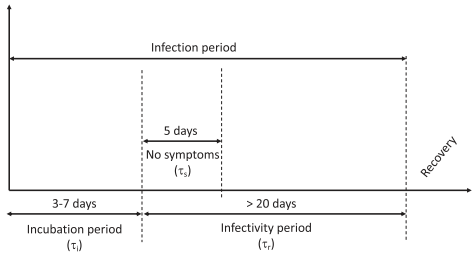

Fig. 2. Observed intra-host disease progression for COVID-19.

length of the incubation period; (ii) h refers to the transition from I_u to I_d and it is $h = 1/\tau_s$, where τ_s is the mean time elapsed until the occurrence of the first recognisable symptoms; (iii) γ models the exit from the infective compartments I_u and I_d due to recovery from the infection and, then, it is $\gamma = 1/\tau_r$ where τ_r is the mean recovery period. Then, according to the meaning of ϕ and to the disease progression, the exit rates from I_u are: ϕh, for that part of I_u that will show symptoms, and $(1-\phi)\gamma$, for the remaining part that will be always asymptomatic or feebly symptomatic. Conversely, an infective patient can exit the compartment I_d after infection recovery, as well as for the death caused by the infection. For the sake of simplicity, we assume the same recovery rate γ for both subpopulations I_u and I_d.

The time-varying variables u_1, u_2, u_3, and u_4 represent control actions (bounded between 0 and 1), modelling intervention measures adopted by the Italian government to contain the disease outbreak (from the first positive notifications). In particular, u_1 represents the action aimed to stimulate, or force, a test campaign on the population (even without any suspect of infection), or to isolate people for a precautionary period because of a suspect of infection. For the sake of simplicity and in the absence of other specific indications, we assume that this action is uniformly distributed among people in compartments S, E and I_u. Then the per capita transit rates from S, E, I_u to Q are all equal to au_1, where a represents the maximal fraction of the entire population that could reasonably be isolated and tested per day, according to the available medical resources and the government investments in buying new ones. The assumption on the fluxes entering Q produces an internal composition of the quarantined compartment that reflects the same proportions of the source populations S, E, I_u. This fact implies that the fraction n, given by Eq. (2), represents the probability of picking up a susceptible individual from Q.

The control u_2 represents the efficacy of the health system in providing the results of the performed swab samples for COVID-19 testing and, again, it depends on medical and economical constraints. The factor u_2 is used to scale the per capita exit rate c, which is the time necessary for the health structures to provide the positive/negative result of a test (i.e. $c = 1/\tau_t$, where τ_t is the mean time for a test result). Disregarding the critical aspect of false positive and false negative test results, the fraction n defined in Eq. (2) is a practical approximation of the probability of getting a negative result when a swab sample is randomly tested inside Q. Therefore, the total outflow resulting from sample testing, cQ, can be split into the portion $c(1-n)Q$ entering the diagnosed infective compartment I_d, and the portion cnQ entering the susceptible compartment S. Furthermore, b is the per capita exit rate from Q after waiting the precautionary isolation period suggested to people suspected of infection ($b = 1/\tau_q$, where τ_q is the quarantine period, usually equal to or longer than the period required for symptom emergence after the infection). So, assuming that the part nQ of the total quarantined population Q is actually susceptible, the return rate into S is bnQ. Conversely, the remaining part $(1-n)Q$, if not selected for a test, could exit Q because of the emergence of symptoms. Assuming again that only a fraction ϕ of the population $(1-n)Q$ will develop recognisable symptoms, the flux of people exiting Q to enter I_d is expressed by $h\phi(1-n)Q$.

Moreover, the control u_3 represents the effect on the relative infectivity β produced by the precautionary measurements assumed by the government to keep the health population far from the possible contagious sources. It accounts for all the government decrees introduced to limit the physical interactions among people, but also for the informative campaign for hygienic measures, TV/radio announcements, and so on.

The last control u_4 refers to the efficacy of therapies in curing side effects of COVID-19. The introduction of u_4 is intended to model the reduction of the observed value of the per capita death rate from I_d.

We finally notice that the fraction $(1-\phi)$ of asymptomatic (or feebly symptomatic) infectives in I_u not entering I_d to be cured is actually unknown. Studies reported in [21] try to evaluate such a quantity, which is of great interest since it represents the quota of undiagnosed infective population that can be circulating and then responsible for the epidemic spread.

The above model formulation has been previously proposed and discussed in particularised to the initial outbreak of the epidemic spread in Hubei, investigating its asymptotic properties in the uncontrolled case; in [18] the same model is used to provide qualitative evaluations of the impact of different control strategies on the future trend of the epidemic.

III. Assessment of the Model Parameters

The model parameters have been fixed according to a priori knowledge, coming from the literature, or have been inferred from official Italian data sources, like the Italian National Institute of Statistics (ISTAT) and the National Institute of Health of Italy (ISS). The ISS data are provided by the national Civil Protection Department and are reported on the data repository GitHub [19], which is updated daily since February 24.

At the moment of the manuscript revision, the available data were updated up to May 4. However, in the analysis of the following sections, we refer to two different notification periods: 1) a short period from February 24 up to March 23; this period includes two weeks after the first strong Italian decree limiting social contacts (March 9, 2020) and it was used for investigating the crucial role of the parameter ϕ on the disease evolution; 2) a long time interval (whole notification period) from February 24 until May 4 used for the estimation of the model parameters.

TABLE I
VALUES OF THE A PRIORI FIXED PARAMETERS

Parameters	Value	Source
B	$1.69 \cdot 10^3$ persons $\cdot$ day^{-1}	[23]
μ	$2.81 \cdot 10^{-5}$ day^{-1}	[23]
a	$5.12 \cdot 10^{-4}$	[20]
b	$6.67 \cdot 10^{-2}$ day^{-1}	[24], [16]
c	0.5 day^{-1}	[25]
k	$1.67 \cdot 10^{-1}$ day^{-1}	[15], [16]
h	$2.0 \cdot 10^{-1}$ day^{-1}	[15], [16]

TABLE II
ESTIMATED MODEL PARAMETERS OBTAINED WITH $u_3^{\max} = 0.99$

Parameters	Value	Source
β	$7.56 \cdot 10^{-9}$ persons^{-1} $\cdot$ day^{-1}	Estimated
μ_{I_d}	$1.63 \cdot 10^{-2}$ day^{-1}	Estimated
γ	$1.83 \cdot 10^{-2}$ day^{-1}	Estimated
ϕ	0.12	Estimated

A. Parameter Tuning

The parameters B and μ have been evaluated from ISTAT demographic data from 2011 up to the last available year, 2018 [22]. Concerning the per capita death rate μ, it has been fixed to the mean value over the period 2011–2018 of the ratio between the number of deaths per year and the number of Italians at the end of the same year, $\mu = 2.81 \cdot 10^{-5}$ days^{-1}. As the Italian population size can be considered constant over the period of interest, the net input rate B has been approximated by the product of the total number of Italians as of the 1st of January 2020, $It_{2020} = 60.317 \cdot 10^6$ [24], and the estimated value of μ, as follows

$$B = It_{2020} \cdot \mu \approx 1.69 \cdot 10^3 \,\text{persons} \cdot \text{day}^{-1}. \tag{3}$$

We exploited ISS epidemiological data [19] to get an indication on the maximal fraction of the population that is isolated and tested per day. So, denoting by δ_j the j-th notification day, with δ_1 representing February 24, we fixed a to the mean value of the ratio

$$\rho(\delta_j) = \frac{\#\,\text{admin. tests at } \delta_j}{It_{2020}}, \quad j = 1, 2, \ldots, \tag{4}$$

along the considered notification period. Then, two different values of a are obtained in the chosen notification intervals: $1.57 \cdot 10^{-4}$ for interval 1) and $5.12 \cdot 10^{-4}$ for interval 2). Table I reports the value of a obtained for the second period that we used for the final estimation of β, μ_{Id}, γ and ϕ (see Table II).

The per capita rates b and c, that allow people to exit the quarantine compartment Q, are fixed on the basis of the current policy adopted by the government or the local institutions. Since a precautionary quarantine period of 15 days (almost corresponding to the period required for symptoms emergence after the infection) is suggested to suspected people, we fixed $b = 1/\tau_q = 1/15$ days^{-1} [16], [23]. Moreover, we set $c = 1/\tau_t = 1/2$ days^{-1} since the mean time τ_t required for the test result is currently of almost two days, as specified by the Italian Ministry of Health [24].

Concerning the disease progression, the parameters k and h are fixed on the basis of known time constants given by the World Health Organization and confirmed by the literature [15], [16]. In particular, since an exposed individual becomes infective after nearly 3–7 days, we fixed $k = 1/\tau_i = 1/6$ days^{-1}. Similarly, since about 5 days are required from the end of the incubation period up to the first symptoms appearance, we set $h = 1/\tau_s = 1/5$ days^{-1}. On the other hand, we decided to estimate the recovery rate γ directly from the available epidemiological data.

The fixed parameter values are reported in Table I.

Concerning the relative infectivity β, the per capita death rate μ_{I_d}, the recovery rate γ and the fraction ϕ of symptomatic infectives in I_u, they are estimated by a least square fitting of the following ISS data: i) daily number of diagnosed individuals that are currently positive, ii) total number of recoveries among all diagnosed positives, iii) total number of notified deaths. Data i)-iii) can be simulated, for each notification day δ_j, by means of the following quantities coming from model (1):

i) $I_d(\delta_j)$,
ii) $\displaystyle\int_{\sigma=\delta_0}^{\sigma=\delta_j} \gamma I_d(\sigma) d\sigma$,
iii) $\displaystyle\int_{\sigma=\delta_0}^{\sigma=\delta_j} \mu_{I_d}(1 - u_4(t)) I_d(\sigma) d\sigma$,

where δ_0 is January 1.

Since the period of notification is strongly influenced by an increasing number of government restrictions but also by an increasing health risk awareness within the population, we estimated β, μ_{I_d}, γ and ϕ by accounting for rapidly increasing control actions. More in details, we assumed u_1 and u_2 linearly increasing, starting from the minimum value 0 on February 24 and achieving the maximal value 1 on March 9, in correspondence to the decrees adopted by the Italian government to force the people to stay at home and limit their social contacts. Conversely, the control action u_3 is assumed slightly increasing from February 24 to March 9 and rapidly increasing afterwards as a consequence of the mentioned government decree, reaching the saturation value $u_3^{\max}$ about two weeks after the official Italian government act. In the following sections, we considered maximal values of u_3 ranging in [0.8, 0.99]. In particular, the extreme values of u_3 are used to evaluate the influence of ϕ on the disease evolution (see Section III-B). The highest value $u_3^{\max} = 0.99$ is instead used to obtain a good data fitting of the notified positives (Section III-C). Consistently with the latest available observations, we assume that the increase of u_4 (which models the efficiency of therapies against COVID-19 side effects) is delayed with respect to the other inputs. Also, we assume that u_4 reaches the maximum value of 0.7. Such a dynamical behaviour of u_4 was suggested by the slowdown of the number of deaths shown by the data during the last notification days (see Fig. 4).

Although the available data start from February 24 (first day of notification), all the simulations reported in the following are

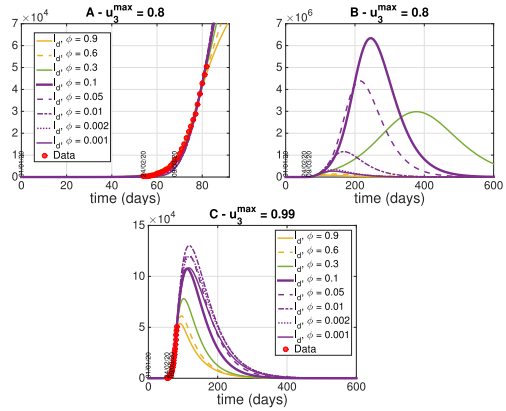

Fig. 3. Time course of diagnosed infectives I_d for different values of ϕ in [0, 1]. Panels A, B: $u_3^{\max} = 0.8$; time interval [0, 90] (panel A) and [0, 600] days (panel B). Panel C: $u_3^{\max} = 0.99$; time interval [0, 90] days. Red dots: daily number of diagnosed positives in the short interval 1) [19].

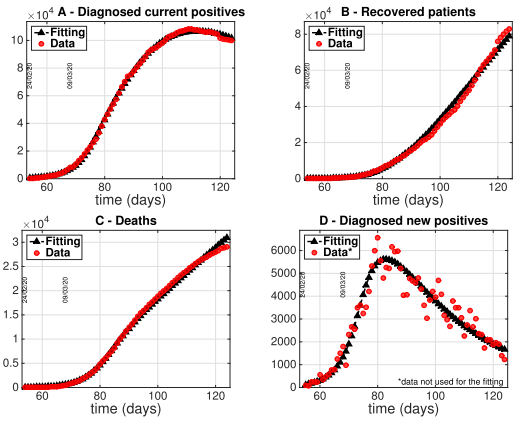

Fig. 4. Panel A: Time-course of the daily number of diagnosed positives. Panel B: Total number of diagnosed recoveries. Panel C: Total number of diagnosed deaths. Panel D: Number of daily new cases ($\int_{\sigma=\delta_j}^{\sigma=\delta_{j+1}} I_d(\sigma)d\sigma$). Red dots: ISS data [19]; data of panel D not used for the fitting. Black triangles: model prediction. Simulations obtained setting $u_3^{\max} = 0.99$.

obtained by setting the initial state value on January 1st (δ_0 =1-Jan-2020), assuming that the first infected (exposed) individual came to Italy on that day. So, the initial state is given by $S(\delta_0) = It_{2020}$, $E(\delta_0) = 1$ and $I_u(\delta_0) = I_d(\delta_0) = Q(\delta_0) = R(\delta_0) = 0$.

B. Crucial Role of the Parameter ϕ

Let us now highlight the effect of the value of the symptomatic fraction ϕ on the dynamical evolution of the epidemic. The evaluation of this effect has been made by simulating changes of ϕ in the admissible range [0, 1]. We remark that the actual value of this quantity could have a crucial impact on the long-term disease evolution, especially when not very efficient lockdown measures are accomplished. Moreover, the estimation of ϕ proved to be critical at the beginning of the outbreak, i.e. when the epidemic is increasing exponentially. The aim of the present section is to highlight the difficulty of estimating ϕ when only few initial data are available, as it was the case for interval 1) ending on March 23. At the same time, our aim is to evidence the strong impact that the parameter ϕ could have on long-term predictions. So, the results reported in this section show how an inaccurate estimation of ϕ could in principle lead to scarcely reliable epidemic predictions. The evaluation of the fraction ϕ can indeed be made more accurate implementing extensive COVID-19 test campaigns for the population screening by direct measurements, like done in a small Italian district [25]. In Section III-C, we show that ϕ can actually be identified provided that a sufficient number of data is available (e.g. notification period 2)).

To investigate how ϕ affects the future disease evolution, while analysing some critical issues of its estimation, in the present section we restrict the parameter identification on the shorter interval 1). At the beginning of the outbreak, ϕ is scarcely identifiable and it actually plays a minor role on the data fitting. Moreover, provided that β is suitably tuned, any value in [0, 1] can be chosen to obtain a quite satisfactory fit of the notified positives. Nevertheless, the long-term prediction strongly depends on the value of ϕ and completely different scenario can be obtained choosing different values. Going into the details, we performed the following trial and error procedure to simulate the effect of the variability of ϕ: (a) ϕ is fixed in [0, 1]; (b) for each fixed ϕ, an estimation of β, μ_{I_d} and γ is provided according to the epidemiological data i)-iii); (c) the impact of the value of ϕ is evaluated by inspecting the consequent disease evolution.

Fig. 3 depicts the simulated I_d course for different ϕ values in [0, 1]) and for different u_3 maximal levels (0.99, highly effective; 0.8 not very effective). Indeed, as it is clear from panel B of Fig. 3, when $u_3^{\max} = 0.8$ the peak of I_d can change remarkably depending on ϕ. The peak amounts to about 100–200 thousand of infectives either for high ϕ (let us say higher than or equal to about 0.6) or for very small ϕ (less then or equal to about 0.001), while it reaches about 6 millions of infectives when ϕ is around 0.1. Also the peak position can change considerably with the value of ϕ. The maximum time displacement of the peak is obtained for intermediate values of ϕ (around 0.3), while it is evidently shortened for ϕ high or very small. We notice that quantifying the peak of I_d is actually an important predictive aspect of the epidemic course, since it gives the maximal concomitant number of infectives showing severe symptoms and needing treatments or medical ventilation, hence representing the most urgent problem that the national health system must cope with.

The influence of ϕ is strongly reduced if a more efficient lockdown is performed, i.e. if u_3 reaches the highest value $u_3^{\max} = 0.99$. Then, the peak could vary from about 50000 to 130000 (see panel C of Fig. 3).

C. Estimation of the Model Parameters From Data Fitting

Considering all the epidemiological data on the notification period 2), from 24-Feb to 4-May, we provide an estimation of the parameters β, μ_{I_d}, γ and ϕ. The other parameters are fixed as suggested in Table I while the maximal value of the control u_3 has been fixed to 0.99. The results of the estimation are reported

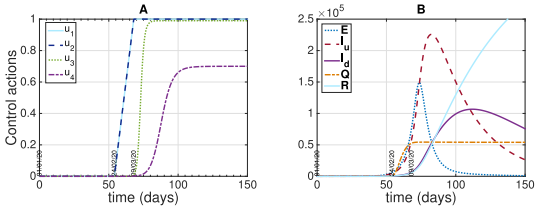

Fig. 5. Panel A: control actions used for the fitting. Panel B: time course of the state variables.

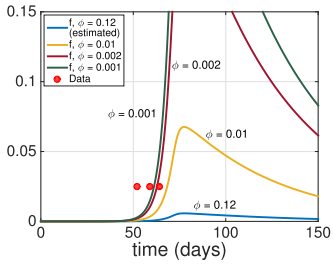

Fig. 6. Time course of $f(t)$ for different values of ϕ in [0, 1] and $u_3^{\max} = 0.99$. Red dots: data reported in the study [25]; the estimated fraction was reported at the beginning of the study, i.e. 22-Feb, after one week (29-Feb), and after almost two weeks (5-Mar).

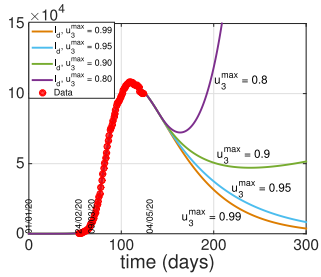

Fig. 7. Time-course of the diagnosed infectives I_d. Simulations obtained with $u_3^{\max} = 0.99$ until May 4 and with $u_3^{\max} = 0.8, 0.9, 0.95, 0.99$ from that day on.

in Table II. The related optimal curves obtained by least square fitting of the epidemiological data i)-iii) are reported in panels A-C of Fig. 4, while the model reconstruction of the daily new cases is reported in panel D of the same figure. The control actions exploited for the fitting and the time course of state variables are reported in Fig. 5.

From the estimation of ϕ given in Table II ($\phi = 0.12$) it emerges that there is approximately one symptomatic patient out of 10 infectives within I_u. We also notice that if the lockdown were not sufficiently strict and properly performed, this estimated value would represent a critical value since it could produce some millions of concomitant infectives in I_d needing medical treatments (so causing the collapse of the Italian health system). This can be deduced from Fig. 3 where the highest peak of I_d is obtained for $\phi = 0.1$, $u_3^{\max} = 0.8$.

We finally note that, in principle, the value of the critical parameter ϕ could be measured directly by means of extensive screening campaigns on the entire Italian population. An example of such a kind of campaign is reported in a recent study on the local population of the small Italian district Vò Euganeo [25]. According to that study, an extensive screening campaign was performed on the entire population of the district, starting from February 22 and collecting data during about one week. The results of the study revealed that the 2.5 % of the tested population, turned out to be positive. This value is in line with the results in [26]. Since Vò Euganeo is considered as one of the first crucial Italian foci of COVID-19, the sample cannot be assumed as representative of the entire Italian population, which probably had a lower diffusion of the virus at the time of the study and, consequently, a lower percentage of positives. Denoting by $f(t)$ the fraction of the entire Italian population that is actually positive at time t, according to the compartmental model (1), we get

$$f(t) = \frac{E(t)+I_u(t)+I_d(t)+(1-n)Q(t)}{S(t)+R(t)+E(t)+I_u(t)+I_d(t)+Q(t)}. \quad (5)$$

Fig. 6 depicts the behaviour of $f(t)$ for different values of ϕ. The lowest curve is related to the fitting case with $\phi = 0.12$, $u_3^{\max} = 0.99$ (Figs. 4, 5), while the remaining curves are model predictions obtained supposing smaller ϕ values. In Fig. 6, data from the Vò Euganeo study are also reported [25]. To account for some spreading delay in the nationwide diffusion of the epidemic with respect to the Vò Euganeo case, three different time points are displayed: the beginning of the study (February 22), one week later (February 29, the last day of the screening), and nearly two weeks later (March 5). Our prediction of the positive fraction in Italy on March 5 turns out to be approximately 20 times lower than the one of the small district. The picture also shows that to obtain a value of f close to the data [25], it would be required a ϕ not larger than 0.01.

IV. Model Predictions After May 4

The prediction of the future evolution of COVID-19 in Italy starts from May 4, that is the last notification day available at the time of the present manuscript revision, but also the first day of the lockdown relaxation in Italy. The prediction is obtained as of May 4 fixing the model parameters to the values of Tables I, II and assuming different values for $u_3^{\max}$ so to represent different effectiveness levels in the contact limitation implemented as of that day in Italy. In particular, we present three different scenarios obtained by reducing $u_3^{\max}$ from 0.99 to 0.95, 0.9 and 0.8.

The numerical simulations are reported in Fig. 7. We note that the number of positives would keep on decreasing, and the epidemic would fade away within about one year, if the so-called new phase II will be able to keep $u_3^{\max}$ sufficiently high, i.e. around 0.99-0.95. On the contrary, a more sensible reduction of $u_3^{\max}$ could produce a new increase of the diagnosed positives I_d and, in principle, a second wave of the disease if no additional restrictions were timely imposed. The lower $u_3^{\max}$ the higher the speed of the restart, and the shorter the time interval to reach the second peak. Indeed, as shown by Fig. 7, if $u_3^{\max}$ were 0.9 the second increase would be very slow and it would be quite easy to take additional restrictions to contain the situation. Conversely,

if it were $u_3^{\max} \geq 0.8$ the increase could be too sharp to allow timely restrictions. Such results highlight to what extent the current planning activity of the Italian government is crucial in identifying efficient intervention measures to safely leave the lockdown.

V. Concluding Remarks

A dynamical model specifically designed for the COVID-19 is used in this paper to describe the epidemic evolution in Italy. Different kinds of control actions (social, political, and medical) are explicitly modeled, so that it is possible to separate the intrinsic characteristics of the disease from the effects of interventions, such as isolation, quarantine and test campaigns. Some crucial parameters are identified on the basis of the Italian data. Our numerical simulations by best fitting of national epidemiological data agree rather well with available official data up to May 4. Along with interesting results for what concerns the contagious and the death rates, the most important aspect enlightened in the results is a contribution to the characterisation of the number of asymptomatic individuals, problem still open in the scientific community and of great interest to better understand the present and, more important, the future evolution of the disease. The possibility of using the model here proposed for prediction of the short and long time evolution is also illustrated showing some possible scenarios.

Some generalizations of the present formulation can be the object of our future work. As the model structure is modular, additional compartments and parameters could be included or some restrictive assumptions could be relaxed, in order to describe further epidemic aspects of COVID-19 in our country and to predict new updated scenarios.

In view of its rather general formulation, the model presented here could in principle be adapted to describe the COVID-19 epidemic in other countries.

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