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COVID-19 has forced quarantine measures in several countries across the world. These measures have proven to be effective in significantly reducing the prevalence of the virus. To date, no effective treatment or vaccine is available. In the effort of preserving both public health as well as the economical and social textures, France and Italy governments have partially released lockdown measures. Here we extrapolate the long-term behavior of the epidemics in both countries using a Susceptible-Exposed-Infected-Recovered (SEIR) model where parameters are stochastically perturbed with a log-normal distribution to handle the uncertainty in the estimates of COVID-19 prevalence and to simulate the presence of super-spreaders. Our results suggest that uncertainties in both parameters and initial conditions rapidly propagate in the model and can result in different outcomes of the epidemics leading or not to a second wave of infections. Furthermore, the presence of super-spreaders adds instability to the dynamics, making the control of the epidemics more difficult. Using actual knowledge, asymptotic estimates of COVID-19 prevalence can fluctuate of order of ten millions units in both countries.

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## I. LEAD PARAGRAPH

**COVID-19 pandemic poses serious threats to public health as well as economic and social stability of many countries. A real time extrapolation of the evolution of COVID-19 epidemics is challenging both for the nonlinearities undermining the dynamics and the ignorance of the initial conditions, i.e., the number of actual infected individuals. Here we focus on France and Italy, which have partially released initial lockdown measures. The goal is to explore sensitivity of COVID-19 epidemic evolution to the release of lockdown measures using dynamical (Susceptible-Exposed-Infected-Recovered) stochastic models. We show that the large uncertainties arising from both poor data quality and inadequate estimations of model parameters (incubation, infection and recovery rates) propagate to long term extrapolations of infections counts. Nonetheless, distinct scenarios can be clearly identified, showing either a second wave or a quasi-linear increase of total infections.**

## II. INTRODUCTION

SARS-CoV-2 is a zoonotic virus of the coronavirus family[1] emerged in Wuhan (China) at the end of 2019[2] and rapidly propagated across the world until it has been declared a pandemic by the World Health Organization on March 11, 2020[3]. SARS-CoV-2 virus provokes an infectious disease known as COVID-19 that has an incredibly large spectrum of symptoms or none depending on the age, health status and the immune defenses of each individuals[4]. SARS-CoV-2 causes potentially life-threatening form of pneumonia and/or cardiac injuries in a non-negligible patients fraction[5,6].

To date, no treatment of vaccine is available for COVID-19[7]. Efforts to contain the virus and to not overwhelm intensive care facilities are based on quarantine measures which have proven very effective in several countries[8–10]. These predictions were based on statistical and epidemiological models that, despite their simplicity, well captured the growths of the epidemics[11–13]. Despite this, lockdown measures entail enormous economical, social and psychological costs. Recent estimates of the International Monetary Fund recently announced a global recession that will drag global GDP lower by 3% in 2020, although continuously developing and changing as well as significantly depending country-by-country[14]. More than 20 million people have lost their job in United States[15] and a large percentage of Italians have developed psychological disturbances

such as insomnia or anxiety due to the strict lockdown measures[16]. Those measures have been taken on the basis of epidemics models, which are fitted on the available data[17]. In Italy, initial lockdown measures started on February 23rd for 11 municipalities in both Lombardia and Veneto which were identified as the two main Italian clusters. After the initial spread of the epidemics into different regions all Italian territory was placed into a quarantine on March 9th, with total lockdown measures including all commercial activities (apart supermarkets and pharmacies), non-essential businesses and industries, and severe restrictions to transports and movements of people at regional, national, and extra-national levels[18]. People were asked to stay at home or near for sporting activities and dog hygiene (within 200 m from home), to reduce as much as possible their movements (only for food shopping and care reasons), and smart-working was especially encouraged in both public and private administrations and companies. At the early stages of epidemics intensive cares were almost saturated with a peak of 4000 people on April 3rd and a peak of hospitalisations of 30000 on April 4th, significantly reducing after these dates, reaching 1500 and 17000, respectively, at the beginning of phase 2 on May 4th, and 750 and 1000 on May 18th when lockdown measures on commercial activities were relaxed. These numbers, continuously declining during the next days and weeks, confirmed the benefit of lockdown measures[19].
Alarmed by the exponential growth of new infections and the saturation of the intensive care beds, also France introduced strict lockdown measures on March 17th[20]. The French government restricted travels to food shopping, care and work when teleworking was not possible, outings near home for individual sporting activity and/or dog hygiene, and it imposed the closure of the Schengen area borders as well as the postponement of the second round of municipal elections. The number of patients in intensive care, like the number of hospitalisations overall peaked in early April and then started to decline, showing the benefits of lockdown measures. On Monday, May 11th, France began a gradual easing of COVID-19 lockdown measures[21]. Trips of up to 100 kilometres from home are allowed without justification, as will gatherings of up to 10 people. Longer trips will still be allowed only for work or for compelling family reasons, as justified by a signed form. Guiding the government's plans for easing the lockdown is the division of the country into two zones, green and red, based on health indicators. Paris region (Ile de France), with about 12 millions inhabitants is flagged, to date, as an orange zone.

In both countries, the release of lockdown measures has been authorised by authorities after consulting scientific committees which were monitoring the behavior of the curve of infections using COVID-19 data. Those data are provided daily, following a request of the WHO. To date,

the WHO guidelines require countries to report, at each day $t$, the total number of infected patients $I(t)$ as well as the number of deaths $D(t)$. Large uncertainties have been documented in the count of $I(t)$[22]. Whereas in the early stage of the epidemic several countries tested asymptomatic individuals to track back the infection chain, recent policies to estimate $I(t)$ have changed. Most of the western countries have previously tested only patients displaying severe SARS-CoV-2 symptoms[23]. In an effort of tracking all the chain of infections, Italy and France are now testing all individuals displaying COVID-19 symptoms and those who had strict contacts with infected individuals. The importance of tracking asymptomatic patients has been proven in a recent study[24]. The authors have estimated that an enormous part of total infections were undocumented (80% to 90%) and that those undetected infections were the source for 79% of documented cases in China. Tracking strategies have proven effective in supporting actions to reduce the rate of new infections, without the need of lockdown measures, as in South Korea[25].

The goal of this paper is to explore possible future epidemics scenarios of the long term behavior of the COVID-19 epidemic[26] but taking into account the role of uncertainties in both the parameters value and the infection counts to investigate different outcomes of the epidemics leading or not to a second wave of infections. To this purpose we use a stochastic Susceptible-Exposed-Infected-Recovered (SEIR) model[27] which consists in a set of ordinary differential equations where control parameters are time-dependent and modelled via a stochastic process. This allows to mimic the dependence on control parameters on some additional/external factors as super-spreaders[28] and the enforcing/relaxing of confinement measures[27]. As for the classical SEIR models[29] the population is divided into four compartmental groups, i.e., Susceptible, Exposed, Infected, and Recovered individuals. The stochastic SEIR model shows that long-term extrapolation is sensitive to both the initial conditions and the value of control parameters[27], with asymptotic estimates fluctuating on the order of ten millions units in both countries, leading or not a second wave of infections. This sensitivity arising from both poor data quality and inadequate estimations of model parameters has been also recently investigated by means of a statistical model based on a generalized logistic distribution[30,31]. The paper is organised as follows: in Section III we discuss the various sources of data for COVID-19 and their shortcomings, and then we discuss in detail the SEIR model and its statistical modelling. In Section IV we discuss the results focusing on the statistical sensitivity of the modelling, and apply it to data from France and Italy. We finish, in Section V, with some remarks and point out some limitations of our study.

## III. DATA AND MODELLING

### A. Data

This paper relies on data stored into the Visual Dashboard repository of the Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE) supported by ESRI Living Atlas Team and the Johns Hopkins University Applied Physics Lab (JHU APL). Data can be freely accessed and downloaded at `https://systems.jhu.edu/research/public-health/ncov/`, and refers to the confirmed cases by means of a laboratory test[3]. Nevertheless there are some inconsistencies between countries due to different protocols in testing patients (suspected symptoms, tracing-back procedures, wide range tests)[32,33], as well as, to local management of health infrastructures and institutions. As an example due to the regional-level system of Italian healthcare data are collected at a regional level and then reported to the National level via the Protezione Civile transferring them to WHO. These processes could be affected by some inconsistencies and delays[34], especially during the most critical phase of the epidemic diffusion that could introduce errors and biases into the daily data. These incongruities mostly affected the period between February 23rd and March 10th, particularly regarding the counts of deaths due to a protocol change from the Italian Ministry of Health[35]. A similar situation occurs in France where the initial testing strategy was based only on detecting those individuals experiencing severe COVID19 symptoms[36]. In the post lockdown phase, France has extended its testing capacity to asymptomatic individuals who have been in contact with infected patients[37].

### B. A Stochastic epidemiological Susceptible-Exposed-Infected-Recovered model

One of the most used epidemiological models is the so-called Susceptible-Exposed-Infected-Recovered (SEIR) model belonging to the class of compartmental models[29]. It assumes that the total population $N$ can be divided into four classes of individuals that are susceptible $S$, exposed $E$, infected $I$, and recovered or dead $R$ (assumed to be not susceptible to reinfection). The model is based on the following assumptions:

1. the total population does not vary in time, e.g., $dN/dt = dS/dt + dE/dt + dI/dt + dR/dt = 0, \ \forall t \geq 0$;

2. susceptible individuals become infected that then can only recover or die, e.g., $S \rightarrow I \rightarrow R$;

3. exposed individuals $E$ encountered an infected person but are not yet themselves infectious;

4. recovered or died individuals $R$ are forever immune. Although the longevity of the antibody response is still unknown, it is known that antibodies to other coronaviruses wane over time typically after 52 weeks from the onset of symptoms[38]. Concerning SARS-CoV-2 it has been shown that antibody levels may remain over the course of almost 2-3 months[39]. Nevertheless, not only antibodies are important for investigating immunity but also other immune cells named T cells play a crucial role for long-term immunity[40,41]. Recently Kissler et al.[42] found that the duration of protective immunity may last 6 to 12 months. Our assumption seems therefore justified at least to study the dynamics of a second wave. We remark also that the basic SEIR model does not distinguish between immune and deaths and it cannot therefore be used to estimate the number of deceased people from COVID-19.

Thus, the model reads as

$$\frac{dS}{dt} = -\lambda S(t)I(t), \tag{1}$$

$$\frac{dE}{dt} = \lambda S(t)I(t) - \alpha E(t), \tag{2}$$

$$\frac{dI}{dt} = \alpha E(t) - \gamma I(t), \tag{3}$$

$$\frac{dR}{dt} = \gamma I(t), \tag{4}$$

where $\gamma > 0$ is the recovery/death rate, $\lambda = \lambda_0/S(0) > 0$ is the infection rate rescaled by the initial number of susceptible individuals $S(0)$, and $\alpha$ is the inverse of the incubation period. Its discrete version can be simply obtained via an Euler Scheme as

$$S(t+1) = S(t) - \lambda S(t)I(t), \tag{5}$$

$$E(t+1) = (1-\alpha)E(t) + \lambda S(t)I(t), \tag{6}$$

$$I(t+1) = (1-\gamma)I(t) + \alpha E(t), \tag{7}$$

$$R(t+1) = R(t) + \gamma I(t). \tag{8}$$

in which we fixed $dt = 1$ day that is the time resolution of COVID-19 counts. By means of $\gamma$ and $\lambda_0$ the model also allows to derived the so-called $R_0$ parameter, e.g., $R_0 = \lambda_0/\gamma$, representing the average reproduction number of the virus. It is related to the number of cases that can potentially (on average) be caused from an infected individual during its infectious period ($\tau_{inf} = \gamma^{-1}$).

Early estimates in Wuhan[43] on January 2020 reported $R_0 = 2.68^{2.86}_{2.47}$ which lead to $\gamma = \gamma_0 = 0.37$ fixing $\lambda \simeq 1$ as in[44] and a 95% confidence level range for the incubation period between 2 and 11 days[45]. Here we set $\alpha = \alpha_0 = 0.27$ (corresponding to an incubation period between 3 and 4 days). This value has been extracted as median period by [45]. However, the $R_0$ parameter as well as models parameters $\lambda$, $\gamma$, and $\alpha$ can vary in time during the epidemics due to different factors as the possible presence of the so-called super-spreaders[28], intrinsic changes of the SARS-CoV-2 features, lockdown measures, asymptomatic individuals who are not tracked out, counting procedures and protocols, and so on[46]. The fact that all the time-scales considered for the parameters are larger than one day also justifies the use of the discrete version of the model in Eqs. 5-8.

To deal with uncertainties in long-term extrapolations and with the time-dependency of control parameters a stochastic approach could provide new insights in modeling epidemics[47–49], especially when epidemics show a wide range of spatial and temporal variability [50–52]. However, instead of investigating how to get a realistic behavior by stochastically perturbing control parameters, here we investigate how uncertainties into the final counts $C(t)$ are controlled by model parameters[27]. Thus, we use a stochastic version of the SEIR model in which the set of control parameters $\kappa \in \{\alpha, \gamma, \lambda\}$ are extracted at each timestep from random distributions. In the ODE model (Eqs 1-4) the introduction of stochastic terms corresponds to replacing $\{\alpha, \gamma, \lambda\}$ with $\{\alpha(t), \gamma(t), \lambda(t)\}$ and adding three more differential equations of the type:

$$\frac{d\kappa}{dt} = -\kappa(t) + \kappa_0 + \varsigma_\kappa \xi(t), \tag{9}$$

where $\kappa_0 \in \{\alpha_0, \gamma_0, \lambda_0\}$, $\xi(t)$ is a random number extracted from a normal distribution for $\alpha, \gamma$ and from a log-normal distribution for $\lambda$ (see below). The stochastic model therefore reads as:

$$dS = -\lambda(t)S(t)I(t)dt, \tag{10}$$

$$dE = [\lambda(t)S(t)I(t) - \alpha(t)E(t)]dt, \tag{11}$$

$$dI = [\alpha(t)E(t) - \gamma I(t)]dt, \tag{12}$$

$$dR = \gamma(t)I(t)dt, \tag{13}$$

$$d\lambda = \lambda_0 dt + \varsigma_\lambda dW(t), \tag{14}$$

$$d\alpha = \alpha_0 dt + \varsigma_\alpha dW(t), \tag{15}$$

$$d\gamma = \gamma_0 dt + \varsigma_\gamma dW(t), \tag{16}$$

where $dW(t) = \xi(t)dt$ is the differential form of the Brownian motion. In order to test the stability of our model integrated with the Euler scheme (see MATLAB code in the Appendix), we perform 30 realisations of Eqs 10-16 with the aforementioned parameters and initial conditions $S(1) = 67 \cdot 10^6$ (French population), $I(1) = 1$, $E(1) = R(1) = 0$. We vary $dt$ in the range $0.1 < dt < 2$. Results are displayed in Figure 1 in terms of daily infections $I(t)$. They show the typical bell-shaped curve of an epidemic wave. We get high stability of the integration when $dt \leq 1$. For larger values, the epidemic peak is first delayed ($dt = 1.5$) and the model diverges (not shown) for $dt = 2$. In the following, we decide to stick to $dt = 1$, which will be convenient to compare our results with those released by the national health agencies as in both the countries data are provided on a daily basis.

With the choice of $dt = 1$ day, one trivially gets that Eq. 9 is equivalent to sampling $\alpha(t) \in \mathcal{N}(\alpha_0, \varsigma_\alpha^2; t)$, $\gamma(t) \in \mathcal{N}(\gamma_0, \varsigma_\gamma^2; t)$ and

$$\log(\lambda(t)) \in \mathcal{N}(\log(\lambda_0 - \sigma^2/2), \sigma; t). \tag{17}$$

In this way we can introduce instantaneous daily discrete jumps (e.g., take into account daily uncertainties) in the control parameters to properly model detection errors on infection counts, appropriately described through a discrete process[53] rather than a continuous one[54]. For $\alpha$ and $\gamma$ we follow[27] and allow for Gaussian fluctuations of the parameters, with intensity $\varsigma_\alpha = 0.2\alpha_0$ and $\varsigma_\gamma = 0.2\gamma_0$. These fluctuations simulate the range of uncertainties obtained in previous studies for the incubation time and the recovery time and discussed in[27]. With respect to[27], we model the infection rate $\lambda(t)$ using a log-normal distribution[55] to take into account the possible presence of super-spreaders, namely individuals who can infect quickly a large number of susceptible people by having several strict social interactions[56]. Super-spreaders can be modelled by introducing heavy right tails for the distribution of $\lambda$. The location and the scale parameters chosen in Eq. 17 ensures that the mean of the distribution does not change, while $\sigma$ is modified to explore super-spreaders influence. In the following, we will only consider three cases:i) $\sigma = 0.2$ for which the log-normal distribution tends to be symmetric and the fluctuations of $\lambda$ are quasi-Gaussian around $\lambda_0$, ii) $\sigma = 0.4$ which models the effect of some possible super-spreaders and $\sigma = 0.6$ where several super-spreaders may be active at the same time.

## IV. RESULTS

### A. Model validation: first wave

We begin this section by validating the SEIR stochastic model on the first wave of infections. We have therefore to chose the initial conditions, and then introduce the lockdown measures in the parameters.

*a. France*

In France, the first documented case of COVID-19 infections goes back to December 27th, 2019. Doctors at a hospital in the northern suburbs of Paris retested samples from patients between December 2nd, 2019, and January 16th, 2020. Of the 14 patient samples retested, one sample, from a 42-year-old man came back positive[57]. As initial condition for the SEIR model, we therefore set $I(t=1)=1$ and $t=1$ corresponds to December 27th, 2019. We then use $R_0 = 2.68^{2.86}_{2.47}$ which lead to $\gamma = 0.37$ fixing $\lambda_0 \simeq 1$. Strict lockdown measures are introduced at $t=80$ (i.e., March 17th, 2020). First wave modelling results are shown in Figure 2. Figure 2a) shows the modelled value of $R_0$. During confinement, we reduce the value of $\lambda_0$ by a factor 1/4. We base this new infection rate on the mobility data for France during confinement, which have shown a drop by $\sim 75\%$ according to the INSERM report #11[58]. The resulting confinement $R_0 \simeq 0.75$, with an error in the range of values compatible with that published by the Pasteur Institute[59], for all values of $\sigma$ of the log-normal distribution of $\lambda$ introduced (Eq. 17). The cumulative number of infections is shown in Figure 2b) and shows, on average, between 6 and 8 millions people have been infected by SARS-CoV-2 in France, depending on whether super-spreaders effects are taken into account via heavy tails in the distribution of $\lambda$. The uncertainty range is extremely large, according to the error propagation given by the stochastic fluctuations of the parameters (see[27] for explanations). It extends from few hundred thousands individuals up to 15 millions. The error range is larger when super-spreaders are modelled. The average is however close to the value proposed by the authors in [60], who estimate a prevalence of $\sim 6\%$ of COVID-19 in the French population. Another realistic feature of the model is the presence of an asymmetric behavior of the right tail of daily infections distributions (Figure 2c) that has also been observed in real COVID-19 published data[61].

*b. Italy*

For Italy, the first suspect COVID-19 case goes back to December 22nd, 2019, a 41-year-old woman who could only be tested positive for SARS-CoV-2 antibodies in April 2020[62]. As initial

condition we therefore set $I(t=1)=1$ and $t=1$ corresponds to December 22nd, 2019. As for France we use $R_0 = 2.68^{2.86}_{2.47}$ leading to $\gamma = 0.37$ if fixing $\lambda_0 \simeq 1$. A first semi-lockdown was set in Italy on March 9th, 2020 ($t=78$) and enforced on March 22nd, 2020 ($t=89$). To simulate these two-steps lockdown we again base our reduction in $R_0$ on the mobility data for Italy which show for the first part of the confinement a reduction of about 50 % and a similar reduction to France (75%) for the strict lockdown phase. Figure 3 shows the results for the first wave. The initial condition on susceptible individuals is fixed to $S(1) = 6.0 \cdot 10^7$ corresponding to the estimate of the Italian population. A clear difference emerges with respect to the case of France in the behavior of $R_0$ which shows an intermediate reduction near $t=80$, corresponding to March 11th, 2020, to $R_0 \simeq 1.4$ before reaching the final value of $R_0 \simeq 0.7$. This sort of "step" into the $R_0$ time behavior corresponds to the time interval between semi- and full-lockdown measures, whose efficiency significantly increases after March 24th, 2020, also corresponding to the peak value of infections. This is confirmed by looking at daily infections distributions (Figure 3c) that shows a peak value near March 24th, 2020, also observed in real COVID-19 data[30]. Note that, as for France, the magnitude of the fluctuations depends on the presence of super-spreaders. The cumulative number of infections (Figure 3b) shows that, on average, almost 10 millions people have been infected by SARS-CoV-2 in Italy, ranging between few hundred thousands up to 15 millions due to the the error propagation by the stochastic fluctuations of model parameters (see[27] for explanations), with the range depending on the presence of super-spreaders. Nevertheless the wide range of uncertainty the average value is close to the value estimated from a team of experts of the Imperial College London according to which the 9.6% of Italian population has been infected, with a 95% confidence level ranging between 3.2% and 26%[63]. These estimates correspond to cumulative infections of $\sim$6 millions, ranging from $\sim$2 and $\sim$16 millions, well in agreement with our model and other statistical estimates[64].

## B. Future epidemics scenarios

After lockdown measures are released, for both countries, we model three different scenarios: a first one where all restrictions are lifted (back to normality), a second one where strict distancing measures are taken and a third one where the population remains mostly confined (partial lockdown).

*a. France*

Results for France are shown in Figure 4. From top to bottom panels we increase $\sigma$ of the log-normal distribution (Eq. 17) to model the presence of super-spreaders. Lockdown is released at $t = 136$, corresponding to May 11th, 2020. The back to normality (red) scenario clearly shows a second wave of infections peaking in summer (early July) and forcing group immunity in the French population. The distancing measures (green) scenario, corresponding to a reduction of the mobility of about 50%, leads to a second wave as intense as the first wave, but longer, at the end of August. As in the previous scenario, the distancing measures scenario allows to reach a group immunity in France. A third partial lockdown scenario is modelled (blue). This latter scenario simulates an $R_0 \simeq 1$, that can be achieved by imposing strict distancing measures, partial lockdowns in cities with active clusters and contact tracking. It results in a linear modest increase of the total number of infections that does not produce a proper wave of infections. As in the first wave modelling, large uncertainties are also present in future scenarios although the three distinct behaviors clearly appear. Finally, the presence of super spreaders may introduce an additional difficulties in controlling partial lockdown scenarios. By comparing Figure 4b) and h) we observe that super-spreaders can trigger an important growth of infections during positive fluctuations of $R_0$ although its mean value is kept, by construction, constant. Another important effect of super-spreaders is to increase the uncertainty on the infection counts: error bars for $\sigma = 0.6$ (Figure 4g,h,i) are two times wider than those for $\sigma = 0.2$ (Figure 4a,b,c).

*b. Italy*

Figure 5 shows the results for modeling future epidemic scenarios for Italy. The first relaxation of lockdown measures started at $t = 131$, corresponding to May 4th, 2020, while strict measures were finally released at $t = 146$, corresponding to May 18th, 2020. The back to normality (red) scenario moves towards a second wave of infections whose peak occurs at $t = 193$, corresponding to July 4th, 2020, exactly three months after initial lockdown measures were released (May 4th, 2020). This would lead the so-called herd immunity for the whole Italian population (see Figure 5b), with a peak of daily infections near 5 millions of people (Figure 5c), and $R_0$ re-approaching the initial value ($R_0 = 2.68$). The distancing measures (green) scenario produces a second wave mostly similar, in terms of intensity, as the first wave, but occurring at $t = 246$, e.g., August 26th, 2020. This scenario will lead to 40 millions infected people, spanning between 25 and 55 millions, thus producing a group immunity in Italy. A third scenario is modelled in which partial lockdown measures are taken (blue). This latter scenario leads to a more controlled evolution of cumula-

tive infections which still remain practically unchanged with respect to the first wave cumulative number. It has been obtained by simulating an $R_0 \simeq 1$, resulting from strict distancing measures and reduced mobility, and does not produce a proper wave of infections. However, all scenarios are clearly characterized by a wide range of uncertainties, although producing three well distinct behaviors in both cumulative and daily infections. The same conclusions made for France apply to Italy when it comes to the role of super-spreaders.

## C. Phase Diagrams

In the previous section we have seen that increasing $R_0$ above 1 can or not produce a second wave of infections and introduce also a time delay in the appearance of a second wave of infections. We now analyse this effect in a complete phase diagram fashion. Phase diagrams are a standard tool used in statistical physics to visualize allowed and forbidden states for selected variables of complex systems and they have already been used in epidemiology[65]. Phase diagrams will help us to visualize for which values of $R_0$ we will observe a second wave of infections. Figures 6-7 show the phase diagrams for France and for Italy, respectively. Panels a,b) show results for $\sigma = 0.2$, c,d) for $\sigma = 0.4$ and e,f) for $\sigma = 0.6$. The diagrams are built in terms of ensemble averages of number of infections per day $I(t)$ versus the average value of $R_0$ after the confinement (panels a), and the errors (represented as standard deviation of the average $I(t)$ over the 30 realisations) are shown in panels b. First we note that despite some small differences in the delay of the COVID-19 second wave of infections peak, the diagrams are very similar. In order to avoid a second wave, $R_0$ could fluctuate on values even slightly larger than one only if super-spreaders are not included. If super-spreaders are active, even small fluctuations of $R_0 > 1$ can trigger a second wave. Furthermore, for $1.5 < R_0 < 2$, the second wave is delayed in Autumn or Winter 2020/2021 months. The uncertainty follows the same behavior as the average and it peaks when the number of daily infections is maximum. This means that the ability to control the outcome of the epidemics is significantly reduced if $R_0$ is too high. The addition of super-spreaders also enhances the uncertainty in the infection counts, inducing large fluctuations which might be difficult to control with partial lockdown measures.

## V. DISCUSSION

France and Italy have faced a long phase of lockdown with severe restrictions in mobility and social contacts. They have managed to reduce the number of daily COVID-19 infections drastically and released almost simultaneously lockdown measures. This paper addresses the possible future scenarios of COVID-19 infections in those countries by using one of the simplest possible model capable to reproduce the first wave of infections and to take into account uncertainties, namely a stochastic SEIR model with fluctuating parameters.

We have first verified that the model is capable to reproduce the behavior of the first wave of infections and provide an estimate of COVID-19 prevalence that is coherent with a-posteriori estimates of the prevalence of the virus. The introduction of stochasticity accounts for the large uncertainties in both the initial conditions as well as the fluctuations in the basic reproduction number $R_0$ originating from changes in virus characteristics, mobility or misapplication in confinement measures. 30 realisations of the model have been produced and they show very different COVID-19 prevalence after the first wave. The range goes from thousands of infected to tens of millions of infections in both countries. Average values are compatible with those found in other studies[60,63] whose aim was to estimate the prevalence of the virus. Nevertheless, we would like to stress that the corresponding number of infected people that was detected in France and Italy during the first wave was, according to the official released data, around 200 thousand people. This discrepancy mostly comes from undetected cases, that can be a number many times bigger than the detected cases. The lower bound provided by the error-bars of the realisations of the stochastic SEIR models is therefore a limit for how many COVID-19 cases occurred in reality and it is at least as big as the number of detected cases for that period, for which data are available, plus the number of undetected cases, which can only be estimated.

Then, we have modelled future epidemics scenarios by choosing specific fluctuating behaviors for $R_0$ and performing again 30 realisations of the stochastic SEIR model. Despite the very large uncertainties, distinct scenarios clearly appear from the noise. In particular, they suggest that a second wave can be avoided even with $R_0$ values slightly larger than one. This means that actual distancing measures which include the use of surgical masks, the reduction in mobility and the active contact tracking can be effective in avoiding a second peak of infections without the need

of imposing further strict lockdown measures. The analysis of phase diagrams show that there is a sharp transition between observing or not a second wave of infections when the value of $R_0$ is larger than 1 and that the exact value depends on the presence or not of super-spreaders. Moreover, the models show that the higher $R_0$, the lower the ability to control the number of infections in the epidemics. Similarly, if super-spreaders are particularly active, the infection counts are difficult to control and a second wave can be triggered more easily.

This model has also evident deficiencies in representing the COVID-19 infections. First of all, the choice of the initial conditions is conditioned by our ignorance on the diffusion of the virus in France and Italy in December 2019. Furthermore, we are unable to verify on an extensive dataset the outcome of the first wave: on one side antibodies blood tests have still a lower reliability[66] and on the other they have not been applied on an extensive number of individuals to get reliable estimates. On top of the data-driven limitations, we have those introduced by the use of compartment models, as there are geographic, social and age differences in the spread of the COVID-19 disease in both countries[21]. Furthermore, we also assume that fluctuations on the parameters of the SEIR model are Gaussian (for the incubation and recovery rate) or log-normal (for the infection rate), in order to simulate heavy tailed distributions[61,67] however the underling (skewed) distribution is unknown. Another interesting research pathway is related to include the different psychological perception on the need of distancing measures depending, e.g. from the media coverage of the COVID-19 epidemics[68,69]. We would like to remark however that, to overcome these limitations, one would need to fit more complex models and introduce additional parameters which can, at the present stage, barely be inferred by the data.

Our choice to stick to the stochastic SEIR model is indeed driven by few factors: i) despite its simplicity our model allows for the possibility of modeling realistically the uncertainties with the stochastic fluctuations instead of adding new parameters whose inference may affect the results; ii) despite regional differences, national infections counts during the first wave have followed, for both France and Italy, a sigmoid function that could be modeled with the mean field SEIR model introduced in the present study. iii) unlike the UK or the US, both France and Italy have dealt with the epidemics with a national centralized approach: whenever intensive care facilities were saturating in one region, patients' transfers have been operated to other national hospitals. iv) lockdown measures have been applied uniformly on all the countries. v) introducing a spatial model also introduces several additional parameters namely the interaction (exchange) coefficients among re-

gions (at least 20x20 coefficients for Italy and 13x13 coefficients for France). The deficiencies of the COVID-19 testing capacities in many regions of both countries during the first phase prevent from having a reasonable estimation of the parameters, introducing uncontrollable errors. However, we acknowledge that, while the above mentioned factors were homogeneous across the different regions of France and Italy, the evolution of the epidemic was very heterogeneous between different regions and even departments in Italy and France, with certain departments having undergone saturation of the health care system (e.g. Lombardy and Bergamo in particular in Italy, or Strasburg and the Grand-Est region in France), and others remaining almost untouched by the epidemic. Moreover, geographical differences in Italy are present also in the measures after the removal of the lockdown, with masks being compulsory only in certain areas. There are therefore also several good reasons to go beyond the presented mean field SEIR models whenever high quality data will be available at a regional level.

This study can be applied to other countries, and this is why we publish the code of our analysis alongside with the paper. To date, Northern Europe, UK, US and other American countries are still facing the first wave of infections, so that future scenarios cannot be devised with the same clarity as those outlined in this study for France and Italy. Other studies are currently focusing on the second-wave modeling with different approaches. In[70–72], deterministic SIR models are employed to forecast the second wave of COVID-19 infections for Washtenaw County, Iran and France. These models are extended to include other variables which represent explicitly the number of patients taken to hospital or to intensive care units. However, their deterministic nature does not allow for propagating the uncertainty in the variables and therefore to get an estimate of the fluctuations in the number of hospitalized patients. In future studies, it could be interesting to add the kind stochasticity suggested in the present study, to the extended SIR models proposed by[70–72] in order to estimate range of uncertainties for hospitals and intensive care units.

## VI. ACKNOWLEDGMENTS

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## VII. DATA AVAILABILITY

The data that support the findings of this study are openly available in https://systems.jhu.edu/research/public-health/ncov/, maintained by Johns Hopkins University Center for Systems Science. All figures scripts are available at https://mycore.core-cloud.net/index.php/s/x8Wm4YyDVqEF2Xa.

## VIII. APPENDIX A: NUMERICAL CODE

```
% This appendix contains the MATLAB code used to perform
% the analysis contained in the paper via a stochastic
% SEIR model

%%VARIABLES INITIALIZATION
S=zeros(1,tmax);
E=zeros(1,tmax);
I=zeros(1,tmax);
R=zeros(1,tmax);
C=zeros(1,tmax);
%%PARAMETERS
%\lambda Infection Rate is equal to 1
lambda0=1;
% alpha is the inverse of the incubation period (1/t_incubation)
alpha0=0.27;
% R0 is equal to 2.68
R0=2.68;
% gamma is the inverse of the mean infectious period
gamma0=lambda0./R0;

% INITIAL CONDITIONS
S(1)=67000000;
I(1)=1;
```

```
R(1)=0;
T(1)=0;
C(1)=0;
gamma(1)=gamma0;
alpha(1)=alpha0;
lambda(1)=lambda0./S(1);

% EULER SCHEME FOR THE SDEs
for t=1:1:tmax./dt

R0(t+1)=lambda(t)./gamma0;
T(t+1)=t.*dt^2;
S(t+1)=S(t)-(lambda(t)*S(t)*I(t)).*dt;
E(t+1)=E(t)+((lambda(t)*S(t)*I(t))-alpha(t)*E(t)).*dt;
I(t+1)=I(t) +(alpha(t)*E(t)  -gamma(t)*I(t)).*dt;
R(t+1)=R(t)+(gamma(t)*I(t)).*dt;
lambda(t+1)=(lambda0*dt+lambda0./5Ty*randn*sqrt(dt))./S(1);
gamma(t+1)=gamma0*dt+gamma0./5*randn*sqrt(dt);
alpha(t+1)=alpha0*dt+alpha0./5*randn*sqrt(dt);

%cumulative infected
C(t+1)=gamma0.*sum(I);

end
```

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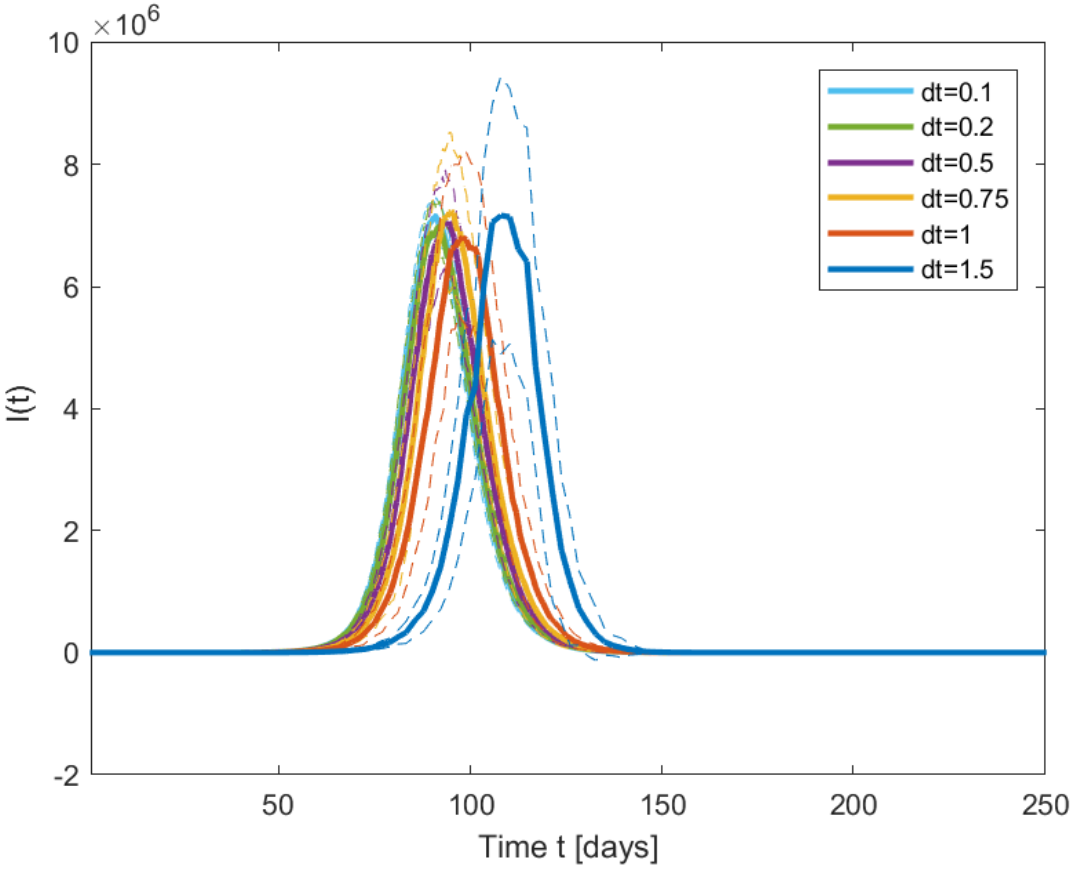


FIG. 1. Test of stability for the Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for France (Eqs 10-16) with $\lambda = 1./S(0)$, $\alpha = 0.27$, $\gamma = 0.37$. Initial conditions are set to $I(1) = 1$, $S(1) = 6.7 \cdot 10^7$ (French Population), $E(1) = R(1) = 0$. The SEIR model is integrated with different $0.1 < dt < 1.5$. Solid lines show the average for 30 realisations of the SEIR stochatic models, dotted lines extend to one standard deviation of the mean.

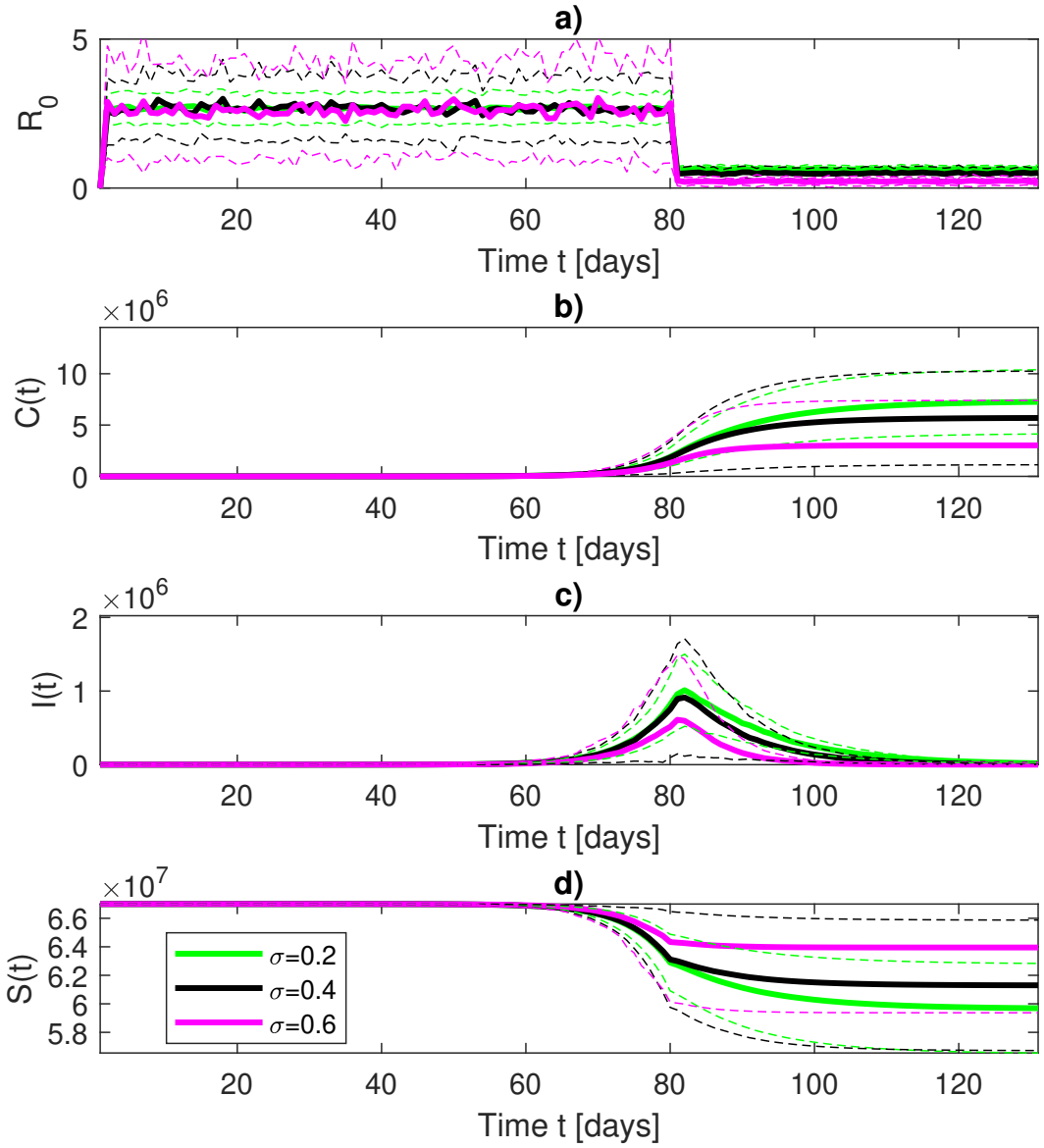


FIG. 2. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for France (Eqs 10-16) with $\lambda = 1./S(0)$, $\alpha = 0.27$, $\gamma = 0.37$, $dt = 1$. Initial conditions are set to $I(1) = 1$, $S(1) = 6.7 \cdot 10^7$, $E(1) = R(1) = 0$. $t = 1$ corresponds to Dec 27, 2019. Confinement is introduced at $t = 78$ (Mar 17, 2020). Time evolution for a) the basic reproduction number $R_0$, (b) the cumulative number of infections $C(t)$, (c) the daily infected individuals $I(t)$, (d) the number of susceptible individuals $S(t)$. Solid lines show the average for 30 realisations of the SEIR stochatic models, shadings extend to one standard deviation of the mean. Colors represent different values of $\sigma$ in the lognormal distribution of $\lambda$ (Eq. 17 from light to heavy tails).

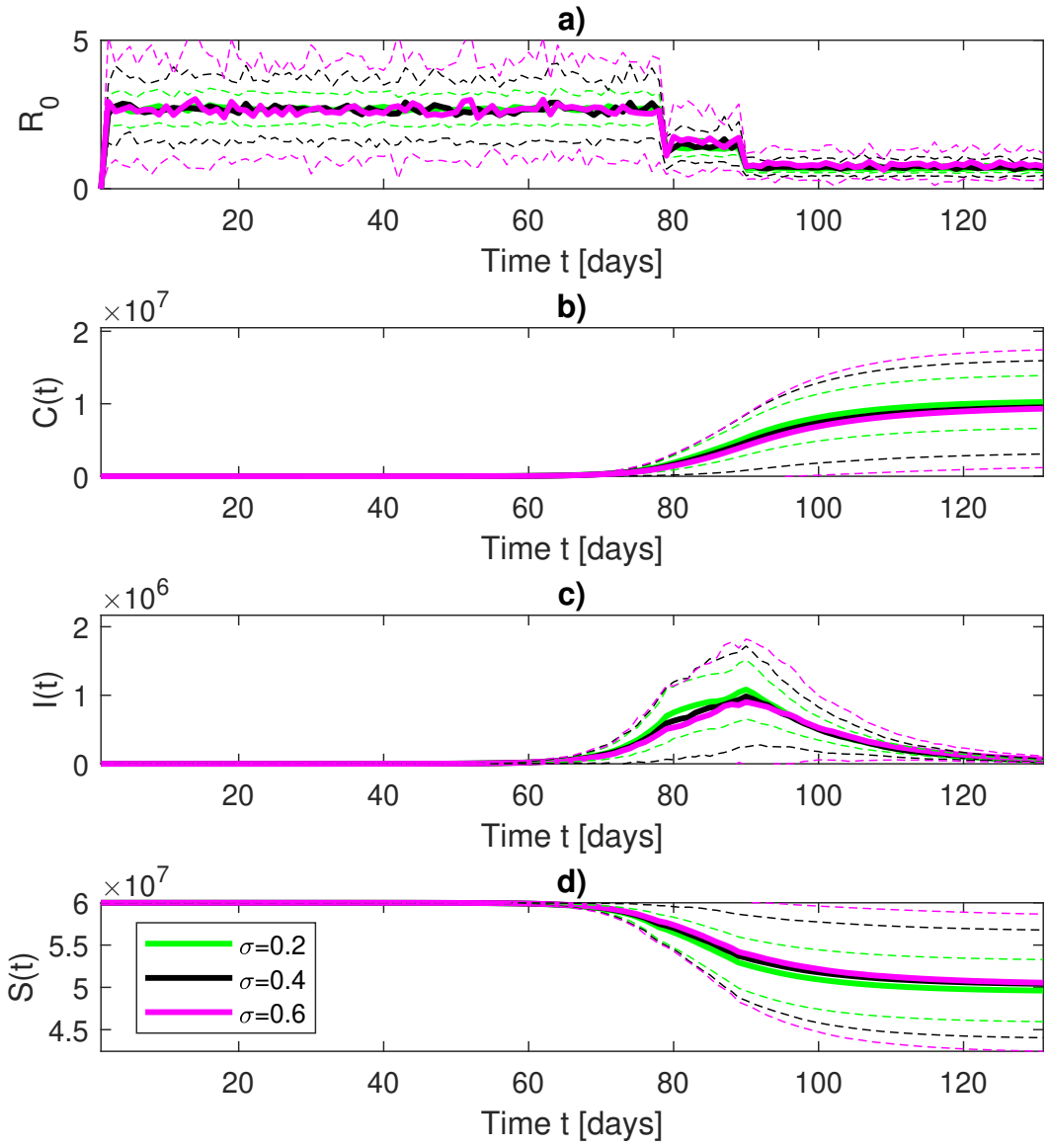


FIG. 3. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for Italy (Eqs 10-16) with $\lambda = 1./S(0)$, $\alpha = 0.27$, $\gamma = 0.37$, $dt = 1$. Initial conditions are set to $I(1) = 1$, $S(1) = 6.0 \cdot 10^7$, $E(1) = R(1) = 0$. $t = 1$ corresponds to Dec 22, 2019. First confinement measures are introduced at $t = 80$ (Mar 9, 2020) and enforced at $t = 89$ (Mar 22, 2020). Time evolution for a) the basic reproduction number $R_0$, (b) the cumulative number of infections $C(t)$, (c) the daily infected individuals $I(t)$, (d) the number of susceptible individuals $S(t)$. Solid lines show the average for 30 realisations of the SEIR stochatic models, shadings extend to one standard deviation of the mean. Colors represent different values of $\sigma$ in the lognormal distribution of $\lambda$ (Eq. 17 from light to heavy tails).

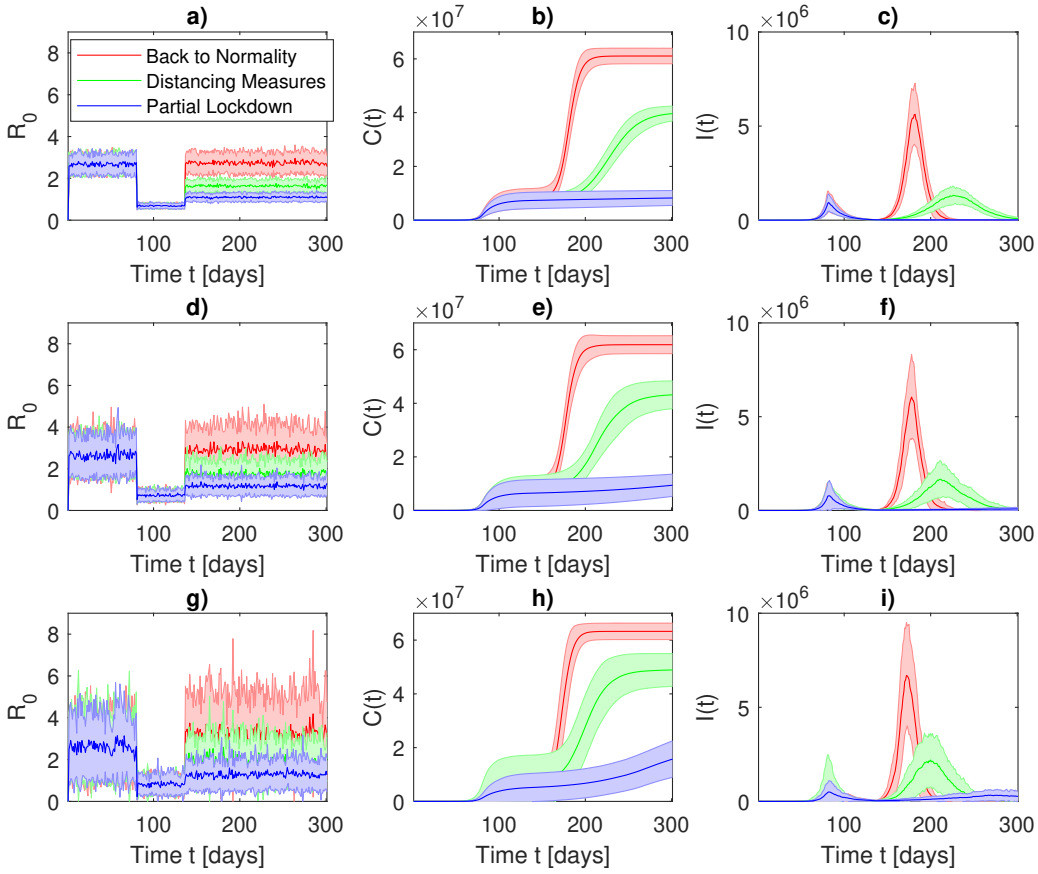


FIG. 4. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in France. Initial conditions are set as in Figure 2. After the confinement is released ($t = 136$, May 11, 2020) three scenarios are modelled: back to normality (red), distancing measures (green), partial lockdown (blue). a,d,g) Time evolution for the basic reproduction number $R_0$, b,e,h) Time evolution for the cumulative number of infections $C(t)$, c,f,i) Time evolution for the daily infected individuals $I(t)$. a,b,c) $\sigma = 0.2$ in, d,e,f) $\sigma = 0.4$, g,h,i) $\sigma = 0.6$ in the lognormal distribution for $\lambda$ (Eq. 17). Solid lines show the average for 30 realisations of the SEIR stochatic models, shadings extend to one standard deviations of the mean.

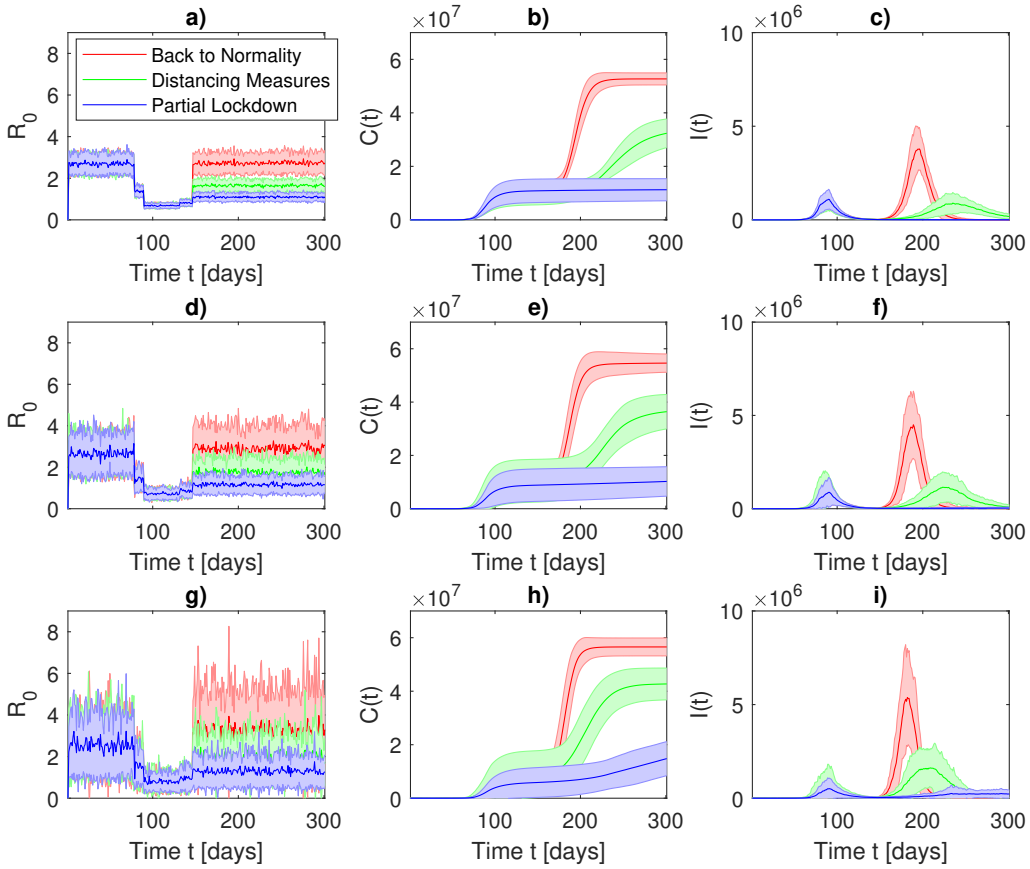


FIG. 5. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in Italy. Initial conditions are set as in Figure 3. After the confinement is released ($t = 131$, May 4, 2020 and $t = 146$, May 18, 2020) three scenarios are modelled: back to normality (red), distancing measures (green), partial lockdown (blue). a,d,g) Time evolution for the basic reproduction number $R_0$, b,e,h) Time evolution for the cumulative number of infections $C(t)$, c,f,i) Time evolution for the daily infected individuals $I(t)$. a,b,c) $\sigma = 0.2$ in, d,e,f) $\sigma = 0.4$, g,h,i) $\sigma = 0.6$ in the lognormal distribution for $\lambda$ (Eq. 17). Solid lines show the average for 30 realisations of the SEIR stochatic models, shadings extend to one standard deviations of the mean.

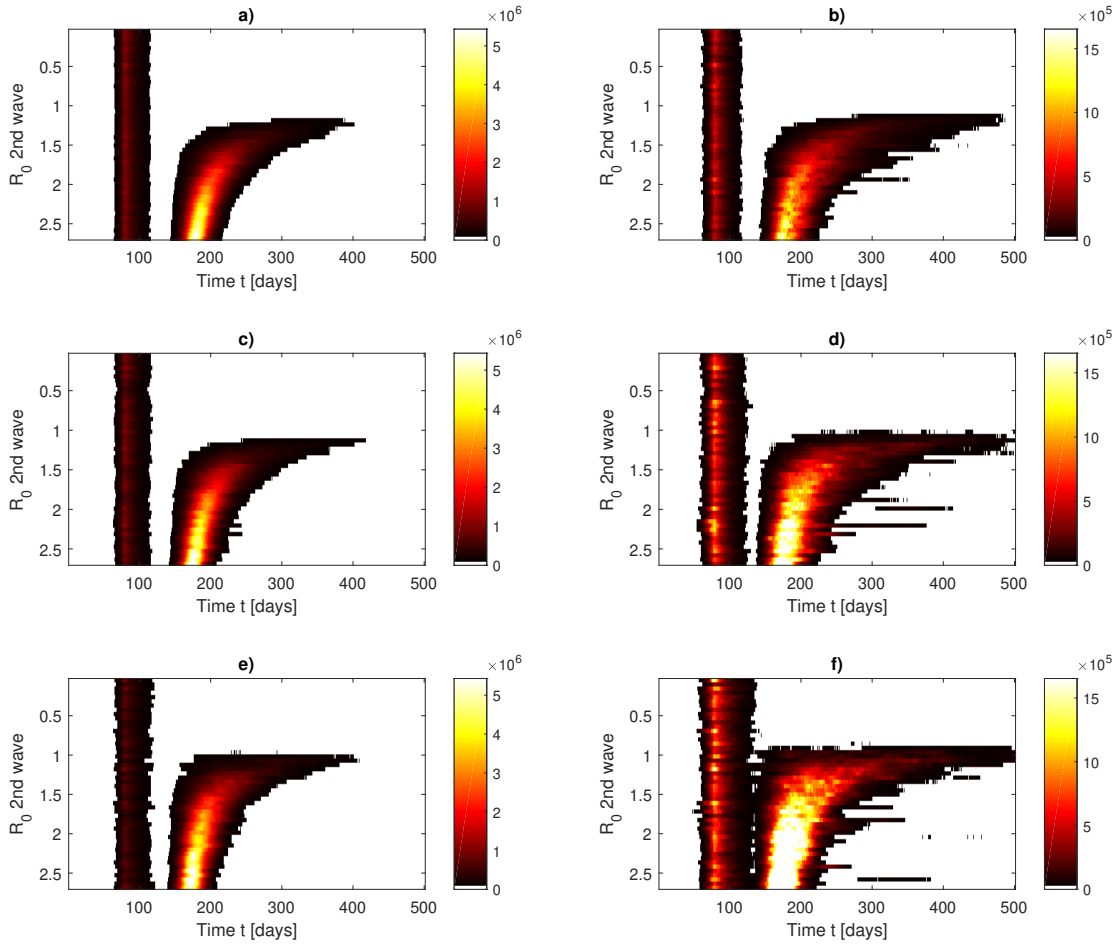


FIG. 6. Phase diagram for the Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in France. Initial conditions are set as in Figure 2. After the confinement is released ($t = 136$, May 11, 2020) all possible $R_0$ are modelled. a,c,e) Average of daily infected individuals $I(t)$. b,d,f) Standard deviation of daily infected individuals. Diagrams are obtained using 30 realisations of the SEIR models. a,b) $\sigma = 0.2$ in, c,d) $\sigma = 0.4$, e,f) $\sigma = 0.6$ in the lognormal distribution for $\lambda$ (Eq. 17).

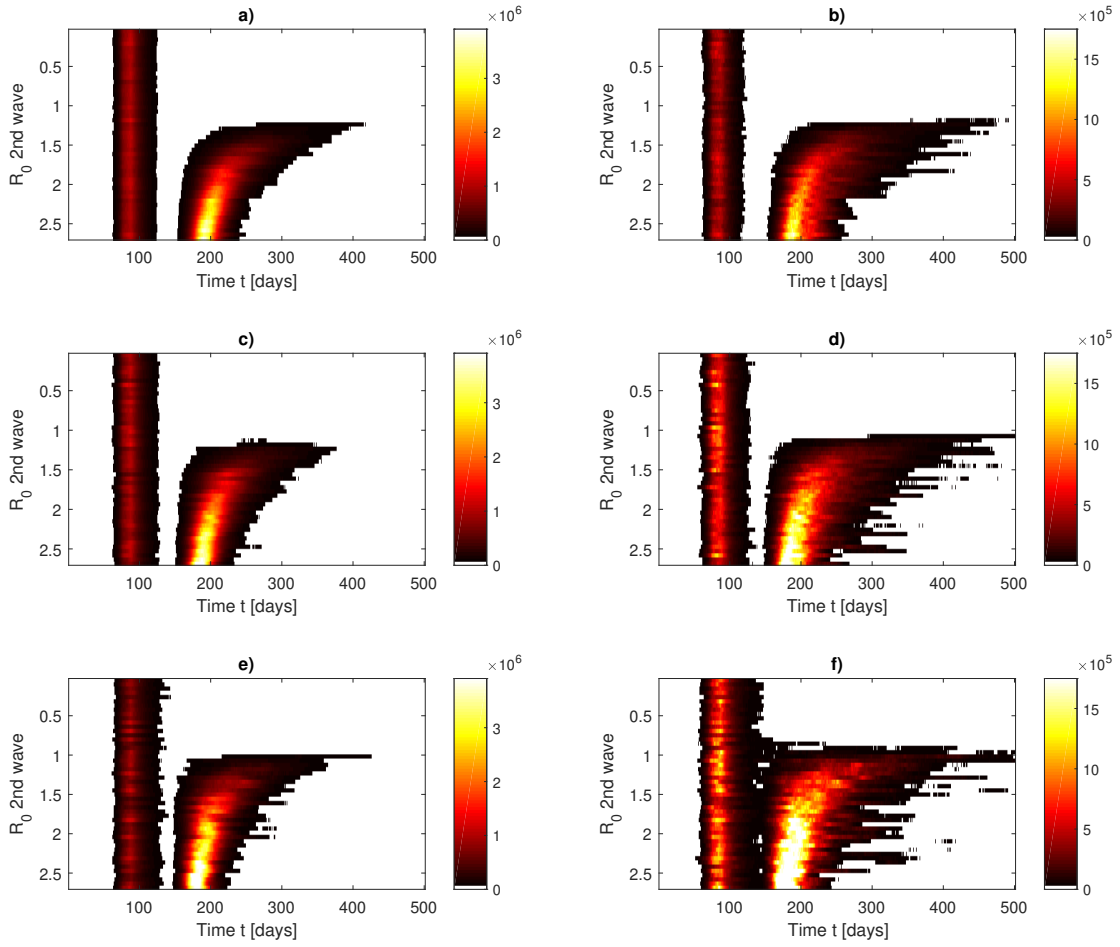


FIG. 7. Phase diagram for the Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in Italy. Initial conditions are set as in Figure 3. After the confinement is released ($t = 131$, May 4, 2020 and then $t = 146$ May 18, 2020) all possible $R_0$ are modelled. a,c,e) Average of daily infected individuals $I(t)$. b,d,f) Standard deviation of daily infected individuals. Diagrams are obtained using 30 realisations of the SEIR models. a,b) $\sigma = 0.2$ in, c,d) $\sigma = 0.4$, e,f) $\sigma = 0.6$ in the lognormal distribution for $\lambda$ (Eq. 17).