

# Modelling the second wave of COVID-19 infections in France and Italy via a Stochastic SEIR model 2

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<sup>2</sup> Stochastic SEIR model

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COVID-19 has forced quarantine measures in several countries across the world. These 14 measures have proven to be effective in significantly reducing the prevalence of the virus. 15 To date, no effective treatment or vaccine is available. In the effort of preserving both 16 public health as well as the economical and social textures, France and Italy governments 17 have partially released lockdown measures. Here we extrapolate the long-term behav-18 ior of the epidemics in both countries using a Susceptible-Exposed-Infected-Recovered 19 (SEIR) model where parameters are stochastically perturbed with a log-normal distribu-20 tion to handle the uncertainty in the estimates of COVID-19 prevalence and to simulate 21 the presence of super-spreaders. Our results suggest that uncertainties in both parameters 22 and initial conditions rapidly propagate in the model and can result in different outcomes 23 of the epidemics leading or not to a second wave of infections. Furthermore, the presence 24 of super-spreaders add instability to the dynamics, making the Using actual knowledge, 25 asymptotic estimates of COVID-19 prevalence can fluctuate of order of ten millions units 26 in both countries. 27

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#### 28 I. LEAD PARAGRAPH

COVID-19 pandemic poses serious threats to public health as well as economic and so-29 cial stability of many countries. A real time extrapolation of the evolution of COVID-19 30 epidemics is challenging both for the nonlinearities undermining the dynamics and the ig-31 norance of the initial conditions, i.e., the number of actual infected individuals. Here we 32 focus on France and Italy, which have partially released initial lockdown measures. The 33 goal is to explore sensitivity of COVID-19 epidemic evolution to the release of lockdown 34 measures using dynamical (Susceptible-Exposed-Infected-Recovered) stochastic models. We 35 show that the large uncertainties arising from both poor data quality and inadequate estima-36 tions of model parameters (incubation, infection and recovery rates) propagate to long term 37 extrapolations of infections counts. Nonetheless, distinct scenarios can be clearly identified, 38 showing either a second wave or a quasi-linear increase of total infections. 39

## 40 II. INTRODUCTION

SARS-CoV-2 is a zoonotic virus of the coronavirus family<sup>1</sup> emerged in Wuhan (China) at the end of 2019<sup>2</sup> and rapidly propagated across the world until it has been declared a pandemic by the World Health Organization on March 11, 2020<sup>3</sup>. 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<sup>4</sup>. SARS-CoV-2 causes potentially life-threatening form of pneumonia and/or cardiac injuries in a non-negligible patients fraction<sup>5,6</sup>.

To date, no treatment of vaccine is available for COVID-19<sup>7</sup>. Efforts to contain the virus and 48 to not overwhelm intensive care facilities are based on quarantine measures which have proven 49 very effective in several countries<sup>8–10</sup>. Despite this, lockdown measures entail enormous econom-50 ical, social and psychological costs. Recent estimates of the International Monetary Fund recently 51 announced a global recession that will drag global GDP lower by 3% in 2020, although contin-52 uously developing and changing as well as significantly depending country-by-country<sup>11</sup>. More 53 than 20 million people have lost their job in United States<sup>12</sup> and a large percentage of Italians 54 have developed psychological disturbances such as insomnia or anxiety due to the strict lockdown 55 measures<sup>13</sup>. Those measures have been taken on the basis of epidemics models, which are fitted 56

on the available data<sup>14</sup>. In Italy, initial lockdown measures started on February 23rd for 11 mu-57 nicipalities in both Lombardia and Veneto which were identified as the two main Italian clusters. 58 After the initial spread of the epidemics into different regions all Italian territory was placed into a 59 quarantine on March 9th, with total lockdown measures including all commercial activities (apart 60 supermarkets and pharmacies), non-essential businesses and industries, and severe restrictions to 61 transports and movements of people at regional, national, and extra-national levels<sup>15</sup>. People were 62 asked to stay at home or near for sporting activities and dog hygiene (within 200 m from home), 63 to reduce as much as possible their movements (only for food shopping and care reasons), and 64 smart-working was especially encouraged in both public and private administrations and compa-65 nies. At the early stages of epidemics intensive cares were almost saturated with a peak of 4000 66 people on April 3rd and a peak of hospitalisations of 30000 on April 4th, significantly reducing 67 after these dates, reaching 1500 and 17000, respectively, at the beginning of phase 2 on May 4th, 68 and 750 and 1000 on May 18th when lockdown measures on commercial activities were relaxed. 69 These numbers, continuously declining during the next days and weeks, confirmed the benefit of 70 lockdown measures<sup>16</sup>. 71

Alarmed by the exponential growth of new infections and the saturation of the intensive care beds, 72 also France introduced strict lockdown measures on March 17th<sup>17</sup>. The French government re-73 stricted travels to food shopping, care and work when teleworking was not possible, outings near 74 home for individual sporting activity and/or dog hygiene, and it imposed the closure of the Schen-75 gen area borders as well as the postponement of the second round of municipal elections. The 76 number of patients in intensive care, like the number of hospitalisations overall peaked in early 77 April and then started to decline, showing the benefits of lockdown measures. On Monday, May 78 11th, France began a gradual easing of COVID-19 lockdown measures<sup>18</sup>. Trips of up to 100 kilo-79 metres from home are allowed without justification, as will gatherings of up to 10 people. Longer 80 trips will still be allowed only for work or for compelling family reasons, as justified by a signed 81 form. Guiding the government's plans for easing the lockdown is the division of the country into 82 two zones, green and red, based on health indicators. Paris region (Ile de France), with about 12 83 millions inhabitants is flagged, to date, as an orange zone. 84

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 89 of  $I(t)^{19}$ . 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 91 the western countries have previously tested only patients displaying severe SARS-CoV-2 symp-92 toms<sup>20</sup>. In an effort of tracking all the chain of infections, Italy and France are now testing all 93 individuals displaying COVID-19 symptoms and those who had strict contacts with infected indi-94 viduals. The importance of tracking asymptomatic patients has been proven in a recent study<sup>21</sup>. 95 The authors have estimated that an enormous part of total infections were undocumented (80% to 96 90%) and that those undetected infections were the source for 79% of documented cases in China. 97 Tracking strategies have proven effective in supporting actions to reduce the rate of new infections, ٩p without the need of lockdown measures, as in South Korea<sup>22</sup>. 99

The goal of this paper is to explore possible future epidemics scenarios of the long term behav-100 ior of the COVID-19 epidemic<sup>23</sup> but taking into account the role of uncertainties in both the pa-101 rameters value and the infection counts to investigate different outcomes of the epidemics leading 102 or not to a second wave of infections. To this purpose we use a stochastic Susceptible-Exposed-103 Infected-Recovered (SEIR) model<sup>24</sup> which consist in a set of ordinary differential equations where 104 control parameters are time-dependent modelled via a stochastic process. This allows to mimic the 105 dependence on control parameters on some additional/external factors as super-spreaders<sup>25</sup> and the 106 enforcing/relaxing of confinement measures<sup>24</sup>. As for the classical SEIR models<sup>26</sup> the population 107 is divided into four compartmental groups, i.e., Susceptible, Exposed, Infected, and Recovered 108 individuals. The stochastic SEIR model shows that long-term extrapolation is sensitive to both the 109 initial conditions and the value of control parameters<sup>24</sup>, with asymptotic estimates fluctuating on 110 the order of ten millions units in both countries, leading or not a second wave of infections. This 111 sensitivity arising from both poor data quality and inadequate estimations of model parameters 112 has been also recently investigated by means of a statistical model based on a generalized logistic 113 distribution<sup>27,28</sup>. The paper is organised as follows: in Section III we discuss the various sources 114 of data for COVID-19 and their shortcomings, and then we discuss in detail the SEIR model and 115 its statistical modelling. In Section IV we discuss the results focusing on the statistical sensitivity 116 of the modelling, and apply it to data from France and Italy. We finish, in Section V, with some 117 remarks and point out some limitations of our study. 118

#### 119 III. DATA AND MODELLING

#### 120 A. Data

This paper relies on data stored into the Visual Dashboard repository of the Johns Hopkins Uni-121 versity Center for Systems Science and Engineering (JHU CSSE) supported by ESRI Living Atlas 122 Team and the Johns Hopkins University Applied Physics Lab (JHU APL). Data can be freely 123 accessed and downloaded at https://systems.jhu.edu/research/public-health/ncov/, 124 and refers to the confirmed cases by means of a laboratory test<sup>3</sup>. Nevertheless there are some 125 inconsistencies between countries due to different protocols in testing patients (suspected symp-126 toms, tracing-back procedures, wide range tests)<sup>29,30</sup>, as well as, to local management of health 127 infrastructures and institutions. As an example due to the regional-level system of Italian health-128 care data are collected at a regional level and then reported to the National level via the Protezione 129 Civile transferring them to WHO. These processes could be affected by some inconsistencies and 130 delays<sup>31</sup>, especially during the most critical phase of the epidemic diffusion that could introduce 131 errors and biases into the daily data. These incongruities mostly affected the period between Febru-132 ary 23rd and March 10th, particularly regarding the counts of deaths due to a protocol change from 133 the Italian Ministry of Health<sup>32</sup>. A similar situation occurs in France where the initial testing strat-134 egy was based only on detecting those individuals experiencing severe COVID19 symptoms<sup>33</sup>. 135 In the post lockdown phase, France has extended its testing capacity to asymptomatic individuals 136 who have been in contact with infected patients $^{34}$ . 137

# 138 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<sup>26</sup>. 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 =145 0,  $\forall t \ge 0$ ;

<sup>146</sup> 2. susceptible individuals become infected that then can only recover or die, e.g.,  $S \rightarrow I \rightarrow R$ ;

<sup>147</sup> 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 148 response is still unknown, it is known that antibodies to other coronaviruses wane over time 149 typically after 52 weeks from the onset of symptoms<sup>35</sup>. Concerning SARS-CoV-2 it has 150 been shown that antibody levels may remain over the course of almost 2-3 months<sup>36</sup>. Never-151 theless, not only antibodies are important for investigating immunity but also other immune 152 cells named T cells play a crucial role for long-term immunity<sup>37,38</sup>. Recently Kissler et al.<sup>39</sup> 153 found that the duration of protective immunity may last 6 to 12 months. Our assumption 154 seems therefore justified at least to study the dynamics of a second wave. 155

<sup>156</sup> Thus, the model reads as

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

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

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

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

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

 $S(t+1) = S(t) - \lambda S(t)I(t), \qquad (5)$ 

165 
$$E(t+1) = (1-\alpha)E(t) + \lambda S(t)I(t),$$
 (6)

166 
$$I(t+1) = (1-\gamma)I(t) + \alpha E(t),$$
 (7)

167 
$$R(t+1) = R(t) + \gamma I(t).$$
 (8)

<sup>168</sup> in which we fixed dt = 1 day that is the time resolution of COVID-19 counts. By means of  $\gamma$  and <sup>169</sup>  $\lambda_0$  the model also allows to derived the so-called  $R_0$  parameter, e.g.,  $R_0 = \lambda_0 / \gamma$ , representing the <sup>170</sup> average reproduction number of the virus. It is related to the number of cases that can potentially <sup>171</sup> (on average) caused from an infected individual during its infectious period ( $\tau_{inf} = \gamma^{-1}$ ). Early <sup>172</sup> estimates in Wuhan<sup>40</sup> on January 2020 reported  $R_0 = 2.68^{2.86}_{2.47}$  which lead to  $\gamma = 0.37$  fixing  $\lambda \simeq 1$ <sup>173</sup> as in<sup>41</sup> and a 95% confidence level range for the incubation period between 2 and 11 days<sup>42</sup>. 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<sup>25</sup>, intrinsic changes of the SARS-CoV-2 features, lockdown measures, asymptomatic individuals who are not tracked out, counting procedures and protocols, and so on<sup>43</sup>. 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 180 parameters a stochastic approach could provide new insights in modeling epidemics<sup>44-46</sup>, espe-181 cially when epidemics show a wide range of spatial and temporal variability <sup>47–49</sup>. However, 182 instead of investigating how to get a realistic behavior by stochastically perturbing control pa-183 rameters, here we investigate how uncertainties into the final counts C(t) are controlled by model 184 parameters<sup>24</sup>. Thus, we use a stochastic version of the SEIR model in which the set of control 185 parameters  $\{\alpha, \gamma\lambda\}$  are extracted at each timestep from random distributions. Specifically we set 186  $\alpha(t) \in \mathcal{N}(\alpha_0, \varsigma^2_{\alpha}; t), \, \gamma(t) \in \mathcal{N}(\gamma_0, \varsigma^2_{\gamma}; t)$  and 187

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$$\log(\lambda(t)) \in \mathcal{N}(\log(\lambda_0 - \sigma^2/2), \sigma; t).$$
(9)

In this way we can introduce instantaneous daily discrete jumps (e.g., take into account daily 189 uncertainties) in the control parameters to properly model detection errors on infection counts, 190 appropriately described through a discrete process<sup>50</sup> than a continuous one<sup>51</sup>. For  $\alpha$  and  $\gamma$  we 191 follow<sup>24</sup> and allows for Gaussian fluctuations of the parameters, with intensity  $\zeta_{\alpha}=0.2\alpha_0$  and 192  $\varsigma_{\gamma} = 0.2\gamma_0$ . These fluctuations simulates the range of uncertainties obtained in previous studies 193 for the incubation time and the recovery time and discussed in<sup>24</sup>. With respect to<sup>24</sup>, we model the 194 infection rate  $\lambda(t)$  using a log-normal distribution<sup>52</sup> to take into account the possible presence of 195 super-spreaders, namely individuals who can infect quickly a large number of susceptible people 196 by having several strict social interactions<sup>53</sup>. Super-spreaders can be modelled by introducing 197 heavy right tails for the distribution of  $\lambda$ . The location and the scale parameters chosen in Eq. 9 198 ensures that the mean of the distribution does not change, while  $\sigma$  is modified to explore super-199 spreaders influence. In the following, we will only consider three cases:i)  $\sigma = 0.2$  for which the 200 log-normal distribution tends to be symmetric and the fluctuations of  $\lambda$  are quasi-Gaussian around 201  $\lambda_0$ , ii)  $\sigma=0.4$  which models the effect of some possible super-spreaders and  $\sigma=0.6$  where 202 several super-spreaders may be active at the same time. 203

#### 204 IV. RESULTS

### 205 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.

209 a. France

In France, the first documented case of COVID-19 infections goes back to December 27th, 2019. 210 Doctors at a hospital in the northern suburbs of Paris retested samples from patients between De-211 cember 2nd, 2019, and January 16th, 2020. Of the 14 patient samples retested, one sample, from 212 a 42-year-old man came back positive<sup>54</sup>. As initial condition for the SEIR model, we therefore set 213 I(t = 1) = 1 and t = 1 corresponds to December 27th, 2019. We then use  $R_0 = 2.68^{2.86}_{2.47}$  which 214 lead to  $\gamma = 0.37$  fixing  $\lambda_0 \simeq 1$ . Strict lockdown measures are introduced at t = 80 (i.e., March 215 17th, 2020). First wave modelling results are shown in Figure 1. Figure 1a) shows the modelled 216 value of  $R_0$ . During confinement, we reduce the value of  $\lambda_0$  by a factor 1/4. We base this new 217 infection rate on the mobility data for France during confinement, which have shown a drop by 218 ~ 75% according to the INSERM report #11<sup>55</sup>. The resulting confinement  $R_0 \simeq 0.75$ , with an 219 error in the range of values compatible with that published by the Pasteur Institute<sup>56</sup>, for all values 220 of  $\sigma$  of the log-normal distribution of  $\lambda$  introduced (Eq. 9). The cumulative number of infections 221 is shown in Figure 1b) and shows, on average, between 6 and 8 millions people have been infected 222 by SARS-CoV-2 in France, depending on whether super-spreaders effects are taken into account 223 via heavy tails in the distribution of  $\lambda$ . The uncertainty range is extremely large, according to the 224 error propagation given by the stochastic fluctuations of the parameters (see<sup>24</sup> for explanations). It 225 extends from few hundred thousands individuals up to 15 millions. The error range is larger when 226 super-spreaders are modelled. The average is however close to the value proposed by the authors 227 in <sup>57</sup>, who estimate a prevalence of  $\sim 6\%$  of COVID-19 in the French population. Another realistic 228 feature of the model is the presence of an asymmetric behavior of the right tail of daily infections 229 distributions (Figure 1c) that has also been observed in real COVID-19 published data<sup>58</sup>. 230

231 *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<sup>59</sup>. As initial

condition we therefore set I(t = 1) = 1 and t = 1 corresponds to December 22nd, 2019. As 234 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 235 was set in Italy on March 9th, 2020 (t = 78) and enforced on March 22nd, 2020 (t = 89). To 236 simulate these two-steps lockdown we again base our reduction in  $R_0$  on the mobility data for 237 Italy which show for the first part of the confinement a reduction of about 50 % and a similar 238 reduction to France (75%) for the strict lockdown phase. Figure 2 shows the results for the first 239 wave. The initial condition on susceptible individuals is fixed to  $S(1) = 6.0 \cdot 10^7$  corresponding 240 to the estimate of the Italian population. A clear difference emerges with respect to the case of 241 France in the behavior of  $R_0$  which shows an intermediate reduction near t = 80, corresponding to 242 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 243 the  $R_0$  time behavior corresponds to the time interval between semi- and full-lockdown measures, 244 whose efficiency significantly increases after March 24th, 2020, also corresponding to the peak 245 value of infections. This is confirmed by looking at daily infections distributions (Figure 2c) that 246 shows a peak value near March 24th, 2020, also observed in real COVID-19 data<sup>27</sup>. Note that, 247 as for France, the magnitude of the fluctuations depends on the presence of super-spreaders. The 248 cumulative number of infections (Figure 2b) shows that, on average, almost 10 millions people 249 have been infected by SARS-CoV-2 in Italy, ranging between few hundred thousands up to 15 250 millions due to the the error propagation by the stochastic fluctuations of model parameters (see<sup>24</sup> 251 for explanations), with the range depending on the presence of super-spreaders. Nevertheless the 252 wide range of uncertainty the average value is close to the value estimated from a team of experts of 253 the Imperial College London according to which the 9.6% of Italian population has been infected, 254 with a 95% confidence level ranging between 3.2% and  $26\%^{60}$ . These estimates correspond to 255 cumulative infections of  $\sim$ 6 millions, ranging from  $\sim$ 2 and  $\sim$ 16 millions, well in agreement with 256 our model and other statistical estimates<sup>61</sup>. 257

## **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). 263 a. France

Results for France are shown in Figure 3. From top to bottom panels we increase  $\sigma$  of the 264 log-normal distribution (Eq. 9) to model the presence of super-spreaders. Lockdown is released 265 at t = 136, corresponding to May 11th, 2020. The back to normality (red) scenario clearly shows 266 a second wave of infections peaking in summer (early July) and forcing group immunity in the 267 French population. The distancing measures (green) scenario, corresponding to a reduction of the 268 mobility of about 50%, leads to a second wave as intense as the first wave, but longer, at the end 269 of August. As in the previous scenario, the distancing measures scenario allows to reach a group 270 immunity in France. A third partial lockdown scenario is modelled (blue). This latter scenario sim-271 ulates an  $R_0 \simeq 1$ , that can be achieved by imposing strict distancing measures, partial lockdowns 272 in cities with active clusters and contact tracking. It results in a linear modest increase of the total 273 number of infections that does not produce a proper wave of infections. As in the first wave mod-274 elling, large uncertainties are also present in future scenarios although the three distinct behaviors 275 clearly appear. Finally, the presence of super spreaders may introduce an additional difficulties in 276 controlling partial lockdown scenarios. By comparing Figure 3b) and h) we observe that super-277 spreaders can trigger an important growth of infections during positive fluctuations of  $R_0$  although 278 its mean value is kept, by construction, constant. Another important effect of super-spreaders is 279 to increase the uncertainty on the infection counts: error bars for  $\sigma = 0.6$  (Figure 3g,h,i) are two 280 times wider than those for  $\sigma = 0.2$  (Figure 3a,b,c). 281

<sup>282</sup> b. Italy

Figure 4 shows the results for modeling future epidemic scenarios for Italy. The first relaxation 283 of lockdown measures started at t = 131, corresponding to May 4th, 2020, while strict measures 284 were finally released at t = 146, corresponding to May 18th, 2020. The back to normality (red) 285 scenario moves towards a second wave of infections whose peak occurs at t = 193, correspond-286 ing to July 4th, 2020, exactly three months after initial lockdown measures were released (May 287 4th, 2020). This would lead the so-called herd immunity for the whole Italian population (see Fig-288 ure 4b), with a peak of daily infections near 5 millions of people (Figure 4c), and  $R_0$  re-approaching 289 the initial value ( $R_0 = 2.68$ ). The distancing measures (green) scenario produces a second wave 290 mostly similar, in terms of intensity, as the first wave, but occurring at t = 246, e.g., August 26th, 291 2020. This scenario will lead to 40 millions infected people, spanning between 25 and 55 millions, 292 thus producing a group immunity in Italy. A third scenario is modelled in which partial lockdown 293 measures are taken (blue). This latter scenario leads to a more controlled evolution of cumula-294

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.

#### 301 C. Phase Diagrams

In the previous section we have seen that increasing  $R_0$  above 1 can or not produce a second 302 wave of infections and introduce also a time delay in the appearance of a second wave of infec-303 tions. We now analyse this effect in a complete phase diagram fashion. Figures 5-6 show the 304 phase diagrams for France and for Italy, respectively. Panels a,b) show results for  $\sigma = 0.2$ , c,d) 305 for  $\sigma = 0.4$  and e,f) for  $\sigma = 0.6$ . The diagrams are built in terms of ensemble averages of number 306 of infections per day I(t) versus the average value of  $R_0$  after the confinement (panels a), and the 307 errors (represented as standard deviation of the average I(t) over the 30 realisations) are shown 308 in panels b. First we note that despite some small differences in the delay of the COVID-19 sec-309 ond wave of infections peak, the diagrams are very similar. In order to avoid a second wave,  $R_0$ 310 could fluctuate on values even slightly larger than one only if super-spreaders are not included. 311 If super-spreaders are active, even small fluctuations of  $R_0 > 1$  can trigger a second wave. Fur-312 thermore, for  $1.5 < R_0 < 2$ , the second wave is delayed in Autumn or Winter 2020/2021 months. 313 The uncertainty follows the same behavior as the average and it peaks when the number of daily 314 infections is maximum. This means that the ability to control the outcome of the epidemics is sig-315 nificantly reduced if  $R_0$  is too high. The addition of super-spreaders also enhances the uncertainty 316 in the infection counts, inducing large fluctuations which might be difficult to control with partial 317 lockdown measures. 318

#### 319 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.

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We have first verified that the model is capable to reproduce the behavior of the first wave of 327 infections and provide an estimate of COVID-19 prevalence that is coherent with clinical tests 328 and other studies. The introduction of stochasticity accounts for the large uncertainties in both 329 the initial conditions as well as the fluctuations in the basic reproduction number  $R_0$  originating 330 from changes in virus characteristics, mobility or misapplication in confinement measures. 30 331 realisations of the model have been produced and they show very different COVID-19 prevalence 332 after the first wave. The range goes from thousands of infected to tens of millions of infections in 333 both countries. Average values are compatible with those found in other studies<sup>57,60</sup>. 334

335

Then, we have modelled future epidemics scenarios by choosing specific fluctuating behaviors 336 for  $R_0$  and performing again, 30 realisations of the stochastic SEIR model. Despite the very large 337 uncertainties, distinct scenarios clearly appear from the noise. In particular, they suggest that a 338 second wave can be avoided even with  $R_0$  values slightly larger than one. This means that actual 339 distancing measures which include the use of surgical masks, the reduction in mobility and the 340 active contact tracking can be effective in avoiding a second peak of infections without the need 341 of imposing further strict lockdown measures. The analysis of phase diagrams show that there is 342 a sharp transition between observing or not a second wave of infections when the value of  $R_0$  is 343 larger than 1 and that the exact value depends on the presence or not of super-spreaders. Moreover, 344 the models show that the higher  $R_0$ , the lower the ability to control the number of infections in the 345 epidemics. Similarly, if super-spreaders are particularly active, the infection counts are difficult to 346 control and a second wave can be triggered more easily. 347

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<sup>62</sup> 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<sup>18</sup>. 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<sup>58,63</sup> however the underling (skewed) distribution is
unknown. 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 inferred by the data.

361

Our choice to stick the stochastic SEIR model is indeed driven by few factors: i) despite its 362 simplicity our model allows for the possibility of modeling realistically the uncertainties with the 363 stochastic fluctuations instead of adding new parameters whose inference may affect the results; 364 ii) despite regional differences, national infections counts during the first wave have followed, for 365 both France and Italy, a sigmoid function that could be modeled with the mean field SEIR model 366 introduced in the present study. iii) unlike the UK or the US, both France and Italy have dealt with 367 the epidemics with a national centralized approach: whenever intensive care facilities were saturat-368 ing in one region, patients' transfers have been operated to other national hospitals. iv) lockdown 369 measures have been applied uniformly on all the countries. v) introducing a spatial model also 370 introduces several additional parameters namely the interaction (exchange) coefficients among re-371 gions (at least 20x20 coefficients for Italy and 13x13 coefficients for France). The deficiencies of 372 the COVID-19 testing capacities in many regions of both countries during the first phase prevent 373 from having a reasonable estimation of the parameters, introducing uncontrollable errors. 374

This study can be applied to other countries, and this is why we publish along 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.

### 379 VI. ACKNOWLEDGMENTS

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# 383 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.

### 387 VIII. APPENDIX A: NUMERICAL CODE

```
% This appendix contains the MATLAB code used to perform
388
   % the analysis contained in the paper via a stochasitc
389
   % SEIR model
390
391
   %% PARAMETER DEFINITIONS
392
   %tmax: number of day of integrations
393
   tmax=500;
394
   %nrel: number of realisations of the model
395
   nrel=30;
396
   %tconf: lockdown day
397
   tconf=50
398
   %tconf2: lockdown release
399
   tconf2=100
400
401
   %% LOOP ON DIFFERENT VALUES OF LAMBDA, INFECTION RATE
402
   for la=1:50
403
        lambdaconf=0.25;
404
        lambdares=la.*0.02;
405
406
        %% LOOP ON REALIZATIONS
407
        for rel=1:nrel
408
            S=zeros(1,tmax);
409
            E=zeros(1,tmax);
410
            I=zeros(1,tmax);
411
```

412	R=zeros(1,tmax);
413	C=zeros(1,tmax);
414	<pre>lambda=zeros(1,tmax);</pre>
415	%S Susceptible individuals (France population)
416	S(1)=67000000;
417	%I Infected individuals
418	I(1)=585;
419	% Recovered
420	R(1)=0;
421	% Inital time
422	T(1)=0;
423	% Cumulative infections
424	C(1)=0;
425	$\%$ alpha is the inverse of the incubation period (1/t_incubation)
426	alpha0=0.27;
427	% RO is equal to 2.68
428	R0=2.68;
429	% gamma is the inverse of the mean infectious period
430	gamma0=lambda0./R0;
431	% uncertainty in gamma and lambda
432	<pre>coeff_gamma=0.5;</pre>
433	<pre>coeff_lambda=0.005;</pre>
434	
435	%% LOOP ON TIME, INTEGRATION OF SEIR MODELS
436	for t=1:1:tmax
437	%gamma=1/Tr where Tr is the recovery time (2 weeks)
438	%Stochastic gamma
439	gamma=gamma0+gamma0./5*randn;
440	%Change lambda for confinement
441	if t==tconf
442	lambda0=lambdaconf;
443	end

444	if t==tconf2
445	lambda0=lambdares;
446	end
447	%Stochastic lambda with lognormal distribution
448	sigmalogn=0.2
449	mulogn=log(lambda0-sigmalogn^2./2)
450	<pre>lambda(t+1)=lognrnd(mulogn,sigmalogn)/S(1);</pre>
451	%Stochastic alpha
452	alpha=alpha0+alpha0./5*randn;
453	%Computation of RO
454	RO(t+1)=lambda(t+1)./gamma0;
455	%Iteration of the model
456	T(t+1)=t;
457	S(t+1)=S(t)-(lambda(t+1)*S(t)*I(t));
458	E(t+1)=E(t)+(lambda(t+1)*S(t)*I(t))-alpha*E(t);
459	I(t+1)=I(t) +alpha*E(t) -gamma*I(t);
460	R(t+1)=R(t)+(gamma*I(t));
461	%cumulative infected
462	C(t+1)=gamma0.*sum(I);
463	%Variables for different realisations
464	<pre>Irel(rel,t+1)=I(t+1);</pre>
465	<pre>lambdarel(rel,t+1)=lambda(t+1);</pre>
466	end
467	
468	end
469	
470	%% AVERAGING OVER DIFFERENT REALIZATIONS
471	<pre>lambdamoy(la,:)=mean(lambdarel,1);</pre>
472	<pre>Imoy(la,:)=mean(Irel,1);</pre>
473	<pre>Istd(la,:)=std(Irel,1);</pre>
474	<pre>lambdavec(la)=lambdares;</pre>
475	ROmoy(la,:)=lambdamoy(la,:)./gamma0.*S(1);

476	

477 end

478

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FIG. 1. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for France (Eqs 5-8) with  $\lambda = 1./S(0)$ ,  $\alpha = 0.27$ ,  $\gamma = 0.37$ . Initial conditions are set to I(1) = 1,  $S(1) = 6.7 \cdot 10^7$ , E(1) = R(1) = 0. t = 1 corresponds to Dec 27, 2019. Confinement is introduced at t = 78 (Mar 17, 2020). a) Time evolution for the basic reproduction number  $R_0$ , b) Time evolution for the cumulative number of infections C(t), c) Time evolution for the daily infected individuals I(t). Solid line shows the average for 30 realisation of the SEIR stochatic models, shading extends to one standard deviations of the mean. Colors represent different values of  $\sigma$  in the lognormal distribution of  $\lambda$  (Eq. 9 from light to heavy tails).



FIG. 2. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for Italy (Eqs 5-8) with  $\lambda = 1./S(0)$ ,  $\alpha = 0.27$ ,  $\gamma = 0.37$ . 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). a) Time evolution for the basic reproduction number  $R_0$ , b) Time evolution for the cumulative number of infections C(t), c) Time evolution for the daily infected individuals I(t). Solid line shows the average for 30 realisation of the SEIR stochatic models, shading extends to one standard deviations of the mean. Colors represent different values of  $\sigma$  in the lognormal distribution of  $\lambda$  (Eq. 9 from light to heavy tails).



FIG. 3. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in France. Initial conditions are set as in Figure 1. 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. 9). Solid line shows the average for 30 realisations of the SEIR stochatic models, shading extends to one standard deviations of the mean.



FIG. 4. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in Italy. Initial conditions are set as in Figure 2. 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. 9). Solid line shows the average for 30 realisations of the SEIR stochatic models, shading extends to one standard deviations of the mean.



FIG. 5. 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 1. After the confinement is released (t = 136, May 11, 2020) all possible  $R_0$  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. 9).



FIG. 6. 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 2. After the confinement is released (t = 131, May 4, 2020 and then t = 146 May 18, 2020) all possible  $R_0$  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. 9).