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

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

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28 I. LEAD PARAGRAPH

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

40 II. INTRODUCTION

41 SARS-CoV-2 is a zoonotic virus of the coronavirus family¹ emerged in Wuhan (China) at the
42 end of 2019² and rapidly propagated across the world until it has been declared a pandemic by
43 the World Health Organization on March 11, 2020³. SARS-CoV-2 virus provokes an infectious
44 disease known as COVID-19 that has an incredibly large spectrum of symptoms or none depending
45 on the age, health status and the immune defenses of each individuals⁴. SARS-CoV-2 causes
46 potentially life-threatening form of pneumonia and/or cardiac injuries in a non-negligible patients
47 fraction^{5,6}.

48 To date, no treatment of vaccine is available for COVID-19⁷. Efforts to contain the virus and
49 to not overwhelm intensive care facilities are based on quarantine measures which have proven
50 very effective in several countries⁸⁻¹⁰. Despite this, lockdown measures entail enormous econom-
51 ical, social and psychological costs. Recent estimates of the International Monetary Fund recently
52 announced a global recession that will drag global GDP lower by 3% in 2020, although contin-
53 uously developing and changing as well as significantly depending country-by-country¹¹. More
54 than 20 million people have lost their job in United States¹² and a large percentage of Italians
55 have developed psychological disturbances such as insomnia or anxiety due to the strict lockdown
56 measures¹³. Those measures have been taken on the basis of epidemics models, which are fitted

57 on the available data¹⁴. In Italy, initial lockdown measures started on February 23rd for 11 mu-
58 nicipalities in both Lombardia and Veneto which were identified as the two main Italian clusters.
59 After the initial spread of the epidemics into different regions all Italian territory was placed into a
60 quarantine on March 9th, with total lockdown measures including all commercial activities (apart
61 supermarkets and pharmacies), non-essential businesses and industries, and severe restrictions to
62 transports and movements of people at regional, national, and extra-national levels¹⁵. People were
63 asked to stay at home or near for sporting activities and dog hygiene (within 200 m from home),
64 to reduce as much as possible their movements (only for food shopping and care reasons), and
65 smart-working was especially encouraged in both public and private administrations and compa-
66 nies. At the early stages of epidemics intensive cares were almost saturated with a peak of 4000
67 people on April 3rd and a peak of hospitalisations of 30000 on April 4th, significantly reducing
68 after these dates, reaching 1500 and 17000, respectively, at the beginning of phase 2 on May 4th,
69 and 750 and 1000 on May 18th when lockdown measures on commercial activities were relaxed.
70 These numbers, continuously declining during the next days and weeks, confirmed the benefit of
71 lockdown measures¹⁶.

72 Alarmed by the exponential growth of new infections and the saturation of the intensive care beds,
73 also France introduced strict lockdown measures on March 17th¹⁷. The French government re-
74 stricted travels to food shopping, care and work when teleworking was not possible, outings near
75 home for individual sporting activity and/or dog hygiene, and it imposed the closure of the Schen-
76 gen area borders as well as the postponement of the second round of municipal elections. The
77 number of patients in intensive care, like the number of hospitalisations overall peaked in early
78 April and then started to decline, showing the benefits of lockdown measures. On Monday, May
79 11th, France began a gradual easing of COVID-19 lockdown measures¹⁸. Trips of up to 100 kilo-
80 metres from home are allowed without justification, as will gatherings of up to 10 people. Longer
81 trips will still be allowed only for work or for compelling family reasons, as justified by a signed
82 form. Guiding the government's plans for easing the lockdown is the division of the country into
83 two zones, green and red, based on health indicators. Paris region (Ile de France), with about 12
84 millions inhabitants is flagged, to date, as an orange zone.

85 In both countries, the release of lockdown measures has been authorised by authorities after
86 consulting scientific committees which were monitoring the behavior of the curve of infections
87 using COVID-19 data. Those data are provided daily, following a request of the WHO. To date,
88 the WHO guidelines require countries to report, at each day t , the total number of infected patients

89 $I(t)$ as well as the number of deaths $D(t)$. Large uncertainties have been documented in the count
90 of $I(t)$ ¹⁹. Whereas in the early stage of the epidemic several countries tested asymptomatic indi-
91 viduals to track back the infection chain, recent policies to estimate $I(t)$ have changed. Most of
92 the western countries have previously tested only patients displaying severe SARS-CoV-2 symp-
93 toms²⁰. In an effort of tracking all the chain of infections, Italy and France are now testing all
94 individuals displaying COVID-19 symptoms and those who had strict contacts with infected indi-
95 viduals. The importance of tracking asymptomatic patients has been proven in a recent study²¹.
96 The authors have estimated that an enormous part of total infections were undocumented (80% to
97 90%) and that those undetected infections were the source for 79% of documented cases in China.
98 Tracking strategies have proven effective in supporting actions to reduce the rate of new infections,
99 without the need of lockdown measures, as in South Korea²².

100 The goal of this paper is to explore possible future epidemics scenarios of the long term behav-
101 ior of the COVID-19 epidemic²³ but taking into account the role of uncertainties in both the pa-
102 rameters value and the infection counts to investigate different outcomes of the epidemics leading
103 or not to a second wave of infections. To this purpose we use a stochastic Susceptible-Exposed-
104 Infected-Recovered (SEIR) model²⁴ which consist in a set of ordinary differential equations where
105 control parameters are time-dependent modelled via a stochastic process. This allows to mimic the
106 dependence on control parameters on some additional/external factors as super-spreaders²⁵ and the
107 enforcing/relaxing of confinement measures²⁴. As for the classical SEIR models²⁶ the population
108 is divided into four compartmental groups, i.e., Susceptible, Exposed, Infected, and Recovered
109 individuals. The stochastic SEIR model shows that long-term extrapolation is sensitive to both the
110 initial conditions and the value of control parameters²⁴, with asymptotic estimates fluctuating on
111 the order of ten millions units in both countries, leading or not a second wave of infections. This
112 sensitivity arising from both poor data quality and inadequate estimations of model parameters
113 has been also recently investigated by means of a statistical model based on a generalized logistic
114 distribution^{27,28}. The paper is organised as follows: in Section III we discuss the various sources
115 of data for COVID-19 and their shortcomings, and then we discuss in detail the SEIR model and
116 its statistical modelling. In Section IV we discuss the results focusing on the statistical sensitivity
117 of the modelling, and apply it to data from France and Italy. We finish, in Section V, with some
118 remarks and point out some limitations of our study.

119 III. DATA AND MODELLING

120 A. Data

121 This paper relies on data stored into the Visual Dashboard repository of the Johns Hopkins Uni-
122 versity Center for Systems Science and Engineering (JHU CSSE) supported by ESRI Living Atlas
123 Team and the Johns Hopkins University Applied Physics Lab (JHU APL). Data can be freely
124 accessed and downloaded at <https://systems.jhu.edu/research/public-health/ncov/>,
125 and refers to the confirmed cases by means of a laboratory test³. Nevertheless there are some
126 inconsistencies between countries due to different protocols in testing patients (suspected symp-
127 toms, tracing-back procedures, wide range tests)^{29,30}, as well as, to local management of health
128 infrastructures and institutions. As an example due to the regional-level system of Italian health-
129 care data are collected at a regional level and then reported to the National level via the Protezione
130 Civile transferring them to WHO. These processes could be affected by some inconsistencies and
131 delays³¹, especially during the most critical phase of the epidemic diffusion that could introduce
132 errors and biases into the daily data. These incongruities mostly affected the period between Febru-
133 ary 23rd and March 10th, particularly regarding the counts of deaths due to a protocol change from
134 the Italian Ministry of Health³². A similar situation occurs in France where the initial testing strat-
135 egy was based only on detecting those individuals experiencing severe COVID19 symptoms³³.
136 In the post lockdown phase, France has extended its testing capacity to asymptomatic individuals
137 who have been in contact with infected patients³⁴.

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

139 One of the most used epidemiological models is the so-called Susceptible-Exposed-Infected-
140 Recovered (SEIR) model belonging to the class of compartmental models²⁶. It assumes that the
141 total population N can be divided into four classes of individuals that are susceptible S , exposed
142 E , infected I , and recovered or dead R (assumed to be not susceptible to reinfection). The model
143 is based on the following assumptions:

- 144 1. the total population does not vary in time, e.g., $dN/dt = dS/dt + dE/dt + dI/dt + dR/dt =$
145 $0, \forall t \geq 0$;
- 146 2. susceptible individuals become infected that then can only recover or die, e.g., $S \rightarrow I \rightarrow R$;

147 3. exposed individuals E encountered an infected person but are not yet themselves infectious;
148 4. recovered or died individuals R are forever immune. Although the longevity of the antibody
149 response is still unknown, it is known that antibodies to other coronaviruses wane over time
150 typically after 52 weeks from the onset of symptoms³⁵. Concerning SARS-CoV-2 it has
151 been shown that antibody levels may remain over the course of almost 2-3 months³⁶. Never-
152 theless, not only antibodies are important for investigating immunity but also other immune
153 cells named T cells play a crucial role for long-term immunity^{37,38}. Recently Kissler et al.³⁹
154 found that the duration of protective immunity may last 6 to 12 months. Our assumption
155 seems therefore justified at least to study the dynamics of a second wave.

156 Thus, the model reads as

$$157 \quad \frac{dS}{dt} = -\lambda S(t)I(t), \quad (1)$$

$$158 \quad \frac{dE}{dt} = \lambda S(t)I(t) - \alpha E(t), \quad (2)$$

$$159 \quad \frac{dI}{dt} = \alpha E(t) - \gamma I(t), \quad (3)$$

$$160 \quad \frac{dR}{dt} = \gamma I(t), \quad (4)$$

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

$$164 \quad S(t+1) = S(t) - \lambda S(t)I(t), \quad (5)$$

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

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

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

168 in which we fixed $dt = 1$ day that is the time resolution of COVID-19 counts. By means of γ and
169 λ_0 the model also allows to derived the so-called R_0 parameter, e.g., $R_0 = \lambda_0/\gamma$, representing the
170 average reproduction number of the virus. It is related to the number of cases that can potentially
171 (on average) caused from an infected individual during its infectious period ($\tau_{inf} = \gamma^{-1}$). Early
172 estimates in Wuhan⁴⁰ on January 2020 reported $R_0 = 2.68_{2.47}^{2.86}$ which lead to $\gamma = 0.37$ fixing $\lambda \simeq 1$
173 as in⁴¹ and a 95% confidence level range for the incubation period between 2 and 11 days⁴².

174 However, the R_0 parameter as well as models parameters λ , γ , and α can vary in time during
 175 the epidemics due to different factors as the possible presence of the so-called super-spreaders²⁵,
 176 intrinsic changes of the SARS-CoV-2 features, lockdown measures, asymptomatic individuals
 177 who are not tracked out, counting procedures and protocols, and so on⁴³. The fact that all the
 178 time-scales considered for the parameters are larger than one day also justifies the use of the
 179 discrete version of the model in Eqs. 5-8.

180 To deal with uncertainties in long-term extrapolations and with the time-dependency of control
 181 parameters a stochastic approach could provide new insights in modeling epidemics⁴⁴⁻⁴⁶, espe-
 182 cially when epidemics show a wide range of spatial and temporal variability⁴⁷⁻⁴⁹. However,
 183 instead of investigating how to get a realistic behavior by stochastically perturbing control pa-
 184 rameters, here we investigate how uncertainties into the final counts $C(t)$ are controlled by model
 185 parameters²⁴. Thus, we use a stochastic version of the SEIR model in which the set of control
 186 parameters $\{\alpha, \gamma, \lambda\}$ are extracted at each timestep from random distributions. Specifically we set
 187 $\alpha(t) \in \mathcal{N}(\alpha_0, \zeta_\alpha^2; t)$, $\gamma(t) \in \mathcal{N}(\gamma_0, \zeta_\gamma^2; t)$ and

$$188 \quad \log(\lambda(t)) \in \mathcal{N}(\log(\lambda_0 - \sigma^2/2), \sigma; t). \quad (9)$$

189 In this way we can introduce instantaneous daily discrete jumps (e.g., take into account daily
 190 uncertainties) in the control parameters to properly model detection errors on infection counts,
 191 appropriately described through a discrete process⁵⁰ than a continuous one⁵¹. For α and γ we
 192 follow²⁴ and allows for Gaussian fluctuations of the parameters, with intensity $\zeta_\alpha = 0.2\alpha_0$ and
 193 $\zeta_\gamma = 0.2\gamma_0$. These fluctuations simulates the range of uncertainties obtained in previous studies
 194 for the incubation time and the recovery time and discussed in²⁴. With respect to²⁴, we model the
 195 infection rate $\lambda(t)$ using a log-normal distribution⁵² to take into account the possible presence of
 196 super-spreaders, namely individuals who can infect quickly a large number of susceptible people
 197 by having several strict social interactions⁵³. Super-spreaders can be modelled by introducing
 198 heavy right tails for the distribution of λ . The location and the scale parameters chosen in Eq. 9
 199 ensures that the mean of the distribution does not change, while σ is modified to explore super-
 200 spreaders influence. In the following, we will only consider three cases: i) $\sigma = 0.2$ for which the
 201 log-normal distribution tends to be symmetric and the fluctuations of λ are quasi-Gaussian around
 202 λ_0 , ii) $\sigma = 0.4$ which models the effect of some possible super-spreaders and $\sigma = 0.6$ where
 203 several super-spreaders may be active at the same time.

204 IV. RESULTS

205 A. Model validation: first wave

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

209 a. France

210 In France, the first documented case of COVID-19 infections goes back to December 27th, 2019.
211 Doctors at a hospital in the northern suburbs of Paris retested samples from patients between De-
212 cember 2nd, 2019, and January 16th, 2020. Of the 14 patient samples retested, one sample, from
213 a 42-year-old man came back positive⁵⁴. As initial condition for the SEIR model, we therefore set
214 $I(t = 1) = 1$ and $t = 1$ corresponds to December 27th, 2019. We then use $R_0 = 2.68_{2.47}^{2.86}$ which
215 lead to $\gamma = 0.37$ fixing $\lambda_0 \simeq 1$. Strict lockdown measures are introduced at $t = 80$ (i.e., March
216 17th, 2020). First wave modelling results are shown in Figure 1. Figure 1a) shows the modelled
217 value of R_0 . During confinement, we reduce the value of λ_0 by a factor 1/4. We base this new
218 infection rate on the mobility data for France during confinement, which have shown a drop by
219 $\sim 75\%$ according to the INSERM report #11⁵⁵. The resulting confinement $R_0 \simeq 0.75$, with an
220 error in the range of values compatible with that published by the Pasteur Institute⁵⁶, for all values
221 of σ of the log-normal distribution of λ introduced (Eq. 9). The cumulative number of infections
222 is shown in Figure 1b) and shows, on average, between 6 and 8 millions people have been infected
223 by SARS-CoV-2 in France, depending on whether super-spreaders effects are taken into account
224 via heavy tails in the distribution of λ . The uncertainty range is extremely large, according to the
225 error propagation given by the stochastic fluctuations of the parameters (see²⁴ for explanations). It
226 extends from few hundred thousands individuals up to 15 millions. The error range is larger when
227 super-spreaders are modelled. The average is however close to the value proposed by the authors
228 in⁵⁷, who estimate a prevalence of $\sim 6\%$ of COVID-19 in the French population. Another realistic
229 feature of the model is the presence of an asymmetric behavior of the right tail of daily infections
230 distributions (Figure 1c) that has also been observed in real COVID-19 published data⁵⁸.

231 b. Italy

232 For Italy, the first suspect COVID-19 case goes back to December 22nd, 2019, a 41-year-old
233 woman who could only be tested positive for SARS-CoV-2 antibodies in April 2020⁵⁹. As initial

234 condition we therefore set $I(t = 1) = 1$ and $t = 1$ corresponds to December 22nd, 2019. As
 235 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
 236 was set in Italy on March 9th, 2020 ($t = 78$) and enforced on March 22nd, 2020 ($t = 89$). To
 237 simulate these two-steps lockdown we again base our reduction in R_0 on the mobility data for
 238 Italy which show for the first part of the confinement a reduction of about 50 % and a similar
 239 reduction to France (75%) for the strict lockdown phase. Figure 2 shows the results for the first
 240 wave. The initial condition on susceptible individuals is fixed to $S(1) = 6.0 \cdot 10^7$ corresponding
 241 to the estimate of the Italian population. A clear difference emerges with respect to the case of
 242 France in the behavior of R_0 which shows an intermediate reduction near $t = 80$, corresponding to
 243 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
 244 the R_0 time behavior corresponds to the time interval between semi- and full-lockdown measures,
 245 whose efficiency significantly increases after March 24th, 2020, also corresponding to the peak
 246 value of infections. This is confirmed by looking at daily infections distributions (Figure 2c) that
 247 shows a peak value near March 24th, 2020, also observed in real COVID-19 data²⁷. Note that,
 248 as for France, the magnitude of the fluctuations depends on the presence of super-spreaders. The
 249 cumulative number of infections (Figure 2b) shows that, on average, almost 10 millions people
 250 have been infected by SARS-CoV-2 in Italy, ranging between few hundred thousands up to 15
 251 millions due to the the error propagation by the stochastic fluctuations of model parameters (see²⁴
 252 for explanations), with the range depending on the presence of super-spreaders. Nevertheless the
 253 wide range of uncertainty the average value is close to the value estimated from a team of experts of
 254 the Imperial College London according to which the 9.6% of Italian population has been infected,
 255 with a 95% confidence level ranging between 3.2% and 26%⁶⁰. These estimates correspond to
 256 cumulative infections of ~ 6 millions, ranging from ~ 2 and ~ 16 millions, well in agreement with
 257 our model and other statistical estimates⁶¹.

258 B. Future epidemics scenarios

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

263 *a. France*

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

282 *b. Italy*

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

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

301 C. Phase Diagrams

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

319 V. DISCUSSION

320 France and Italy have faced a long phase of lockdown with severe restrictions in mobility and
321 social contacts. They have managed to reduce the number of daily COVID-19 infections drasti-
322 cally and released almost simultaneously lockdown measures. This paper addresses the possible

323 future scenarios of COVID-19 infections in those countries by using one of the simplest possible
324 model capable to reproduce the first wave of infections and to take into account uncertainties,
325 namely a stochastic SEIR model with fluctuating parameters.

326

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

335

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

348 This model has also evident deficiencies in representing the COVID-19 infections. First of all,
349 the choice of the initial conditions is conditioned by our ignorance on the diffusion of the virus in
350 France and Italy in December 2019. Furthermore, we are unable to verify on an extensive dataset
351 the outcome of the first wave: on one side antibodies blood tests have still a lower reliability⁶² and
352 on the other they have not been applied on an extensive number of individuals to get reliable esti-
353 mates. On top of the data-driven limitations, we have those introduced by the use of compartment
354 models, as there are geographic, social and age differences in the spread of the COVID-19 disease

355 in both countries¹⁸. Furthermore, we also assume that fluctuations on the parameters of the SEIR
356 model are Gaussian (for the incubation and recovery rate) or log-normal (for the infection rate),
357 in order to simulate heavy tailed distributions^{58,63} however the underlying (skewed) distribution is
358 unknown. We would like to remark however that, to overcome these limitations, one would need
359 to fit more complex models and introduce additional parameters which can, at the present stage,
360 barely be inferred by the data.

361

362 Our choice to stick to the stochastic SEIR model is indeed driven by few factors: i) despite its
363 simplicity our model allows for the possibility of modeling realistically the uncertainties with the
364 stochastic fluctuations instead of adding new parameters whose inference may affect the results;
365 ii) despite regional differences, national infection counts during the first wave have followed, for
366 both France and Italy, a sigmoid function that could be modeled with the mean field SEIR model
367 introduced in the present study. iii) unlike the UK or the US, both France and Italy have dealt with
368 the epidemics with a national centralized approach: whenever intensive care facilities were saturat-
369 ing in one region, patients' transfers have been operated to other national hospitals. iv) lockdown
370 measures have been applied uniformly on all the countries. v) introducing a spatial model also
371 introduces several additional parameters namely the interaction (exchange) coefficients among re-
372 gions (at least 20x20 coefficients for Italy and 13x13 coefficients for France). The deficiencies of
373 the COVID-19 testing capacities in many regions of both countries during the first phase prevent
374 from having a reasonable estimation of the parameters, introducing uncontrollable errors.
375 This study can be applied to other countries, and this is why we publish along with the code of our
376 analysis alongside with the paper. To date, Northern Europe, UK, US and other American coun-
377 tries are still facing the first wave of infections, so that future scenarios cannot be devised with the
378 same clarity as those outlined in this study for France and Italy.

379 VI. ACKNOWLEDGMENTS

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383 VII. DATA AVAILABILITY

384 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
385 for Systems Science.
386

387 VIII. APPENDIX A: NUMERICAL CODE

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

```

412     R=zeros(1,tmax);
413     C=zeros(1,tmax);
414     lambda=zeros(1,tmax);
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     % R0 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     coeff_gamma=0.5;
433     coeff_lambda=0.005;
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=lambdacnf;
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         lambda(t+1)=lognrnd(mulogn,sigmalogn)/S(1);
451         %Stochastic alpha
452         alpha=alpha0+alpha0./5*randn;
453         %Computation of R0
454         R0(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         Ire1(rel,t+1)=I(t+1);
465         lambdarel(rel,t+1)=lambda(t+1);
466     end
467
468     end
469
470 %% AVERAGING OVER DIFFERENT REALIZATIONS
471 lambdamoy(la,:)=mean(lambdarel,1);
472 Imoy(la,:)=mean(Ire1,1);
473 Istd(la,:)=std(Ire1,1);
474 lambdavec(la)=lambdares;
475 R0moy(la,:)=lambdamoy(la,:)./gamma0.*S(1);

```

476

477 end

478

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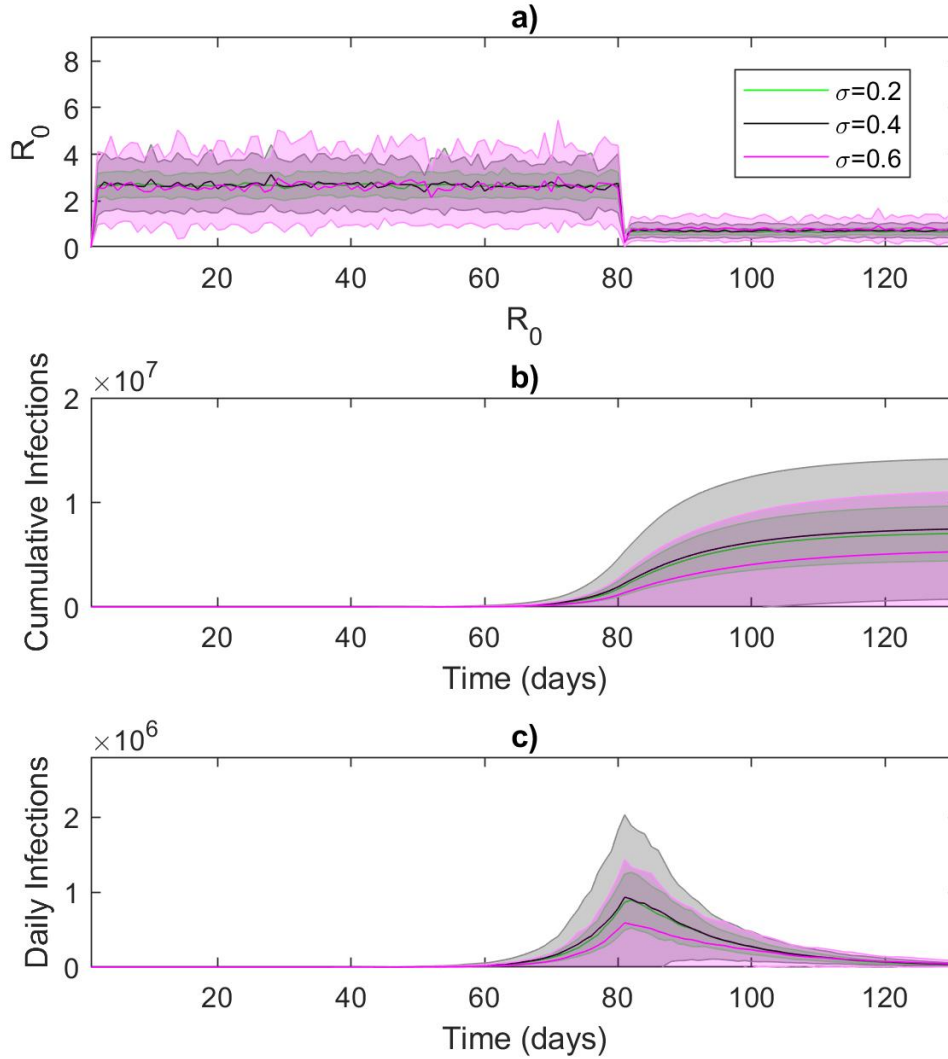


FIG. 1. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for France (Eqs 5-8) with $\lambda = 1./S(0)$, $\alpha = 0.27$, $\gamma = 0.37$. Initial conditions are set to $I(1) = 1$, $S(1) = 6.7 \cdot 10^7$, $E(1) = R(1) = 0$. $t = 1$ corresponds to Dec 27, 2019. Confinement is introduced 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 stochastic models, shading extends to one standard deviations of the mean. Colors represent different values of σ in the lognormal distribution of λ (Eq. 9 from light to heavy tails).

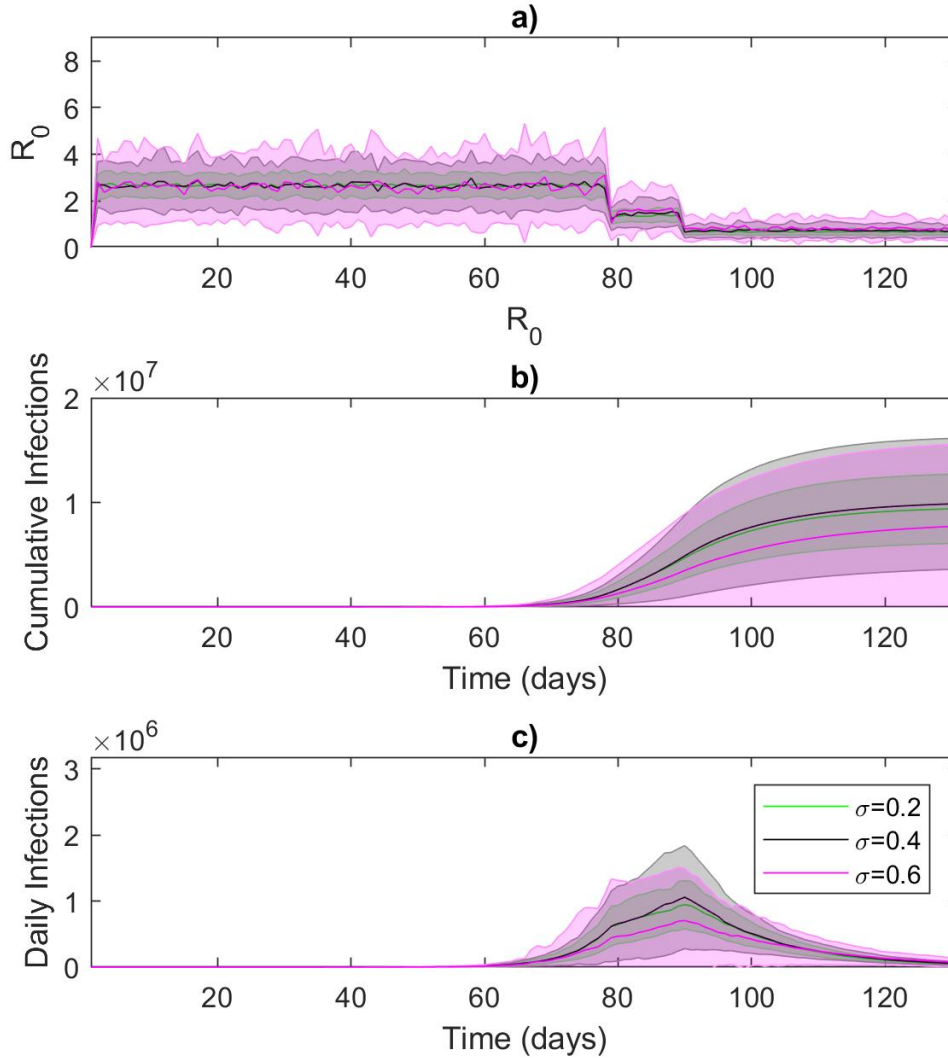


FIG. 2. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for Italy (Eqs 5-8) with $\lambda = 1./S(0)$, $\alpha = 0.27$, $\gamma = 0.37$. Initial conditions are set to $I(1) = 1$, $S(1) = 6.0 \cdot 10^7$, $E(1) = R(1) = 0$. $t = 1$ corresponds to Dec 22, 2019. First confinement measures 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 stochastic models, shading extends to one standard deviations of the mean. Colors represent different values of σ in the lognormal distribution of λ (Eq. 9 from light to heavy tails).

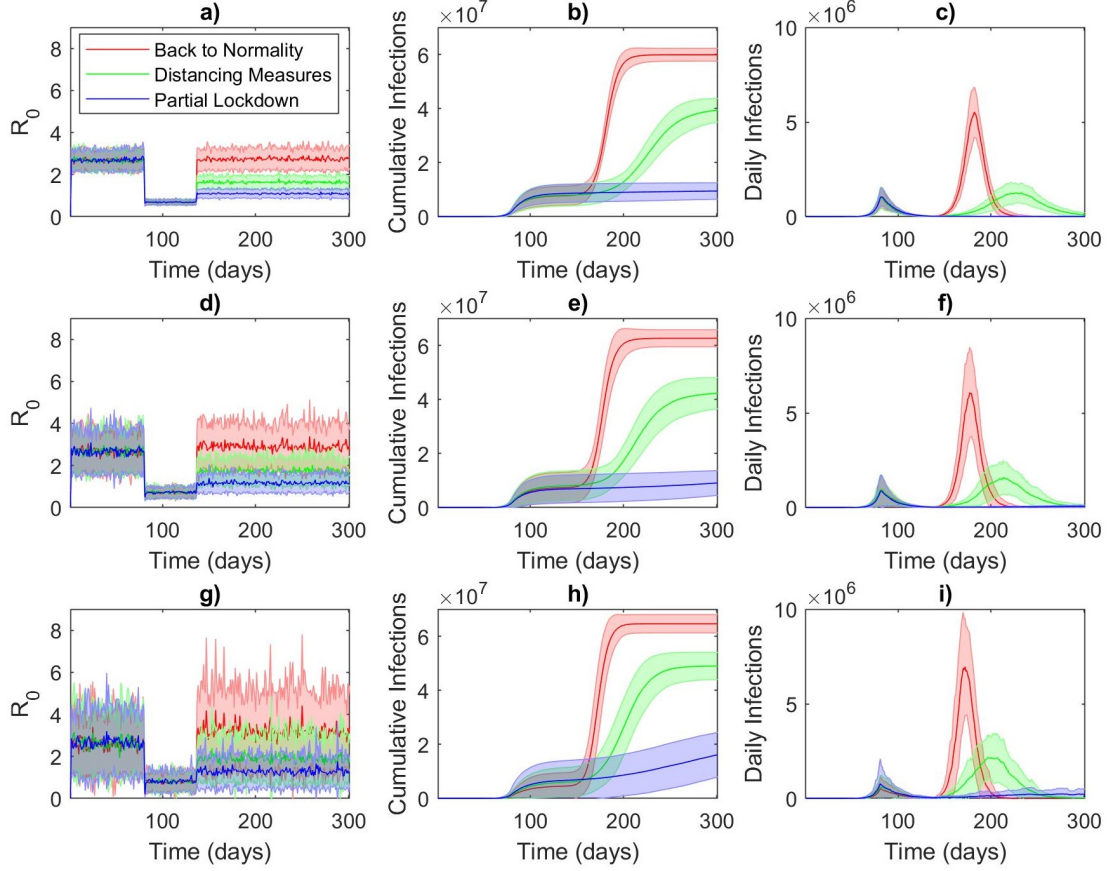


FIG. 3. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in France. Initial conditions are set as in Figure 1. After the confinement is released ($t = 136$, May 11, 2020) three scenarios are modelled: back to normality (red), distancing measures (green), partial lockdown (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 λ (Eq. 9). Solid line shows the average for 30 realisations of the SEIR stochastic models, shading extends to one standard deviations of the mean.

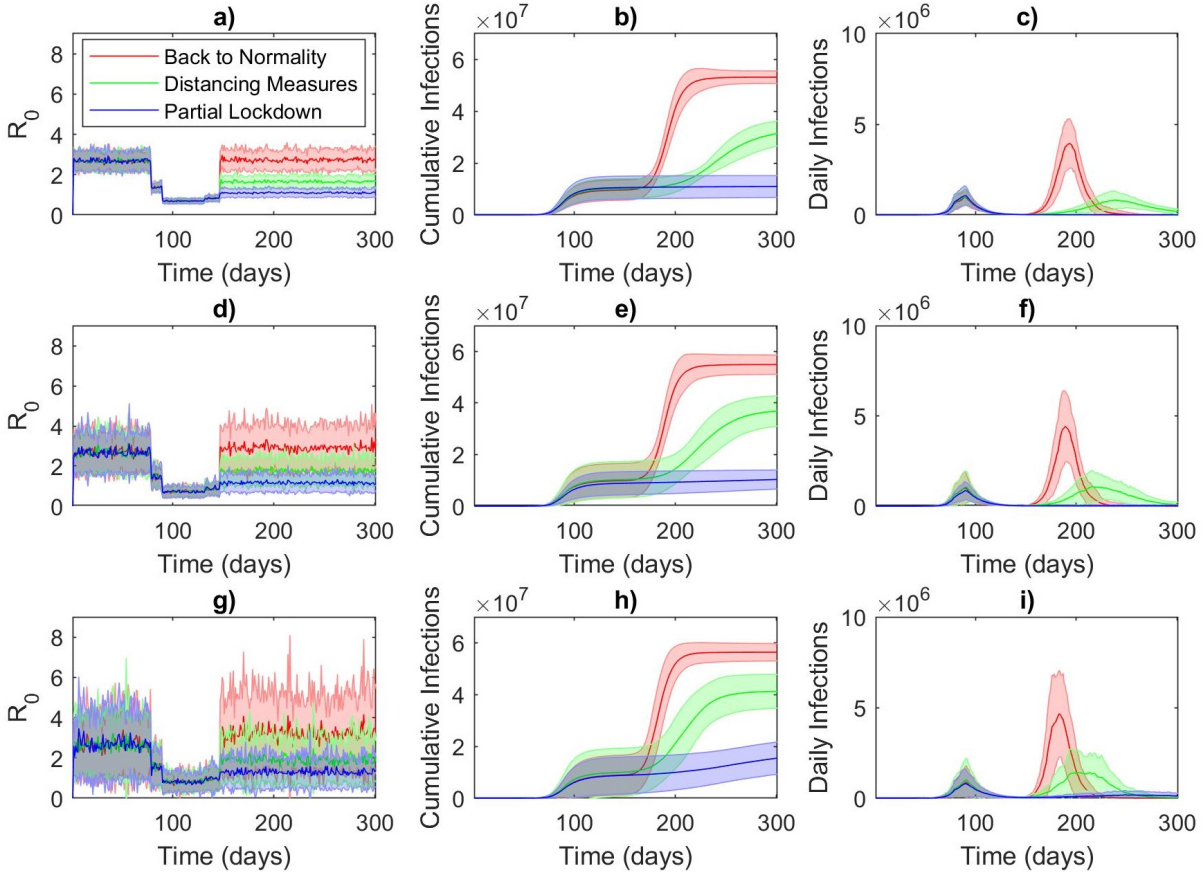


FIG. 4. Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in Italy. Initial conditions are set as in Figure 2. After the confinement is released ($t = 131$, May 4, 2020 and $t = 146$, May 18, 2020) three scenarios are modelled: back to normality (red), distancing measures (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 λ (Eq. 9). Solid line shows the average for 30 realisations of the SEIR stochastic models, shading extends to one standard deviations of the mean.

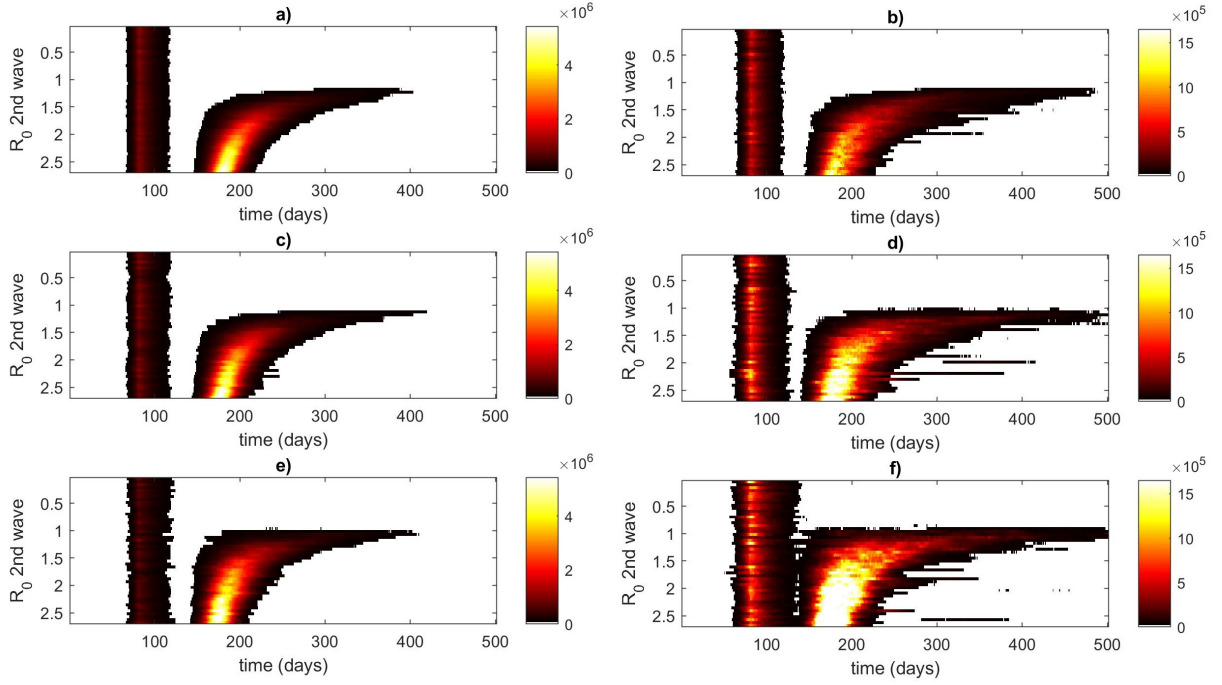


FIG. 5. Phase diagram for the Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in France. Initial conditions are set as in Figure 1. After the confinement is released ($t = 136$, May 11, 2020) all possible R_0 modelled. a,c,e) Average of daily infected individuals $I(t)$. 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 λ (Eq. 9).

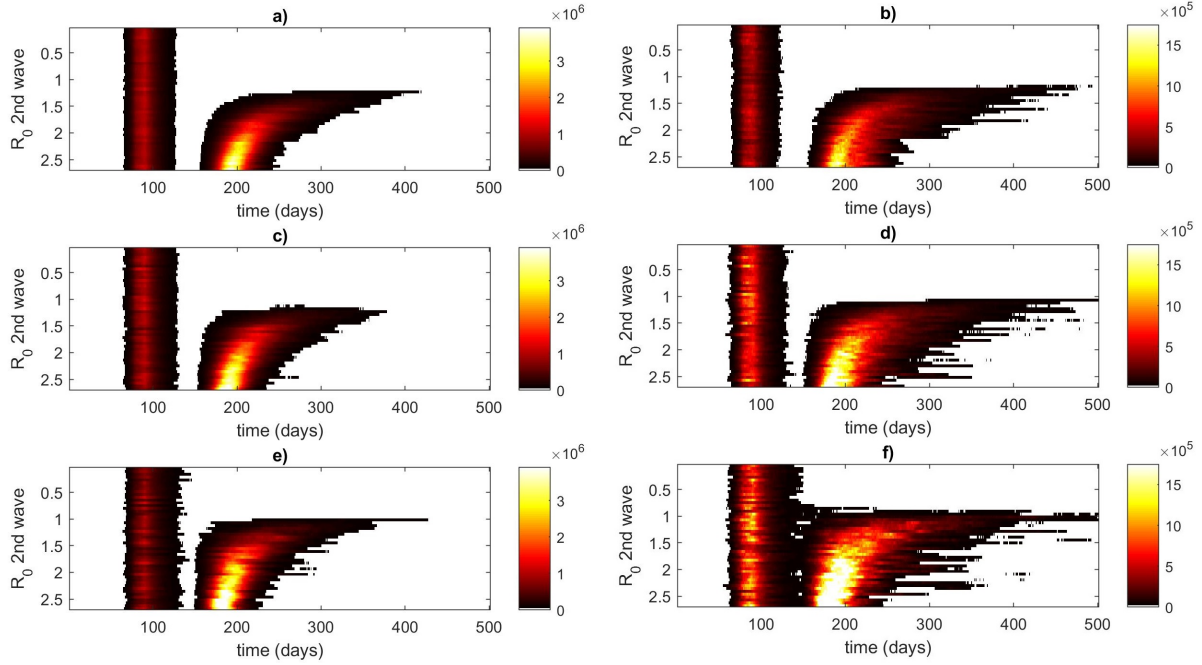


FIG. 6. Phase diagram for the Susceptible-Exposed-Infected-Recovered (SEIR) model of COVID-19 for the second wave in Italy. Initial conditions are set as in Figure 2. After the confinement is released ($t = 131$, May 4, 2020 and then $t = 146$ May 18, 2020) all possible R_0 modelled. a,c,e) Average of 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 λ (Eq. 9).