PREDICTION OF CONFINEMENT EFFECTS ON THE NUMBER OF COVID-19 OUTBREAK IN ALGERIA

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Ali Moussaoui[1] and Pierre Auger[2, 3]

Abstract. The first case of coronavirus disease 2019 (COVID-19) in Algeria was reported on 25 February 2020. Since then, it has progressed rapidly and the number of cases grows exponentially each day. In this article, we utilize $SEIR$ modelling to forecast COVID-19 outbreak in Algeria under two scenarios by using the real-time data from March 01 to April 10, 2020. In the first scenario: no control measures are put into place, we estimate that the basic reproduction number for the epidemic in Algeria is 2.09, the number of new cases in Algeria will peak from around late may to early june and up to 82% of the Algerian population will likely contract the coronavirus. In the second scenario, at a certain date T, drastic control measures are taken, people are being advised to self-isolate or to quarantine and will be able to leave their homes only if necessary. We use $SEIR$ model with fast movements between compartments. We prove that the final size of the epidemic depends strongly on the cumulative number of cases at the date when we implement intervention and on the fraction of the population in confinement. Our analysis shows that the longer we wait, the worse the situation will be and this very quickly produces.

Mathematics Subject Classification. 92B05,92C60.

1. Introduction

The cumulative number since 25 February, when the first case was diagnosed, to present day, is 1761 cases, including 529 from the city of Blida and 310 from Algiers. Since then, the infection has become more virulent, and the number of cases has been increasing. It should be noted that screening remains very low in relation to the means available. Figure 1 shows the cumulative number of detected cases of coronavirus in Algeria between March 01 and April 10, 2020. Between these two dates, the cumulative number of cases increased from 03 to 1761. The spread of the epidemic adjusts very well (which is well known in epidemiology) with an exponential growth for the number of contaminated cases I over time:

$$I(t) = I_0 e^{\lambda t} \tag{1}$$

Keywords and phrases. COVID-19, $SEIR$ compartmental model, basic reproduction number, time scales, Aggregation of variables

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By using a least-squares fit for the exponential function (1) for the number of contaminated cases with the data shown in Figure 2, we find for Algeria $\lambda \approx 0.16$. If this rhythm of growth continues, Algeria will be faced with tens, even hundreds of thousands of cases in the space of a few weeks, including thousands of patients requiring intensive care.

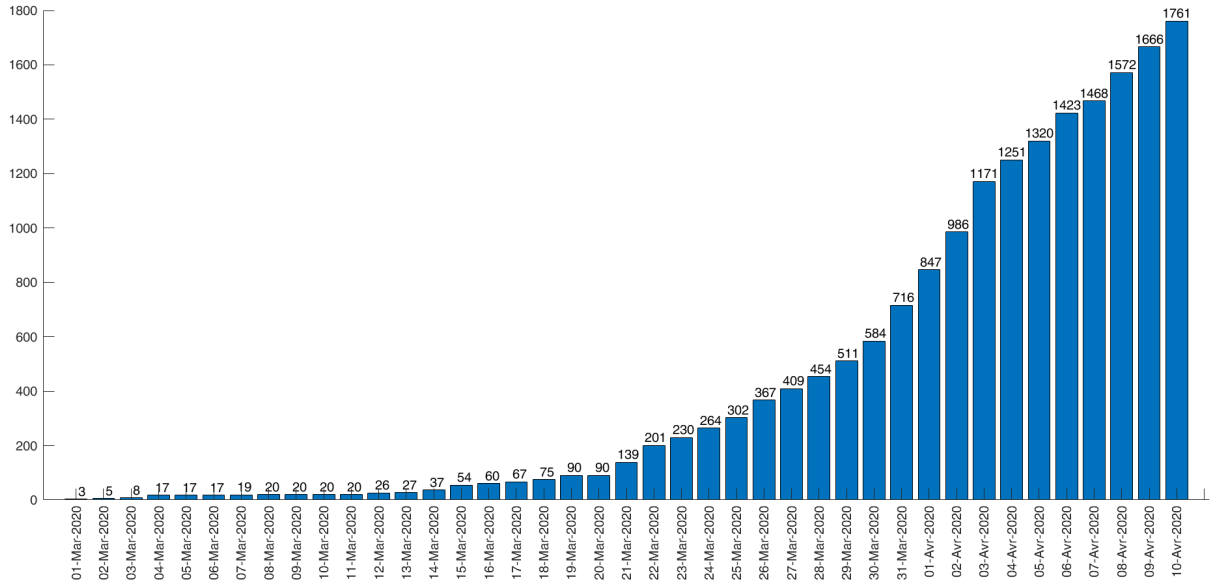


FIGURE 1. COVID-19 cases in Algeria, [1, 2].

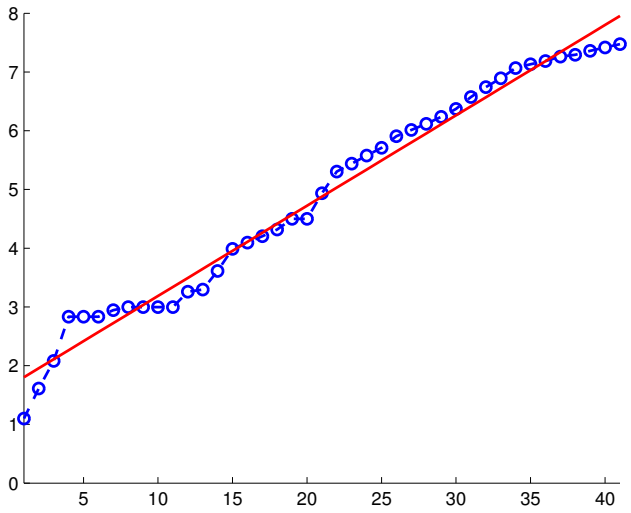


FIGURE 2. Neperian logarithm of the cumulative number of cases and linear regression lines.

2. The model without intervention

Multiple epidemiological models have been proposed to predict the spread of COVID-19 epidemic, we cite here the works of Liu et *al.* [10], where the authors developed a model of the COVID-19 epidemic in Wuhan, China. Magal and Webb [12] studied the spread of the epidemic in South Korea, Italy, France and Germany. Rong et *al.* [13] evaluated effects of delay in diagnosis on transmission of COVID-19. Kuniya [8] studied the prediction of the epidemic Peak of COVID-19 in Japan.

2.1. **Estimation of the $SEIR$ model parameters**

To model the dynamic of the disease and predict the number of COVID-19 cases in Algeria, we use a standard $SEIR$ model. We let $S(t)$, denote the fraction of individuals who are susceptible to the disease, that is, who are not (yet) infected at time t, $E(t)$ denotes the fraction of exposed or latent individuals that is, who are infected but not yet infectious at time t, $I(t)$ denotes the fraction of infected individuals, assumed infectious and able to spread the disease by contact with susceptible at time t. $R(t)$ corresponds to the fraction of cumulative number of known cases (infectious but confined at home, in hospital, recover or die from the disease) at time t.
The $SEIR$ model can be written as follows:

$$\frac{dS}{dt} = -\beta S(t)I(t), \tag{2}$$
$$\frac{dE}{dt} = \beta S(t)I(t) - kE(t), \tag{3}$$
$$\frac{dI}{dt} = kE - \alpha I, \tag{4}$$
$$\frac{dR}{dt} = \alpha I, \tag{5}$$
$$S(t) + E(t) + I(t) + R(t) = 1, \tag{6}$$

where β is the transmission rate per infectious individual, k is the infection rate calculated by the inverse of the average incubation period, based on the previous studies [8,9,14], we fix $1/k = 5$, and thus, $k = 0.2$. $1/\alpha$ is the average time in compartment "I" before isolation. It is more difficult to estimate α because, it depends not only on the biological characteristics of the virus but also on the promptness of isolation after symptom onset. Let's assume as in [5] that it's on the order of 1 day because when the patient senses the symptoms, he calls the medical center to come and take care of him on the same day.
Infected case data can then be used to estimate unknown epidemiological parameters, including the transmission rate β and the basic reproduction ratio $\mathcal{R}_0$. In the case of the $SEIR$ model, the predicted exponential growth rate, can be derived from a solution of the linearized dynamics near the Disease-Free Equilibrium (DFE) $(1, 0, 0, 0)$ [11,16]. The equations for E and I are decoupled and we obtain a linear system of the form

$$\frac{dE}{dt} = -kE + \beta I, \tag{7}$$
$$\frac{dI}{dt} = kE - \alpha I. \tag{8}$$

The predicted exponential growth rate, λ correspond to the largest eigenvalue of the Jacobian:

$$J = \begin{bmatrix} -k & \beta \\ k & -\alpha \end{bmatrix}. \tag{9}$$

It can be shown that the growth of the number of infected cases is an exponential of the form $I(t) \sim I_0 e^{\lambda t}$ where

$$\lambda = \frac{-(k+\alpha) + \sqrt{(k-\alpha)^2 + 4k\beta}}{2}. \tag{10}$$

In addition, initially, $S \approx 1$, thus, the incidence rate (number of new cases per day) $C = \beta SI$ also increases exponentially.
The basic reproduction number $\mathcal{R}_0$, which means the expected number of secondary cases produced by a single (typical) infection in a completely susceptible population [7] is calculated as the maximum eigenvalue of the next generation matrix FV^{-1} [11], where

$$J = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} \quad , \quad V = \begin{bmatrix} k & 0 \\ -k & \alpha \end{bmatrix}, \tag{11}$$

then

$$\mathcal{R}_0 = \frac{\beta}{\alpha}. \tag{12}$$

Note that β and $\mathcal{R}_0$ ca be inferred from λ. In fact, from (10), express β in terms of λ and substitute it into $\mathcal{R}_0$, we get

$$\beta = \big(\lambda + \alpha\big)\Big(1 + \frac{\lambda}{k}\Big) \quad \text{and} \quad \mathcal{R}_0 = \Big(1 + \frac{\lambda}{\alpha}\Big)\Big(1 + \frac{\lambda}{k}\Big). \tag{13}$$

Thus, it is possible to estimate β and $\mathcal{R}_0$ using the data set, we get,

$$\mathcal{R}_0 \approx 2.09 \quad , \ \beta = 2.09.$$

Adding (7) and (8), we obtain

$$\frac{d(E+I)}{dt} = (\beta - \alpha)I = (\mathcal{R}_0 - 1)\frac{dR}{dt}.$$

Hence, at the beginning of the epidemic, we obtain the same form as in [5]:

$$E(t) + I(t) + R(t) \approx \mathcal{R}_0 R(t). \tag{14}$$

2.2. **The final sizes of S_∞, R_∞ when no control measures are put into place.**

The final size relation gives a relationship between the basic reproduction number and the size of the epidemic, that is the number of members of the population who are infected over the corse of the epidemic [6].
Integration of the sum of the three equations (2), (3) and (4) from 0 to ∞ gives

$$R_\infty = 1 - S_\infty = \alpha \int_0^\infty I(t)dt. \tag{15}$$

Division of the equation (2) by S followed by integration from 0 to ∞ gives

$$-\log \frac{S_\infty}{S_0} = \beta \int_0^\infty I(t)dt = \mathcal{R}_0\big(1 - S_\infty\big). \tag{16}$$

Equation (16) gives implicitly S_∞ and therefore also the final epidemic size $R_\infty = 1 - S_\infty$. At the beginning of the epidemic, the initial fraction of infected people I_0 is small compared with the population size, so $S_0 \approx 1$, formula (16) can be rewritten using $S_\infty = 1 - R_\infty$ as

$$1 - R_\infty \approx e^{-\mathcal{R}_0 R_\infty}. \tag{17}$$

The number of new cases in Algeria will peak from around late may to early june and up to 82% of the Algerian population will likely contract the coronavirus if no measures were imposed, see Figure 3.

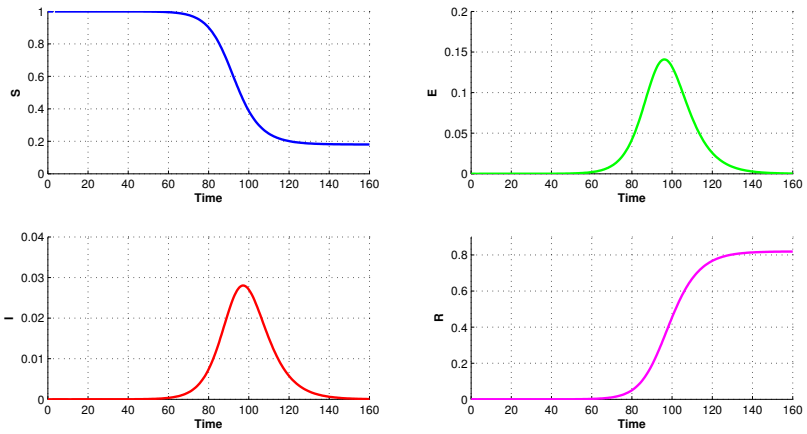


FIGURE 3. Solutions of $SEIR$ system (2)-(6), $S_0 = 1 - 10^{-7}, E_0 = 0, I_0 = 10^{-7}, R_0 = 0$. The total resident population in Algeria reached 43 million.

3. Integration of intervention strategies

In order to avoid this catastrophic situation and limit the exposure to the virus, partial "confinement" measures were imposed on some cities that have reported a highest number of contaminated cases. More people are being advised to self-isolate or to quarantine, they leave their homes only to buy essential items like food and medicine. Effects of the adopted policies on March 23 are not yet known. To help in the evaluation, we are using the fraction of individuals, susceptible, exposed and infectious outside the home u as a control variable, we generated different scenarios with varying values of this fraction in order to evaluate the effect of confinement and shelter-in-place measures on the spread of the coronavirus.

The susceptible individuals are divided into two sub-populations: unconfined (S_1): those individuals capable of contracting the disease and becoming themselves infectious, and self-quarantine susceptible (S_2) who are confined to their homes. Let $S(t) = S_1(t) + S_2(t)$, $E(t) = E_1(t) + E_2(t)$ and $I(t) = I_1(t) + I_2(t)$ be the fraction of total susceptible, exposed and infected individuals, respectively. All individuals, susceptible, exposed and infected can move to compartments S_1, E_1 and I_1, respectively, at rate m_2 by staying at home for quarantine. The self-quarantined individuals are released from quarantine at rate m_1. Thus the time scale of the movements of a typical individual is the day while the epidemic takes place on a time scale of several weeks. Therefore, we assume fast exchanges between the compartments with respect to the dynamics of the epidemics. Figure 4 shows how the disease is progressing from one sub-population to another.

In reality, the population is very heterogeneous. It includes different individuals, some in hospital or aged in a retirement home never moving. Others who are younger can go to work every day. Some may go out once or twice a day to play sports or shop. All these individuals, depending on their age, frequent various places where the risks of contact with other individuals and of infection can vary greatly. In the absence of precise information on the movements of the various age classes and categories of individuals, we have chosen to model the individual behavior of a super individual supposed to be representative on average of the entire population. The individual behavior of a typical individual is modeled with frequent exits from his home (compartment S_1) to the outside (compartment S_2) to go to work, to go shopping or to perform various tasks followed by daily returns to his home. For simplicity, we assume that the infection only occurs in compartment S_2. We neglect infections at home.

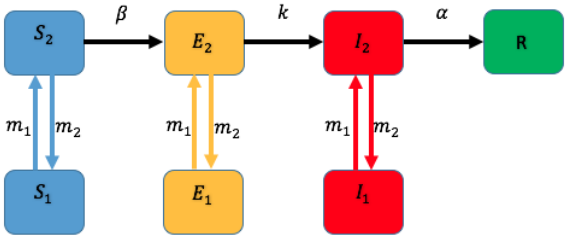


FIGURE 4. Flow diagram of the transmission dynamics of COVID-19.

The following complete model describes the time evolution of the epidemic:

$$\frac{dS_1}{d\tau} = m_2 S_2 - m_1 S_1, \tag{18}$$
$$\frac{dS_2}{d\tau} = m_1 S_1 - m_2 S_2 - \varepsilon\big(\beta S_2(t) I_2(t)\big), \tag{19}$$
$$\frac{dE_1}{d\tau} = m_2 E_2 - m_1 E_1 + \varepsilon\big(- kE_1\big), \tag{20}$$
$$\frac{dE_2}{d\tau} = m_1 E_1 - m_2 E_2 + \varepsilon\big(\beta S_2(t) I_2(t) - kE_2\big), \tag{21}$$
$$\frac{dI_1}{d\tau} = m_2 I_2 - m_1 I_1 + \varepsilon\big(kE_1 - \alpha I_1\big), \tag{22}$$
$$\frac{dI_2}{dt} = m_1 I_1 - m_2 I_2 + \varepsilon\big(kE_2 - \alpha I_2\big), \tag{23}$$
$$\frac{dR}{d\tau} = \varepsilon\big(\alpha I_1 + \alpha I_2\big), \tag{24}$$

where τ is the fast time, $t = \varepsilon\tau$ is the slow time and where $\varepsilon << 1$ is a small dimensionless parameter. The previous complete model can be reduced. As a first step, we consider the fast system which is obtained by setting $\varepsilon = 0$ in the complete system. In our case, the fast equilibrium can be easily calculated and is given by:

$$S_1^* = vS \quad , \quad S_2^* = uS, \quad E_1^* = vE \quad , \quad E_2^* = uE, \quad I_1^* = vI \quad , \quad I_2^* = uI, \tag{25}$$

where $v = \frac{m_2}{m_1+m_2}$ is the fraction of confined individuals at home and $u = (1 - v)$ is the fraction of individuals outside homes.
Using aggregation of variables methods [3, 4], a reduced model is obtained by substituting the fast stable equilibrium into the complete system and by adding two equations for susceptible populations. This leads to the following aggregated model at the slow time which is valid when the reduced system is structurally stable and for small value of $\varepsilon << 1$:

$$\frac{dS}{dt} = -\beta_1 S(t) I(t), \tag{26}$$
$$\frac{dE}{dt} = \beta_1 S(t) I(t) - kE(t), \tag{27}$$
$$\frac{dI}{dt} = kE - \alpha I, \tag{28}$$
$$\frac{dR}{dt} = \alpha I, \tag{29}$$

where $\beta_1 = u^2\beta$. This system is exactly the same as in the previous section except that the constant proportion u appears in the equations via the parameter β_1.
The total number of infected individuals since the beginning of the epidemic can easily be calculated based on the date of confinement T. We can repeat the same study by integrating between T and ∞, we obtain the following result:

$$\log \frac{S(\infty)}{S(T)} = -u^2\mathcal{R}_0\big(R(\infty) - R(T)\big), \tag{30}$$

and this leads to the form

$$1 - R(\infty) = S(T)e^{-u^2\mathcal{R}_0\left(R(\infty)-R(T)\right)}. \tag{31}$$

As control measures steps were taken at the beginning of the epidemic, we can combine (31) with (14) and we obtain

$$1 - R(\infty) \approx \big(1 - \mathcal{R}_0 R(T)\big)e^{-u^2\mathcal{R}_0\left(R(\infty)-R(T)\right)}, \tag{32}$$

which still cannot be solved explicitly. Nevertheless, since $u^2\mathcal{R}_0 < 1$ and $0 < R(\infty) - R(T) << 1$, the approximation $e^{-x} \approx 1 - x$ gives

$$1 - R(\infty) \approx \big(1 - \mathcal{R}_0 R(T)\big)(1 - u^2\mathcal{R}_0\big(R(\infty) - R(T)\big). \tag{33}$$

We finally obtained a result similar to that obtained in [5]

$$R(\infty) \approx \mathcal{R}_0 R(T)\frac{1-u^2}{1-u^2\mathcal{R}_0}. \tag{34}$$

When $u \to 0$, (corresponding to lockdown measures), the final size of the epidemic will be

$$R(\infty) \approx \mathcal{R}_0 R(T). \tag{35}$$

In order to manage the epidemic by confinement measures, it is very important to find out the unconfinement level u that is needed at time T_1 in order to stop definitively the epidemic, i.e. by avoiding a second peak after the first one.
In that frame, it is important to estimate the effective reproduction number $\mathcal{R}_0(t)$, defined by the expression

$$\mathcal{R}_0(t) = \begin{cases} \mathcal{R}_0 S(t) \ \text{ if } \ t < T. \\ \\ u^2\mathcal{R}_0 S(t) \ \text{ if } \ t \geq T. \end{cases} \tag{36}$$

The prevalence of the infection increases or decreases according to whether $\mathcal{R}_0(t)$ is greather than or less than one. We note

$$\mathcal{R}_0^\infty = \lim_{t\to\infty} \mathcal{R}_0(t) \approx u^2\mathcal{R}_0 S(\infty) = u^2\mathcal{R}_0(1 - R(\infty)).$$

Using (34), the effective reproduction number at ∞ is given as

$$\mathcal{R}_0^\infty \approx u^2\mathcal{R}_0\Big(1 - \mathcal{R}_0 R(T)\frac{1-u^2}{1-u^2\mathcal{R}_0}\Big). \tag{37}$$

Hence, if $\mathcal{R}_0^\infty < 1$, the epidemic is declining and is under control (vice versa if $\mathcal{R}_0^\infty > 1$). Consequently, there exists an unconfinement threshold u^* below which u must be chosen in order to stop the epidemic. Above that threshold, the epidemic is likely to reoccur:

$$u^* :\approx \frac{1}{\sqrt{\mathcal{R}_0}} \approx 0.69. \tag{38}$$

4. Discussion and conclusion

We can predict what will happen in Algeria according to the date of our partial and total confinement. The blue curves in Figures 5a, 5b, 5c and 5d simulate what could happen without any intervention, the worst-case scenario, the number of new cases in Algeria will peak from around late may to early june and up to 82% of the Algerian population will likely contract the coronavirus. The other two curves (red and green) in Figure 5a correspond to the prediction if partial confinement will be carried out moderately end-April ($v = 10\%$ in green) or severe ($v = 50\%$ in red).

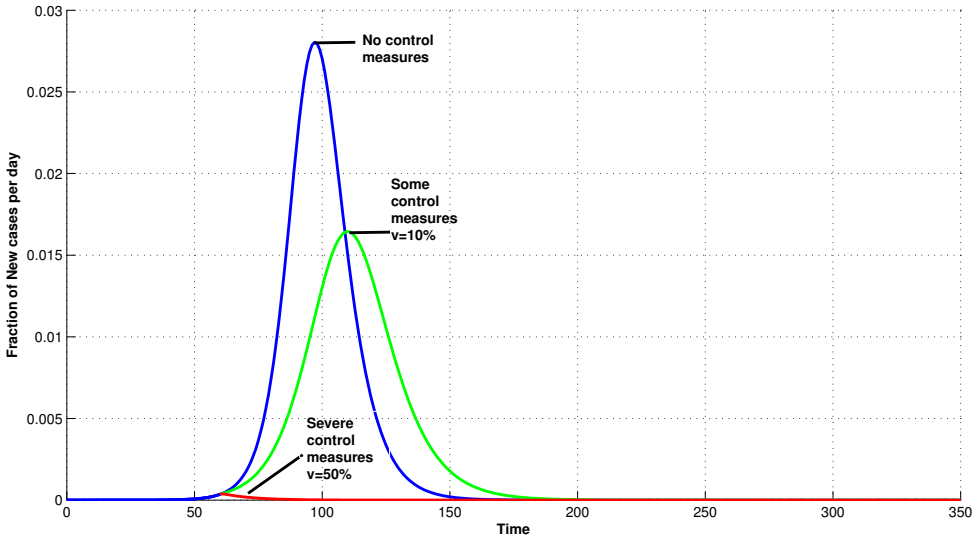
Figure 5b shows that the choice of the confinement date is very important. Indeed, an early date of partial confinement provokes a delay in the epidemic peak which is not desirable. From the economic point of view, we would favor a situation with an epidemic lasting less time in order to restart the economics faster. However, Figure 5b also shows that an early date of confinement decreases the amplitude of the peak which is of course very desirable from the point of view of hospitals and medicists which would be confronted to less patients at the same time and would be able to take care of all of them. Therefore, there is a balance to find between economic and medical needs. This balance is to be considered by decision makers.

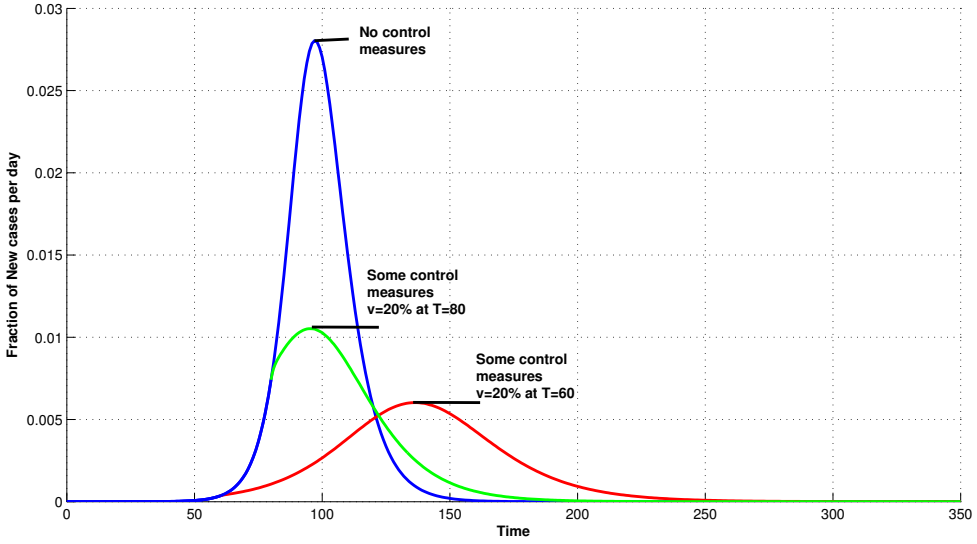
The curves in red in Figures 5c and 5d correspond to the lockdown. However, in the case of a lockdown at $T = 80$, when people are going to be unconfined, a second peak with large amplitude can occur if the proportion of unconfined persons is too large, that is if $u > u^*$. Figure 5c shows two cases of unsuccessful unconfinement, ($u = 0.8$ and $u = 0.9$ at $T = 110$), after lockdown with occurence of a second peak. Therefore, it is needed to unconfine at a level below the threshold $u < u^*$ in order to control definitively the epidemic. Figure 5d shows such a case of lockdown at $T = 80$ followed by successful unconfinement at $T = 110$ without resurgence of the epidemic. Our simulation shows that with confinement of only 35% of the population, it is possible to avoid a second epidemic peak. Taking into account, the proportion of people already contaminated by the first peak and cured, confining people at risk and elderly could be enough to prevent a resurgence of the epidemic after the first peak.

The confinement might also focus on persons who are not very involved in the economic activity (aged, retired, scholars, students, teachers) and those who can do teleworking. The confinement in each cluster should be done at the maximum level $v = 1 - u$ that would maintain a good level of the economic activity and allowing to avoid a second peak.

Our model aims to provide information on the dynamics of the epidemic in Algeria. It also makes it possible to study in general the effects of containment policies and what is very important and current of the measures to be taken for deconfinement. Our model is very simplified compared to reality. It models the set of individual behaviors by that of a super individual type who is believed to be representative of the entire population. We also assume that individuals are only infected in the outer compartment and that no infection occurs at home. We hope, however, that this simplified model provides insights and information for decision-makers.

In perspective, we would like to take into account different categories of individuals and model their movements in various places where the risks of contagion are different. For this, it would be necessary to consider several compartments S_1 instead of just one. Taking into account age classes also seems very important.


No control measures
Some control measures v=10%
Severe control measures v=50%
Fraction of New cases per day
Time
0.03
0.025
0.02
0.015
0.01
0.005
0
0
50
100
150
200
250
300
350


No control measures
Some control measures v=20% at T=80
Some control measures v=20% at T=60
Fraction of New cases per day
Time
0.03
0.025
0.02
0.015
0.01
0.005
0
0
50
100
150
200
250
300
350

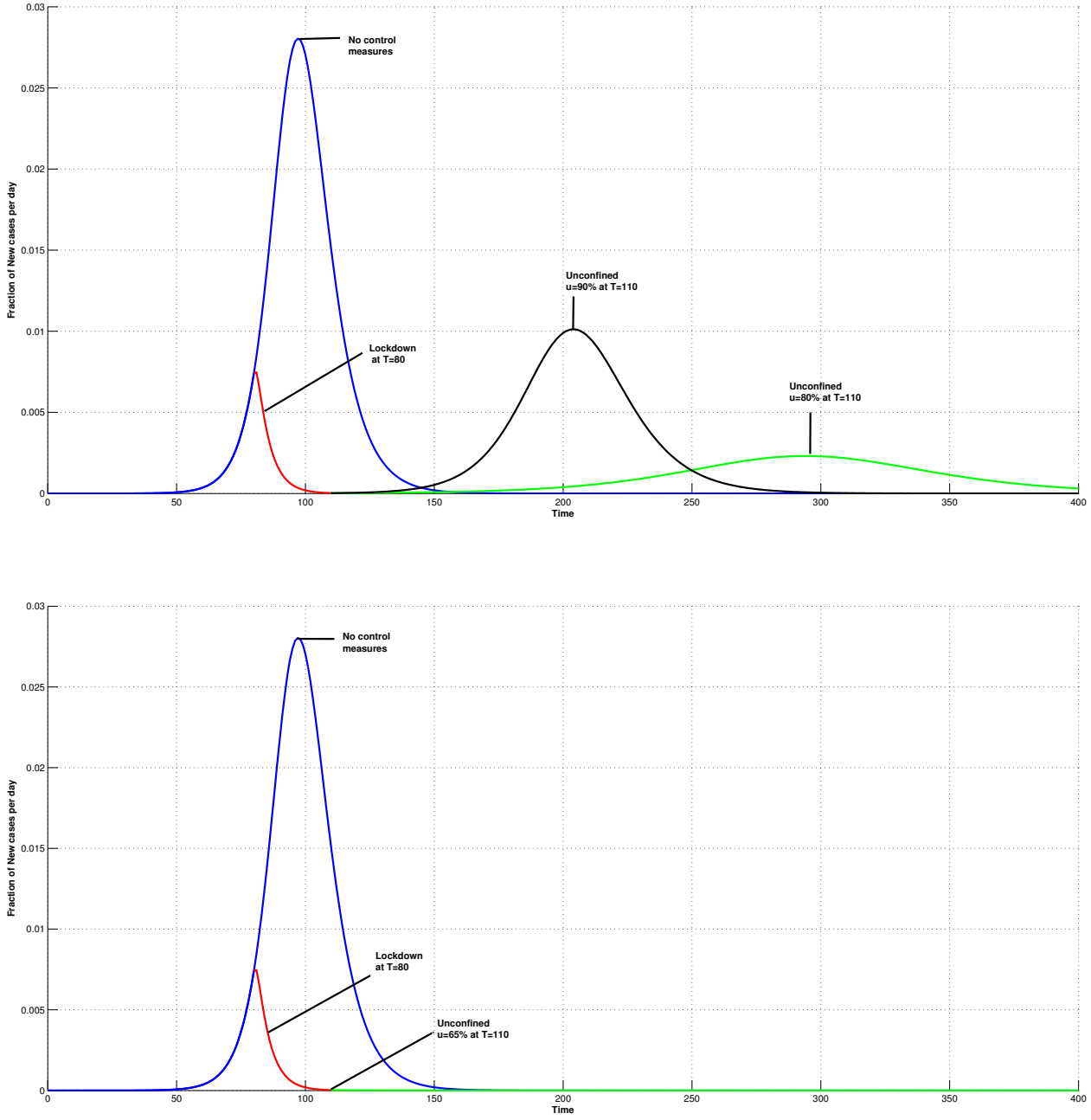


FIGURE 5. How Control Measures Could Slow the Outbreak. Without action (blue).
(5a) Some control measures ($v = 10\%$, green), severe control measures ($v = 50\%$, red).
(5b) Some control measures at $T = 60$ ($v = 20\%$, red), some control measures at $T = 80$ ($v = 20\%$, green).
(5c) Lockdown ($v = 100\%$, red) at $T = 80$ followed with unsuccessful unconfinement, either $u = 0.8$ or $u = 0.9$ at $T = 110$.
(5d) Lockdown ($v = 100\%$, red) at $T = 80$ followed with successful unconfinement at $T = 110$ ($u = 0.65$, green).

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