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The effect of quarantine measures in COVID-19

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Abstract

We consider deterministic SEIQR epidemic model for novel coronavirus (COVID-19). In addition to the classical SIR model, it takes into account the exposed and quarantined states. The objective of the study is to estimate epidemiological parameters for COVID-19 in the United Kingdom and understand the effect of various quarantine measures. The basic reproduction number is estimated to be 3.622. The findings suggest that weaker quarantine measures may be insufficient to fight with the disease.

Keywords: Dynamical systems, epidemic models, COVID-19, quarantine, parameter estimation, United Kingdom

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Mathematics is a very powerful interdisciplinary research tool that can be applied to various fields and life sciences is one of them. Especially starting with Kermack–McKendrick epidemic model (1927) the dynamical systems modeling of an infectious disease provides good insights on the prediction and simulation of epidemics. More specifically, Kermack–McKendrick divides the population at time moment t into three compartments S(t), I(t), and R(t) which are susceptible, infectious, and recovered individuals respectively. Assuming that the population is homogenously well mixed, the *Mass Action Law* gives that the rate of transmission of the disease is proportional to the product of S and I. The rate of removed individuals either due to death or recovery is assumed to be proportional to the current number of infectious individuals I. With these assumptions, using the model can be described mathematically as a system of nonlinear ordinary differential equations

$$\frac{dS}{dt} = -\beta SI/N$$

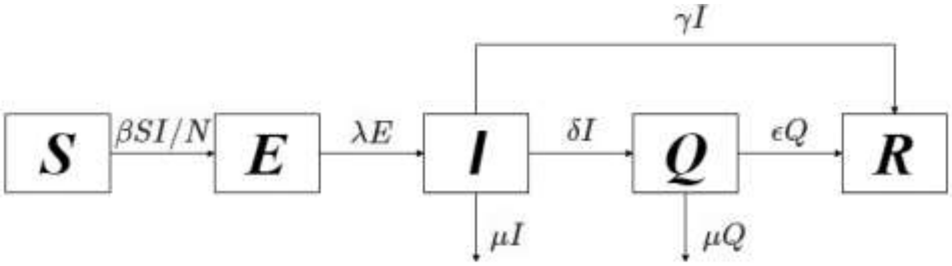
$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I$$

Here, N=S+I+R is the total population where the outbreak occurred, parameters $\beta, \gamma > 0$ are transmission and recovery rates, respectively, and $\mu > 0$ is the death rate due to the disease. One of the main questions of interest in the field of infectious diseases is to find out whether a particular disease is becoming an epidemic (or even worse a pandemic) or whether it will shortly disappear by itself. This question can be answered by estimating the so called *Basic Reproduction Number*, denoted by R_0, which is defined to be the average number of individuals (secondary cases) infected by one infectious individual. This means, when $R_0 > 1$, the number of infectious I will increase and cause and epidemic, while R_0<1 implies the disease will die out and epidemic does not occur. For I to increase, its derivative w.r.t. time should be positive. From the SIR model above, this implies that the term $\beta SI/N - \gamma I$ must be positive, that is, $\beta S/N > \gamma$. In the beginning of the disease we may safely assume that $S \approx N$, which in tern gives β/γ >1. In fact, formula for the reproduction number is given by $R_0 = \beta/\gamma$.

In December 2019, the first human cases of a novel coronavirus COVID-19, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), were identified in Wuhan, the capital city of Hubei province, China. After a while the COVID-19 pandemic is declared to be Public Health Emergency of International Concern by the World Health Organization (WHO). As of June 1, 2020 the total confirmed cases of COVID-19 is 5,976,360 with the death toll 364,523.

While it is possible to consider SIR to model COVID-19, we consider a more general and realistic version with five compartments instead of three. First of all, COVID-19 is found to have an incubation period, a time interval between exposure to the disease and showing first symptoms. Indeed, the mean incubation period is estimated to be 6.4 days (Backer, Klinkenberg, & Wallinga, 2020). We let E denote the compartment of exposed individuals. This means, it takes about 6.4 days on average until the exposed individuals transfer from E to I. Various early reports of the basic reproduction number for COVIS-19 ranges from 1.4 to 6.49, see e.g. (Liu, Gayle, Wilder-Smith, & Rocklöv, 2020) and references therein. Compared to previous coronaviruses SARS-COV (1.7–1.9) and MERS-COV (<1) these findings suggest that more stringent measures should be employed by the governments including lockdowns and quarantines for control and prevention of COVID-19. To this end, we include quarantine compartment, Q in our model. Below is the transmission diagram of the general model.



As a system of ordinary differential equation we have we obtain the following *SEIQR* model:

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \lambda E$$

$$\frac{dI}{dt} = \lambda E - \delta I - \gamma I - \mu I$$

$$\frac{dQ}{dt} = \delta I - \epsilon Q - \mu Q$$

$$\frac{dR}{dt} = \gamma I + \epsilon Q$$

Here, $\lambda > 0$ is the incubation rate which is taken to be the inverse of incubation period., $\delta \geq 0$ is the rate of transfer of infectious individuals to quarantine, $\epsilon > 0$ is the recovery rates from quarantine.

Our goal in this article is to calculate the formula for basic reproduction number R_0 and carry data analysis to estimate the model parameters. Finally, we show how the quarantine parameter δ affects the control of the disease and final value of confirmed cases.

In the next section we use the next-generation matrix to calculate the formula for R_0. We then fix some of the model parameters as reported in early studies and estimate remaining parameters using the up to date dataset provided by Johns Hopkins University. We then vary the parameter δ to simulate possible scenarios. Finally, we end with a discussion section interpreting the results and findings.

Formula for basic reproduction number

We note that in the literature there are many generalities of *SIR* model and our model *SEIQR* is not an exception. Following (Allen & Van den Driessche, 2008) we use next-generation matrix to find the formula for the basic reproduction number. To this end, we let

$$\mathcal{F} = (\beta SI/N, 0,0) \text{ and } \mathcal{V} = (\lambda E, -\lambda E + (\delta + \gamma + \mu)I, -\delta I + (\epsilon + \mu)Q).$$

Next, we compute Jacobian matrices at the disease free equilibrium: $S = N, E = 0, I = 0, Q = 0$. It gives

$$\partial\mathcal{F} = \begin{pmatrix} 0 & \frac{\beta S}{N} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and } \partial\mathcal{V} = \begin{pmatrix} \lambda & 0 & 0 \\ -\lambda & \delta + \gamma + \mu & 0 \\ 0 & -\delta & \epsilon + \mu \end{pmatrix}.$$

Setting $S = N$ and computing the spectral radius of $\partial\mathcal{F}(\partial\mathcal{V})^{-1}$ we see that

$$R_0 = \frac{\beta}{\delta + \gamma + \mu}.$$

Epidemic parameter estimation

For incubation rate we let $\lambda = 1/6.4 = 0.156$ (Backer, Klinkenberg, & Wallinga, 2020). On the other hand, the recovery rate, the inverse of recovery period, is taken to be $\gamma = \epsilon = 1/10.91$ (You, et al., 2020). We consider United Kingdom COVID-19 data provided by Johns Hopkins University (Coronavirus 2019-nCoV, 2020). Figure 1a shows the I(t) since the first occurrence of the positive case in UK. For the death rate we simply consider the ratio of deaths in UK to total confirmed cases to the date. This gives $\mu = 37460/267240 = 0.14$. To estimate β we restrict ourselves for the first 60 days of the data when approximately exponential increase occurred with almost no quarantine measures, that is, $\delta = 0$. The UK population is taken to be *N*= 66,650,000. The nonlinear least square curve fit is shown in Figure1b and β is estimated to be 0.8404, mean square error 35.

Infectious individuals in UK and least square fit

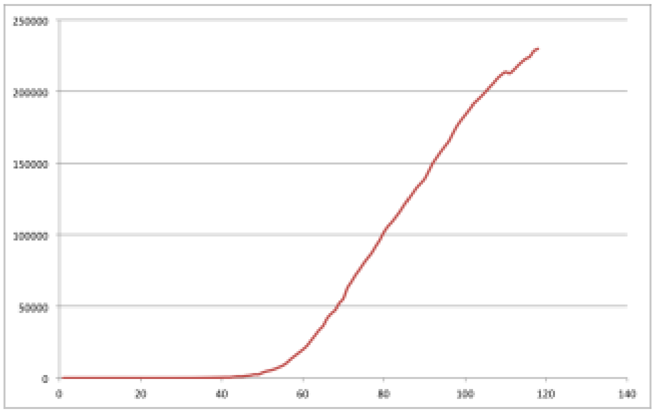


Figure 1a. Number of infectious individuals in UK at time *t*, starting from January 31, 2020

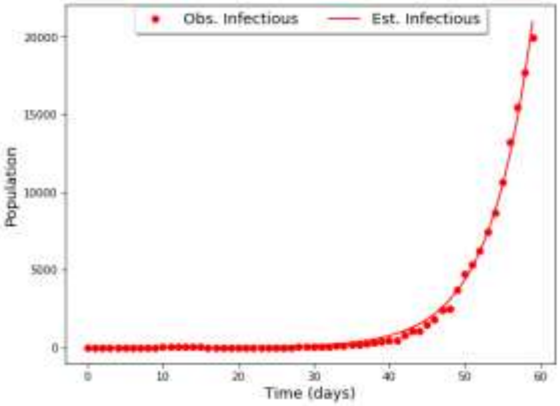


Figure 1b. Nonlinear least square curve fitting to the first 60 days of the data

Putting all the parameters together we have following result, Table 1.

Table 1. Epidemiological parameters for COVID-19 in UK.

Parameter	Value
Transmission rate β	0.8404
Incubation rate λ	0.156
Death rate μ	0.14
Recovery rate γ	0.092
Reproduction number R_0	3.622

Here the basic reproduction number is calculated using the formula from the previous section. The two-hundred-day prediction of the COVID-19 since January 31 without any quarantine measures is shown in Figure 2.

SEIQR forecasting: COVID-19 in UK starting at January 31

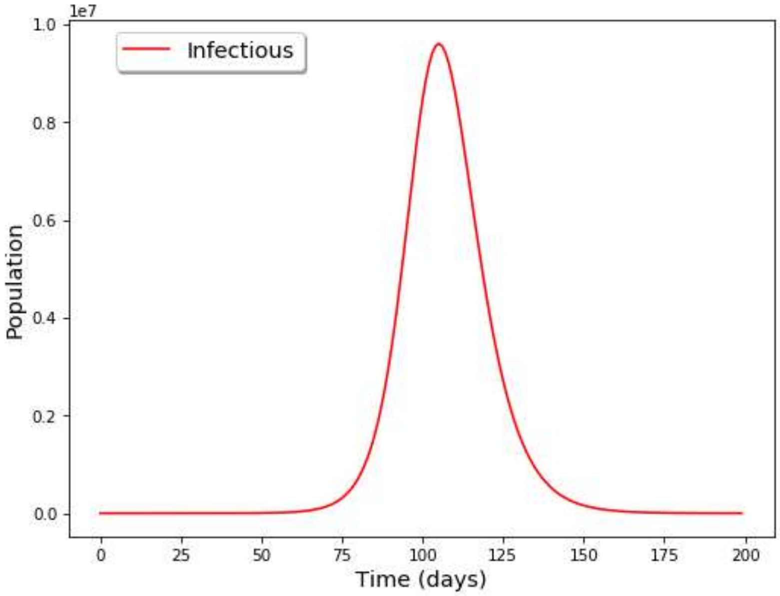


Figure 2. The simulation of SEIQR model with $\delta = 0$.

Quarantine effect

We now turn to see how the change in quarantine measures δ affects the size of the confirmed cases. We vary δ in the range of [0.1, 1] where 0.1 means almost no quarantine measures and 1 means strict quarantine measures. Results are depicted in Figure 3 and 4.

Weaker quarantine measures

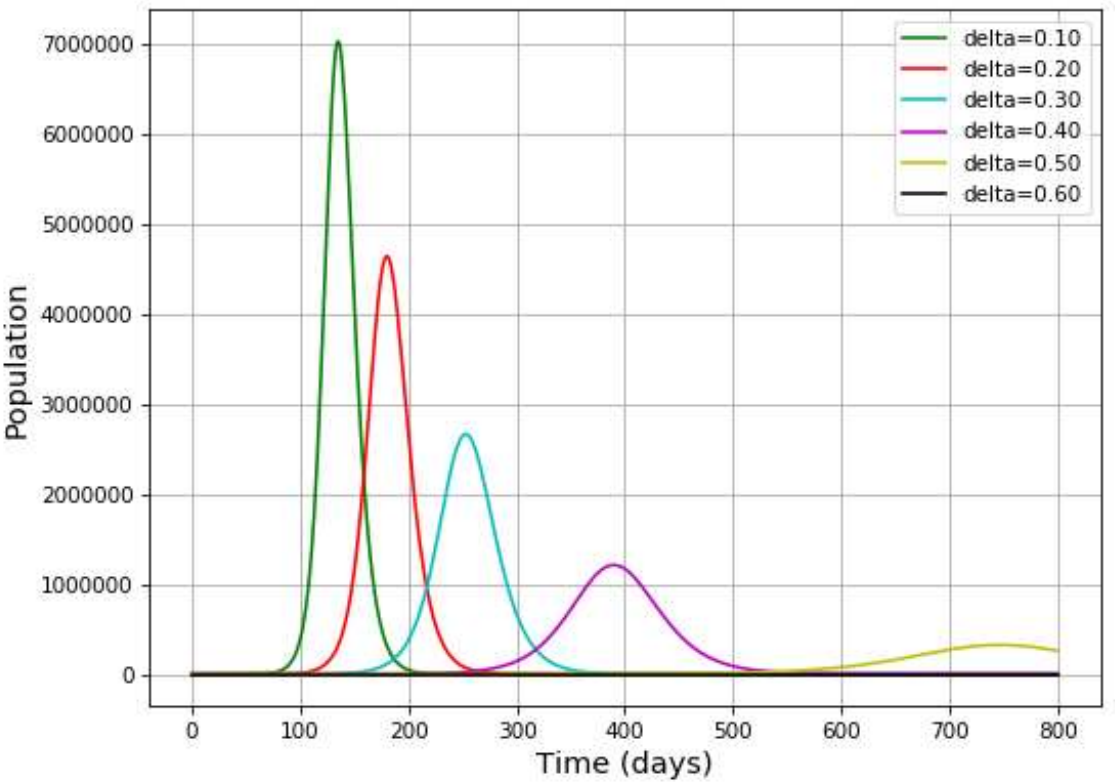


Figure 3. Infectious individuals I(t) for smaller delta values.

Stricter quarantine measures

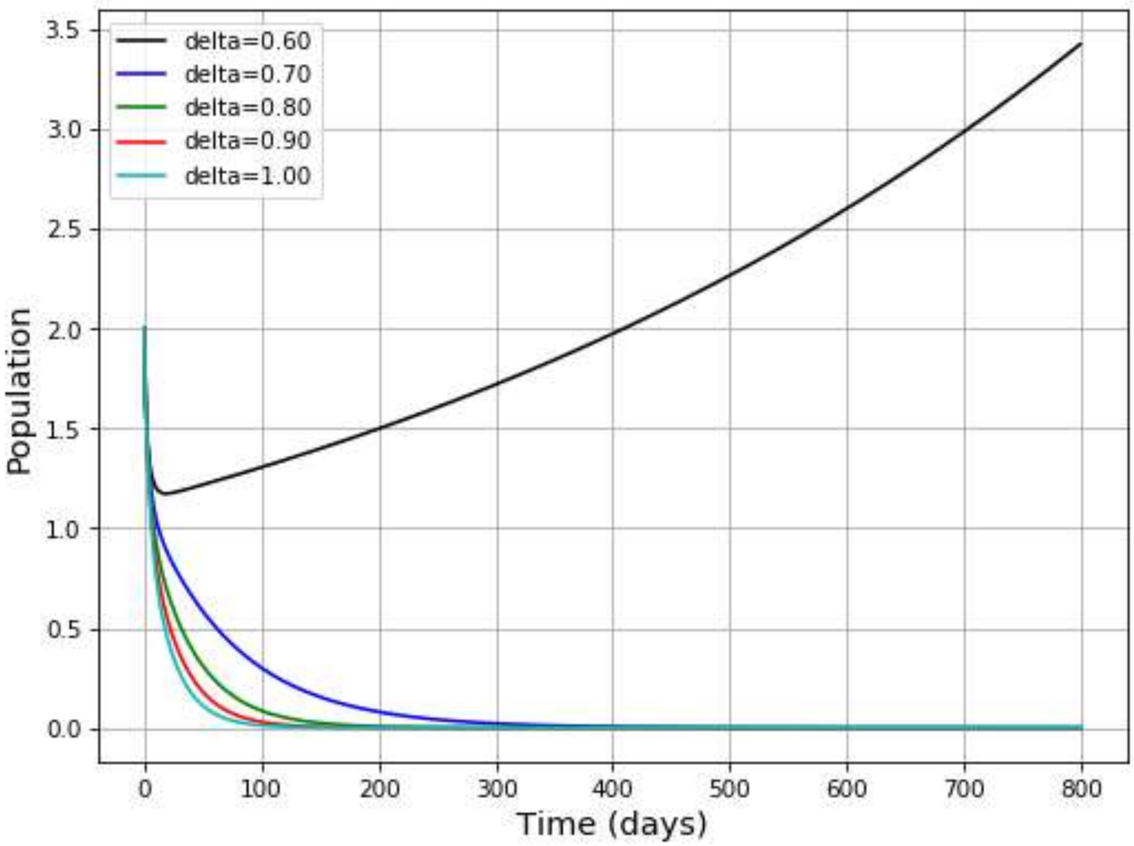


Figure 4. Infectious individuals I(t) for larger delta values.

We see from two figures that there is a threshold value (bifurcation) around $\delta \approx 0.6$.

Discussion and conclusion

In this article we studied SEIQR mathematical epidemic modeling of COVID-19 with real data. The estimated reproduction number $R_0 = 3.622$ is within the range reported in early results from different countries. Without any quarantine measure, the disease would eventually die out within 175 days since the start of January 31, that is, until mid July. However, if there are some mild quarantine measures applied then the disease may persist over a year, however this may help to sustain the epidemic within healthcare capacity. With the stricter quarantine measure the COVID-19 can be overcome within a very short period as shown in Figure 4. Recall that the basic reproduction number is given by $R_0 = \beta/(\delta + \gamma + \mu)$, and that our reported parameters from Table 1 are $\beta = 0.8404, \gamma = 0.092, \mu = 0.14$. This gives,

$$R_0 = \frac{0.8404}{\delta + 0.232}.$$

Hence, if $\delta < 0.8404 - 0.232 = 0.6084$, then $R_0 > 1$ and we have the epidemic, otherwise if $\delta \geq 0.6084$ we have $R_0 \leq 1$ and hence the epidemic is controlled. So, $\delta = 0.6084$ is the threshold (bifurcation) and to win the virus the quarantines rate must be more than $\delta = 0.6084 = 60.84\%$.

Lock down or quarantine measure cannot be applied indefinitely and hence a better model would be to consider a time-dependent quarantine rate. This makes the model non-autonomous and theoretical approach may be no so easy.

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