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*Quantitative Effects of COVID-19 Pandemic Containment Policies*

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## **Title: Quantitative Effects of COVID-19 Pandemic Containment Policies**

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### **Abstract:**

Countries are implementing containment policies to fight the coronavirus 2019 pandemic. We extend the susceptible-exposed-infectious-recovered (SEIR) model to include asymptomatic cases, which account for around 20%. We consider the cumulative confirmed and death cases in Italy and South Korea for our model estimation. The data for Italy, collated up to March 14, 2020, are not affected by any containment policy, whereas the data for South Korea collated up to the end of April 2020 reflect four containment policies: social distancing, preemptive quarantine, testing and quarantine of symptomatic or asymptomatic patients. Our policy experiments show that the testing and quarantine of symptomatic patients are very effective to contain, but not enough to extinguish, the epidemic. Thus, testing and quarantine should include the asymptomatic cases as well.

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## 1. Introduction

The World Health Organization (WHO) declared the coronavirus disease 2019 (COVID-19) a pandemic on March 11, 2020. As of June 23, the world had reported 9.2 million confirmed cases and 474,425 deaths (1). Most countries are still affected by the virus. Even worse, some experts are expecting a second wave of the pandemic later this year (2).

To reduce the COVID-19 transmission, policymakers have introduced a variety of non-pharmaceutical interventions. However, these interventions are often adopted without rigorous empirical evidence (3). A distinguishing feature of COVID-19 is the presence of asymptomatic patients. This could change the transmission channel dramatically. Lack of symptoms renders the existing susceptible-exposed-infectious-recovered (SEIR) models incapable of projecting the virus spread and evaluating the policy interventions for the current pandemic. We extended the SEIR model to include asymptomatic cases and found that the policy of tracking, testing, and quarantining both symptomatic and asymptomatic patients is most effective.

## 2. Methods

The scientific community is continuously gaining knowledge on the COVID-19 virus but still remains far from fully understanding its features. One feature not yet fully understood is how the virus transmits the disease. On June 11, 2020, the WHO stated that asymptomatic patients are much less likely to transmit the virus than those with symptoms (4), but the next day a top WHO official clarified that scientists have not yet determined how frequently the asymptomatic cases, which may include mild symptoms that are not recognized as COVID-19 infection, transmit the virus. (5).

Asymptomatic cases should not be ignored. South Korean public health officials have estimated that 20% to 30% of infected patients can be asymptomatic and yet show a very high transmission rate (6). Iceland

tested a random sample of 17,900 persons for COVID-19 and found that 50% of the infected had no symptoms (7). Although controversial and yet to be confirmed, the transmissibility of asymptomatic cases is an important distinguishing feature of the COVID-19 virus; this is quite different from the other coronaviruses that spread earlier, such as the Severe Acute Respiratory Syndrome (SARS) or Middle East Respiratory Syndrome (MERS) viruses.

The SEIR model has been used to project the spread of epidemic diseases but it has a serious drawback to apply to the current pandemic – the lack of asymptomatic infected in the model. Asymptomatic patients experience mild symptoms, if any, but do not recognize themselves as COVID-19 infected. Because of their little or no symptoms, they tend to remain untested and still spread the virus.

Our model extends the standard SEIR model to cover the infectious asymptomatic patients as in Figure 1. The right-hand side of Figure 1 with a square box shows the quarantined status that cannot transmit the virus. The left-hand side of the figure with a circle presents the patients who can transmit the virus. The standard SEIR model nested in our extended model is shown with a red circle in Figure 1. Asymptomatic cases are presented with a gray background ( $I_A$ ,  $Q_A$ ).

Those infected with the virus are divided into four groups: (1) symptomatic patients who are not yet tested and confirmed ( $I_S$ ); (2) asymptomatic patients who are not yet tested and confirmed ( $I_A$ ); (3) symptomatic patients who are tested and confirmed ( $Q_S$ ); and (4) asymptomatic patients who are tested and confirmed ( $Q_A$ ). All confirmed patients are assumed quarantined and so do not transmit the disease anymore.

An individual belongs to one of the following eleven distinctive states evolving over time and characterized by a set of first-order differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= -(b_A + q(1 - b_A))kS(t)I_A(t) - (b_S + q(1 - b_S))kS(t)I_S(t) + q(1 - b_A)kS(t - \tau_Q)I_A(t - \tau_Q) \\
&\quad + q(1 - b_S)kS(t - \tau_Q)I_S(t - \tau_Q) \\
\frac{dS_Q}{dt} &= q(1 - b_A)kS(t)I_A(t) + q(1 - b_S)kS(t)I_S(t) - q(1 - b_A)kS(t - \tau_Q)I_A(t - \tau_Q) \\
&\quad - q(1 - b_S)kS(t - \tau_Q)I_S(t - \tau_Q) \\
\frac{dE}{dt} &= (1 - q)b_AkS(t)I_A(t) + (1 - q)b_SkS(t)I_S(t) - \gamma_E E(t) \\
\frac{dE_Q}{dt} &= qb_AkS(t)I_A(t) + qb_SkS(t)I_S(t) - \gamma_E E_Q(t) \\
\frac{dI_A}{dt} &= (1 - \psi_E)\gamma_E E(t) - (\gamma_I + d_A)I_A(t) \\
\frac{dQ_A}{dt} &= (1 - \psi_E)\gamma_E E_Q(t) + d_A I_A(t) - \gamma_I Q_A(t) \\
\frac{dI_S}{dt} &= \psi_E \gamma_E E(t) - (\gamma_I + d_S)I_S(t) \\
\frac{dQ_S}{dt} &= \psi_E \gamma_E E_Q(t) + d_S I_S(t) - \gamma_I Q_S(t) \\
\frac{dR_A}{dt} &= \gamma_I I_A(t) + \gamma_I Q_A(t) \\
\frac{dR_S}{dt} &= (1 - \delta_S)\gamma_I I_S(t) + (1 - \delta_S)\gamma_I Q_S(t) \\
\frac{dD}{dt} &= \delta_S \gamma_I I_S(t) + \delta_S \gamma_I Q_S(t)
\end{aligned}$$

An individual starts a day as susceptible to the virus ( $S$ ) and makes  $k$  contacts with infected patients, both symptomatic and asymptomatic. The individual becomes infected with probability  $b_S$  following contact with an  $I_S$  patient and with probability  $b_A$  following contact with an  $I_A$  patient. A fraction  $q$  of the contacted population, that is,  $q(kS(t)I_A(t) + kS(t)I_S(t))$ , are quarantined as a preemptive measure. Of these,  $q(1 - b_A)kS(t)I_A(t) + q(1 - b_S)kS(t)I_S(t)$  cases turn out uninfected, while ( $S_Q(t)$ ) cases are released to state  $S(t)$  in  $\tau_Q$  days.

The remaining  $qb_AkS(t)I_A(t) + qb_SkS(t)I_S(t)$  cases are exposed to the virus and enter the presymptomatic (incubation) period; they are in state  $E_Q$ . Of these cases, those not preemptively quarantined, that is,  $(1 - q)b_AkS(t)I_A(t) + (1 - q)b_SkS(t)I_S(t)$  cases, are infected, and are in state  $E$ . An individual in incubation, whether in state  $E_Q$  or  $E$ , exits with probability  $\gamma_E$ . On exit, the individual in state  $E_Q$  either develops symptoms and transits to the quarantined symptomatic state  $Q_S$  with probability

$\psi_E$ , or does not develop symptoms and transits to the quarantined asymptomatic state  $Q_A$  with probability  $1 - \psi_E$ . An individual in state  $E$  faces the same situation. She becomes a symptomatic infected patient ( $I_S$ ) with probability  $\psi_E$ , or an asymptomatic infected patient ( $I_A$ ) with probability  $1 - \psi_E$ . A symptomatic (asymptomatic) infected patient has the probability  $d_S$  ( $d_A$ ) of being tested, confirmed, and quarantined, and hence switches to state  $Q_S$  ( $Q_A$ ).

All infected persons, whether in state  $Q_S$ ,  $Q_A$ ,  $I_S$ , or  $I_A$ , have the same probability of  $\gamma_I$  to exit from their respective states. Those exiting from asymptomatic states  $I_A$  and  $Q_A$  fully recover and become immune to the disease ( $R_A$ ). However, those exiting from symptomatic states  $I_S$  and  $Q_S$  either recover fully and become immune to the disease ( $R_S$ ) with probability  $1 - \delta_S$  or succumb to the disease ( $D$ ) with probability  $\delta_S$ .

Model parameters  $\psi_E$ ,  $\gamma_E$ ,  $\gamma_I$ ,  $b_A$ , and  $b_S$  are disease characteristics assumed to be universally constant. The mortality of the infected,  $\delta_S$ , depends on the virus-specific characteristics and the medical environment.

Some parameters depend on the containment policies ( $k, q, \tau_Q, d_A, d_S$ ). Parameter  $k$  depends on the socio-economic factors and containment policies, such as social distancing or lockdown. The probability and period of preemptive quarantine,  $q$  and  $\tau_Q$ , reflect the intensity of the precautionary measures. Model parameter  $d_A$  is non-zero if and only if asymptomatic patients are aggressively tracked, tested, and quarantined. However, parameter  $d_S$  would be non-zero even with no containment measure since some symptomatic patients will be confirmed and quarantined when they are hospitalized. We denote this un-intervened parameter  $d_S$  as  $d_S^0$ . Parameter  $d_S$  would increase as the society continues to intensively track, test, and quarantine.

Let us next define the newly confirmed asymptomatic and symptomatic cases  $F_A$  and  $F_S$  and the cumulative confirmed asymptomatic and symptomatic cases  $C_A^F(t)$  and  $C_S^F(t)$ , respectively. From the equations of  $\frac{dQ_A}{dt}$  and  $\frac{dQ_S}{dt}$ , we have

$$F_A(t) = (1 - \psi_E)\gamma_E E_Q(t) + d_A I_A(t) \text{ and } F_S(t) = \psi_E \gamma_E E_Q(t) + d_S I_S(t).$$

Therefore,  $C_A^F(t) = C_A^F(0) + \int_0^t F_A(s)ds$  and  $C_S^F(t) = C_S^F(0) + \int_0^t F_S(s)ds$ . The  $C_A^F(t)$  and/or  $C_S^F(t)$  are ones we will match with observed data to fit the model.

By taking the next-generation matrix approach, we can derive the basic reproduction number ( $R_0$ ) of our model as follows:

$$R_0 = (1 - q)k \left( \frac{b_A}{\gamma_I + d_A} (1 - \psi) + \frac{b_S}{\gamma_I + d_S} \psi \right).$$

When un-intervened  $k$  becomes  $k^0$  with no policy intervention, we have

$$R_0^{ref} = k^0 \left( \frac{b_A}{\gamma_I} (1 - \psi) + \frac{b_S}{\gamma_I + d_S^0} \psi \right).$$

The data provide the cumulative number of positive cases and deaths for the two countries on a daily basis. Some characteristic disease parameters are adopted from earlier studies; for example,  $\gamma_E$  and  $\gamma_I$  are adopted from Wang et al. (2020) (8). Parameter  $\tau_Q$  is set to 14 days, representing the prevailing practice. We estimate the model assuming  $\psi_E = 0.8$ , which means that the fraction of asymptomatic patients is 20%.

We choose Italy and South Korea (Korea hereafter) because they contrast in terms of containment measures, at least at the initial stage of the COVID-19 spread. The data for Italy that we use are up to March 14, 2020. The Italian government implemented country wide quarantine on March 9, 2020 but it took some time to show the effects. Therefore, we assume that Italy did not adopt any active containment measures during this period. Thus, the Italian data parameter values for this period are not affected by containment policy measures such as  $(k^0, d_S^0, \delta_{S,Italy})$ .

In contrast, Korea adopted aggressive measures to identify and quarantine the infected. The Korean data we use are up to April 30, 2020. Since January 20, 2020, when the first patient was identified in Korea,

the Korea Center for Disease Control (KCDC) has been conducting complete epidemiologic surveys and testing all those who had contacts with confirmed patients. In addition, those who had any contact with confirmed patients are advised to go on a 14-day self-quarantine. The daily increase in confirmed cases continued in one-digit numbers until February 18, 2020, but a super spread in the Daegu area abruptly raised the newly confirmed cases to 20 on February 19. The daily increase in confirmed cases soared to 813 at the peak. Still, the KCDC continued the procedure of complete epidemiologic surveys and testing. When a patient is confirmed, epidemiologists track all the possible contacts of the patient from two days prior to symptom development and notify the contacts to immediately take polymerase chain reaction (PCR) tests. The confirmed patient's movement information during the potentially dangerous time are publicly released so that people with possible contact can have themselves tested. To accommodate the sharp increase in test demand, a coronavirus drive-through testing station was introduced on February 26 (9). An enormous number of PCR tests and quarantines continued each day until the newly confirmed cases in the Daegu area went down to one-digit numbers. Those found positive were quarantined in government facilities, and those who tested negative were advised to go on self-quarantine for 14 days.

We find that the data from Korea reflect the effects of the containment measures. For further analysis, we divide the data into two subperiods, up to February 26, 2020 (February 26 included), and from February 27 to April 30, 2020, and then estimate the Korean parameters  $(q^1, k^1, d_{S,1}, d_{S,2}, d_{A,1}, d_{A,2}, \delta_{S,Korea})$ . We keep Korea's parameters  $q$  and  $k$  constant over the periods because Korea adopted no policies that could change them drastically. Parameters  $b_A, b_S$  are set equal in both countries.

The number of cumulative positive cases in Italy and Korea during the sample periods reflects the intensities of their respective containment measures. Italy did not adopt aggressive steps to identify infected people. Those with symptoms were tested and confirmed positive only when they visited a hospital. Therefore, the confirmed cases in Italy capture only the symptomatic patients. In contrast, Korea

adopted intensive testing and tracking based on epidemiological surveys, and so their confirmed cases include both symptomatic and asymptomatic patients.

We used a fourth-order Runge–Kutta method solve our model numerically with given set of parameters.

We denote the equations for parameters  $(k^0, d_S^0, \delta_{S,Italy})$  and  $(b_A, b_S)$  with subscript “*Italy*,” such as

$C_{S,Italy}^F(t)$  and  $D_{Italy}(t)$ , for notational brevity. Likewise, we denote the equations with subscript

“*Korea*,” such as  $C_{S,Korea}^F(t)$ ,  $C_{A,Korea}^F(t)$ , and  $D_{Korea}(t)$ , for parameters

$(q^1, k^1, d_{S,1}, d_{S,2}, d_{A,1}, d_{A,2}, \delta_{S,Korea})$  and  $(b_A, b_S)$ .

We fit  $C_{S,Italy}^F(t)$  to Italy’s reported number of cumulative confirmed cases, and  $C_{S,Korea}^F(t) +$

$C_{A,Korea}^F(t)$  to Korea’s reported number of cumulative confirmed cases. We also fit  $D_{Italy}(t)$  to the

Italian and  $D_{Korea}(t)$  to the Korean cumulative death toll data. All these data are converted into fractions

of the respective countries’ total population. The model parameters are estimated after minimizing the

sum of the root mean squared prediction errors.

### 3. Results

We show the estimated parameter values in Table 1. The number of contacts for parameter  $k$  is 2.07 and

for parameter  $k^0$  is 1.49 for Korea. Parameter  $d_S^0$  is estimated to be 0.0287, implying that less than 3% of

symptomatic patients are tested in Italy. Parameter  $d_{S,1} = 0.0083$  and parameter  $d_{S,2} = 0.8829$ ,

indicating that Korea tested 0.8% and 88% of symptomatic patients before and after February 26,

respectively. Similarly, parameter  $d_{A,1} = 0.0668$  and parameter  $d_{A,2} = 0.2159$ , implying that Korea

tested 6.7% and 21.6% of asymptomatic patients before and after February 26, respectively. From these

estimates, the basic reproduction rates are computed as 7.27 for  $R_0^{ref}$ , and 4.83 and 0.56 respectively for the two periods for Korea.

We show the number of cumulative positive cases in Supplement Figure 1(A) and deaths in Supplement Figure 1(B) for Italy during the first 50 days of the pandemic. The red bars represent the actual data, while the black solid line represents the estimated  $C_{S,Italy}^F(t)$ . Supplement Figures 2(A) and 2(B) give the same parameters for Korea during the first 120 days of the pandemic. As the figures indicate, the estimated model fits the data very well.

We use the estimated model to analyze the effectiveness of the four measures, each of which helped Korea to contain the pandemic without lockdown, unlike other countries. First, Korea strongly encouraged the use of masks and social distancing. These practices are believed to have led to a smaller  $k$  than  $k^0$  in Korea, in line with the estimation. The Korean government strictly implemented the following three containment measures: preemptive quarantine ( $q$ ), intensive testing, and quarantine for both symptomatic ( $d_S$ ) and asymptomatic ( $d_A$ ) patients. The common purpose of social practice (reducing  $k$ ) and the three policy measures is to protect the susceptible from infection.

We carry out a series of policy simulations to evaluate the effectiveness of these measures. An imaginary society whose parameters are initially set at  $(q, k, d_S, d_A) = (0, k^0, d_S^0, 0)$  implements policies that change  $(q, k, d_S, d_A)$  to  $(q^1, k^1, d_{S,2}, d_{A,2})$ . The simulated policies are  $(0, k^0, d_S^0, 0)$  to  $(q^1, k^0, d_S^0, 0)$ ;  $(0, k^0, d_S^0, 0)$  to  $(0, k^1, d_S^0, 0)$ ;  $(0, k^0, d_S^0, 0)$  to  $(0, k^0, d_{S,2}, 0)$ ; and  $(0, k^0, d_S^0, 0)$  to  $(0, k^0, d_{S,2}, d_{A,2})$ . Each of these policies is introduced on the 50th day of the pandemic. The four policies are denoted as “ $q$ ,” “ $k$ ,” “ $d_S$ ,” and “ $(d_S, d_A)$ ” in Figure 2. We used  $\delta_{S,Italy}$  for policy simulations.

The figure compares the policy experiment results with the results with no intervention. Figure 2(A) shows the fraction of newly confirmed cases during the first 150 days. In the absence of containment measures, the fraction of newly confirmed cases would peak on the 70th day to 6.8% of the population. Preemptive quarantine (a higher  $q$ ) does not delay the peak, but lowers it to 4.9%.

The  $d_S$  test and quarantine for symptomatic patients is the most effective containment measure. It would delay the peak to the 103th day and lowers it to 1.9%. However, testing and quarantine of symptomatic patients cannot extinguish the epidemic because the asymptomatic patients would go unnoticed. The final policy experiment ( $d_S, d_A$ ) is to adopt the two containment measures, testing and quarantine, for both symptomatic and asymptomatic patients; this can be implemented only through an epidemiological survey. This combined approach would gradually bring down the newly confirmed cases.

Figure 2(B) shows the fraction of cumulative positive cases in the population during the first 150 days. This graph conveys the same messages as those in the upper panel, but in a cumulative sense. Preemptive quarantine cannot lower the infection rate, but can delay the spread. The quarantine of symptomatic patients lowers the cumulative infection rate to 75% and flattens after infecting 84% of population over 150 days. The quarantine of both symptomatic and asymptomatic patients would lower the cumulative infection rate to 14%.

Figure 2(C) presents the fraction of those who succumbed to COVID-19. Because of the absence of a containment policy, 2.3% of patients lost their lives during the first 150 days. Tracking, testing, and hospitalization of symptomatic patients could reduce the fraction of the cumulative death by 1.5 % during the first 150 days, but the fraction then increased to 1.9%. Tracking, testing, and hospitalization of both symptomatic and asymptomatic patients can reduce the fraction of cumulative death to 0.3%. This finding is in line with the number of newly confirmed and cumulative infected cases.

#### **4. Discussion**

Although we extended the conventional SEIR models to incorporating the asymptomatics, there are a lot to be done for making our model more realistically applicable to the current COVID-19 pandemic. First thing to point out is about the test probabilities ( $d_S$ 's and  $d_A$ 's). They are assumed fixed in our model but clearly are functions of each country's test capacity and have increased over time. If data for each country's test capacity are available, then we can incorporate varying test probabilities and make our model more realistic.

Different strains of COVID-19 may have different transmission rates. When regional distributions of strains are known, our model can be extended to having multiple transmission rates by regions so that we can project the infected more accurately and our model help policy makers design better policies.

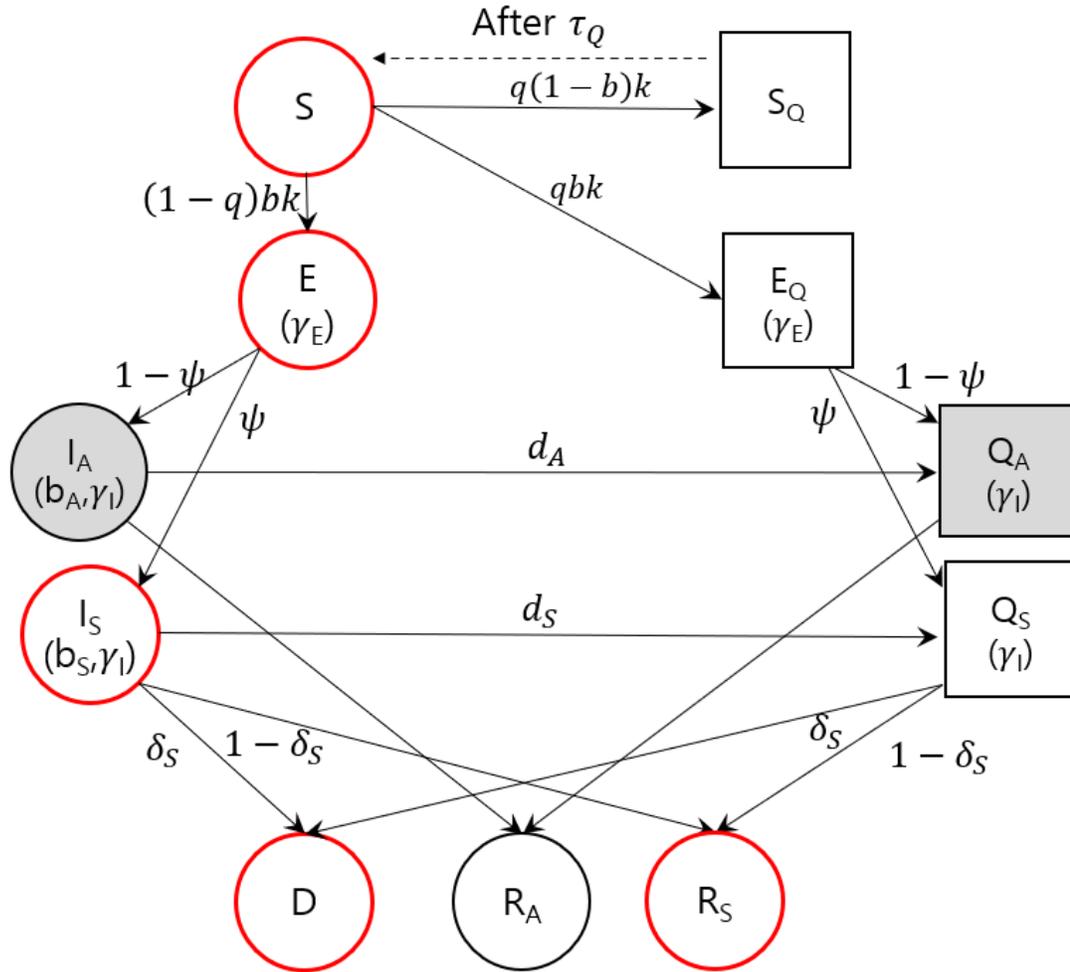
## **5. Conclusion/Policy recommendations.**

We have presented the effects of containment measures with the scenario that the fraction of the asymptomatic among the total infected is 20%. We have also experimented scenarios with the fraction of the asymptomatic being 50%. As the asymptomatic fraction increases, testing and quarantine of the symptomatic alone becomes less effective dramatically. However, testing and quarantining both symptomatic and asymptomatic patients is still effective although the number of cumulative infected is slightly higher than that reported in Figure 2(B).

Our policy experiments show that the testing and quarantine of symptomatic patients are very effective to contain, but not enough to extinguish, the epidemic. Thus, testing and quarantine should include the asymptomatic cases as well.

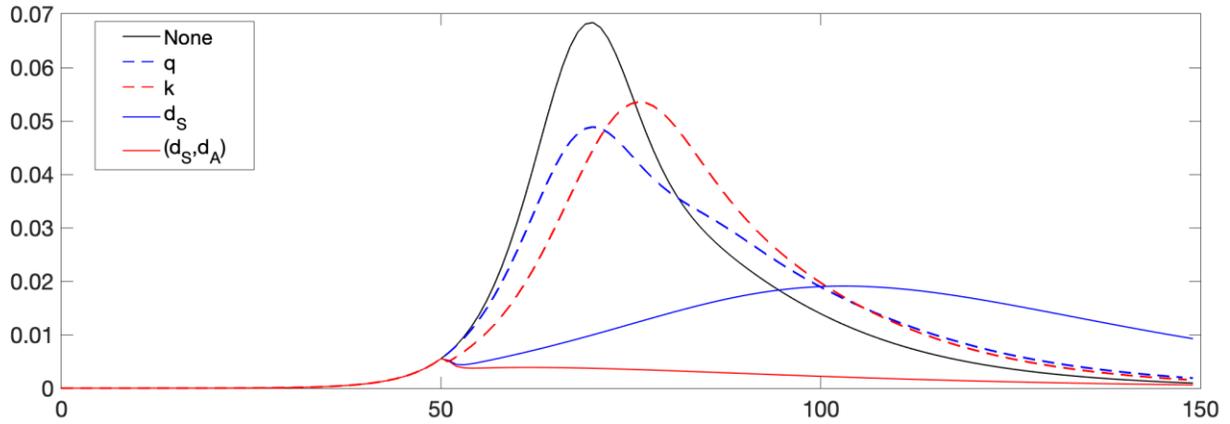
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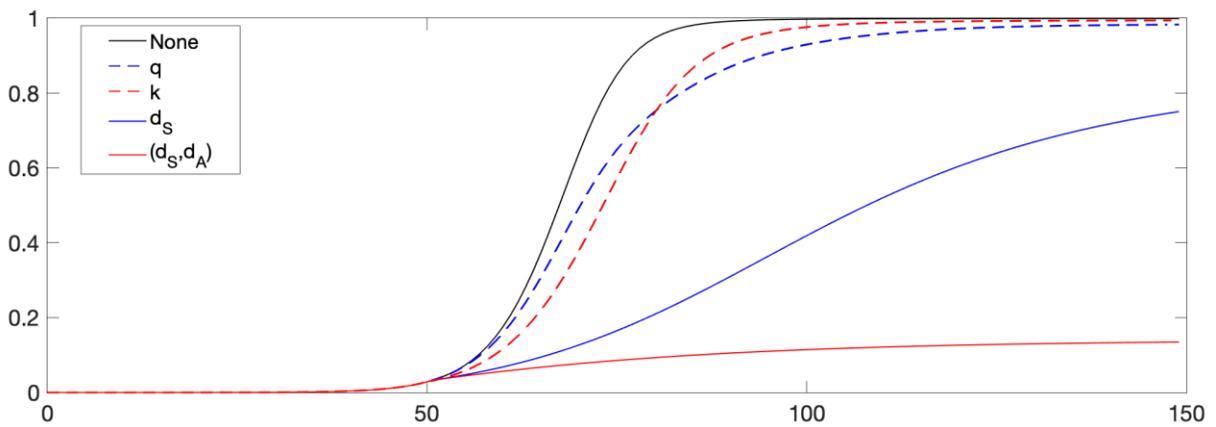


**Fig. 1. SEIR model with asymptomatic patients**

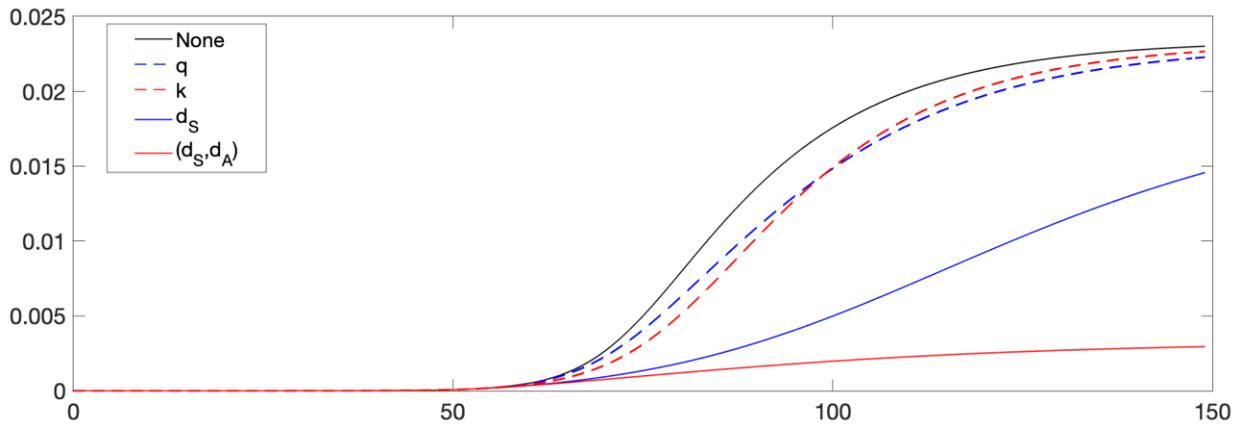
Notes: Red circles represent the basic SEIR model. A square box means quarantined. The model feature added from the basic SEIR is the asymptomatic,  $I_A$ , gray background circle. S means susceptible, E means exposed,  $I_A$  means asymptomatic,  $I_S$  means symptomatic,  $E_Q$  means exposed and quarantined, and  $Q_S$  and  $Q_A$  mean quarantine symptomatic and quarantine asymptomatic, respectively.  $R_A$  and  $R_S$  mean recovered from asymptomatic and symptomatic, respectively. D means dead. Four containment policies are following.  $q$  is the probability of quarantine for the contacted persons, and  $k$  is the frequency of contact.  $d_S$  and  $d_A$  mean the probability of being tested for symptomatic and asymptomatic patients, respectively.  $\psi_E$  is the fraction of symptomatic patients.  $\delta_S$  means the fraction of dead symptomatic patients.



**A.**



**B.**



**C.**

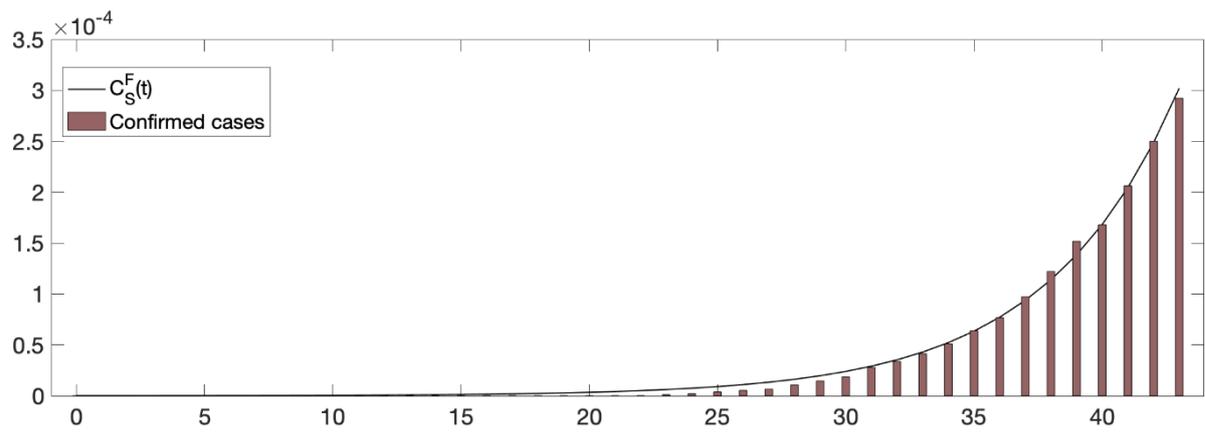
**Fig. 2. Policy simulation on 50th day of outbreak (A) Ratio of newly confirmed patients to population. (B) Ratio of cumulative confirmed patients to population. (C) Ratio of number of dead to population. None means no containment policy intervention; “q” is the containment policy of increasing  $q$  from 0.0 to 0.13; and “k” is the containment policy of lowering the number of contacts from 2.07 to 1.49.**

**Table 1. Parameter estimates,  $\psi=0.8$** 

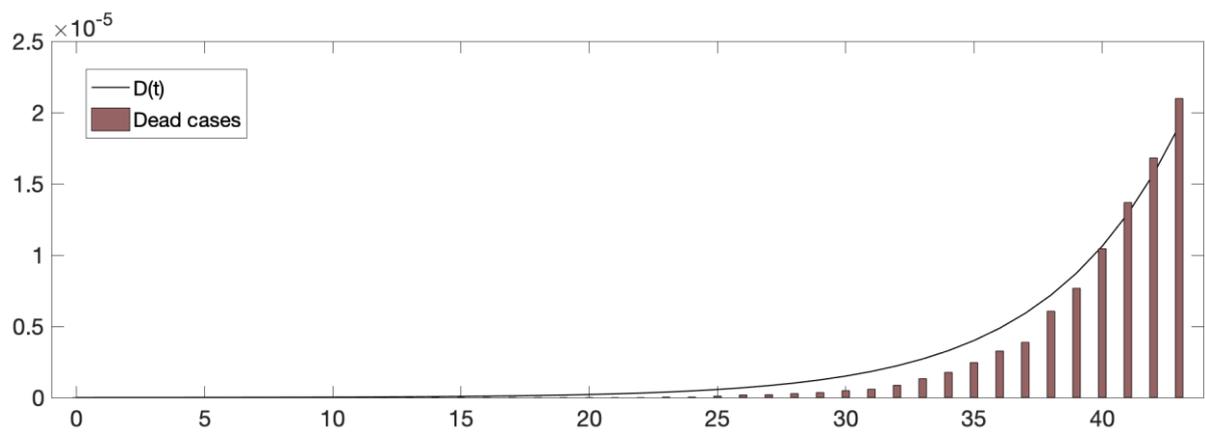
Parameter	Description	Italy	S. Korea
<b>Society-related parameters</b>			
$k^0$	Contact rate	2.0670	.
$k^1$		.	1.4857
$q^1$	Preemptive quarantine rate	.	0.1296
$d_S^0$	Test Probability	0.0287	.
$d_{S1}$		.	0.0083
$d_{S2}$		.	0.8829
$d_{A1}$		.	0.0668
$d_{A2}$		.	0.2159
<b>Virus-specific parameters</b>			
$b_A$	Transmission rate for asymptomatic cases	0.2859	0.2859
$b_S$	Transmission rate for symptomatic cases	0.2612	0.2612
$R_0^{ref}$		7.2515	.
$R_0^1$		.	4.8325
$R_0^2$		.	0.5603

Notes: 20% of cases are assumed asymptomatic. The Italian data are up to March 14 and Korean data are up to April 30, 2020.

### Supplementary Materials: Supplementary Figure and Table

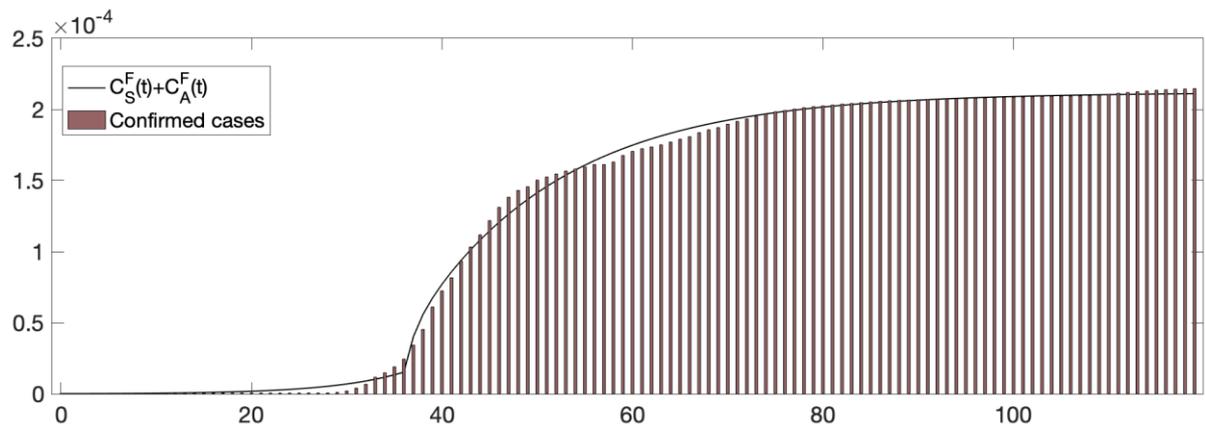


**A.**

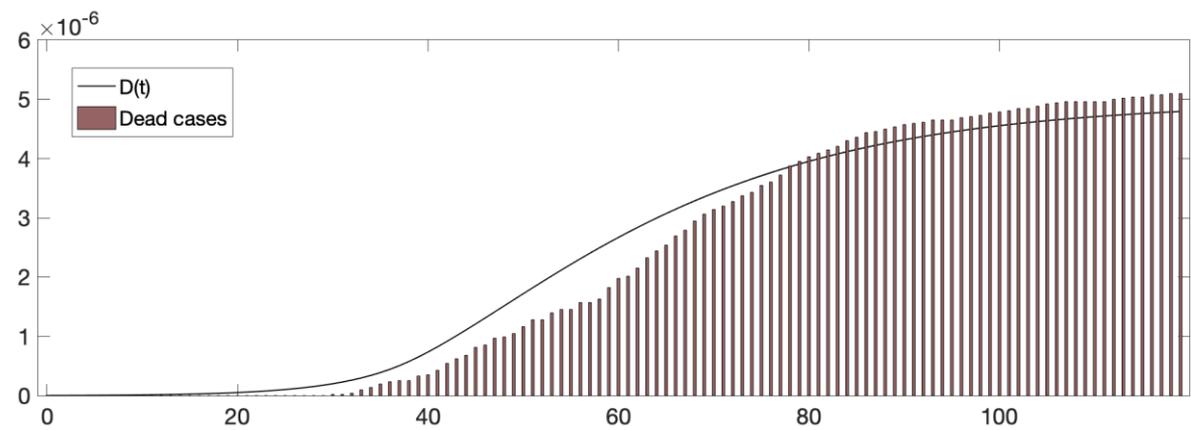


**B.**

**Supplement Fig. 1. Observed data and model estimation for Italy (A) Cumulative number of confirmed cases (only symptomatic) in real data (red bar) and model estimation (black line). (B) Cumulative number of deaths in real data (red bar) and model estimation (black line).**



**A.**



**B.**

**Supplement Fig. 2. Observed data and model estimation for South Korea (A)**

Cumulative number of confirmed cases (symptomatic and asymptomatic) in real data (red bar) and model estimation (black line). **(B)** Cumulative number of deaths in real data (red bar) and model estimation (black line).