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RESEARCH ARTICLE

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Public healthcare system capacity during COVID-19: A computational case study of SARS-CoV-2

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Abstract

Aim: Coronavirus Disease (COVID-19) is spreading typically to the human population all over the world and the report suggests that scientists have been trying to map the pattern of the early transmission of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) since it has been reported as an epidemic. Our main aim is to show if the rise-in-cases proceeds in a gradual and staggered manner instead of soaring quickly then we can suppress the burden of the health system. In this new case study, we are attempting to show how to control the outbreak of the infectious disease COVID-19 via mathematical modeling. We have examined that the method of flattening the curve of the coronavirus, which increases the recovery rate of the infected individuals and also helps to decrease the number of deaths. In this pandemic situation, the countries like Russia, India, the United States of America (USA), South Africa, and the United Kingdom (UK) are leading in front where the virus is spreading in an unprecedented way. From our point of view, we establish that if these countries are following the method of flattening the curve like China and South Korea then these countries can also overcome this pandemic situation.

Method: We propose a Susceptible, Infected, and Recovered (SIR) mathematical model of infectious disease with onset data of COVID-19 in Wuhan and international cases, which has been propagated in Wuhan City to calculate the transmission rate of the infectious virus COVID-19 until now. To understand the whole dynamics of the transmission rate of coronavirus, we portray time series diagrams such as growth rate diagram, flattening the pandemic curve diagram, infected and recovered rate diagram, prediction of the transmission of the disease from the available dataset in Wuhan, and internationally exported cases from Wuhan.

Results: We have observed that the basic reproduction number in Wuhan declined from 2.2 (95% Confidence Interval [CI] 1.15-4.77) to 1.05 (0.41-2.39) and the mean incubation period was 5.2 days (95% [CI], 4.1-7.0). Interestingly the mean value lies between 2 and 2.5 for COVID-19. The doubling time of COVID-19 was registered 7.4 days (95% CI, 5.3-19) in the early stages and now the value decreases to −4.9 days. Similarly, we have observed the doubling time of the epidemic in South Korea decreased to −9.6 days. Currently, the doubling time of the epidemic in

Russia, India, and the USA are 19.4 days, 16.4 days, and 41 days, respectively. We have investigated the growth rate of COVID-19 and plotted the curve flattening diagram against time.

Conclusion: Via flattening the curve method, China and South Korea control the transmission of the fatal disease COVID-19 in the human population. Our results show that these two countries initially sustained pandemics in a large portion of the human population in the form of virus outbreaks that basically prevented the virus from spreading further and created ways to prevent community transmission. The majority portion of the people are perfectly fine, who are quarantined strictly and never get sick, but the portion of people who have developed symptoms is quickly isolated further.

KEYWORDS

epidemic, flattening the curve, mathematical modeling, population dynamics, SARS-CoV-2

1 | INTRODUCTION

All over the world, SARS-CoV-2 is spreading in such a way that it is declared as a pandemic situation. The outburst of COVID-19 has driven the total confirmed cases rose to about 117 602 506 with a death toll of about 2 608 341 and recovered cases 93 089 885 as of 9th March, 2021 and also the active cases are about 21 904 280. Among infected active cases, 99.6% cases are in mild conditions and 0.4% cases are in serious or critical condition. The other two Coronaviruses, which have caused epidemics recently, are Severe Acute Respiratory Syndrome (SARS) in China in 2002-04, and Middle East Respiratory Syndrome (MERS) in Saudi Arabia in 2012. One company, Maryland-based Novavax, has now repurposed those vaccines for SARS-CoV-2, and says several of its candidates are able to enter the human test this spring. SARS-CoV-2 has a genetic similarity of 80% to 90% with the SARS virus and hence the name SARS-CoV-2 comes. Both consist of a strip of Ribonucleic acid (RNA) inside a spherical protein capsule wrapped in a spike. The spike locks the receptors on the surface of the cells of the human lung line. In both cases, the receptor is of the equivalent kind, which is allowing the virus to interrupt into the cell. After the virus attack, it hijacks the cell's reproductive machinery to produce more copies of itself, before breaking out the cell again and killing it.[1] The Chinese City Wuhan is considered the epic-enter of SARS-CoV-2 and is locked down since January 23 and the government banned all the transportation. In South Korea, public and personal laboratories have been established, which provide the medical facility to the affected people via dozens of mobile centers.[2] The effect of MERS virus gave the perfect lesson on how to approach infectious diseases. The centers for disease control of MERS virus found a special department to organize for the worst cases, which was a great movement that appears to have paid off. The country has seen two waves of infection, the primary beginning was on 20 January with the primary confirmed cases, and after that, the second wave comes with mass infections among the people. Now there is a fear that the imported cases could fuel a third wave. The government plans to put in around 20 phone booth-style test facilities inside Incheon Airport to hurry up the method of testing all arrivals from Europe. The trick of success of South Korea is that the medical team has worked so hard to lower the infection rates. This situation is like climbing a mountain without knowing how high the top of the mountain should be or what obstacles might come in the way. The people of Europe are so worried about their dire situation that if they give up even a little bit, it could be extremely unfortunate for them.[3,4] To understand the whole dynamics of the transmission rate of coronavirus, we portray time series diagrams such as growth rate diagram, flattening the pandemic curve diagram, and SIR model diagram. We have observed that the basic reproduction number in Wuhan declined from 2.2 (95% [CI] 1.15-4.77) to 1.05 (0.41-2.39) and the mean incubation period was 5.2 days (95% [CI], 4.1-7.0). Interestingly the mean value of incubation period lies between 2 and 2.5 for COVID-19. The doubling time of COVID-19 was registered 7.4 days (95% CI, 5.3-19) in the early stages and now the value decrease to 4.9 days.

Susceptible (S) individuals are those who have never been infected with and thus have no immunity against COVID-19. Once susceptible people are infected with the disease, they become infectious with the disease. When the individuals become infectious then they experience non-critical symptoms like fever and cough and may even have mild pneumonia but do not require hospitalization. These individuals may either recover or progress to the critical stage of the disease. One step further when the Infected individuals with a critical infection experience respiratory failure, septic shock, and/or multiple organ dysfunction or failure then they must require treatment in an Intensive Care Unit (ICU). These individuals may either recover or die from the disease. Recovered (R) individuals are those who have recovered and are assumed to be immune to future infection with COVID-19. Previously many studies have been done on the natural clinical progression of COVID-19 infection.[5-9] Infected (I) individuals do not immediately develop severe symptoms, but instead go through the mild stages of infection first. In some studies, what we call mild infection is divided into two separate categories, that is, mild and moderate, where individuals with moderate infection show radiographic signs of mild pneumonia. These mild and moderate cases occur at

roughly equal proportions.[10] There is some debate about the role of pre-symptomatic transmission (occurring from exposed cases) and asymptomatic infected cases for coronavirus, which are not include in the present model. We use a compartmental epidemiological model, followed by the traditional SIR model, to illustrate the spread and clinical progression of COVID-19. Tracking the different clinical outcomes of infections is very important because taking care of them requires different levels of healthcare resources and in many cases, isolation may be necessary. The study shows that an individual is most infectious during the stage of non-critical infection period. At this period, population would still be in the community and feeling well enough to interact with others. However, there is also a chance to transmit the disease into the further stage such as critical stage. We cited this phenomenon as an example of an infection between hospitalized patients and their healthcare providers. At a population level, infections are most likely to spread from these non-critical people because most of the patients are not aware at this stage. In the case of COVID-19, we can assume that the period of the first stage starts from the time when the non-critical symptoms start, the time from symptom onset to hospitalization (eg, progress to critical stage), or it is the period of viral shedding through the sputum or throat swabs and from this time onwards the onset of various symptoms start. The probability of progressing to the critical stage is proportional to all infections that end up to critical. Individuals with critical infection need hospitalization. The duration of critical infection could be reported from the time of hospitalization to recovery for individuals or the time from hospital admission to ICU admission (since critical cases require ICU-level care). Since there is no accurate estimate of this period, we instead use the total time estimate from the onset of symptoms to ICU admission (eg, the length of critical infection). Generally, at the critical infection stage of ICU care, mechanical ventilation is required. The duration of this stage is the time from ICU admission to recovery or death. Different case study reports show that the total time from hospital admission to death, which can approximate the duration of the critical stage.[11-19] The case fatality ratio describes the fraction of all symptomatic infected individuals who eventually die. Since individuals must progress to critical infection to die, the conditional probability of someone in the critical stage dying vs recovering is given by the case fatality ratio divided by the fraction of all critical infections.

Generally, such micro-organisms grow at an exponential rate with plenty of resources and thus it has been observed that the decline of the population makes reduction of the resources. In the case of infectious viruses, the primary resource is the existence among the susceptible individuals. The virus can spread rapidly without taking care of enough obstructive measurements in presence of an infected individual in a massive population. At the initial stage, the expansion of the infectious virus is considered exponentially and the total number of infected individuals along with the time is counted at double rate from the initial number. Therefore, if we consider that 10 individuals are infected initially without taking care of obstructive measurements such as putting masks on faces, keeping social distancing, and maintaining hygienic conditions, then the curve of expansion can reach up to 20 individuals over the time. In this exponential way, the number of estimated expansions becomes bigger and bigger such as 10, 20, 40, 80, 160, and so on. This phenomenon seems to be non-identical with the growth of linear curve in which the number of identical cases may grow such as 10, 20, 30, 40, and so on. However, all the exponential growth rates are not similar and thus we can understand how the growth rate is reaching massive and the corresponding situation is going to be the worst. For instance, if the number of cases increases by 1% on a daily basis (a hypothetical situation) then it is important to note that the spread is benign. On the opposite hand, if a situation arises where the infection doubles on a daily basis, it may represent a worrying situation.[20-24]

With the perception of transmission of the infection in human population, we propose a mathematical model termed as SIR model with vital dynamics of infectious disease and show the flattening curve method is a possible way to decrease the spread rate of coronavirus. China and South Korea follow the same way to flatten the curve method of SARS-CoV-2 and control this infectious disease. Here, we endorse if Russia, India, USA, South Africa, UK, and rest of the world can follow the same method like China and South Korea from which they are being benefited and can sustain to transmit this infectious disease from human-to-human population and reduce the number of severe cases, causing less burden on public health systems. The arrangements of the manuscript are as follows: The formulation of model systems and their attributes are elaborately discussed in the Section 2. The computational study of the model formulation has been done in Section 4. Numerical results are discussed in Section 4. In the final, Section 5, conclusion of the study is described.

2 | MODEL FORMULATION

2.1 | Traditional model (without vital dynamics)

The dynamical behavior of an epidemic (eg, flu) model system is often much quicker than the dynamics of birth and death of the population. Therefore, birth and death are often excluded in the traditional compartmental model. The SIR model divides into three compartments such as S (representing the number of susceptible individuals), I (representing the number of infectious individuals), and R (representing the number of recovered or immune individual). The model system is associated with the recovery rate γ and β, which is the average number of contacts per person per time. The SIR system without so-called vital dynamics can be written as following[9]:

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

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

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

where $S(0) \geq 0$, $I(0) \geq 0$, $R(0) \geq 0$. We know from the fundamental theory of functional differential equations, there is a unique solution $(S(t), I(t), R(t))$ of system (1) with above initial conditions.

2.2 | Theoretical simulation of the traditional model

The basic reproduction number is given by $R_0 = \frac{\beta}{\gamma}$. $S(t) + I(t) + R(t) = N$ where N denotes the total population. The contact time between population is $t_c = \frac{1}{\beta}$ and the time until removal is $t_r = \frac{1}{\gamma}$. Therefore, we conclude that $R_0 = \frac{t_r}{t_c}$. If we consider $\frac{S}{N} < 1$, then from $\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$, we obtain $R_0 > 1$. This phenomenon suggests that the epidemic outbreaks along with an increasing number of infected populations.

2.3 | Updated model (with vital dynamics)

This transmission of this infectious disease is about human to human. The model system of SARS-CoV-2 is characterized by a death rate μ and birth rate a, where the communicable disease is spreading. The transmission of this infectious disease (termed as SIR model) is modeled as follows[25,26]:

$$\frac{dS}{dt} = a - \mu S - \frac{\beta SI}{N},$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - (\mu + \gamma)I,$$

$$\frac{dR}{dt} = \gamma I - \mu R.$$

2.4 | Theoretical simulation of the updated model

The disease-free equilibrium points of the above the model is $\left(\frac{a}{\mu}, 0, 0\right)$ and the basic reproduction number $R_0 = \frac{\beta}{(\mu+\gamma)}$ and consider $S(t) + I(t) + R(t) = N$, as total population. From the point view of population biology, we conclude as follows:

1. $R_0 \le 1$, implies the disease-free equilibrium point $\lim_{t\to\infty}(S(t) + I(t) + R(t)) = \left(\frac{a}{\mu}, 0, 0\right)$.
2. $R_0 > 1$ and $I(0) > 0$, indicate the endemic equilibrium point $\lim_{t\to\infty}(S(t) + I(t) + R(t)) = \left(\frac{\gamma+\mu}{\beta}, \frac{\mu(R_0-1)}{\beta}, \frac{\gamma(R_0-1)}{\beta}\right)$.

Overall, one may conclude that R_0 be the average number of infections caused by a single infectious individual in an entire susceptible population and the above inequalities of R_0 biologically suggests that if the basic reproduction number is less than or equal to one then the disease goes to extinct, whereas if basic reproduction number is greater than one the disease will remain permanently endemic in the population.[25,26]

3 | MATHEMATICAL SIMULATIONS

3.1 | Growth rate

We are interested in knowing how the number of active cases is going to change in the near term. We assume that active cases (A_t) follow an exponential growth model such that $E(A_t) = A_0 e^{r_t}$. In reality, the growth dynamics are much more complex than this, but for short time periods, the exponential model may provide a reasonable approximation. To fit this model, we take the natural logarithm of both sides, yielding $\ln A_t = r_t + \ln A_0$ which is showing that we can fit a simple linear regression of $\ln A_t$ against t. The slope of this fit is an estimate of the intrinsic growth rate r. The doubling time (t_d) is an intuitive measure of how fast a population is growing. It reports the number of days for the population to double in size and is calculated by setting $A_t/A_0 = 2$, yielding $t_d = \frac{\ln 2}{r}$. Public health interventions are firmly aimed at the reduction of virus transmission and also in the growth of the number of active cases. Early indications of success will be expressed by reducing the growth rate.

3.2 | Basic reproductive ratio

Generally, the Jacobian method is used to derive the biological significance of R_0 for Susceptible, Infected, Exposed, and Recovered (SEIR) model system. However, the complex compartmental model with multiple infected compartments is difficult to obtain because the mathematical calculation depends on algebraic properties of Routh-Hurwitz criteria for the stability analysis of the Jacobian matrix. There is another scheme, termed as next generation matrix method, to determine R_0 for an Ordinary Differential Equation (ODE) compartmental model.[27,28]

Let $x = (x_1, x_2, \ldots, x_m, x_{m+1} \ldots, x_n)^T$, be the number of individuals in each compartment, where the first $m < n$ compartments are associated to infected individuals and rest of the compartments are the other variables. Let us consider disease-free equilibria remains steady in the absence of the disease. We also assume that the linearized equations for $x_1, \ldots, x_n$ around the disease-free equilibria separate from the other equations. Let us consider, the dynamical presentation of the compartmental model is written as follows:

$$\frac{dx_i}{dt} = \mathcal{F}_i(x) - \mathcal{V}_i(x), \text{for } i = 1, 2, \ldots, m,$$

where $\mathcal{F}_i(x)$ represents the rate of appearance of new infections (the portion of the population, which are either susceptible or had fully recovered, but are becoming infected due to contact with the infected individuals) in compartment i and $\mathcal{V}_i(x)$ is the rate of other transitions between compartment i and other infected compartments, which is including removals from the infected groups and other compartmental transitions. Assumptions are made such that $\mathcal{F}_i(x), \mathcal{V}_i(x) \in C^2$, and $\mathcal{F}_i(x) = 0$ if $i \in [m_{i+1}, n]$. Now we define $F = \frac{\partial \mathcal{F}_i(x_0)}{\partial x_j}$ and $V = \frac{\partial \mathcal{V}_i(x_0)}{\partial x_j}$ for $1 \le i, j \le m$. Biologically, F represents entry wise non-negative and V denotes non-singular M-matrix.[29] Therefore, V^{-1} is entry wise non-negative. Let us consider, initial number of infected individuals be $\chi(0)$. Then $FV^{-1}\chi(0)$ is an entry wise non-negative vector, which denotes the expected number of new infections. Matrix FV^{-1} has (i, j) entry equal to the expected number of secondary infections in compartment i produced by an infected individual introduced in compartment

j. Hence, FV^{-1} is the next generation matrix and the reproduction number is defined as the spectral radius (leading eigenvalue) of the Next Generation Matrix (NGM) V^{-1}, which is denoted as $R_0 = \rho(FV^{-1})$, where ρ represents the spectral radius. Now we apply the NGM scheme in the infected compartment of the model system (1). At the disease-free equilibria, matrices F and V are as follows:

$$F = \begin{bmatrix} \beta \\ 0 \end{bmatrix}, V = [\mu + \gamma]. \text{ Therefore, } FV^{-1} = \frac{\beta}{\mu + \gamma}.$$

3.3 | Well-posed system

Feasible solution set of the system (2) is $\omega = (S, I, R) \in \mathbb{R}^3_+ : 0 \le S + I + R = N \le \frac{a}{\mu}$.

Here $\mathbb{R}^3_+$ denotes the non-negative cone of $\mathbb{R}^3$ with its lower dimensional faces. If $> \frac{a}{\mu}$, we have $\frac{dN}{dt} \le 0$, suggests that the host population decreases asymptotically to the carrying capacity. However, if $N \le \frac{a}{\mu}$, each solution with initial conditions belongs to $\mathbb{R}^3_+$ and the solution of (2) is positive for all values of $t > 0$. So, the region ω is positively invariant and the system (2) is well-posed.

Theorem 3.1. *For $R_0 > 1$, there exists a unique endemic equilibrium E^*.*

Proof. When disease becomes endemic, mathematically we represent $\frac{dI}{dt} > 0$ and $\frac{dS}{dt} > 0$. The following inequalities are obtained from the system (2): $\frac{\beta SI}{N} - (\gamma + \mu)I > 0$,

$$a - \mu S - \frac{\beta SI}{N} > 0.$$

Now we are using the fact $\frac{S}{N} < 1$, we obtain the following inequality:

$$\frac{a\beta}{\mu(\mu + \gamma)} > 1,$$

which follows $R_0 > 1$. This proves the theorem.

3.4 | Epidemic growth rate

Early in the epidemic, before susceptible are depleted, the epidemic grows at an exponential rate r, which can also be described with doubling time $T_2 = \ln(2)/r$. During this phase, all infected classes grow among population level at the same rate as each other and as the deaths and recovered individuals. The cumulative number of infections that have happened because of the outbreak started also grows at the same rate. This rate can be calculated from the dominant eigenvalue of the linearized system of equations in the limit that $S = N$. During this early exponential growth phase, there will be a fixed ratio of individuals between any pair of compartments. This expected ratio could be used to estimate the amount of under reporting data. For example, we might think that all deaths are reported, but some mild infections might not be reported, since these patients might not seek healthcare or might not be prioritized for testing. These ratios have expected values under the model for a fixed set of parameters. They can be calculated by finding the eigen vector corresponding to the dominant eigenvalue (r) for the linearized system described above. Ratios that deviate from these values suggest either the under reporting of cases relative to deaths, or the local differences in the clinical parameters of disease progression. The expected ratio of the system (2) is given as follows:

$$\frac{\text{Infected}}{\text{Death}} = \frac{r(\mu + \gamma + r)}{\mu\beta}.$$

4 | NUMERICAL SIMULATIONS

We validate the analytical results of our model system (2), which are obtained by the numerical simulations. The transmission rates are generally impossible to directly observe or estimate. Instead, these values can be backed out by looking at the early exponential growth rate of an epidemic and choosing transmission rates that recreate these observations. The growth of COVID-19 outbreaks has varied a lot between settings and over time. Some numerical values are given in the Tables 1 to 3.

We consider that the most effective source of infection is people who have non-critical infections and are still moving openly in public, as opposed to being isolated in a hospital. In the Figure 1A, we illustrate the outbreak of coronavirus of the model system (2) and it has been observed that the lifetime immunity has been developed from this viral disease, so there is no sign of returning cases recovered to susceptible compartment. In the Figure 1B,C, we portray the infection rate and recovery rate over the progression of time, respectively. Here, we consider the time span is about 5 months, from the beginning of the epidemic outbreak.

In general, the whole population is initially susceptible (other than for initial cases). Individuals that recover from COVID-19 are subsequently immune. The primary purpose is to explore the dynamics of COVID-19 cases and the associated strain on the health care system in the near future. The outbreak is influenced by infection control measures such as school closures, lock-down, etc. In Figure 2A, we illustrate the effect of lockdown, applied by the government to calculate the infected cases and it gives us a proper idea about the effect of quarantine period and also suggests that the population ratio of infected peaks have decreased after the lockdown period. Here we consider the time period about more than 6 months. However, Figure 2B indicates the mortality rate does not significantly fluctuate after more than the 6 months period of lockdown. After the lockdown period is over, a fraction of the exposed population can again restart the coronavirus spread. In Figure 2C, it is observed that the recovery rate has been increased after the lockdown period and the effect of the significance of this phenomenon plays a major role to fight against COVID-19. In Figure 2D, we investigate the effect of healthcare

system capacity, reaches to its threshold point for the model system (2) during the lockdown period. We consider that the dominant source of transmission is the individuals having non-critical infections who are likely to be in the community, as opposed to isolated in the hospital.

In Figure 3, we portray the realistic scenario of the growth trajectory of China, South Korea, Russia, India, the USA, South Africa, and the UK. Growth in total cases standardized to start when a region reaches 100 cases. In Figure 3, health interventions are rapidly changing the growth rate. This can be seen as deviations from the expected straight line on the log-plot with suggesting positive part is bad, negative part is good. Progress rate from the disease would be indicated by steady decline in growth rate over the progression of time, and holding in negative territory.

TABLE 1 Estimated parameters for COVID-19 clinical progression

Quality	Value
Duration of asymptomatic infections	6 days
Duration of pre-symptomatic infectiousness[30-32]	2 days
Portion of asymptomatic infections[33,34]	30%
Incubation period[35-37]	5 days
Proportion of non-critical infections[38]	80%
Duration of non-critical infections[13,14,19]	5 days
Proportion of critical infections[38]	20%
Time from symptoms to ICU admission[39-41]	12 days
Time from hospital admission to death[42]	14 days
Duration of critical infection[41]	8 days
Time from symptom onset to death[41]	20 days
Case fatality ratio[43]	2%
Serial interval	8 days

TABLE 2 Observed early epidemic growth rates r across different settings, along with the corresponding doubling times

Growth rate r	Doubling time	Location	Dates
0.1	6.9 days	Wuhan	Early January[36]
0.14	5 days	Wuhan	Early January[16]
0.25	2.8 days	Wuhan	January[44]
0.3	2.3 days	Wuhan	January[13]
0.5	1.4 days	Italy	February 24[44]
0.17	4.1 days	Italy	March 9[44]
0.3	2.3 days	Iran	March 2[44]
0.5	1.4 days	Spain	February 29[44]
0.2	3.5 days	Spain	March 9[44]
0.2	3.5 days	France	March 9[44]
0.2	3.5 days	South Korea	February 24[44]
0.5	1.4 days	UK	March 2[44]

Note: There are many other settings where growth rates are now close to zero.

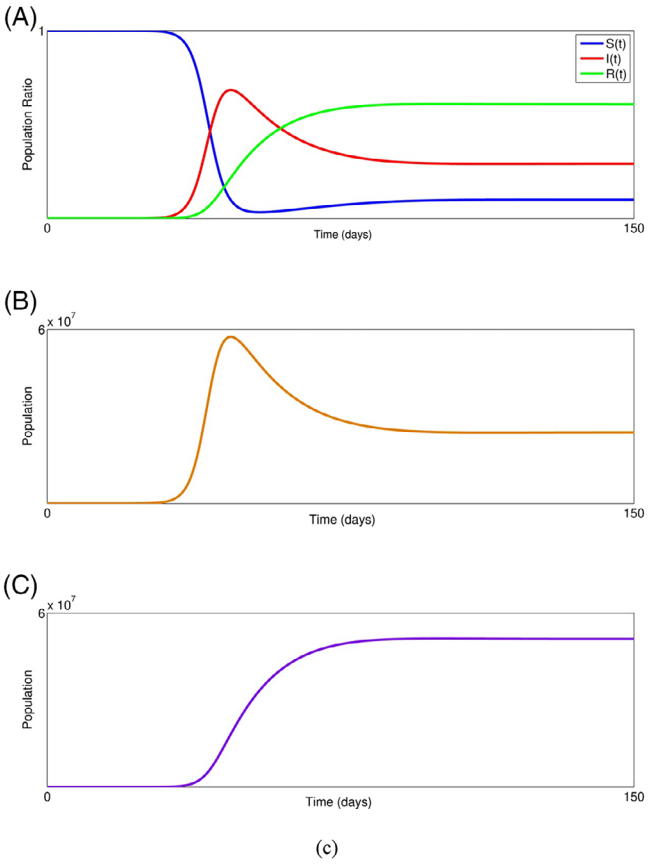


FIGURE 1 A, Time series diagram of the model system (2) is portrayed. B, We depict the infection rate over time of the model system (2). C, The recovery rate over time of the model system (2) is illustrated. Here we consider the time period about 5 months. Parameter values of system (2): $a = 0.01$, $\beta = 0.5$, $\gamma = 0.05$, $\mu = 0.024$

TABLE 3 A sampling of the estimates for epidemic parameters

Reproduction number (R_0)	Incubation period (in days)	Infectious period (in days)	Location
3.0 (1.5-4.5)	5.2	2.9	Wuhan[45]
2.2 (1.4-3.9)	5.2 (4.1-7.0)	2.3 (0.0-14.9)	Wuhan[46]
2.68 (2.47-2.86)	6.1	2.3	Greater Wuhan[47]
4.5 (4.4-4.6)	4.8 (2.2-7.4)	2.9 (0-5.9)	Guangdong[4]
14.8	5	10	Princess Diamond[29]

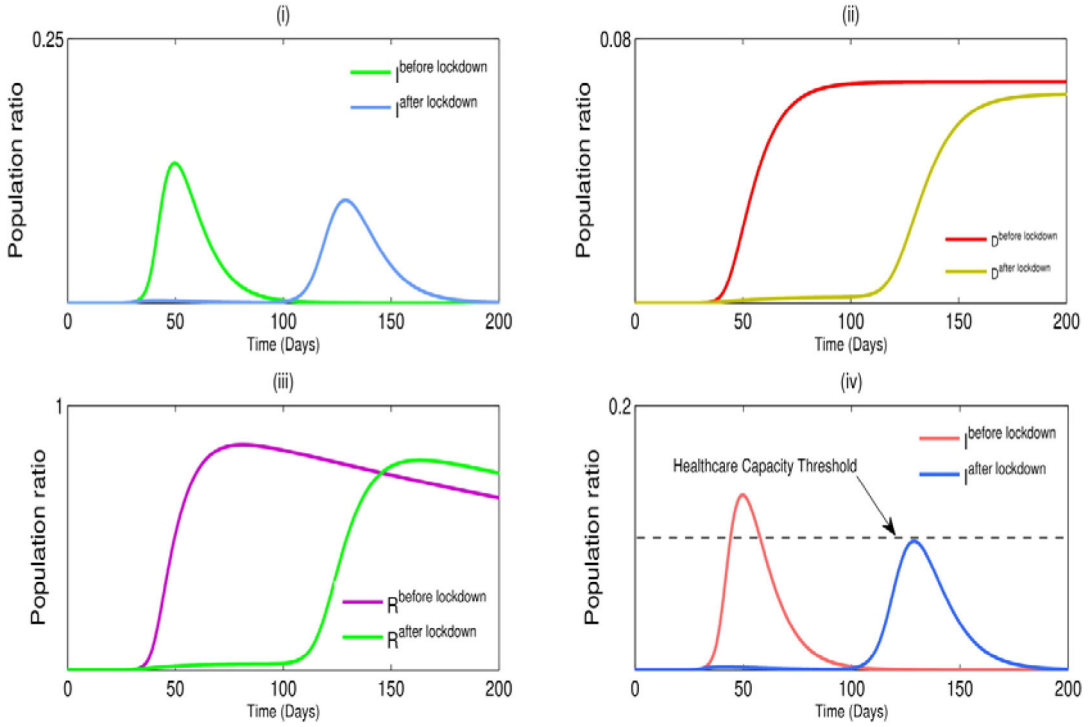


FIGURE 2 A, Simulation of the model system (2) with a lockdown period correspond to the effect of before and after the lockdown. B, The effect of mortality rate before and after the lockdown. C, The effect of recovered rate before and after the lockdown. D, Healthcare capacity system reaches its threshold point at infection (I) = 0.1. Here, *I* represents the infected populations, *D* describes the dead populations and *R* indicates recovered individuals. Parameter values of system (2): $\beta = 0.5$, $a = 0.056$, $\gamma = 0.0025$, $\mu = 0.02$. During the lockdown period β is decreased to 0.1 whilst other parameters are fixed

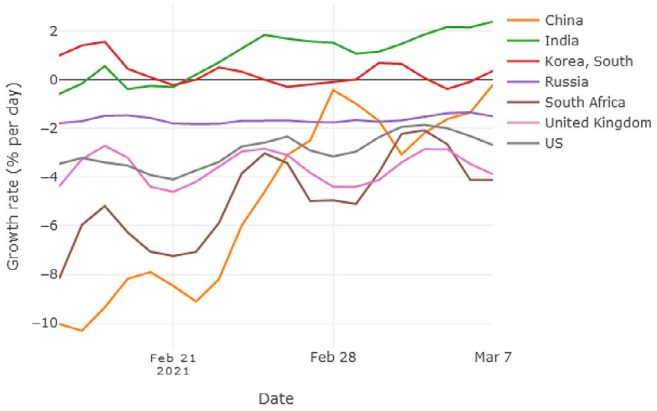


FIGURE 3 Growth rate of COVID-19 of China, South Korea, Russia, USA, India, UK, and South Africa

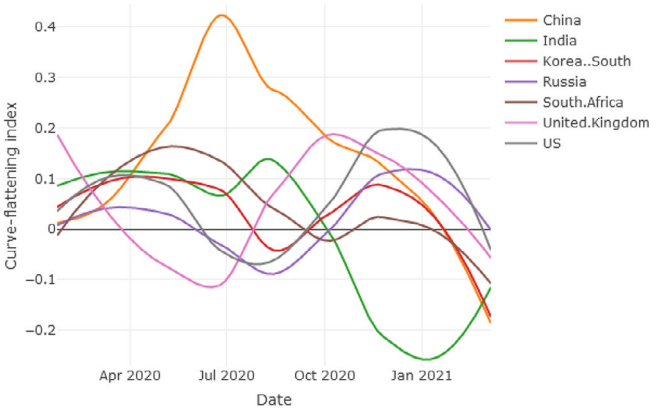
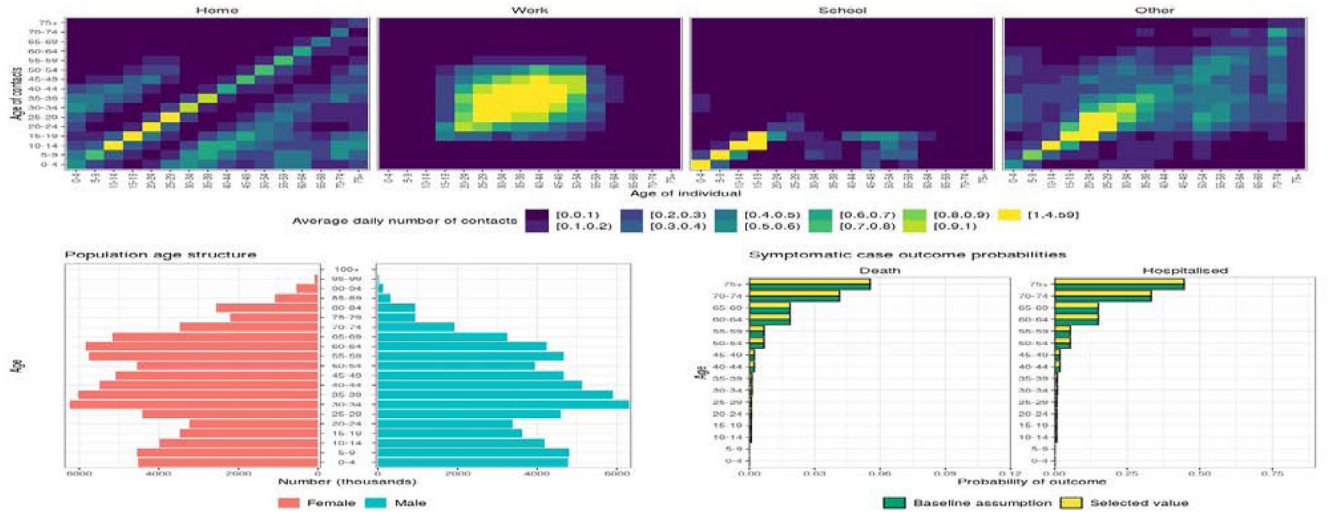


FIGURE 4 Flatten the curve of COVID-19 of China, South Korea, Russia, USA, India, UK, and South Africa

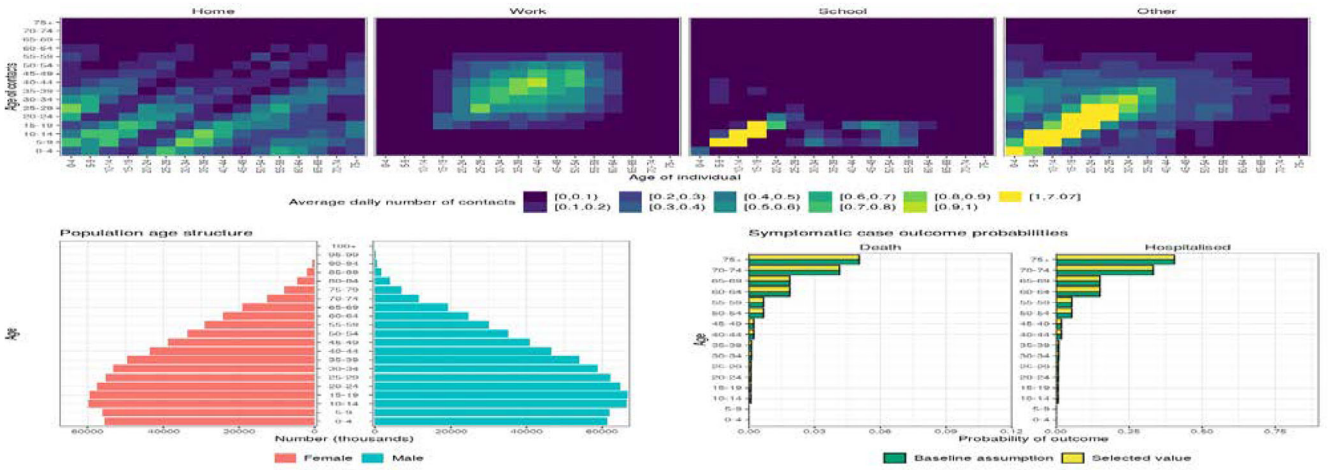
In Figure 4, flattening of the curve illustrates the growth rates are declining rapidly, which implies the curve is flattening, which suggests the forecast from this exponential model will be biased upwards.

In Figure 5, age-specific parameters show the number of contacts in each age group made by each individual in the country at home, work, school, and all other settings. We observe that how SARS-CoV-2 might spread between people of different ages in the countries like Russia, India, and the USA. There is an important impact on the health burdens of COVID-19, since older adults are more likely to be hospitalized or die as a result of COVID-19, while children and younger adults are more likely to have asymptomatic infections, and appear to be less susceptible to infection than adults.[48,49]

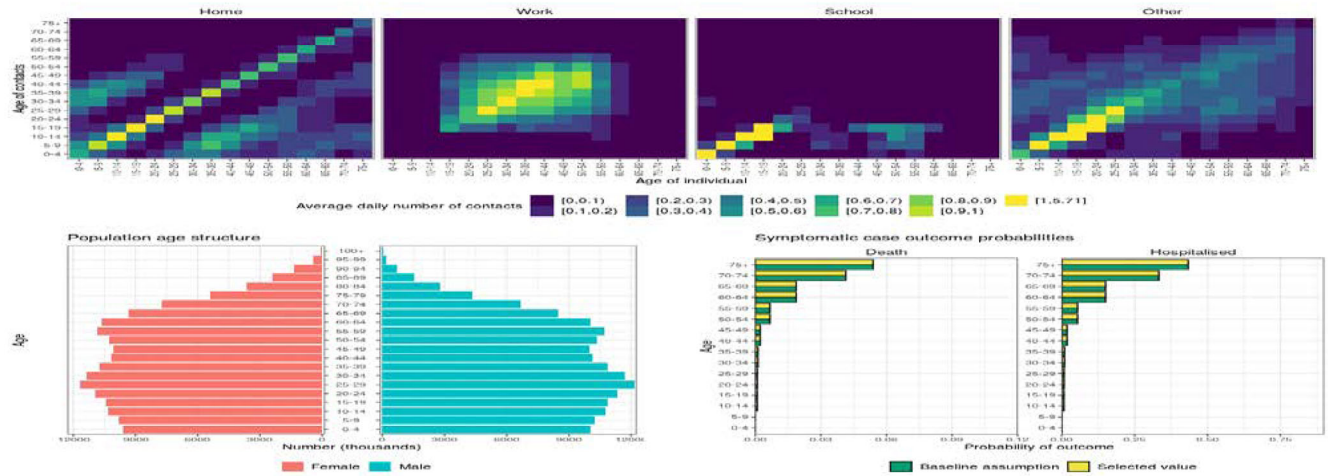
One can expect the estimates to have large uncertainty ranges; however, they do provide working estimates that give a sense of scale. At present, we have not included uncertainty ranges such as confidence intervals but may consider this in future implementations



(A) RUSSIA



(B) INDIA



(C) UNITED STATES OF AMERICA

FIGURE 5 The number of contacts in each age group made by each individual in the country

if feasible. It would require computationally intensive methods such as bootstrapping. We note also that the estimates of undiagnosed infections can also be used as an alternative way to forecast new cases, since future diagnoses depend on past infections. This is another area of possible future development.

5 | CONCLUSION

Some recent reports have suggested that healthcare workers are disproportionally infected with COVID-19, suggesting there is some role to hospital-based transmission (eg, from individuals in infected state, or individuals who are hospitalized with only mild infection). In China, approximately 5% of all infections were in healthcare workers, and in Italy, the number is currently around 10%. One of the biggest dangers of a widespread COVID-19 epidemic is the strain it could place on hospital resources, since individuals with critical infection require hospital care. The critical stage of infection requires mechanical ventilation, which is ICU-level care. Individuals with non-critical infection do not require hospitalization, and could recover at home on their own or can be treated in a regular hospital ward. However, in many countries these individuals have also been hospitalized, likely as a way to isolate them and decrease the transmission rate, as well as to observe them for progression to more aggressive disease stages. In recent studies on COVID-19, it has been noticed that in most of the cases, individuals had symptoms, since the presence of symptoms was used to determine whether someone would be admitted for a test of COVID-19. However, it is possible that some individuals may be infected and able to transmit to others without developing symptoms. Recent studies show that asymptomatic individuals were also screened for infection and tested positive. The model also suggests the possibility of pre-symptomatic transmission. The general compartmental epidemiological models assume that the onset of symptoms and the onset of infectiousness coincide, but recent evidence indicates that symptoms may be delayed relative to when an individual is infectious. Viral loads are measured over time in symptomatic individuals. Studies show that they are at a peak on the first day of symptoms, suggesting that they were already high before symptoms started. Detailed contact tracing studies that have tracked transmission chains, where the infector and the infected are both known, have found the serial interval, which is the time between symptom onset in the infector and infected and this is sometimes less than the incubation period. This means there must be pre symptomatic transmission. A wide range of values for the proportion of all transmission that is pre-symptomatic has been estimated (12%−62%), so we choose an intermediate value of 25%, consistent with.[30] A related line of evidence for the presence of pre symptomatic infection is that the average length of the serial interval is quite close to the average length of the incubation period in a few studies. This suggests either a very short symptomatic and infectious period, or, significant pre-symptomatic transmission. Undetected cases of COVID-19 are the primary incertitude of this pandemic. COVID-19 is new and it has not been observed before as a result, massive number of infected populations are registered day by day in the globe. Effectively, it is impossible for a country to diagnose all the active cases of COVID-19. So naturally, the number of active cases always remains less than the actual cases in the country. We can describe the non-detected cases in two categories such as undiagnosed and undetected. Undiagnosed individuals are considered the infected individuals whose symptoms are yet to visualize and they will come under diagnosis very soon. Undetected individuals never come under the scanner of treatment as they are having mild symptoms. A delay has been noticed between the time period of infection and treatment. If somehow, we are able to know about the delay, then we can be able to investigate about the number of undiagnosed individuals. The most significant time of the delay is the infection's incubation period of time, which can be mathematically modeled with the help of probability distribution, termed as incubation distribution. In general, the average period of incubation is between 5 and 6 days. It has been observed that in 95% of the cases, infections have maximum period of incubation time as 12 to 13 days. Everyday analysis of the COVID-19 in the population has registered a larger section of infected individuals. Here we totally ignore the undetected cases. To calculate these, we consider that the death individuals should not be avoided such as undetected cases. In addition, we have to count the cases of community transmission in a dense population, to figure out the mortality rate of the symptomatic cases. As a result, there are a larger number of death population than the registered cases in the countries associated to undetected cases. As of now, there is no vaccination procedure to overcome this fatal disease. So, we have to emphasize on testing over infected population. The United Nations health agency has urged people across the world to wash their hands in regular interval, avoid touching their eyes, nose and mouth from hands, maintaining social distancing, and make themselves home isolated, practice respiratory hygiene, and seek medical aid if they suffer from a fever, cough, or any difficulty in breathing.

Now the situation becomes more worried as there are observed instability in the community since the outbreak of such pandemic is spreading rapidly. We investigate flatten the curve method and it is one of the suitable ways to control the whole pandemic situation. We offer some proposals to control this fatal epidemic disease:

- Embed maximum lockdown of the entire population in the country, send to quarantine of the infected cases, and impose home isolation of the asymptomatic cases (rest of the people who are not infected) and look after in the application of these above-mentioned cases as soon as possible.
- Figure out the number of exposed cases and distinguish the level of their infectiousness.
- Maximal lockdown remains until as many of all the number of estimated exposed cases are calculated.
- Lift the lockdown and apply strict social distancing upon economic conditions.
- Back to normal life if no new cases have been registered for a long period of time.

- Select a state as a model state and apply all the above regulations and observe the effectiveness. If the results are fruitful then apply the regulations in the whole country.

To understand the whole dynamics of the transmission rate of coronavirus, we portray the time series diagrams such as growth rate diagram, flattening the pandemic curve diagram, infected and recovered rate diagram, and the transmission of the disease from the available dataset in Wuhan and internationally exported cases from Wuhan. Via flatten the curve method, China and South Korea are able to control the fatal disease COVID-19 from the transmission into the human population. We show by our results that the above techniques can sustain the epidemic at an oversized portion of the human population by pruning the virus at the beginning, which basically stops the virus from spreading further and makes a way to prevent community transmission and its effect on the capacity of healthcare system. The condition of human lives is becoming such metastable so that we all need to think unitedly against the deadly coronavirus and make a way through this fatal phase. Except for the parametric conditions, nothing is specified about the coronavirus. So, we can only predict the infected and mortality rates with all possible patterns of the epidemic disease over the progression of time.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

AUTHOR CONTRIBUTIONS

Conceptualization: Saikat Batabyal, Arthita Batabyal
Data Curation: Saikat Batabyal, Arthita Batabyal
Formal Analysis: Saikat Batabyal, Arthita Batabyal
Investigation: Saikat Batabyal, Arthita Batabyal
Methodology: Saikat Batabyal, Arthita Batabyal
Supervision: Saikat Batabyal
Visualization: Saikat Batabyal, Arthita Batabyal
Writing – Original Draft Preparation: Saikat Batabyal, Arthita Batabyal
Writing – Review and Editing: Saikat Batabyal, Arthita Batabyal

All authors have read and approved the final version of the manuscript.

Saikat Batabyal, as the corresponding author, confirms having full access to all of the data and takes complete responsibility for the integrity of the data and the accuracy of the data analysis.

TRANSPARENCY STATEMENT

Saikat Batabyal confirms that the manuscript is an honest, accurate, and transparent account of the study being reported and no important aspects of the study have been omitted.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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REFERENCES

1. Paules CI, Marston HD, Fauci AS. Coronavirus infections-more than just the common cold. *JAMA*. 2020;323:707.
2. Lai S, Bogoch II, Watts A, Khan K, Li Z, Tatem A. Preliminary Risk Analysis of 2019 Novel Coronavirus Spread within and beyond China, WorldPop, (2020).
3. Hellewell J, Abbott S, Gimma A, Bosse NI, Jarvis C. Feasibility of Controlling 2019-nCoV Outbreaks by Isolation of Cases and Contacts, medRxiv. (2020).
4. Li Q, Guan X, Wu P, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. *N Engl J Med*. 2020; 382:1199-1207.
5. Batabyal S, Batabyal A. Mathematical computations on epidemiology: a case study of the novel coronavirus (SARS-CoV-2). *Theory Biosci*. 2021;1-16. https://doi.org/10.1007/s12064-021-00339-5.
6. Zunyou W, McGoogan JM. Characteristics of and important lessons from the coronavirus disease 2019 (COVID-19) outbreak in China: summary of a report of 72 314 cases from the Chinese Center for Disease Control and Prevention. *JAMA*. 2020.
7. Bajiya VP, Bugalia S, Tripathi JP. Mathematical modeling of COVID-19: impact of non-pharmaceutical interventions in India. *Chaos*. 2020; 30(11):113143. https://doi.org/10.1063/5.0021353.
8. Bugalia S, Bajiya VP, Tripathi JP, Li MT, Sun GQ. Mathematical modeling of COVID-19 transmission: the roles of intervention strategies and lockdown. *Math Biosci Eng*. 2020;17(5):5961-5986. https://doi.org/10.3934/mbe.2020318.
9. Batabyal S. COVID-19: perturbation dynamics resulting chaos to stable with seasonality transmission. *Chaos, Solitons Fractals*. 2021;145: 110772. https://doi.org/10.1016/j.chaos.2021.110772.
10. Penghui Y, Ding Y, Xu Z, et al. Epidemiological and Clinical Features of COVID-19 Patients with and without Pneumonia in Beijing, China, medRxiv. (2020).
11. Hiroshi N, Kobayashi T, Miyama T, et al. Estimation of the Asymptomatic Ratio of Novel Coronavirus Infections (COVID-19), medRxiv. (2020).
12. Julien R, Hauser A, Counotte MJ, Althaus CL. Adjusted Age-Specific Case Fatality Ratio during the COVID-19 Epidemic in Hubei, China, January and February 2020, medRxiv. (2020).
13. Steven S, Lin YT, Xu C, Romero-Severson E, Hengartner N, Ke R. The Novel Coron- Avirus, 2019-nCoV, Is Highly Contagious and more Infectious than Initially Estimated, medRxiv. (2020).
14. Lauren T, Coombe M, Stockdale JE, et al. Transmission Interval Estimates Suggest Pre-Symptomatic Spread of COVID-19, medRxiv. (2020).
15. Russell TW, Hellewell J, Jarvis CI, et al. Estimating the Infection and Case Fatality Ratio for COVID-19 Using Age-Adjusted Data from the Outbreak on the Diamond Princess Cruise Ship, CMMID. (2020).
16. Robert V, Okell LC, Dorigatti I, et al. Estimates of the Severity of COVID-19 Disease, medRxiv. (2020).
17. Jiancong W, Zhou M, Liu F. Exploring the reasons for healthcare workers infected with novel coronavirus disease 2019 (COVID-19) in China. *J Hosp Infect*. 2020.
18. Joseph W, Leung K, Bushman M, et al. Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. *Nat Med*. 2020;1-5.
19. Roman W, Corman VM, Guggemos W, et al. Clinical Presentation and Virological Assessment of Hospitalized Cases of Coronavirus Disease 2019 in a Travel-Associated Transmission Cluster, medRxiv, (2020).
20. WHO. Coronavirus disease 2019 (COVID-19), Situation report 24, February 13, 2020. Geneva: World Health Organization. 2020.
21. WHO. Novel Coronavirus (2019-nCoV) situation reports, World Health Organization.
22. 2019 Novel Coronavirus (2019-nCoV) in the U.S., U.S. Centres for Disease Control and Prevention (CDC).
23. Outbreak Notification. National Health Commission (NHC) of the People's Republic of China.

24. Joint Mission. Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19). 2020. https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.pdf (Accessed March 23, 2020).
25. Hethcote HW. The mathematics of infectious diseases. *SIAM Rev*. 2000;42(4):599-653.
26. Kermack WO, McKendrick AG. A contribution to the mathematical theory of epidemics. *Proc R Soc A*. 1927;115(772):700-721.
27. Diekmann O, Heesterbeek JAP, Metz JAJ. On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations. *J Math Biol*. 1990;28(4):365-382.
28. van den Driessche P, Watmough J. Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission. *Math Biosci*. 2002;180:29-48.
29. Kucharski AJ, Russell TW, Diamond C, et al. Early dynamics of transmission and control of COVID-19 in Wuhan. *Lancet Infect Dis*. 2020;20:553-558.
30. Yang L, Funk S, Flasche S. The Contribution of Pre-Symptomatic Transmission to the COVID-19 Outbreak, CMMID. (2020).
31. Zhanwei D, Xu X, Wu Y, Wang L, Cowling BJ, Meyers LA. The Serial Interval of COVID-19 from Publicly Reported Confirmed Cases, medRxiv. (2020).
32. Tapiwa G, Kremer C, Chen D, et al. Estimating the Generation Interval for COVID-19 Based on Symptom Onset Data, medRxiv. (2020).
33. Qifang B, Wu Y, Mei S, et al. Epidemiology and Transmission of COVID-19 in Shenzhen China: Analysis of 391 Cases and 1,286 of their Close Contacts, medRxiv. (2020).
34. Kenji M, Kagaya K, Zarebski A, Chowell G. Estimating the Asymptomatic Ratio of 2019 Novel Coronavirus Onboard the Princess Cruises Ship, 2020, medRxiv. (2020).
35. Stephen L, Grantz KH, Bi Q, et al. The Incubation Period of 2019-nCoV from Publicly Reported Confirmed Cases: Estimation and Application, medRxiv. (2020).
36. Qun L, Guan X, Wu P, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia. *N Engl J Med*. 2020.
37. Natalie L, Kobayashi T, Yang Y, et al. Incubation period and other epidemiological characteristics of 2019 novel coronavirus infections with right truncation: a statistical analysis of publicly available case data. *J Clin Med*. 2020;9(2).
38. Jingyuan L, Liu Y, Xiang P, et al. Neutrophil-to- Lymphocyte Ratio Predicts Severe Illness Patients with 2019 Novel Coronavirus in the Early Stage, medRxiv. (2020).
39. Chaolin H, Wang Y, Li X, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet*. 2020;395(10223):497-506.
40. Xiaobo Y, Yu Y, Xu J, et al. Clinical course and outcomes of critically ill patients with SARS-CoV-2 pneumonia in Wuhan, China: a single-centered, retrospective, observational study. *Lancet Respir Med*. 2020.
41. Fei Z, Yu T, Du R, et al. Clinical course and risk factors for mortality of adult inpatients with COVID-19 in Wuhan, China: a retrospective cohort study. *Lancet*. 2020.
42. Wei-jie G, Ni Z, Hu Y, et al. Clinical characteristics of coronavirus disease 2019 in China. *N Engl J Med*. 2020.
43. David B, Qi X, Nielsen-Saines K, Musso D, Pomar L, Favre G. Real estimates of mortality following COVID-19 infection. *Lancet Infect Dis*. 2020.
44. Abbott S. Temporal Variation in Transmission during the COVID-19 Outbreak, CMMID. (2020).
45. Rocklov J, Sjodin H, Wilder-Smith A. COVID-19 outbreak on the Diamond princess cruise ship: estimating the epidemic potential and effectiveness of public health countermeasures. *J Travel Med*. 2020;27.
46. Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *Lancet*. 2020;395:689-697.
47. Liu T, Hu J, Xiao J, et al. Time-Varying Transmission Dynamics of Novel Coronavirus Pneumonia in China, Biorxiv. (2020).
48. Mossong J, Hens N, Jit M, et al. Social contacts and mixing patterns relevant to the spread of infectious diseases. *PLoS Med*. 2008;5(3):e74.
49. Prem K, Cook AR, Jit M. Projecting social contact matrices in 152 countries using contact surveys and demographic data. *PLoS Comput Biol*. 2017;13(9):e1005697.

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