Estimation of Transmission Risk and Control of COVID-19: A Mathematical Modelling Study

C V Rao

Article Info Article History

Received: April 11, 2021

Accepted:

November 14, 2021

Keywords:

Novel coronavirus; pandemic; mathematical modelling; epidemiologist; Severe Acute Respiratory Syndrome

DOI:

10.5281/zenodo.5700826

Abstract

The current outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has created havoc worldwide. Understanding early transmission risk in asymptomatic individuals and estimating the efficiency of control measures is critical to find out the new infectious cases of transmission in new areas. Applying the susceptible-exposed-infectious-recovered (SEIR) mathematical model with six datasets of countries including USA, Italy, Spain, Germany, France, and Iran, I have estimate the transmission dynamics from the date of onset to the 5 April 2020. The trajectory of the time-dependent population increases initially with the infection at the peak of the graph, afterward it tends to decrease with some interventions. The algorithm reveals a significant result in this pandemic if cases were introduced.

Introduction

As of March 23, 2021, more than 122 536 880 cases of coronavirus 2019 (COVID-19) had been confirmed, and more than 2 703 780 reported deaths globally[1]. The novel coronavirus (2019-nCov or SARS-CoV-2) is the latest from the family of viruses known as coronaviridae. This family is notorious for causing respiratory disease outbreaks, second only to the influenza family of viruses. Control measures havebeen implemented country-wise with full or partial lockdown including 203 countries. In the initial stages of a new contagious pandemic outbreak, it is necessary to understand the transmission flow of the infection, so that essential steps can be taken to prevent the spread of pandemic. Public Health Emergency of International Concern (PHEIC) of the World Health Organization (WHO) already declared its outbreak because it has killed more people than Severe Acute Respiratory Syndrome (SARS). The epidemiologist are inspecting the changes in transmission over time to the wide range of parameters [2] and estimating how contagious a new virus is, in order to identify whether adopted outbreak control measures holds a measurable effect [3,4]. Such analysis parameters can be helpful for the estimate risk to other countries [5] and guide the preparation of alternative arbitrations [6].

However, the whole world is struggling for several challenges to such analyses. There can be a delay to symptom appearance (resulting from incubation period) and delay to confirmation of cases (resulting from detection and treatment capacity) [7]. Henceforth, it is a need of the hour to develop a mathematical model to suppress the causalities due of this contagious COVID-19.As acknowledged by the WHO, mathematical models can play a vital role for policy-makers and provides the health decision, especially in real time. In addition, indeed, modelling can be better to understand: severe-ness of the infection, transmission density, highest infection during the incubation period and effectiveness of interventions. Many developed countries like Italy, Spain, and United States are struggling to meet the healthcare demands COVID-19 has produced. Sometimes the early dataset might be imperfect, or reveals the one aspects of the outbreak dynamics. However, the early stage data of this pandemic are still lacking and available data may have many flaws and unreliability due to substantial uncertainty, concerning, for instance, the accurate timing and natural history of cases. The main aspect and significant challenge to simulate the proposed model is a collection of good data quality. On the contrary, case analysis could help drop out some impractical assumptions, allowing to test different hypotheses. Proposed model, which has a capacity to fit to multiple data sources can reveals more vibrantestimation of the transmission dynamics [8, 9]. Preparing a mathematical model of SARS-CoV-2 transmission with different datasets in the USA, Italy, Spain, Germany, France and Iranregion, I have estimated variation of transmission flow from the first case appeared with country-to-country. Ihave predict the potential aspects for this human-tohuman transmission to occur in provinces outside China on the basis of these estimates, if cases were announced. Human-to-human transmission of COVID-19 is mainly thought to spread among close contacts through respiratory droplets produced by sneezing and coughing [10].

In this report, I have discussed the algorithms of the susceptible-exposed-infectious-recovered (SEIR) model [11].

1. Epidemiological model

The model used in this study is SEIR model, which has been successfully used to accurately predict previous outbreak like SARS. Here, I have discussed the algorithmof SEIR model, more compliance in this time of outbreaks, as described below:

Algorithm

The SEIR model can be described by the following ordinary differential equations, where total population (N) is the sum of four classes S, E, I and R represented as susceptible, exposed, infected and recovered population respectively to describe the model equations [11].

$$\frac{dS}{dt} = -\frac{R_t}{T_{\text{inf}}}. IS$$

$$\frac{dE}{dt} = \frac{R_t}{T_{\text{inf}}}. IS - T_{\text{inc}}^{-1}E$$
(1)

$$\frac{dI}{dt} = T_{\rm inc}^{-1} E - T_{\rm inf}^{-1} I \tag{3}$$

$$\frac{dR}{dt} = T_{\text{inf}}^{-1} I \tag{4}$$

Where R_t represents the effective reproduction number, $T_{\rm inc}$ is an incubation period and $T_{\rm inf}$ denotes the infectious period. The parameter R_t indicates transmissibility of the virus that reveals us about how many personshave get infected in the current state of population, which does not have to be the uninfected state. It is significantly shows the number of new cases a single infected person at time t will cause during their infectious period. The value of R_t can be calculated by multiplying R_0 by the fraction S of the population that is susceptible. It is one of the most important parameters for evaluating any pandemic. The SARS-CoV-2 has R_0 in the range of 2.4–3.4 but it depends on the country involved. Furthermore R_0 will change with time. The R_0 is the basic reproduction number which denotes the ration between frequency of contacts to the frequency of recovery. When R_0 is greater than 1, the epidemic can enter a totally susceptible population and the number of active cases will improve substantially in return, whereas when R_0 is less than 1, the epidemic will always fail to spread.

2. Results and discussion

Since the emergence of COVID-19 in Wuhan, China, in December 2019, the number of infectious cases are increasing gradually day-by-day worldwide. The improvement in the number of cases is shocking and it is obvious the fear of transmission from asymptomatic individuals. The study of the diseases has been such a successful application of mathematical modelling because most diseases imitate to the assumptions behind the simple models. In addition, the contribution of asymptomatic cases in the transmission of SARS-CoV-2 is not well studied and deserve additional work to know the magnitude of occurrence and the role in transmission. It is important to estimate the liability of asymptomatic individuals. Such studies will improve the understanding of these embryonic viruses and will advise the policy-makers to adopt the scientifically proven recommendations. However, it is a challenging task to overcome the spread of outbreaks that have been introduced into SEIR model which allow them to better show the observed dynamics.

WHO is working with its networks of researchers and other experts to coordinate global work on surveillance, epidemiology, mathematical modelling, diagnostics and virology, clinical care and treatment, infection prevention and control, and risk communication. Recent study shows that this SARS-CoV-2 is mutating very fast and have two different strains S- type and L-type [12], in which the L-type is more aggressive

than S-type. On the other hand, some scientist believes that mutations are a natural part of the virus life cycle including RNA-viruses like SARS-CoV-2 and rarely impact outbreaks dramatically [13].

The recent study suggests that there are two strategies which suppresses the graph surprisingly with different interventions as reported by the Imperial College Covid-19 Response Team, explicitly, suppression and mitigation [14]. The first is suppression which aims to reverse the growth of the epidemic, reducing the active cases to a very least number or even wipe out the disease completely. The second is mitigation, which only aims to slow down the growth of the epidemic. As far as mitigation is concerned, the team found that the optimal minimal combination of measures is the combination of home isolation of suspect cases, home quarantine for those living in the same house as suspect cases, and social distancing of those over 70 years of age, which would remain in place for four months.

Figure 1(a-f) expresses the time (in days) dependence of population in the algorithm of SEIR model as described above in Eqs (1) to (4). The simulated outbreaks initiated with 20 initial cases, the basic reproduction number, R₀ is to be taken in the range of 2.4–3.4 depends on the country, particular for SARS-CoV-2, and 1% transmission before symptom start to appear at the first instant even with low transmission infectious rate. At the beginning it seems that the graph is linear but it more likely exponential. The time (in days) dependence of population plot has categorized into four different parameters namely exposed, infectious, hospitalized and death. Here, the exposed refers to the population currently in incubation, infectious means number of infections actively circulating, hospitalized depicts the active hospitalizations, and deaths means the total number of fatalities in the suspected population. The plots are more likely bell in shape but with the trajectory of time it becomes stable. Initially it looks like infectious cases are large but afterwards during the entire outbreak these cases eradicates. The recovery rate has calculated by the ratio of recovered to the active cases while the susceptible-infected parameter was calculated by the ratio of infected to the active cases. The recovery rateevaluated in this study are 6%, 23%, 47%, 41%, 24% and 67% and the susceptible-infected parameter evaluated are 1.3%, 2.0%, 1.5%, 1.4%, 2.0%, and 2.2% for USA, Italy, Spain, Germany, France and Iran, respectively. The delayincubation period has been taken from the first case appeared in the country to the 5 April, 2020.Let us assume we enforce intervention on Day 1. This scenario diminishes the instant effect of exposure of infected people to healthy people. Since the mean incubation period is 5 days, daily new symptomatic patients will start reducing from Day 6. In most scenario, the death rate is constant after 3 months due to an outbreak of COVID-19. It can be seen from Figs 1(a-f), the population of control eradicates with long delays from symptom onset to intervention. This model can be modified to assess the updated transmission dynamics and more realistic results of the current outbreak can be achieved in real time. In this present study, the pure theoretical work have been done with the data available in the WHO website. In order to evaluate the real values, case reports from health workers provides us the real time case scenario which can be best correlate with the theoretical data.

Figure 2(a–f) described the time (in days) dependence of a number of cases plot for major affected countries by using the algorithmof SEIR model. In this graph, I have analyzed four types of the number of cases, namely exposed, infectious, recovered and deaths. All graph represents that these four types of the number of cases are increasing exponentially. Although the deaths are very minimal as compared to the number of exposed, infectious and recovered cases. The slope of these graphs at any given time shows the rate of increase in the number of daily new cases over time. It is remarkable that one thing is common in all the plots that are an inflection point. As we know that it is the point at which the slope of the graph first starts decreasing or flattening out, which is obvious from all the Figures 2(a–f). When we observe that the new cases for a day are less than the new cases on the previous days that mean we have reached the inflection point. It might be possible that absolute number of cases will increase after this, but the rate of increase of cases diminishes. This is the first indication that we are starting to get a hold of the outbreak.

The inflection point can be elaborate in this study by taking the logarithms of the number of daily cases, as can be seen in Figures 3(a–f). It is clear from these plots that all the countries show the inflection before 90 days, except the USA. The USA is the only county which has reached the flattened site of curve very late.

4. Conclusion

Our study has discussed the algorithm tools under the SEIR model for the transmission dynamics of the new COVID-19. The six countries, USA, Italy, Spain, Germany, France and Iran have been taken into account, where the outbreaks are massive as compared to other countries. As per the population size, the recovery rate and susceptible-infected parameter both are evaluated that are least for the USA and highest for the Iran. The basic reproduction number, R_0 have been taken around 2.4–3.4 for SAR-CoV-2 in algorithm of the SEIR model.

The algorithm plays a vital role for the transmission risk of this pandemic disease of COVID-19. In near future, when pandemic trend, the collection of real-time information of data and resources available to intervene the spread of pandemic, not only for the policy-makers but also for the public health workers.

Acknowledgements

This work is supported by the GS Department, Jubail Industrial College (Royal Commission in Jubail) Saudi Arabia.

Data Sharing

http://gabgoh.github.io/COVID/index.html(for algorithm)

References

WHO. Weekly epidemiological update on COVID-19-23 March 2021. https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---23-march-2021.

Camacho A, Kucharski A, Aki-Sawyerr Y, et al. Temporal changes in Ebola transmission in Sierra Leone and implications for control requirements: a real-time modelling study. *PLoSCurr*2015; 7.

Funk S, Ciglenecki I, Tiffany A, et al. The impact of control strategies and behavioural changes on the elimination of Ebola from Lofa County, Liberia. *Philos Trans R SocLond B BiolSci*2017; **372:** 20160302.

Riley S, Fraser C, Donnelly CA, et al. Transmission dynamics of the etiological agent of SARS in Hong Kong: impact of public health interventions. *Science* 2003; **300:** 1961–66.

Cooper BS, Pitman RJ, Edmunds WJ, Gay NJ. Delaying the international spread of pandemic influenza. *PLoS Med* 2006; **3:** e212.

Kucharski AJ, Camacho A, Checchi F, et al. Evaluation of the benefits and risks of introducing Ebola community care centers, Sierra Leone. *Emerg Infect Dis* 2015; **21:** 393–99.

Aylward B, Barboza P, Bawo L, et al. Ebola virus disease in West Africa—the first 9 months of the epidemic and forward projections. *N Engl J Med* 2014; **371:** 1481–95.

Birrell PJ, De Angelis D, Presanis AM. Evidence synthesis for stochastic epidemic models. *Stat Sci*2018; **33**: 34–43.

Baguelin M, Flasche S, Camacho A, Demiris N, Miller E, Edmunds WJ. Assessing optimal target populations for influenza vaccination programmes: an evidence synthesis and modelling study. *PLoS Med* 2013; **10**: e1001527.

"Transmission of Novel Coronavirus (2019-nCoV) CDC". www.cdc.gov. 2020-01-31.

Wu T et. al, The Lancet 2020 395(10225) 689-697

Tang X et.al National Science Review, nwaa036, https://doi.org/10.1093/nsr/nwaa036 (in press)

Grubaugh, N.D., Petrone, M.E. & Holmes, E.C. Nature Microbiology 5, 529-530 (2020).

Neil M Ferguson et. al, Imperial College COVID-19 Response Team, March 2020, DOI: https://doi.org/10.25561/77482

Author Information

C V Rao

Department of General Studies, Jubail Industrial College, P. O. Box - 10099, Jubail Industrial City-31961, Saudi Arabia