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Application of SEIR Model in COVID-19 and The Effect of Lockdown on Reducing The Number of Active Cases

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ABSTRACT

The spread of COVID-19 within a region in South East Asia has been modelled using a compartment model called SEIR (Susceptible, Exposed, Infected, Recovered). Actual number of sick people needing treatments, or the number active case data was used to obtain realistic values of the model parameters such as the reproduction number (R0), incubation, and recovery periods. It is shown that at the beginning of the pandemic where most people were still not aware, the R0 was very high as seen by the steep increase of people got infected and admitted to the hospitals. Few weeks after the lockdown of the region was in place and people were obeying the regulation and observing safe distancing, the R0 values dropped significantly and converged to a steady value of about 3. Using the obtained model parameters, fitted on a daily basis, the maximum number of active cases converged to a certain value of about 2500 cases. It is expected that in the early June 2020 that the number of active cases will drop to a significantly low level.

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1. INTRODUCTION

An outbreak of a corona virus disease was first identified in Wuhan, China, in December 2019. What follows is an increasing number of reported cases internationally with travel histories related to Wuhan, China (http://virological.org/t/epidemiological-data-from-the-ncov-2019-outbreak-early-descriptions-from-publicly-available-data/337/3). This new corona virus has been designated as COVID-19 and later officially named as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by WHO (https://www.who.int/dg/speeches/detail/who-director-general-s-remarks-at-the-media-briefing-on-2019-ncov-on-11-february-2020). Due to its worldwide spread, COVID-19, as it is more well-known, has been declared as a world pandemic by WHO (https://www.who.int/news-room/detail/30-01-

2020-statement-on-the-second-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-ncov)).

Governments around the world have been trying to implement various control measures to contain the virus. Researchers, on the other hand, do whatever they can to help giving information to the governments, as well as helping front liners and societies. One of the most important pieces of information regarding the outbreak of the virus is the estimation of how many people may get infected, fall sick, need treatments, and how health care systems can cope with that. This information is important to be able to develop and evaluate control measures as well as for future prevention (Prem *et al.*, 2020; Wang *et al.,* 2020).

Many researchers have done various modeling efforts using data to model the spread of viruses. As reported in literatures, the model approaches cover stochastic transmission model (Kucharski *et al.*, 2020), polynomial chaos-based nonlinear Bayesian approach(Bavdekar & Mesbah, 2016; Santonja & Chen-Charpentier, 2012), stochastic Galarkin method(Harman & Johnston, 2016), and various compartmental based models such as SEIR (Fang *et al.*, 2020), SIR (Chen-Charpentier & Stanescu, 2010), or SUQC(Zhao & Chen, 2020).

The most commonly used model is what is called as compartmental based models which was developed and used a lot within epidemiological communities to predict the spread of the virus and its severity. Out of many variations of the compartmental based models, such as Susceptible, Exposed, Infectious, Recovery (SEIR), has been used as a general model to work with and modified further.

SEIR model is a population balance type of model where people are moving from one compartment to another compartment. Compartment “S” stands for Susceptible, which is the population that may get infected. Compartment “E” or exposed is the population that are exposed or infected by the virus, but there is no sign of illness yet. They are still in the incubation period. Compartment “I” or Infected population is the population that are infected and fall ill and needs treatment. The compartment “R” or recovered population is the population that has recovered from the illness caused by the virus.

There are few observations that justify the use of SEIR model to better represent the spread of the virus. It is a known fact that people in compartment “E” may not fall sick or just show very light symptoms that they themselves do not notice. This group of people is commonly called as “carrier” where they are moving around spreading the viruses to people with lower level of immunities. This observation is the basis of having the compartment “E”. It is also known that there is no passive or maternal immunity against this virus. Hence, other compartment “M” or population with maternal/passive immunities is not included in the model. And lastly, it is widely assumed that the recovered people have permanent immunity against COVID-19. This assumption necessitates the Recovered group of people and they are not getting back to being ill. Hence, based on these observations and assumptions, the most appropriate model to use is the SEIR model. This model has been used widely and it has been used to model the actual case in China (Fang *et al.*, 2020). Some of the advanced versions of the model can be found online (https://covid19-scenarios.org). The basic of the SEIR model is shown in **Figure 1.**

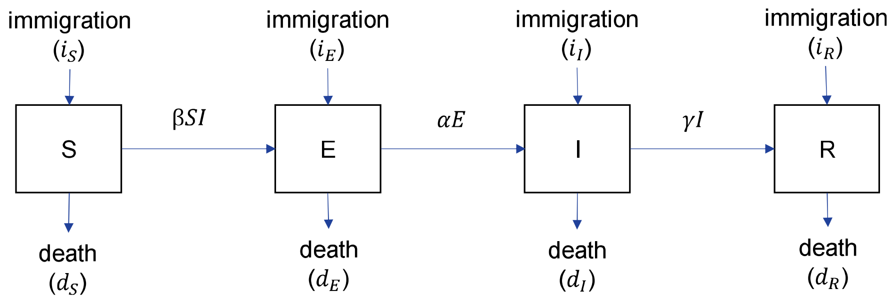

Figure 1. Basic SEIR compartment model

In many cases, the number of people immigrating (i) to the compartments can be assumed to be zero. Death ratios (d) other than the death caused by the virus itself (dI) are also normally neglected as it is not necessarily to be reported during the pandemic period. Hence, taking into account these considerations, equations (1) – (7) describing the SEIR model are shown in **Figure 1**. These are dynamic equations modeling the different compartments (populations) as a function of time and the effect of the virus on their numbers.

$$\frac{dS}{dt} = i_S S - d_S S - \beta SI \quad (1)$$

$$\frac{dE}{dt} = \beta SI - \alpha E + i_E E - d_E E \quad (2)$$

$$\frac{dI}{dt} = \alpha E - \gamma I + i_I I - d_I I \quad (3)$$

$$\frac{dR}{dt} = \gamma I + i_R R - d_R R \quad (4)$$

$$\frac{dR}{dt} = \gamma I + i_R R - d_R R \quad (5)$$

$$\alpha = \frac{1}{T_{incubation}} = Incubation\ period (6)$$

$$\beta = \frac{Reproduction\ Number\ (R_0)}{Recovery\ period} = R_0 \cdot \gamma (7)$$

One of the parameters used in this model is the Reproduction Number (R0). R0 is defined as how many people can be infected from 1 sick person. The higher the R0 can mean many things, which some of them include the more contagious the virus, that it can spread very easily. It may also mean the more unprepared a region/country to prevent the spread of the virus. It means that the virus has been transmitted without being notice and suddenly it has been spreading in an exponential rate. It could also mean the higher the density of the people within a certain area where people are living in a very crowded place where the virus can also be transmitted very easily and rapidly. Lastly, it can also tell about the socio-cultural of the people living within that community (e.g. community closeness, travelling frequencies, events with crowds, etc.). However, its precise value is very difficult to predict given the different circumstances of various communities, events, and regions (Leung *et al*., 2020).

In our previous study, we have developed system for simulating some chemical processes (Putra, 2016). Here, in this work, this SEIR model was used to model the number of infected people needing treatment, or the number of reported active cases at hospitals. Unlike other previous approach on this model where the model parameters were taken from references as typical values (Prem *et al.*, 2020), this work tried to fit the model with the actual data to obtain realistic model parameters for the considered region. These parameters were then used back in the model to predict the maximum number of active cases and when it would be happening, as well as when it would be reaching to a significantly low level. Some observations to the actual case was also going to be discussed further. The effect of the implementation of lockdown would also be discussed. A region within South East Asia was used as the case study.

2. METHODOLOGY

In this work, the SEIR model was fitted against the number of active cases or the number of infected people needing treatment at hospitals on a daily basis. This data fitting was to find the realistic values for the model parameters considering local circumstances of the affected community as mentioned previously. In this model, it was assumed that everybody has the same virus spreading capacity and the same immunity level. Few other parameters used in the models were obtained from the actual reported data as follows:

(i) Number of people infected at the beginning was 4 people as of the data on 25th January 2020

(ii) Death rate was 1.6% of the infected people as the average number from the data

Once the data was fitted to get the model parameters, they were then used to predict how many and when the maximum number of active cases was going to happen, as well as when it would become significantly low. These multivariate differential equations model were solved with Python as the programming language, by using Anaconda as the platform.

3. RESULTS AND DISCUSSION

Fitting active case data until mid of April 2020 is shown in **Figure 2**. It is a fact that every community has different response and preparedness towards the virus, different socio-cultural behavior, and so on, which may make these model parameters unique. From this fitted data, the model parameters of reproduction number (R0), incubation, and recovery periods are obtained. Hence, by fitting the model into the actual data, the obtained model parameters really reflect the actual local reality.

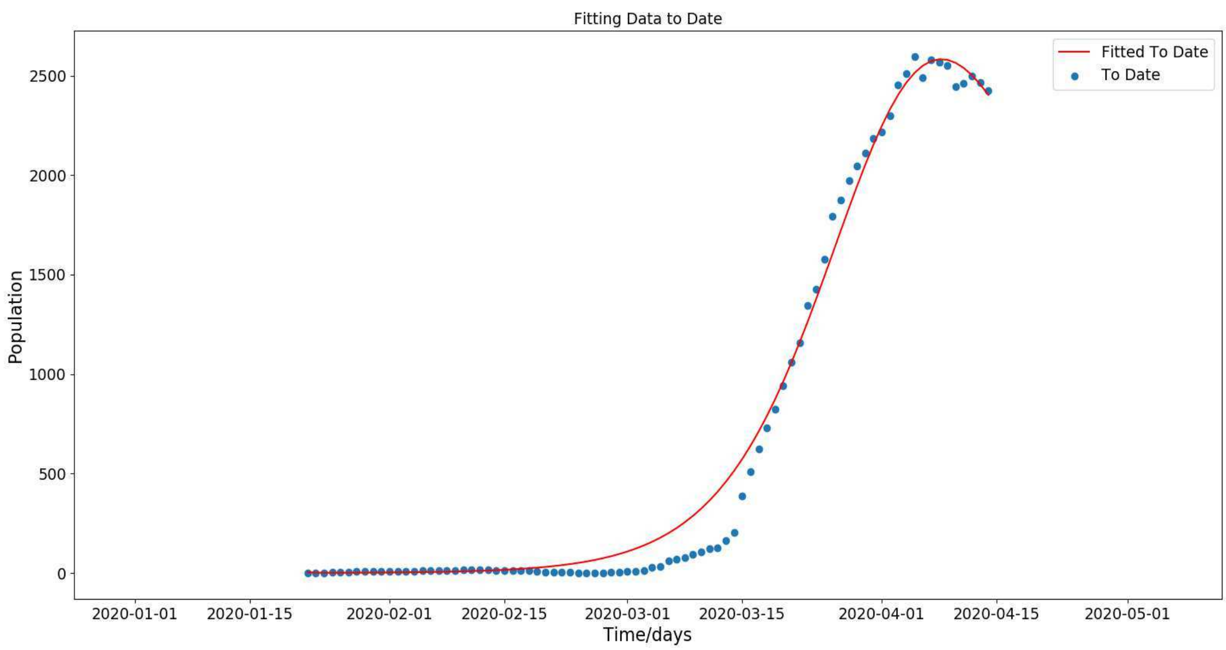

Figure 2. Regression result

Figures 3 and **4** show the estimated Susceptible, Exposed, Infected, and Recovered populations using the parameters obtained by fitting the active case data until mid of April 2020. In **Figure 3**, the shape of the curves shows that many of the exposed population may not need treatment at the hospital and can recover by themselves. Their number is indeed very high, reaching above 20 thousand people. However, only about 2500 people need hospital treatment as shown in the infected population (or number of active cases, in this example).

Figure 5 shows several values of R0 depending on the time frames of the fitted data. It can be seen that at late March 2020, when most people were not fully aware of how this virus spreads and still moving around, the obtained R0 values were very high. This means that when people were still freely moving, the virus is spread very rapidly. One infected person can infect 6 or more people before the 25th of March 2020. The R0 number even went up to about 10 during late March 2020. The last week of March was the time when lockdown was ordered. Once it was ordered, people were rushing to their hometowns, highways were jammed, and many crowds were at public transportation hubs. That was the perfect situation where the virus spread very rapidly. Then, about two weeks after the lockdown was commenced, situation got calm, people are obeying the lockdown situation, the R0 values are dropping substantially until it reaches a steady value of around 3.

Figure 6 shows the expected number of active cases using the parameters obtained from **Figure 5**. It can be seen that for the first two points in **Figure 5** corresponds to the two highest peaks in Figure 6. With high R0 values, many people can get infected, fall sick, and then need further treatments in the hospitals. Few weeks after the lockdown, the number of infected people reduces and the number of active cases also reduces. The maximum active cases are somewhat converging to a fixed value of about 2500 people. By the end of June 2020, the number of active cases is predicted to be at the very low level.

As a general conclusion from the graph, it can be seen that the lockdown and the way it is being observed and controlled seems to be effective in reducing the spread of the virus. The predictions seem to converge consistently to a certain value may also mean that people are obeying this lockdown situation, excellent work done by the government in providing testing and treatment facilities, and amazing work performed by front liners in treating people and maintaining the death ratio lower and relatively constant.

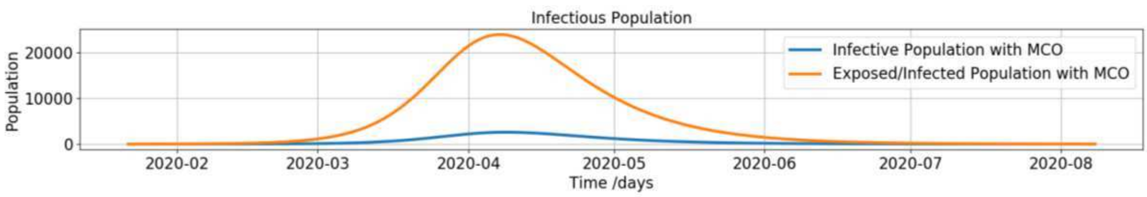

Figure 3. Prediction of Exposed and Infected (needs treatment) populations using the parameters fitted from data until mid of April 2020)

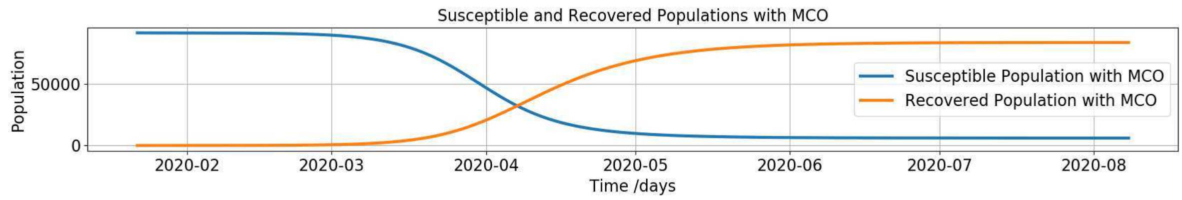

Figure 4. Prediction of Susceptible and Recovered populations using the parameters fitted from data until mid of April 2020

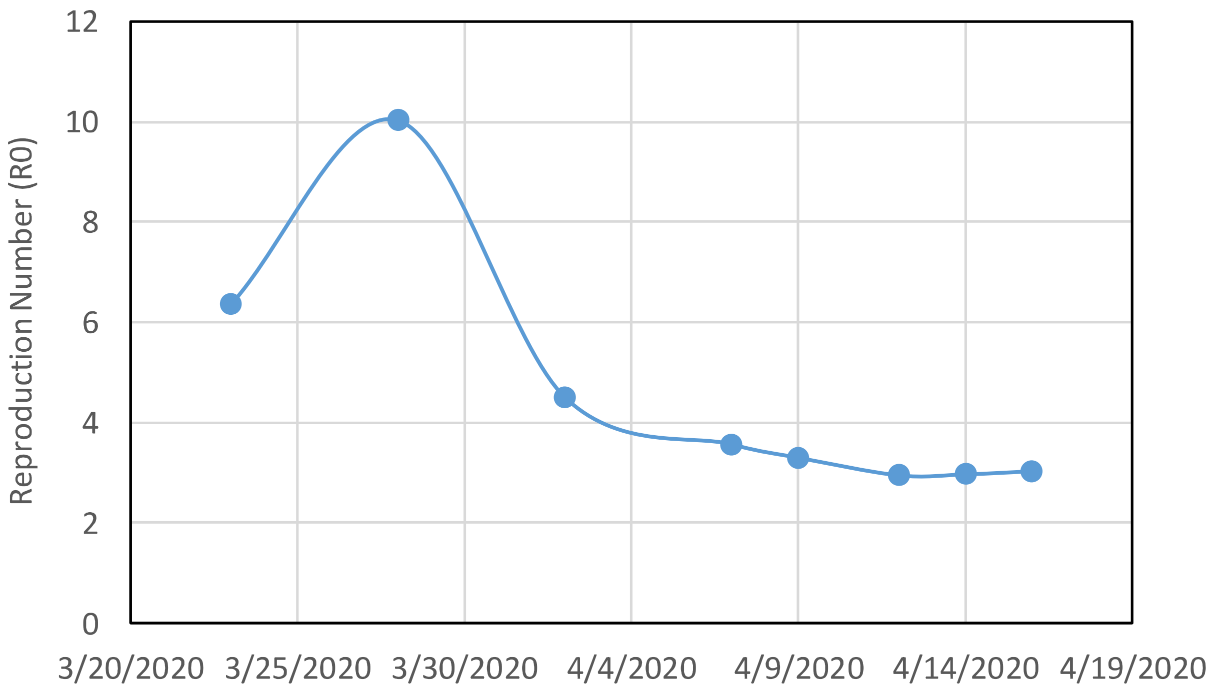

Figure 5. Estimated R0 for different data fitting in various time frames

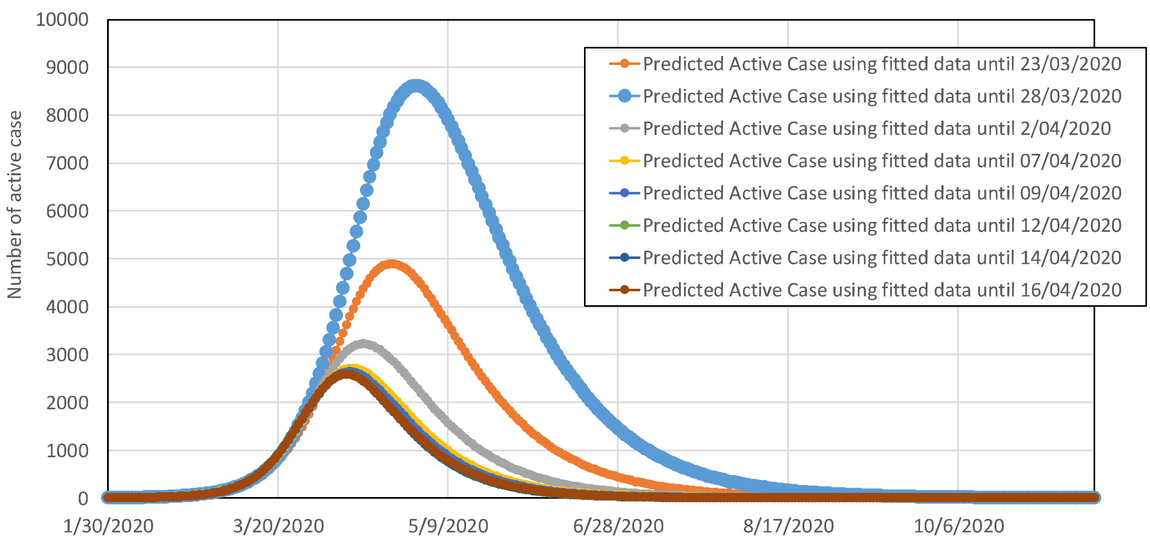

Figure 6. Number of active cases (under hospital treatment) estimated from data fitted using different time frames

4. CONCLUSION

A compartment model called SEIR has been described in this article, demonstrating model for the number of active cases (number of sick people needing treatment) due to COVID19 in an area within South East Asia region. Actual active case data was used to obtain realistic number of the model parameters such as the reproduction number (R0), incubation, and recovery periods. It can be seen that at the beginning of the pandemic where most people were still not aware, the R0 was very high as seen by the steep increase of people got infected and admitted to the hospitals. Few weeks after the lockdown was in place and people were obeying the regulation and observing safe distancing practice, the R0 values dropped significantly and converged to a steady value of about 3. Using the obtained model parameters and fitting on a daily basis, the maximum number of active cases converged to a certain value. It is expected that in the early June 2020 that the number of active cases will drop to a low level.

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6. AUTHORS' NOTE

The author(s) declare(s) that there is no conflict of interest regarding the publication of this article. Authors confirmed that the data and the paper are free of plagiarism.

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