Menemui Matematik (Discovering Mathematics)
Vol. 4, No. 1: 35-52 (2022)

The Impacts of Immigrants' Population on the Dispersal of COVID-19 Infections in Malaysia

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ABSTRACT

This article presents an improved SLEAICR model that considered the impacts of immigration, the lockdown, and the effects of prevention and control measures of infectious diseases on COVID-19 transmission. The specific number of infections in Malaysia is then used in the model to obtain the basic reproduction number in Malaysia. Furthermore, the impacts of immigrants on the dispersal of COVID-19 are analyzed. The number of active cases from the 1st of June to the 11th of August 2021 was intercepted and the curve fitting was done to obtain the relevant model parameters. Finally, the results obtained in this article support the effectiveness of lockdown for immigrants in the process of reducing COVID-19 transmission.

Keywords: COVID-19; Immigrant Population; Impact Reproduction Number; Lockdown

INTRODUCTION

The Coronavirus disease 2019 (COVID-19) virus is a type of positive-chain single-stranded RNA virus (Li et al., 2020a) that is hosted and spread by bats (Shereen et al., 2020). Unfortunately, this virus can be transmitted from the hosts (bats) to humans and when humans are infected, the virus can cause Severe Acute Respiratory Syndrome Coronavirus 2 virus (SARS-CoV-2) which can eventually lead to the death of the infected individual (Pambuccian, 2020). The disease is contagious and can be transmitted by infected humans to other humans through respiratory droplets or aerosols. Apart from human-human transmissions, the virus can also be contracted when contaminated surfaces or fomites are touched or contacted in any form. When humans are infected, the virus targets the lungs and causes severe damages to the lungs (Pambuccian, 2020; Li et al., 2020a).

COVID-19 has become a global pandemic since it was first discovered in Wuhan, China, in December 2019 (WHO, 2020). So far, the number of infected individuals has increased exponentially in different countries worldwide. Patients that test positive for the COVID-19 virus exhibit symptoms such as fever, cough, exhaustion or myalgia, sputum production, and headache (Ma et al., 2020; Zhu et al., 2020; Yang et al., 2020). As of the 27th of July 2020, the total number of reported cases globally has reached 16,481,022 with 653,296 reported deaths (WHO, 2020). The disease caused by this virus has become an epidemic in many parts of the world thereby affecting many countries negatively (WHO, 2020). Malaysia reported its first COVID-19 cases on the 25th of January 2020, in which three Chinese tourists were involved (Ministry of Health Malaysia, 2020). As of March 2020, Malaysia has recorded a total number of 8904 confirmed infections (Ministry of Health Malaysia, 2020). As a result of this alarming situation, the Malaysian government was forced to take strict control measures to reduce human-human transmissions. Some of these measures include the suspension of school activities and university classes, the banning of events, the closing of borders, and a complete lockdown from the 18th of March to the 9th of June 2020. However, considering the recent increase in COVID-19 virus infections and its rapid spread across the globe, it is important to understand and visualize the virus's spread and its impact.

Many scientists are currently working hard to control and limit the spread of this virus, and to find ways of treating those infected. By approaching this pandemic disease from a mathematical perspective, the patterns and common systems in the disease function can be identified and some of the underlying structures that govern outbreaks and epidemics can be found. Recently, a mathematical model describing the spread of the COVID-19 outbreak in humans was introduced by Sardar et al. (2020). The model incorporated the lockdown effect and variability in transmission between symptomatic and asymptomatic populations, with the former being a rapid spreader of the disease. Their result has proven that lockdown in five locations (i.e. Maharashtra, Delhi, Tamil Nadu, Gujarat, and Punjab) impacts the higher percentage of symptomatic infection that exists in the population. Therefore, a great-scale COVID-19 mass testing is necessary to reduce infection in those locations. The modeling with lockdown for COVID-19 has also been explored extensively by Rawson et al. (2020), Ibarra-Vega (2020), and Li et al. (2020b). Although the previous models which incorporated the lockdown effects have contributed immensely to COVID-19 research, these models have omitted the effects of migration which is a significant factor in the spread of the disease.

Recently, human as well as animal migration is an important factor that has contributed to the spread of diseases worldwide. As a result, it is imperative to use migration models for modeling the spread of the disease. According to Aleshkovski and Iontsev (2006), migration models can be classified into two types and these are the static or dynamic migration models. The authors defined static models as models that considered the state of migration processes at a particular point in time, whereas dynamic models consider the interaction between the variables in time. Several kinds of research have been conducted with migration models. For instance, Piccolo and Billings (2005) and Widyaningsih et al. (2018) proposed the addition of an immigration term in an epidemic model with population dispersal. Piccolo and Billings (2005), presented the Susceptible-Infected-Recovery (SIR) immigrant model which considered the effects of immigration on the spread of rubella in a large city. The authors then obtained the minimum vaccination levels required to continue the herd immunity or the natural die-out of the disease. From the results of the numerical simulations, the authors showed that a less vaccinated immigrant population causes the rubella epidemic to thrive through the immigrant population and then spreads to the local citizen’s population.

Furthermore, Widyaningsih et al. (2018) presented a Susceptible-Exposed-Infected-Recovery (SEIR) mathematical model that considered the effects of immigration and how the interaction between the population of local citizens and those of immigrants influences the spread of disease. From the results of the study, the authors showed that the immigrant population contributed to the spread of the disease to the local citizen's population in communities. However, to obtain better results from the COVID-19 mathematical models, it is imperative to improve the mathematical model presented by Sardar et al. (2020) to include the impact of immigration on the spread of COVID-19 infections. With this improvement, more realistic scenarios that will give a better understanding of the spread of COVID-19 infections can be analyzed. Therefore, in this article, an improved mathematical model that considers the impact of the immigrant's population to the spread of COVID-19 infections is introduced. Subsequently, the consequences of the immigrant population when entering communities are explored.

This article is arranged in sections. In Section 2, the method used for the study which includes the formulation of the improved mathematical model, as well as the model analysis and the basic reproduction number, are presented. In Section 3, the model parameters are interpreted and presented. In Section 4, the results of the model simulation are presented and discussed. Lastly, the article is concluded with a summary of the potential implications of this research and suggestions for further research.

THE METHOD

This section presents the method used for the study which includes the formulation of the improved model, the analysis of the model, and the model simulation.

The Immigrant Model

This section presents the new improved immigrant model. However, the basic SLEAICR model and the SEIR model are first presented. The SLEAICR model means the Susceptible, Lockdown, Exposed, Asymptomatic, Symptomatic, Hospitalized and Recovered humans model, and it was proposed and developed by Sardar et al. (2020). The SLEAICR model considered the lock-down effect on the COVID-19 outbreak. The model parameters consist of a homogeneous human population but with a variety of COVID-19 transmission between symptomatic and asymptomatic populations with the latter being the fast spreader of the disease. In the model, the total population of humans at time t is given by the equation below

$$N(t) = S(t) + L(t) + E(t) + A(t) + I(t) + C(t) + R(t)$$

where
S, L, E, A, I, C, and R are the populations of Susceptible, Lockdown, Exposed, Asymptomatic, Symptomatic, Hospitalized, and Recovered humans respectively.

According to Avila-Ponce de Léon (2020), an asymptomatic human is defined as an infected human, but with no visible symptoms of COVID-19 infection while the symptomatic humans have clinical symptoms (Gumel et al., 2004). The hospitalized human can be defined as the patient who was suspected of contracting the COVID-19 virus or had tested positive for the COVID-19 infection (Horby et al., 2020). Therefore, the non-linear differential equation representing the SLEAICR model for COVID-19 transmission with lockdown effect is given below

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Pi_H + \omega L + \frac{\beta IS}{(N-L-C)} - \frac{\rho\beta AS}{(N-L-C)} - (\mu + l)S,\\
\frac{dL}{dt} &= lS - (\mu+\omega)L,\\
\frac{dE}{dt} &= \frac{\beta_1 IS}{(N-L-C)} - \frac{\rho\beta_1 AS}{(N-L-C)} - (\mu+\sigma)E,\\
\frac{dA}{dt} &= (1-k)\sigma E - (\gamma_1+\mu)A,\\
\frac{dI}{dt} &= k\sigma E - (\gamma_2+\tau+\mu)I,\\
\frac{dC}{dt} &= \tau I - (\delta+\gamma_3+\mu)C,\\
\frac{dR}{dt} &= \gamma_1 A + \gamma_2 I + \gamma_3 C - \mu R,
\end{aligned}\right\} \quad (1)$$

The SLEAICR model parameters in Equations (1) are given below in Table 1.

Table 1: The SLEAICR model parameters in Equations (1)

Symbol	Description
Π_H	The average recruitment rate
$\frac{1}{\omega}$	The lockdown period
β_1	The transmission rate of symptomatic infected
ρ	The reduction in COVID-19 transmission for Asymptomatic infected
μ	The natural death rate
l	The average lockdown rate
κ	The fraction of exposed population that become symptomatic infected
γ_1	The recovery rate for asymptomatic infected
γ_2	The recovery rate for symptomatic infected
γ_3	The average recovery rate for COVID-19 hospitalized and notified infection
$\frac{1}{\sigma}$	The disease incubation period
τ	The average notification and hospitalization rate of symptomatic infection
δ	The average case fatality rate

The SEIR model, presented by Widyaningsih et al. (2018), which incorporated the impact of immigration is given below:

$$\left.\begin{aligned}
\frac{dS}{dt} &= \mu N - \frac{\beta S}{N} - (\mu+\eta)S,\\
\frac{dE}{dt} &= \frac{\beta S}{N} - (\mu+\eta)E - \sigma E,\\
\frac{dI}{dt} &= \sigma E + \eta N - \gamma I - (\mu+\eta)I,\\
\frac{dR}{dt} &= \gamma I - (\mu+\eta)R,
\end{aligned}\right\} \qquad (2)$$

with $S(t)\geq 0,\ E(t)\geq 0,\ I(t)\geq 0$ and $I(t)\geq 0$.
where, μ , β, γ, η and σ are all positive parameters.

The total human population $N(t)$ is given below
$\left(N(t)=S(t)+E(t)+I(t)+R(t)\right)$ and it is divided into Susceptible $(S(t))$, Exposed $(E(t))$, Infected $(I(t))$, and Recovered $(R(t))$. Then, μ , β, γ, η and σ are the natural death rate, the effective contact rate, the rate for recovery, the immigrant rate, and the latest period, respectively.

The Improved Model

By using the SEIR model as a reference, the new improved model is formulated with the immigrant theory and is used for the COVID-19 outbreak. The model parameters will incorporate the lockdown effect, asymptomatic humans, symptomatic humans, and hospitalized humans. Therefore, the new COVID-19 outbreak model incorporating the immigrant population is given below

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Pi_H + \theta\omega L - \frac{\beta_1 IS}{(N-L-C)} - \frac{\rho\beta_1 AS}{(N-L-C)} - (\mu+l+\eta)S,\\
\frac{dL}{dt} &= \eta N + lS - (\mu+\omega+\eta)L,\\
\frac{dE}{dt} &= \frac{\beta_1 IS}{(N-L-C)} + \frac{\rho\beta_1 AS}{(N-L-C)} - (\mu+\sigma+\eta)E,\\
\frac{dA}{dt} &= (1-k)\sigma E - (\gamma_1+\mu+\eta)A,\\
\frac{dI}{dt} &= k\sigma E - (\gamma_2+\tau+\mu+\eta)I,\\
\frac{dC}{dt} &= (1-\theta)\omega L + \tau I - (\delta+\gamma_3+\mu+\eta)C,\\
\frac{dR}{dt} &= \gamma_1 A + \gamma_2 I + \gamma_3 C - (\mu+\eta)R,
\end{aligned}\right\} \qquad \ldots(3)$$

where the immigrant rate is denoted by η .

The immigrants assist in the survival of the human population and this facilitates the dispersal of the COVID-19 outbreak.

Analysis of the model

Lemma 1 Let the initial value $F(0) \geq \mathbf{0}$, where

$$F(t) = (S(t), L(t), E(t), A(t), I(t), C(t), R(t)) .$$

Then the solutions $F(t)$ of model (3) are non-negative for all time $t > 0$. Furthermore, all solutions are uniformly bounded.

Proof The total dynamics of the human population is given by

$$\frac{dN}{dt} = \Pi_H - \mu N - \delta C .$$

Then, $\limsup\limits_{t\to\infty} N(t) \leq \dfrac{\Pi_H}{\mu_H}$.

It has also been shown that the region

$$\Omega = \{(S(t), L(t), E(t), A(t), I(t), C(t), R(t)) \in R_+^7 \Big| 0 \leq S(t) + L(t) + E(t) + A(t) + I(t) + C(t) + R(t) \leq \frac{\Pi_H}{\mu_H}\}.$$

is positively invariant for model (3) with non-negative initial conditions in R_+^7.

Basic Reproduction Number and Stability of the Disease-free Equilibrium

When $E(t) = I(t) = A(t) = 0$, then $l = 0$, and it can be inferred that virus is only hosted by some immigrants. For the immigrants, there is a policy of isolation. Therefore, the infected humans will be admitted to the hospital directly and will not be able to spread the virus among the general population. At this point, the virus can be controlled. The model Equation (3) then becomes the following:

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Pi_H + \theta\omega L - (\mu + \eta)S, \\
\frac{dL}{dt} &= \eta N - (\mu + \omega + \eta)L, \\
\frac{dC}{dt} &= (1-\theta)\omega L - (\delta + \gamma_3 + \mu + \eta)C, \\
\frac{dR}{dt} &= \gamma_3 C - (\mu + \eta)R,
\end{aligned}\right\} \qquad \ldots(4)$$

The model Equation (4) is then treated in two cases

Case 1: $\theta = 1$. This means that there are no infected immigrants. The model Equation (4) has a unique equilibrium point $E_0 = (S_0, L_0, C_0, R_0) \; = (\frac{\Pi_H}{\mu} \cdot \frac{\mu + \omega}{\mu + \omega + \eta}, \frac{\Pi_H}{\mu} \cdot \frac{\eta}{\mu + \omega + \eta}, 0, 0)$.

Case 2: $0 < \theta < 1$. The model Equation (4) has a unique equilibrium point $E_0 = (S_0, L_0, C_0, R_0)$, where

$$
\begin{aligned}
S_0 &= \frac{\Pi_H}{\mu+\eta} + \frac{\gamma_3+\eta+\delta+\mu}{\mu+\eta}\frac{\theta}{1-\theta}C_0, \\
L_0 &= \frac{\gamma_3+\eta+\delta+\mu}{(1-\theta)\omega}C_0, \\
R_0 &= \frac{\gamma_3}{\mu+\eta}C_0, \\
C_0 &= \frac{\Pi_H\eta(1-\theta)\omega}{\mu^3+(\omega+\gamma_3+2\eta+\delta)\mu^2+(\gamma_3+\eta+\delta)(\omega+\eta)\mu+\omega\eta\delta(1-\theta)}.
\end{aligned}
$$

The associated Jacobian matrix of the model Equation (4) is given as

$$
J = \begin{pmatrix}
-(\mu+\eta) & \theta\omega & 0 & 0 \\
\eta & -(\mu+\omega) & \eta & \eta \\
0 & (1-\theta)\omega & -(\delta+\gamma_3+\mu+\eta) & 0 \\
0 & 0 & \gamma_3 & -(\mu+\eta)
\end{pmatrix}
$$

One of the eigenvalues of J is $-(\mu+\eta)$. The other two eigenvalues J are the roots of the following equation:

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0,$$

where

$$
\begin{aligned}
a_1 &= \delta+2\mu+\gamma_3+\omega+3\eta, \\
a_2 &= 3\eta^2+(2\delta+4\mu+2\gamma_3+\omega)\eta+\mu^2+(\delta+\gamma_3+2\omega)\mu+\omega(\delta+\gamma_3), \\
a_3 &= \eta^3+(\delta+2\mu+\gamma_3)\eta^2+[\mu^2+(\delta+\gamma_3+\omega)\mu+\omega\delta(1-\theta)]\eta+\omega\mu(\delta+\gamma_3+\mu).
\end{aligned}
$$

The coefficients a_i $(i=1,2,3)$ are positive. Moreover, all the order principal minor determinants are positive, which means all the eigenvalues of J are negative. Therefore as a linear system, when $t \to \infty$, the solution of model Equation (4) will tend to the unique equilibrium point $E_0 = (S_0, L_0, C_0, R_0)$.

Lemma 2 The unique point $E_0 = (S_0, L_0, C_0, R_0)$ of model Equation (4) is asymptotically stable Ω.

Lemma 3 Set $\Omega_1 = \{S \mid S < S_0\} \cap \Omega$， the region Ω_1 is positively invariant for model (3).

Proof Noting

$$
\begin{aligned}
\frac{dS}{dt} &= \Pi_H + \theta\omega L - \frac{\beta_1 IS}{N-L-C} - \frac{\rho\beta_1 AS}{N-L-C} - (\mu+l+\eta)S \\
&\le \Pi_H + \theta\omega L - (\mu+\eta)S = (\mu+\eta)(S_0-S),
\end{aligned}
$$

Thus $S \le S_0 - [S_0 - S(0)]e^{-(\eta+\mu)t}$. Hence if $S(0) < S_0$, for all $t \ge 0$, $S < S_0$. Therefore, by combining with Lemma 1, Lemma 3 is proved.

It can be inferred that if the virus does not spread except in hospitals and isolated places, then the virus has been wiped out in areas of normal activities. Therefore, the disease-free equilibrium of model Equation (3) is

$E^0 = (S_0, L_0, 0, 0, 0, C_0, R_0)$,

where (S_0, L_0, C_0, R_0) is the unique equilibrium point of the model Equation (4).

The local asymptotic stability of E^0 can be established by using the Next-Generation Operator Method on the system (3). The infected compartments are (E, A, I). So, by using the Next-Generation Operator Method, the matrices *F* and *V* are

$$F = \begin{pmatrix} 0 & \dfrac{\beta_1 S_0 \rho}{S_0 + R_0} & \dfrac{\beta_1 S_0}{S_0 + R_0} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, V = \begin{pmatrix} k_1 & 0 & 0 \\ -(1-k)\sigma & k_2 & 0 \\ -k\sigma & 0 & k_3 \end{pmatrix},$$

where $k_1 = \mu + \eta + \sigma, k_2 = \gamma_1 + \mu + \eta, k_3 = \gamma_2 + \mu + \eta + \tau$.

It follows that the basic reproduction number of the model Equation (3), obtained by $\hat{R} = \rho(FV^{-1})$, is given by

$$\hat{R} = \frac{\beta_1[\rho(1-k)k_3 + kk_2][\Pi_H(1-\theta) + (\eta + \delta + \mu + \gamma_3)C_0\theta]\sigma}{k_1k_2k_3[\Pi_H(1-\theta) + (\eta + \delta + \mu)C_0\theta + r_3C_0]}$$

Based on the theorem proposed by van den Driessche and Watmough, (2002), the following theorem is established.

Theorem 1 The disease-free equilibrium $E^0 = (S_0, L_0, 0,0,0, C_0, R_0)$ of model Equation (3), is locally asymptotically stable (LAS) if $\hat{R} < 1$, and unstable if $\hat{R} > 1$.

Moreover, the global stability of $E^0 = (S_0, L_0, 0,0,0, C_0, R_0)$ for the region Ω_1 can be established.

Theorem 2 The disease-free equilibrium $E^0 = (S_0, L_0, 0,0,0, C_0, R_0)$ of model Equation (3) is globally asymptotically stable (GAS) Ω_1 whenever $\hat{R} < 1$.

Proof let $X = (S, L, C, R), Z = (E, A, I)$.

Set $\dfrac{dZ}{dt} = G(X, Z)$,

where $G(X,Z)$ is the right side of E, A, I.

According to Castillo-Chavez et al., 2002 and Agusto et al., 2013; besides condition $\hat{R} < 1$, the disease-free equilibrium $E^0 = (S_0, L_0, 0,0,0, C_0, R_0)$ is globally asymptotically stable (GAS) if $G(X,Z)$ satisfies the two following conditions,

$(A) \quad G(X,0) = 0,$

$(B) \quad G(X,Z) = D_Z\, G(X^*,0)Z - \hat{G}(X,Z), \hat{G}(X,Z) \geq 0,$

where $X^* = (S_0, L_0, C_0, R_0)$, and

$D_Z G(X^*,0)$ is the Jacobian of $G(X,Z)$ at point $(X^*,0)$, which is given by

$$D_Z G(X^*,0)=\begin{pmatrix} -k_1 & \dfrac{\beta_1 S_0 \rho}{N_0-L_0-C_0} & \dfrac{\beta_1 S_0}{N_0-L_0-C_0} \\ (1-k)\sigma & -k_2 & 0 \\ k\sigma & 0 & -k_3 \end{pmatrix}.$$

Therefore,

$$\hat{G}(X,Z)=\begin{pmatrix} \dfrac{\beta_1 S_0(\rho A+I)}{N_0-L_0-C_0}-\dfrac{\beta_1 S\ (\rho A+I)}{N\ -L\ -C} \\ 0 \\ 0 \end{pmatrix}.$$

$$\frac{\beta_1 S_0(\rho A+I)}{N_0-L_0-C_0}-\frac{\beta_1 S\ (\rho A+I)}{N\ -L\ -C}=\frac{\beta_1 S_0(\rho A+I)}{N_0-L_0-C_0}(1-\frac{N_0-L_0-C_0}{N\ -L\ -C}\frac{S}{S_0})>0.$$

So, each element of the matrix $\hat{G}(X,Z)$ is greater than or equal to zero. Therefore, based on the method proposed by Castillo-Chavez et al., (2002) and Agusto et al., (2013), the disease-free equilibrium is globally asymptotically stable.

MODEL SIMULATION

This section presents the model simulation method which includes the data collection method.

Data Source

The Malaysian COVID-19 cases from the 1st of January 2021 to the 11th of August 2021 were obtained from the Ministry of Health Malaysia (MOH) official website at https://www.outbreak.my/. Some model parameters were obtained from previous studies and statistics on the epidemic released by the National Health Council through the media. The average recruitment rate and the natural death rate values were estimated based on the data from the Department of Statistics Malaysia Official Portal (DOSM, 2019).

Data Analysis and Selection

The active COVID-19 cases in Malaysia from the 1st of January 2021 to the 11th of August 2021 are illustrated in Figure 1. The continuous control measures from the government and the vaccination program kept the active cases of infection basically below 50,000. The turning point came in June, with a sudden surge in infections. Therefore, we intercept the data from the 1st of June to the 11th of August for simulation.

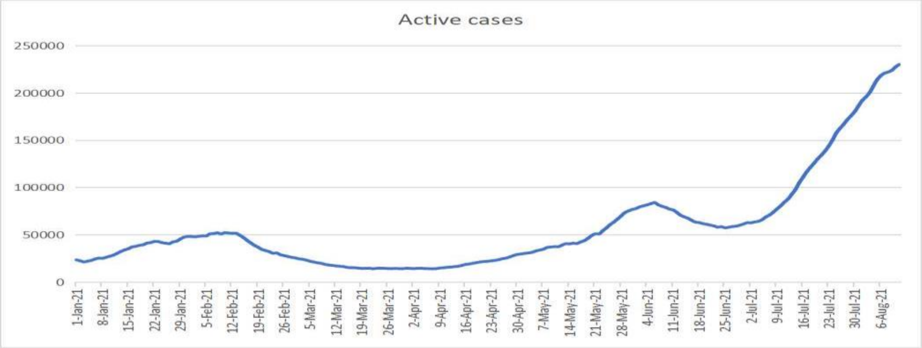


Figure 1 The number of active cases in Malaysia from 1-Jan-2021 to 11-Aug-2021.
(Data is from the Ministry of Health Malaysia (MOH) official website at https://www.outbreak.my/.

Parameter Estimation

The model parameters and their corresponding values are presented below.

(1) Π_H is the average recruitment rate. Malaysia's population growth rate in 2019 was 1.33% (DOSM 2019), with an average daily increase of about 1218 per day based on the total population of 32600000 (DOSM 2019). Thus, $\Pi_H = 1218$.

(2) A study done by researchers at the Peking University in collaboration with the National Institutes of Health (NIH) on the incubation period of novel COVID-19 (Qin et al., 2020) showed that the estimated median incubation period of COVID-19 was 8.13 days, with an average duration of 8.62 days, and about 10% of patients had a latency period longer than 14 days. Therefore, the value of 8.13 days was assigned for the incubation period and the lockdown period was assigned the value of 14 days. It should be noted that the Ministry of Health of Malaysia announced a reduction in the isolation of persons in close contact with infected individuals and those entering Malaysia from 14 to 10 days, starting from the 14th of December 2020. Thus, for the model parameters, before the 14th of December 2020, the values $\omega = \frac{1}{14}$, $\sigma = \frac{1}{8.13}$ were assigned; while after the 14th of December 2020 , $\omega = \frac{1}{10}, \sigma = \frac{1}{8.13}$ were assigned.

(3) The average life expectancy of the Malaysian population is about 74 years, according to DOSM 2019. Thus, the natural death rate was set as $\frac{1}{74 \times 365} \approx 0.000037$ per day.

(4) k is the fraction of the exposed population that later become symptomatically infected. As early as the 28th of January 2020, the definition of "asymptomatic infected person" appeared in the "new coronavirus pneumonia prevention and control program (third edition)" issued by the National Health and Health Commission of China: No clinical symptoms, respiratory specimens of new coronavirus etiology positive. A study from China was published in February 2021 in the “Journal of the American Medical” (Ren et al., 2021). The study found

that from April to mid-October last year, half of the nucleic acid-positive patients who entered China were asymptomatic. And over time, the proportion of asymptomatic patients is increasing. Further analysis showed that about 40% of the 3103 new coronavirus positive patients, that is about 1,354 people, had symptoms when they entered China; 4.4% (137) had no symptoms at the time of entry, but had symptoms during isolation, which were also classified as confirmed cases; whereas 51.9% (1612) of positive patients remained asymptomatic until day 13, which were defined as asymptomatic infections. This data has certain reference significance for other countries. Here, we set $1-k=0.52$ ， that is $k=0.48$.

(5) China's National Health and Health Commission held a press conference at 15:00 on the 4th of February 2020, to introduce the medical treatment of severe pneumonia patients with new Covid-19 infection. In particular, a group of data - the average hospitalization days of discharged patients at that time were counted. In addition to Hubei Province, the shortest time for inpatients in the country was 5 days in Hainan Province, and the longest was 12.75 days in Guangdong Province. The average hospitalization day for discharged patients was more than 9 days. Considering that all critical patients in the confirmed cases should be admitted to the hospital for treatment, those who are not in the hospital had mild symptoms or were asymptomatic. Therefore, the average recovery time without being hospitalized was chosen as 7 days and the average hospitalization day for discharged patients was taken 9 days. Therefore, $r_1=r_2=\frac{1}{7}, r_3=\frac{1}{9}$.

(6) Based on a study by Chen et al., (2020), there is a 5.8-day delay from symptom onset to hospitalization of a case. The authors used 5.8 days (95% CI: 4.3–7.5) Chen et al., (2020). So, in the model, we set $\tau=\frac{1}{5.8}\approx 0.1724$.

(7) According to a group of data announced by the Malaysian Ministry of Health in April 2020, 4817 of the 83488 people at high risk of COVID-19 were positive, with a positive detection rate of 5.8 percent (https://world.huanqiu.com/article/3xpTinMXawi). The isolated population is part of the high-risk population. We assume that the rate of positive detection during the quarantine period also remains the same, that is, $1-\theta=0.058$ .Once a case tested positive during the quarantine period, it should be transferred to the hospital for treatment.

(8) With reference to the Ministry of Health Malaysia (MOH) official website, the average case fatality rate is 0.0086 from the cumulative average mortality rate until 11 August 2021.

The description of the model parameters and their corresponding values are presented in Table 2.

Table 2: Description of the parameters used in the model Equation (1)

Symbol	Description	Value	Source
Π_H	The average recruitment rate	1218	Estimated

$\frac{1}{\omega}$	The lockdown period	14	From actual value
ρ	The reduction transmission for Asymptomatic infected	0.5	Chen et al.,2020
μ	The natural death rate	0.000037	From actual value
k	The fraction of exposed population that become symptomatic infected	0.48	Ren et al., 2021
γ_1	The recovery rate for asymptomatic infected	1/7	Estimated
γ_2	The recovery rate for symptomatic infected	1/7	Estimated
γ_3	The average recovery rate for hospitalized and notified infection	1/9	Estimated
$\frac{1}{\sigma}$	The disease incubation period	8.13	Qin et al., 2020
τ	The average notification and hospitalization rate of symptomatic infection	0.1742	Chen et al.,2020
δ	The average case fatality rate	0.0086	From actual value

The model parameter l is the average lockdown rate which relates to the proportion of those who had close contacts with infected individuals that were traced per day. The parameter β is the transmission rate of symptomatic infected individuals which relates to the manner of people's contact and the circumstance of where they stay. They all need to be calibrated by actual data.

RESULTS AND DISCUSSION

The indicator of viral transmission capacity is the basic reproduction number $\hat{R}$.
From Section 2, we have got $\hat{R}$ model (3), given by

$$\hat{R} = \frac{\beta\ [\rho(1-k)k_3 + kk_2][\Pi_H(1-\theta) + (\eta+\delta+\mu+\gamma_3)C_0\theta]\sigma}{k_1k_2k_3[\Pi_H(1-\theta) + (\eta+\delta+\mu)C_0\theta + r_3C_0]}.$$

To quantify this indicator, the values in Table 1 are used. Thereafter, the schematic diagram of $\hat{R}$ changes with the β under different immigration rates: $\eta = 0.0002,$ $\eta = 0.002,$ $\eta = 0.02,$ and $\eta = 0.2$ is shown in Figure 2. Due to the policy of contact tracing, isolation of infected individuals, and isolation of immigrants; the disease is likely to be controlled even if the infection rate is relatively high. This shows that under isolation, the impact of migration on the transmission of the virus is not significant. But the model is an ideal state, it does not consider the domestic isolation of immigrants， and it assumed that the total number is fixed. Thus, a larger immigration rate is meaningless here. For the next simulation, we choose $\eta = 0.0002.$

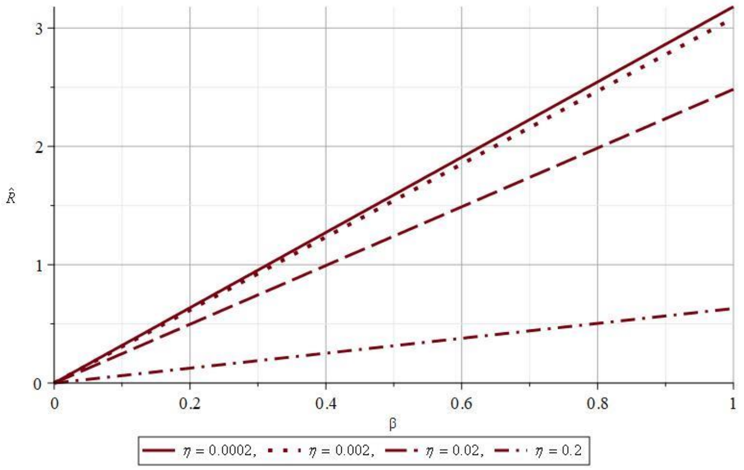


Figure 2 $\hat{R}$ changes with the β under different immigration rates: $\eta = 0.0002$, $\eta = 0.002$, $\eta = 0.02$, and $\eta = 0.2$.

Simulation of Model Equation (3)

The differential equation for the model (Equation (3)) was solved using MATLAB and the model simulations were also done with MATLAB. The curve fitting was done using the least square method and the values $\beta = 0.466, l = 0.0005$ were obtained. The curve fitting results of model Equation (3) are shown in Figure 3.

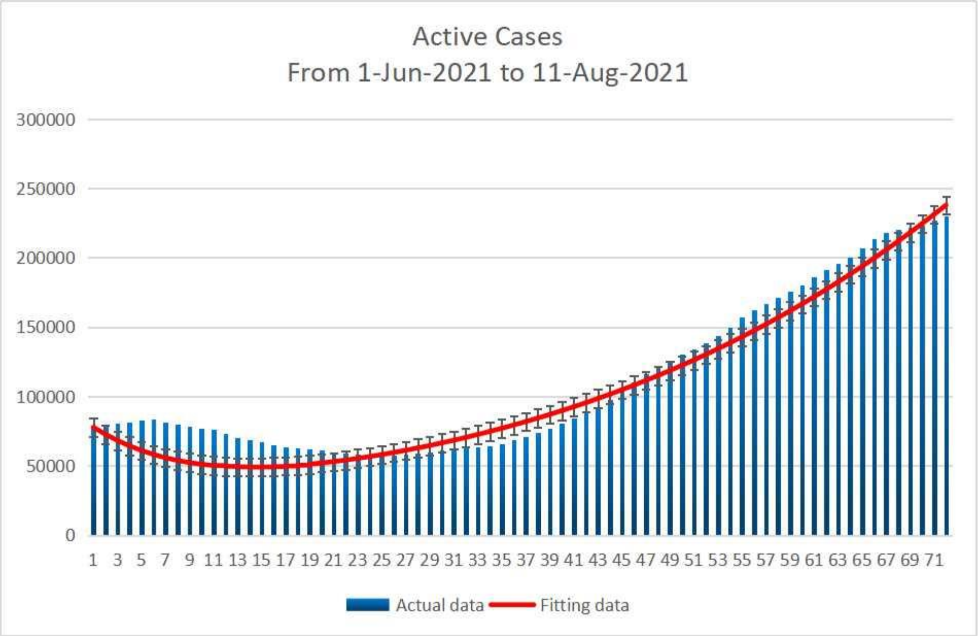


Figure 3 Curve fitting results of model (3) with reported data of active cases in Malaysia.

Let the Y^* be the fitting value, Y be the actual value, then the goodness of fit R_{New} is 0.98899 and it was calculated by the expression below,

$$R_{New} = 1 - \sqrt{\frac{\sum (Y - Y^*)^2}{\sum Y^2}} \text{ (Zhang, 2002).}$$

It implies that by using values of $\beta = 0.466, l = 0.0005$, the model parameters can fit the actual value.

The impact of immigration on the spread of COVID-19

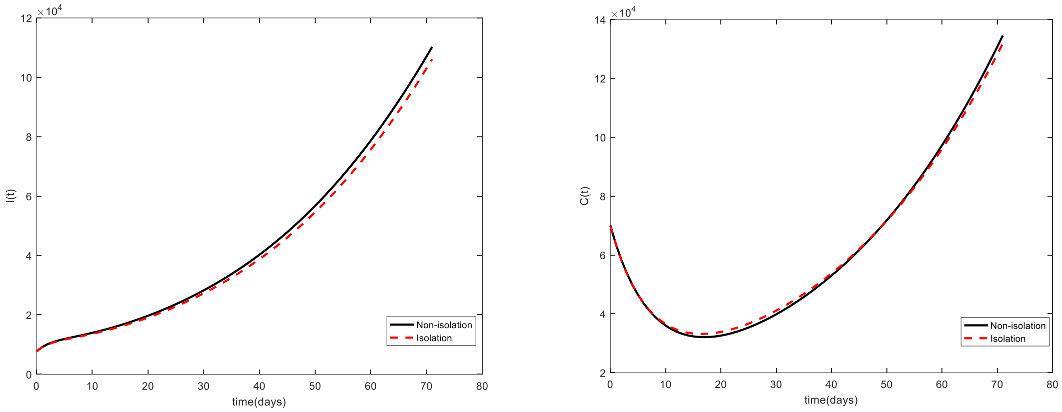
To study the impact of immigration on virus transmission and the importance of immigration isolation policy, the model was modified. Assuming that all immigrants are not isolated, then the immigrants are divided into three parts. The first part is those who are not carriers of the virus and thus become susceptible, the second part is those who are carriers of the virus but without symptoms and thus become exposed, and the third part is those with obvious symptoms that should be sent directly to the hospital. After the modification, the model then becomes

$$\begin{cases} \frac{dS}{dt} = \Pi_H + \theta\omega L + h_1\eta N - \frac{\beta_1 IS}{(N-L-C)} - \frac{\rho\beta_1 AS}{(N-L-C)} - (\mu + l + \eta)S, \\ \frac{dL}{dt} = lS - (\mu + \omega + \eta)L, \\ \frac{dE}{dt} = \frac{\beta_1 IS}{(N-L-C)} + \frac{\rho\beta_1 AS}{(N-L-C)} + h_2\eta N - (\mu + \sigma + \eta)E, \\ \frac{dA}{dt} = (1-k)\sigma E - (\gamma_1 + \mu + \eta)A, \\ \frac{dI}{dt} = k\sigma E - (\gamma_2 + \tau + \mu + \eta)I, \\ \frac{dA}{dt} = (1-k)\sigma E - (\gamma_1 + \mu + \eta)A, \\ \frac{dC}{dt} = (1-\theta)\omega L + \tau I + h_3\eta N - (\delta + \gamma_3 + \mu + \eta)C, \\ \frac{dR}{dt} = \gamma_1 A + \gamma_2 I + \gamma_3 C - (\mu + \eta)R, \end{cases} \tag{5}$$

where $h_i, i = 1,2,3$ is the proportion of weights assigned to three chambers for migrants, and $0 \le h_i \le 1, h_1 + h_2 + h_3 = 1.$

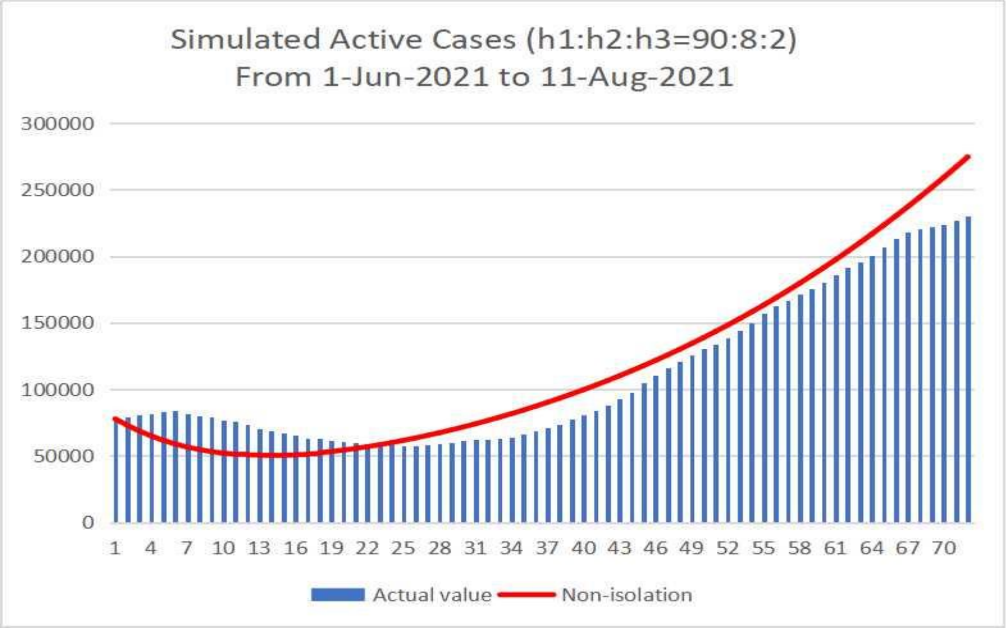
Noting that the active cases reported by officials are a combination of the infected cases and the cases in hospitals, then some changes are in the infected compartment $I(t)$ and the hospitalized compartment $C(t)$. If $h_1 = 0.98, h_2 = 0.01, h_3 = 0.01$, it means that only one immigrant is exposed out of 100 immigrants, one is infected out of 100, the rest belongs to the susceptible compartment. As shown in Figure 4(a), from 1-Jun to 11-Aug, the non-isolation causes the number of $I(t)$ increase. Although the cases in hospitals decreased, as shown in Figure 4(b), the cases without admission into hospitals would increase the number of late infections.

As the proportion of h_2 and h_3 increases, the fermentation time will be shortened and confirmed cases will increase significantly. For example, by setting the values of $h_1 = 0.9$, $h_2 = 0.08$, and $h_3 = 0.02$, the virtual infections are higher than actual infections (as shown in Figure 4(c)). Total cases increased by 4.589% within 71 days from the 1st of June to the 11th of August 2021. Therefore, the use of a segregation policy for immigrants is very necessary.



(4a) The comparison of infected cases with $h_1 = 0.98, h_2 = 0.01, h_3 = 0.01$.

(4b) The comparison of hospital cases with $h_1 = 0.98, h_2 = 0.01, h_3 = 0.01$.



(4c) The comparison of active cases with $h_1 = 0.90, h_2 = 0.08, h_3 = 0.02$.

Figure 4 Comparison of the number of confirmed cases under isolated and non-isolated conditions

In disease control, the basic reproduction number $\hat{R}$ in response to the capability of disease transmission is an important factor. Therefore, in this article, the estimate $\hat{R}$ for the COVID-19 outbreak in Malaysia from the 1st of June 2021 to the 11th of August 2021 was obtained as 1.4823. This suggested that the disease remains in a low prevalence. However, in a previous study by Gill et al. (2020), the effects of epidemic control measures in preventing the transmission of COVID-19 in Malaysia were modeled and $\hat{R}$ was obtained as 1.68 which is higher than the $\hat{R}$ presented in this article. The difference in values may be due to the methods used, the parameters selected (especially the immigrant rate η), and the data intercepted. As shown in Figure 2, the smaller the value of η, the higher the value of $\hat{R}$ at the same contact rate β. Similarly, a team of researchers used different methods to calculate $\hat{R}$ the flu outbreak for the same set of data, and the results were quite different with different methods (Chen et al., 2016). But in this article, although the probability of contact infection used in the model was 0.466, the basic regeneration number was not large. It can be assumed that Malaysia's MCO played an important role in controlling the speed of transmission.

CONCLUSION

In this study, the SLEAICR model was constructed. The model considered the impacts of immigration, the characteristics of COVID-19 transmission, the number of infections in Malaysia, and the prevention and control measures of the diseases. The data of Malaysia’s COVID-19 cases from the 1st of June 2021 to the 11th of August 2021were used for the curve fitting. By using the model, the importance of isolation control measures for immigrants was analyzed. Generally, due to the limitation of model principle and data, this study still has some limitations. First, the propagation dynamics model is a deterministic parameter model. Once the model parameters are determined, future trends can be determined. Therefore, certain requirements are required for data when key parameters are to be fitted. Secondly, the model assumed an ideal state, which cannot respond to the sudden change of environmental background in time. Despite these limitations, the findings of this study support the effectiveness of isolation measures for immigrants in the process of suppressing COVID-19 transmission.

REFERENCES

Agusto, F. B., Del Valle, S. Y., Blayneh, K. W., Ngonghala, C. N., Goncalves, M. J., Li, N., et al. (2013). The impact of bed-net use on malaria prevalence. *Journal of Theoretical Biology*, **320**: 58-65.

Aleshkovski, I. & Iontsev, V. (2006). Mathematical Models of Migration. *Systems analysis and Modeling of Integrated World Systems*, II, Encyclopedia of Life Support Systems (EOLSS).

Avila-Ponce de Léon, U. A. P. D, Pérez, A. G. C. & Avila-Vales, E. (2020). A data driven analysis and forecast of an SEIARD epidemic model for COVID-19 in Mexico. arxiv.org -Quantitative Biology, arxiv:2004.08288.

Aziz, N. A., Othman, J., Lugova, H. & Suleiman, A. (2020). Malaysia's approach in handling COVID-19 onslaught: Report on the Movement Control Order (MCO) and targeted screening to reduce community infection rate and impact on public health and economy. *Journal of Infection and Public Health*, **13(12)**: 1823-1829.

Castillo-Chavez, C., Blower, S., van den Driessche, P., Kirschner, D., & Yakubu, A.A. (2002). Mathematical approaches for emerging and reemerging infectious diseases. New York: Springer-Verlag.

Chen, T., Chen, Q. P., Liu, R. C., Szot, A., Chen, S. L., Zhao, J. & Zhou, S. (2016). The transmissibility estimation of influenza with early stage data of small-scale outbreaks in Changsha，China，2005-2013. *Epidemiology and Infection*, **145(3)**: 424-433.

Chen, T. M.，Rui, J.，Wang, Q. P., Zhao, Z. Y., Cui, J. A. & Yin, L. (2020). A mathematical model for simulating the phase-based transmissibility of a novel coronavirus. *Infectious Diseases of Poverty*, **9(24)**: 1-8.

Gill B. S., Jayaraj, V. J., Singh, S., Mohd Ghazali, S., Cheong, Y. L., Md Iderus, N. H., Murali Sundram, B., Aris, T., Mohd Ibrahim, H., Hong, B. H. & Labadin, J. (2020). Modelling the Effectiveness of Epidemic Control Measures in Preventing the Transmission of COVID-19 in Malaysia. *International Journal of Environmental Research*. **17(15)**: 1-13. 10.3390/ijerph17155509.

Gumel, A. B., Ruan S., Day T., Watmough J., Brauer F., Van den Driessche, P., Gabrielson, D., Bowman, C., Alexander, M. E., Ardal, S., Wu, J. & Sahai, B. M. (2004). Modelling strategies for controlling SARS outbreaks. Proceeding of the Royal Society B: Biological Sciences, **271(1554)**: 2223-2232.

Horby, P., Lim, W. S., Emberson, J. R., Haynes, R. & Landray, M. J. (2020). Dexamethasone in Hospitalized Patients with Covid-19 - Preliminary Report. *The New England Journal of Medicine*. DOI: 10.1056/NEJMoa2021436.

Ibarra-Vega (2020). Lockdown, one, two, none, or smart. Modeling containing covid-19 infection. A conceptual model. *Science of the Total Environment*. **730**: 138917.

Qin, J., You, C., Lin, Q., Hu, T., Yu, S. & Zhou, X. H. (2020). Estimation of incubation period distribution of COVID-19 using disease onset forward time: a novel cross-sectional and forward follow-up study, *Science Advances*, **6(33)**: 1-7.

Liu, Z., Magal, P., Seydi, O. & Webb, G. (2020). Understanding Unreported Cases in the COVID-19 Epidemic Outbreak in Wuhan, China, and the Importance of Major Public Health Interventions. *Biology*, **9(3)**: 50.

Li, G., Hu, R. & Gu, X. (2020a). A close-up on COVID-19 and cardiovascular diseases. *Nutrition, Metabolism and Cardiovascular Diseases, Journal pre-proof*.

Li, Y, Wu, Y., Wang, X., Guo, C., Wang, L., Li, J. & Wang, S. (2020b). Modelling the effect of lockdown on COVID-19 pandemic in 22 countries and cities. *Research Square, Infectious Diseases*.

Ma, K., Chen, T., Han, M. F., Guo, W., & Ning, Q. (2020). Management and clinical thinking of Coronavirus Disease 2019. *Zhonghua gan zang bing za zhi= Zhonghua ganzangbing zazhi= Chinese journal of hepatology*, 28, E002-E002.

Ministry of Health Malaysia. Kenyataan Akhbar Ketua Pengarah Kesihatan Malaysia Pada 24 Januari 2020 - Tindakan KKM Bagi Pengesanan Kontak (Contact Tracing) Kepada Kes Pertama Positif Novel Coronavirus Di Negara Singapura Pada 24 Januari 2020. In: Ministry of Health Malaysia Official Website. 2020 Jan 24 [Cited 2020 March 26]. Available from: http://www.moh.gov.my/index.php/database_stores/store_view_page/21/1300

Ministry of Health Malaysia. Press Statement: Updates on 27 July 2020. Situasi Semasa Pandemik COVID-19 Di Malaysia.

Available online: http://covid-19.moh.gov.my (accessed on 27th July 2020)

Pambuccian, S. E. (2020). The COVID-19 pandemic: implications for the cytology laboratory. *Journal of the American Society of Cytopathology*, **xx**: 1-10.

Piccolo, C. & Billings, L. (2005). The Effect of Vaccinations in an Immigrant Model. *Mathematical and Computer Modelling*, **42(3)**: 291-299.

Rawson, T., Brewer, T., Veltcheva, D., Huntingford, C. & Bonsall, M. B. (2020). How and When to End the COVID-19 Lockdown: An Optimization Approach. *Frontiers Public Health*. https://doi.org/10.3389/fpubh.2020.00262

Ren. R., Zhang Y. & Li, Q. (2021). Asymptomatic SARS-CoV-2 Infections Among Persons Entering China From April 16 to October 12, 2020. *JAMA*.325(5):489-492. DOI: 10.1001/jama.2020.23942.

Sardar, T., Nadim, Sk. S., Rana, S. & Chattopadhyay, J. (2020). Assessment of Lockdown Effect in Some States and Overall India: A Predictive Mathematical Study on COVID-19 Outbreak. *Chaos, Solitons and Fractals*, 110078.

Shereen, M. A., Khan, S., Kazmi, A., Bashir, N. & Siddique, R. (2020). COVID-19 infection: Origin, transmission, and characteristics of human coronaviruses. *Journal of Advanced Research Volume*, **24**: 91-98.

Widyaningsih, P., Saputro, D. R. S. & Nugroho, A. W. (2018). Susceptible exposed infected recovery (SEIR) model with immigration: Equilibria points and its application. International Conference on Science and Applied Science (ICSAS) 2018, AIP Conference Proceedings **2014(1)**: 020165-1–020165-7.

Worldometer. COVID-19 Coronavirus Pandemic. Last updated: July 27, 2020, Available online: https://www.worldometers.info/coronavirus/?utm_campaign=homeAdvegas1?

World Health Organization (WHO). Coronavirus Disease 2019 (COVID-19): situation report, 75. Available online: https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200404 -sitrep-75-covid-19.pdf?sfvrsn=99251b2b_2. (accessed on 25th April 2020)

Yang, H. Y., & Duan, G. C. (2020). Analysis on the epidemic factors for the corona virus disease. *Zhonghua yu Fang yi xue za zhi [Chinese Journal of Preventive Medicine]*, **54**: E021-E021.

Zhang, S. Q. (2002). Approach on the Fitting Optimization Index of Curve Regression, *Chinese Journal of Health Statistics (in Chinese)*, **19(1)**: 9-11.

Zhu, Z. B., Zhong, C. K., Zhang, K. X., Dong, C., Peng, H., Xu, T. & Zhang, Y. H. (2020). Epidemic trend of corona virus disease 2019 (COVID-19) in mainland China. *Zhonghua yu fang yi xue za zhi [Chinese journal of preventive medicine]*, **54**: E022-E022.