A Mathematical Model to Study the Effect of Travel Between Two Regions on the Covid-19 Infections

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Abstract

COVID-19 has attracted a lot of researchers’ attention since it has emerged in Wuhan, China in December 2019. Numerous model predictions on the COVID-19 epidemic have been created in case of Wuhan and the other regions. In this paper, a new COVID-19 epidemic model between two regions is proposed. The model differentiates asymptomatic infectious compartment and symptomatic infectious compartment. It is assumed that the symptomatic population cannot infect the susceptible population due to direct isolation, but the asymptomatic population can. The symptomatic population is also assumed to be unable to travel between regions. We analyze the stability of the model using Lyapunov Function. The Basic Reproduction Number for the model is presented. The numerical simulation and sensitivity analysis are explored to determine the significant parameter of the model.

Keywords: Covid 19, Stability, symptomatic population, Lyapunov function

1. Introduction

In December 2019 Coronavirus Disease (COVID-19) was first reported in Wuhan City, China (Huang et al., 2020). As of June 3, 2020, there have been 6.3 million confirmed cases and 380 thousand deaths. To reduce the rate of COVID-19 spread, a policy that corresponds to the risk of transmission is needed. The virus is spread through droplets so contact between infected people and healthy people should be avoided. If a person is in contact with the infected, then the person must be quarantined independently so as not to spread to others (Ghinai et al., 2020). So that contact between COVID-19 sufferers and populations that have not been exposed to COVID-19 can be minimized and have an impact on the decrease in the rate of growth of COVID-19 cases.

COVID-19 epidemiological models have been extensively researched by various researchers. Peng et al. (2020) constructed the SEIR COVID-19 model that was generalized for china. Chen et al. (2020) also examined COVID-19 cases in China using fractional time delay dynamic system. Shao et al. (2020)
calculates the $R_0$ value of COVID-19 with statistical time delay dynamical system model. Salim et al. (2020) has researched the impact of lockdown or quarantine of territory in Malaysia with dynamic models. There are also several papers to discuss about the spread of COVID-19 in Indonesia. Adila et al. (2020) use optimal control to calculate the effect of population awareness on the spread COVID-19 in Indonesia. Ndii and Adi (2020) also use control optimal to calculate the control strategies on COVID-19 transmission. The control strategies are the reducing the transmission rate and detecting the infection. Ndii et al. (2020) analyze the COVID-19 transmission with infected undetected and infected detected in Indonesia and Saudi Arabia.

The spread of diseases between regions has also been widely studied by various researchers. Xu, McCluskey and Cressman (2013) researched the model of the spread of disease through the public transport system. Zhu and Zhu (2020) also researched the relationship between the region and the spread of COVID-19 in China using SEIQR heterogeneous spatial model.

Based on the above description, the authors are interested in researching the spread of COVID-19 disease between regions using dynamical system analysis. The analysis was used to determine the dynamics of COVID-19 disease transmission with the help of numerical simulations.

2. Methods

In this section, we introduce a SEIR model with asymptomatic and symptomatic case to characterize the epidemic of COVID-19 with travel between two regions. The model consists five states for each region: susceptible cases ($S(t)$), exposed cases ($E(t)$) (infected but not yet infectious to susceptible), asymptomatic cases ($I_a(t)$), symptomatic cases ($I_s(t)$) (infected but do not infectious due to treatment), and recovered cases ($R(t)$). In this model, people who do not infected by disease travel to other regions. The asymptomatic cases can still travel to other region too and can transmit the disease to others, but symptomatic cases are not. The We also assume that the two regions are identical. So, the parameters in the model are same for all regions. The schematic diagram is shown in the following Figure 1. The parameters of the model are described in Table 1.
Figure 1: The schematic diagram of the model

| Parameter | Description |
|-----------|-------------|
| \(\Lambda\) | The birth rate of the population |
| \(\beta\) | Local transmission coefficient |
| \(\gamma\) | Transmission coefficient between two regions |
| \(\alpha\) | The rate of transportation between two regions |
| \(c\) | The rate coefficient of the transfer from latent to infected |
| \(q\) | The fraction of the newly infected to symptomatic compartment |
| \((1-q)\) | The fraction of the newly infected to asymptomatic compartment |
| \(d\) | The recovering rate of infected population |
| \(\varepsilon\) | The transition rate from asymptomatic to symptomatic compartment |
| \(\mu\) | The natural death rate |
| \(\mu_1\) | The disease-related death rate |

The dynamical equation for two regions is:

\[
\begin{align*}
\frac{dS_1}{dt} &= \Lambda - \mu S_1 - \beta S_1 I_1 - \alpha S_1 + \alpha S_2 - \gamma \alpha S_1 I_1 \\
\frac{dE_1}{dt} &= \beta S_1 I_1 - (\mu + c)E_1 - \alpha E_1 + \alpha E_1 + \gamma \alpha S_2 I_2 \\
\frac{dI_1}{dt} &= (1-q)cE_1 - \mu I_1 - dI_1 - \alpha I_1 + \alpha I_2 - \varepsilon I_1 \\
\frac{dS_1}{dt} &= qE_1 - \mu S_1 - dS_1 + \varepsilon I_1 \\
\frac{dR_1}{dt} &= dI_1 + dS_1 - \mu R_1 - \alpha R_1 + \alpha R_2 \\
\frac{dS_2}{dt} &= \Lambda - \mu S_2 - \beta S_2 I_2 - \alpha S_2 + \alpha S_1 - \gamma \alpha S_1 I_2
\end{align*}
\]
\[
\frac{dE_2}{dt} = \beta S_2 I a_2 - (\mu + c)E_2 - \alpha E_2 + \alpha E_2 + \gamma_0 S_1 I a_1
\]
\[
\frac{dl a_2}{dt} = (1 - q) c E_2 - \mu_l a_2 - dl a_2 - al a_2 + al a_1 - \epsilon l a_2
\]
\[
\frac{dl s_2}{dt} = q c E_2 - \mu_1 l s_2 - dl s_2 + \epsilon l a_2
\]
\[
\frac{dR_2}{dt} = dl a_2 + dl s_2 - \mu R_2 - \alpha R_2 + \alpha R_1
\]

2.1 Positivity of solution

\textbf{Lemma 1.} If the initial values for model (1) \(S_1(0) > 0, E_1(0) > 0, I a_1(0) > 0, I s_1(0) > 0, R_1(0) > 0, S_2(0) > 0, E_2(0) > 0, I a_2(0) > 0, I s_2(0) > 0\) and \(R_2(0) > 0\), the solutions \(S_1(t), E_1(t), I a_1(t), I s_1(t), R_1(t), S_2(t), E_2(t), I a_2(t), I s_2(t), R_2(t)\) of system 1 are positive for all \(t > 0\).

\textbf{Proof.} Let \(W(t) = \min \{S_1(t), E_1(t), I a_1(t), I s_1(t), R_1(t), S_2(t), E_2(t), I a_2(t), I s_2(t), R_2(t)\}\), for all \(t > 0\). It is clear that \(W(0) > 0\). Assuming that there exists a \(t_1 > 0\) such that \(W(t_1) = 0\) and \(W(t) > 0\), for all \(t \in [0, t_1]\).

If \(W(t) = S_1(t)\), then \(E_1(0) > 0, I a_1(0) > 0, I s_1(0) > 0, R_1(0) > 0, S_2(0) > 0, E_2(0) > 0, I a_2(0) > 0, I s_2(0) > 0\) and \(R_2(0) > 0\) for all \(t \in [0, t_1]\). From the first equation of model 1, we can obtain
\[
\frac{dS_1}{dt} > -\mu S_1 - \beta S_1 I a_1 - \alpha S_1 - \gamma S_1 I a_1, \quad t \in [0, t_1]
\]
Thus, we have
\[
0 = S_1(t_1) \geq S_1(0) e^{\int_{t_1}^{t} [-\mu - \beta I a_1 - \alpha - \gamma I a_1] dt} > 0
\]
which contradicts with the assumption. Thus \(S_1(t) > 0\) for all \(t \geq 0\).

Similarly, we can also prove that \(E_1(0) > 0, I a_1(0) > 0, I s_1(0) > 0, R_1(0) > 0, S_2(0) > 0, E_2(0) > 0, I a_2(0) > 0, I s_2(0) > 0\) and \(R_2(0) > 0\) for all \(t \geq 0\). 

2.2 Invariant region

\textbf{Lemma 2.} If \(N(t) = S_1(t) + E_1(t) + I a_1(t) + I s_1(t) + R_1(t) + S_2(t) + E_2(t) + I a_2(t) + I s_2(t) + R_2(t)\). The feasible region \(\Omega\) defined by
\[
\Omega = \{(S_1(t), E_1(t), I a_1(t), I s_1(t), R_1(t), S_2(t), E_2(t), I a_2(t), I s_2(t), R_2(t)) \in R_{+}^{10} : N(t) \leq \frac{2N}{\mu} \}
\]
with initial conditions \(S_1(0) > 0, E_1(0) > 0, I a_1(0) > 0, I s_1(0) > 0, R_1(0) > 0, S_2(0) > 0, E_2(0) > 0, I a_2(0) > 0, I s_2(0) > 0\) and \(R_2(0) > 0\) is positively invariant for system 1.
**Proof.** Adding the equation of model (1), we obtain

\[
\frac{dN}{dt} = 2\Lambda - \mu (S_1 + E_1 + Ia_1 + R_1 + S_2 + E_2 + Ia_2 + R_2)
\]

\[\leq 2\Lambda - \mu N\]

It follows that

\[0 \leq N(t) \leq \frac{2\Lambda}{\mu} + N(0)e^{-\mu t}\]

where \(N(0)\) represents the initial values of total population in all regions. Thus \(\lim_{t \to \infty} \sup N(t) \leq \frac{2\Lambda}{\mu}\). It implies that the region \(\Omega = \{(S_1(t), E_1(t), Ia_1(t), Is_1(t), R_1(t), S_2(t), E_2(t), Ia_2(t), Is_2(t), R_2(t)) \in \mathbb{R}_+^{10} : N(t) \leq \frac{2\Lambda}{\mu}\}\) is positively invariant set for model (1) □.

### 3. Result and Discussion

#### 3.1 Basic Reproduction Number

The basic reproduction number \((R_0)\) is an important threshold number to analyze the epidemiology model. To find basic reproduction number based on Driessche, we need know a disease-free equilibrium of the model. The disease free equilibrium is \(x^0 = (S_1^0, E_1^0, \ldots, S_2^0, E_2^0, Ia_2^0, Is_2^0, R_2^0)\) and the next generation matrix (Van den Driessche and Watmough, 2002).

Let \(x = (E_1, Ia_1, Is_1, E_2, Ia_2, Is_1, S_1, R_1, S_2, R_2)\), then the model 1 can be written as

\[
\frac{dx}{dt} = \mathcal{F}(x) - \mathcal{V}(x)
\]

where
The Jacobian matrix of \( \mathcal{F}(x) \) and \( \mathcal{V}(x) \) at the disease-free equilibrium \( x^0 \) are

\[
\begin{pmatrix}
(\mu + c)E_1 + \alpha E_1 - \alpha E_1 \\
-(1 - q)cE_1 + \mu l a_1 + d l a_1 + \alpha l a_1 - \alpha l a_2 + \epsilon l a_1 \\
\end{pmatrix}
\]

\[
(\mu + c)E_2 + \alpha E_2 - \alpha E_2 \\
-(1 - q)cE_2 + \mu l a_2 + d l a_2 + \alpha l a_2 - \alpha l a_1 + \epsilon l a_2 \\
\end{pmatrix}
\]

\[
= 
\begin{pmatrix}
(\mu + c)E_1 + \alpha E_1 - \alpha E_1 \\
-(1 - q)cE_1 + \mu l a_1 + d l a_1 + \alpha l a_1 - \alpha l a_2 + \epsilon l a_1 \\
\end{pmatrix}
\]

\[
(\mu + c)E_2 + \alpha E_2 - \alpha E_2 \\
-(1 - q)cE_2 + \mu l a_2 + d l a_2 + \alpha l a_2 - \alpha l a_1 + \epsilon l a_2 \\
\end{pmatrix}
\]

\[
\frac{\Lambda + \mu s_1 + \beta s_1 l a_1 + \alpha s_1 - \alpha s_2 + \gamma \alpha s_1 l a_1}{\mu} \\
\frac{\Lambda + \mu s_2 + \beta s_2 l a_2 + \alpha s_2 - \alpha s_1 + \gamma \alpha s_2 l a_2}{\mu}
\]

\[
\frac{d l a_1 - d l s_1 + \mu r_1 + \alpha r_1 - \alpha r_2}{\mu} \\
\frac{d l a_2 - d l s_2 + \mu r_2 + \alpha r_2 - \alpha r_1}{\mu}
\]

The Jacobian matrix of \( \mathcal{F}(x) \) and \( \mathcal{V}(x) \) at the disease-free equilibrium \( x^0 \) are

\[
D\mathcal{F}(x^0) = \begin{pmatrix} F_{6 \times 6} & 0 \\ 0 & 0 \end{pmatrix}, D\mathcal{V}(x^0) = \begin{pmatrix} V_{6 \times 6} & 0 \\ 0 & 0 \end{pmatrix}
\]

where

\[
F = \begin{pmatrix}
\frac{\beta \Lambda}{\mu} & 0 & 0 & \frac{\gamma \alpha \Lambda}{\mu} & 0 \\
0 & \mu & 0 & 0 & 0 \\
0 & 0 & 0 & \mu & 0 \\
0 & \gamma \alpha \Lambda & 0 & \frac{\beta \Lambda}{\mu} & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0
\end{pmatrix}
\]
The derivative of equilibrium is stable. Otherwise, the endemic equilibrium is stable.

3.2 Global stability of the disease-free equilibrium

**Theorem 1.** For model (1), the disease-free equilibrium $X_0$ is globally stable if $R_0 \leq 1$

**Proof.** We construct Lyapunov function for model (1) (Feng et al., 2020).

$$V = \begin{pmatrix} \mu + c + \alpha & 0 & 0 & -\alpha & 0 & 0 \\ (q - 1)cd & d + \mu + \alpha + \epsilon & 0 & 0 & -\alpha & 0 \\ -qc & -\epsilon & d + \mu_1 & 0 & 0 & 0 \\ -\alpha & 0 & 0 & \mu + c + \alpha & 0 & 0 \\ 0 & -\alpha & 0 & (q - 1)cd & d + \mu + \alpha + \epsilon & 0 \\ 0 & 0 & 0 & -qc & -\epsilon & d + \mu_1 \end{pmatrix}$$

The basic reproduction number is thus given by

$$R_0 = \rho(FV^{-1}) = \frac{\Lambda c(\alpha \gamma + \beta)(1 - q)}{\mu(d + \epsilon + \mu)(\mu + c)}$$

(6)

If the value of $R_0 \leq 1$, then the disease-free equilibrium is stable. Otherwise, the endemic equilibrium is stable.

$$V = \left(S_1 - S_1^0 - S_1^0 \ln \left(\frac{S_1}{S_1^0}\right)\right) + \left(S_1 - S_1^0 - S_1^0 \ln \left(\frac{S_1}{S_1^0}\right)\right) + E_1 + E_2 + \frac{\mu + c}{(1 - q)c} \alpha a_1$$

$$+ \frac{\mu + c}{(1 - q)c} \alpha a_2$$

(7)

The derivative of $V$ is given by

$$V' = (S_1 - S_1^0) \left(\frac{\Lambda}{S_1} - \mu - \beta l a_1 - \alpha + \frac{\alpha S_2}{S_1} - \gamma \alpha a_1\right)$$

$$+ (S_1 - S_1^0) \left(\frac{\Lambda}{S_1} - \mu - \beta l a_1 - \alpha + \frac{\alpha S_2}{S_1} - \gamma \alpha a_1\right) + \beta S_1 l a_1 - (\mu + c)E_1 - \alpha E_1$$

$$+ \alpha E_1 + \gamma a S_2 l a_2 + \beta S_2 l a_2 - (\mu + c)E_2 - \alpha E_2 + \alpha E_2 + \gamma \alpha S_1 l a_1$$

$$+ \frac{\mu + c}{(1 - q)c} ((1 - q)c E_1 - \mu l a_1 - d l a_1 - \alpha l a_1 + \alpha l a_2 - \epsilon l a_1)$$

$$+ \frac{\mu + c}{(1 - q)c} ((1 - q)c E_2 - \mu l a_2 - d l a_2 - \alpha l a_2 + \alpha l a_1 - \epsilon l a_2)$$

(8)

$$= \left(\frac{\Lambda}{\mu}(\beta + \gamma \alpha) - \frac{\mu + c}{1 - q}(\mu + d + \epsilon)\right) l a_1 + \left(\frac{\Lambda}{\mu}(\beta + \gamma \alpha) - \frac{\mu + c}{1 - q}(\mu + d + \epsilon)\right) l a_2 + F(S_1, S_2)$$

$$= (\mu + c)(\mu + d + \epsilon) (R_0 - 1)l a_1 + (\mu + c)(\mu + d + \epsilon) (R_0 - 1)l a_2 + F(S_1, S_2)$$

where
\[ F(S_1, S_2) = (S_1 - S_1^0) \left( \Lambda - \frac{\mu}{S_1} \right) + (S_2 - S_2^0) \left( \Lambda - \frac{\mu}{S_2} \right) + \alpha S_1^0 \left( 1 - \frac{S_2}{S_1} \right) + \alpha S_2^0 \left( 1 - \frac{S_1}{S_2} \right) \]  \hspace{1cm} (9)

We have \( F(S_1, S_2) \leq 0 \) for \( S_1, S_2 \geq 0 \) and \( F(S_1, S_2) = 0 \) if and only if \( S_1 = S_2 = S_1^0 = S_2^0 = \frac{\Lambda}{\mu} \). Since \( R_0 \leq 1 \) then \( V' \leq 0 \). So, the disease-free equilibrium \( x_0 \) is globally asymptotically stable when \( R_0 \leq 1 \).

### 3.3 Numerical Simulation

In this section, numerical examples are shown to verify our analytical finding. For this purpose, we have taken the following parameter values by assuming in model system: \( \Lambda = 0.3, \mu = 0.2, c = 0.3, \mu_1 = 0.4, \beta = 0.6, a = 0.9, \gamma = 1, d = 0.1, q = 0.3 \) and \( \epsilon = 0.1 \) with the initial value: \( S_1(0) = 0.5, E_1(0) = 0.2, I_{a1}(0) = 0, I_{s1}(0) = 0, R_1(0) = 0, S_2(0) = 0.3, E_2(0) = 0.1, I_{a2}(0) = 0, I_{s2}(0) = 0 \) and \( R_2(0) = 0 \).

Using this set of parameters, it can be checked the \( R_0 \) of the model (1).

\[ R_0 = \frac{\Lambda c (a \gamma + \beta) (1 - q)}{\mu (d + \epsilon + \mu)(\mu + c)} = 2.3625 \]

The value \( R_0 > 1 \). So, the dynamical system of model (1) is stable at endemic equilibrium as shown at Figure 2. Otherwise, if the value \( R_0 < 1 \), the dynamical system of model (1) is stable at disease-free equilibrium as shown at Figure 3.
Figure 2. The schematic diagram of the model if $R_0 > 1$

Figure 3: The schematic diagram of the model if $R_0 < 1$

3.4 Sensitivity Analysis

In this section, we show sensitivity analysis of the model by using the combination of Latin Hypercube sampling (LHS) and Partial Rank Correlation Coefficient (PRCC) using 5000 samples (Marino et al., 2008). We measure against the increasing number of asymptomatic infections and symptomatic infection, and the result are given in Figure 4.a and 4.b respectively.

Figure 4.a shows that the influential parameter for all time is $\mu$. This parameter has negative relationship. This means if the value of $\mu$ increase, the number of asymptomatic infections decrease. The other parameter like $c$, $d$, and $\gamma$ have significant impact for the number of asymptomatic infections but
the impact decreases over time.

Figure 4.b shows that the influential parameters for all time are $\mu$ and $d$. These parameters have negative relationship. So, the result implies that when the values of $\mu$ and $d$ increase, the number of symptomatic infections decrease. The other parameters like $c$, $q$, and $\beta$ have significant impact for the number of asymptomatic infections but the impact decreases over time.

![Figure 4: Plot of PRCC value for model](image)

4. Conclusion

In this paper we constructed a mathematical model of COVID-19 transmission with the effect of travel between two regions, where the model follows classical SEIR model with asymptomatic and symptomatic cases. The analysis model and the numerical system have shown that the equilibrium of the system is affected by the value of $R_0$. If $R_0 > 1$ then the dynamical system of model is stable at endemic equilibrium. Otherwise, if the value $R_0 < 1$, the dynamical system of model is stable at disease-free equilibrium. A global sensitivity analysis has been performed to know the influential parameter in the model. The parameter $\mu$ determine a decrease in number of asymptomatic and symptomatic infections.

Acknowledgments

This research is funded by Hibah Riset Internal Universitas Padjadjaran with scheme Academic Leadership Grant, with contract number 1427/UN6.3.1/LT/2020.
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