Stability Analysis of the Corona Virus (Covid-19) Dynamics SEIR Model in Indonesia

L P Sinaga¹, H Nasution², D Kartika³
¹,²,³Department of Mathematics, Universitas Negeri Medan, Jalan Willem Iskandar Pasar V, Medan 20221, Indonesia

¹lazer_integral@yahoo.com, ²hamidah_math@yahoo.com, ³dindakartika@unimed.ac.id

Abstract. Covid-19 is a type of virus that infects the respiratory tract or is also known as severe acute respiratory syndrome Corona virus-2 (SARS-CoV-2). Researchers through this study were trying to build a mathematical model of the spread of the Covid-19 virus and analyzed the stability of its critical points. This virus dynamic model was built based on the interaction between the suspect group with the exposed group and the interaction with the infected group. The virus spread model in this study consists of two critical points, namely a disease-free critical point and a disease endemic critical point. The two critical points will be stable if they meet the requirements for certain parameter values. Numerical simulations of virus dynamics in Indonesia were carried out using data on the number of susceptible people, the number under monitoring, the number of infected, the number of cures and the number of deaths due to the virus. These data were obtained from the Ministry of Health of the Republic of Indonesia. Based on the data obtained, it was found that the simulation model of stability reached a critical point in a very long time. Therefore, treatment or vaccines are needed as a step to reduce the dynamics of Covid-19.

1. Introduction
Corona virus or severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) is a virus that attacks the respiratory system. The virus causes this disease is called Covid-19 (Corona Virus Disease 2019). The ICTV Corona virus disease Study Group stated that this virus is a species associated with severe acute respiratory syndrome. Covid-19 was first discovered in humans in December 2019. The outbreak was first detected in Wuhan City, Hubei Province, China in mid-December 2019. In the end, the outbreak due to SARS-CoV-2 was declared a global health emergency or pandemic by the Health Organization. World (WHO) on January 30, 2020. The Chinese government conducted quarantine in the city of Wuhan on January 23, 2020 as a step to control the pandemic [2].

Based on data from BPS (Statistics Indonesia), it is known that the total population in 2020 is projected to be 271,066,400 people [1]. The discovery of Covid-19 was first confirmed in Indonesia on March 02, 2020. At that time it was declared that there were 2 people who were positively infected, of which 0 recovered and 0 died [7]. The investigators suggest that the main reason for the high number of cases may be due to a lack of testing so that many cases go undetected. The Indonesian Ministry of Health officially changed the terms ODP, PDP, OTG and confirmed cases to be suspect cases, probable cases, close contacts and confirmed cases. This change is contained in the Decree of
the Minister of Health Number HK 01.07/MENKES/413/2020 concerning Guidelines for the Prevention and Control of Covid-19.

Criteria so the case can be classified as case of suspect is in the form of cases of acute respiratory infection where within 14 days before illness, the person concerned comes from/lives in an area where local transmission has occurred and the person concerned in the last 14 days has had contact with a positive confirmed case or close contact with the probable case. Furthermore, probable cases are defined as cases that have criteria in the form of clinical cases believed to be Covid-19, the patient's condition is severe with ARDS or severe ARD and respiratory problems that can be seen clearly, but laboratory tests through RT-PCR have not been carried out. The criteria in the case of close contact is that someone has had contact with a positive confirmation case or with a probable case. The last one is the confirmation case, which is a case where a person has been confirmed positive after going through the RT-PCR laboratory examination. There are 2 criteria for confirmatory cases, namely confirmation cases with symptoms and confirmatory cases without symptoms [4-6].

Various fields engaged in health have tried to prevent the spread of this virus. One of them is pharmacologists who are struggling to find a vaccine that can paralyze this virus. Mathematicians and researchers in other fields from various countries also contributed to researching the characteristics of the virus and the nature of its spread. Mathematical modeling is used to understand the characteristics of an outbreak epidemic, predict its infection, and make decisions to break the chain of spread.

One of the researches was conducted by [3] in his writing entitled "A Simulation on Potential Secondary Spread of Novel Coronavirus in an Exported Country Using a Stochastic Epidemic SEIR Model". This research discusses a simulation to estimate the impact of a potential viral outbreak outside China. The simulation is performed using a stochastic SEIR model assuming one patient will interact with a community. This study provides the results that proper control can reduce the risk of outbreaks to a certain degree. Some other results about mathematical modelling of Covid-19 can be found in [5,6,8].

2. Research methodology
The procedures in conducting this research consisted of:

1. Building a SEIR mathematical model for the spread of the corona virus (Covid-19).
2. Find the disease-free and endemic critical points in the modified SEIR model of the spread of the corona virus (Covid-19).
3. Linearize the model and determine the Jacobi matrix at each equilibrium point.
4. Find the equations of characteristics and eigen values.
5. Determine the equilibrium point stability by using Routh Hurwitz Criteria.
6. Collect the data (number of suspects, monitoring, confirmed, died, and recovered) from the Covid-19 Response Task Force at the Ministry of Health Republic of Indonesia.
7. Process data and determine the model parameters and build numerical simulation.
8. Draw conclusions.

3. Results and discussion

3.1. Modification of The SEIR Model for The Spread of Covid-19
The SEIR model for the spread of Covid-19 infection consists of 4 subpopulations, namely Susceptible, Exposed, Infected and Recovered that was built based on the following scheme:
The assumptions in the modification of the SEIR model are:
1. The population size is constant.
2. The population is homogeneous where every individual has the same opportunity to make contact with other individuals.
3. The spread of the corona virus occurs from person to person.
4. Individuals who have recovered cannot be reinfected.

Based on the modified SEIR Model scheme, a system of differential equations is obtained as follows:

\[
\begin{align*}
\frac{dS}{dt} &= \Lambda - \alpha S(\theta E + (1-\theta)I) - \mu_1 S \\
\frac{dE}{dt} &= \alpha S(\theta E + (1-\theta)I) - (\mu_2 + \beta)E \\
\frac{dI}{dt} &= \beta E - (\mu_3 + \gamma)I \\
\frac{dR}{dt} &= \gamma I - \mu_4 R
\end{align*}
\]  

(1)

**Table 1. Definition of model variables**

| Variable | Description |
|----------|-------------|
| S        | Group of healthy individuals who are susceptible to infection. |
| E        | Group of individuals who have been positive for the virus during the incubation period |
| I        | Group of individuals who have tested positive for the virus and may transmit it on to other individuals. |
| R        | Group of individuals who have recovered and are immune to the virus. |

**Table 2. Definition of model parameters**

| Parameter | Description |
|-----------|-------------|
| \( \Lambda \) | The rate regarding the increase in suspect cases |
| \( \alpha \) | The rate of change from suspect to exposed classes due to interaction with infected individuals |
| \( \beta \) | The rate at which individuals become infected |
| \( \gamma \) | Recovery rate |
| \( \mu \) | Death rate |
| \( \theta \) | The proportion of the suspected individuals amount who have direct contact with the monitoring group |
| \( 1-\theta \) | The proportion of the suspected individuals amount who have direct contact with the positive confirmed group |
3.2. The Critical Points of SEIR Model for the Spread of Covid-19

The critical point of the system can be found if it satisfies
\[ \frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0 \].
Thus, the model critical point is processed as follows:

\[ \Lambda - \alpha S(\theta E + (1 - \theta)I) - \mu_s S = 0 \]  \hspace{1cm} (2)
\[ \alpha S(\theta E + (1 - \theta)I) - (\mu_s + \beta)E = 0 \]  \hspace{1cm} (3)
\[ \beta E - (\mu_i + \gamma)I = 0 \]  \hspace{1cm} (4)
\[ \gamma I - \mu_s R = 0 \]  \hspace{1cm} (5)

From (2) it is obtained
\[ S^* = \frac{\Lambda}{\alpha(\theta E + (1 - \theta)I) + \mu_s} \]  \hspace{1cm} (6)

From (4) it is obtained
\[ I^* = \frac{\beta}{\mu_i + \gamma} E^* \]  \hspace{1cm} (7)

Furthermore, Equation (7) is substituted into Equation (6) as follows
\[ S^* = \frac{(\mu_i + \gamma)\Lambda}{\alpha(\mu_i + \gamma)\theta + (1 - \theta)\beta)E + \mu_s(\mu_i + \gamma)} \]  \hspace{1cm} (8)

Equation (7) and Equation (8) is substituted into Equation (3) as follow:
\[ \alpha S(E + I) - \mu_s E - \beta E = 0 \]

\[ \alpha \left( \frac{(\mu_i + \gamma)\Lambda}{\alpha(\mu_i + \gamma)\theta + (1 - \theta)\beta)E + \mu_s(\mu_i + \gamma)} \right) (\theta E + (1 - \theta)\beta) - \frac{\beta}{\mu_i + \gamma} E^* - (\mu_s + \beta)E^* = 0 \]

\[ E^* \left( \frac{\alpha \Lambda((\mu_i + \gamma)\theta + (1 - \theta)\beta)}{\alpha((\mu_i + \gamma)\theta + (1 - \theta)\beta)E^* + \mu_s(\mu_i + \gamma)} - (\mu_s + \beta) \right) = 0 \]

so that it is obtained:
\[ E^* = 0 \text{ and } E^* = \frac{\alpha \Lambda((\mu_i + \gamma)\theta + (1 - \theta)\beta) - \mu_s(\mu_i + \gamma)(\mu_s + \beta)}{\alpha((\mu_i + \gamma)\theta + (1 - \theta)\beta)}(\mu_i + \gamma) \]  \hspace{1cm} (9)

For \( E^* = 0 \), the \( S^*, I^*, R^* \) obtained are as follows:
\[ S^* = \frac{\Lambda}{\mu_i} \]
\[ I^* = 0 \]
\[ R^* = 0 \]

Thus, the disease-free critical point obtained is \( E_0 = (\frac{\Lambda}{\mu_i}, 0, 0, 0) \).

And for \( E^* = \frac{\alpha \Lambda((\mu_i + \gamma)\theta + (1 - \theta)\beta) - \mu_s(\mu_i + \gamma)(\mu_s + \beta)}{\alpha((\mu_i + \gamma)\theta + (1 - \theta)\beta)}(\mu_i + \gamma) \) the \( S^*, I^*, R^* \) obtained are as follows:
\[ S^* = \frac{\Lambda(\mu_i + \gamma)(\mu_s + \beta)}{\alpha \Lambda((\mu_i + \gamma)\theta + (1 - \theta)\beta)} \]
\[ E^* = \frac{\Lambda}{(\mu_i + \gamma)} - \frac{\mu_s(\mu_i + \gamma)}{\alpha((\mu_i + \gamma)\theta + (1 - \theta)\beta)} \]
\[ I^* = \frac{\beta \Lambda}{(\mu_s + \beta)(\mu_i + \gamma)} - \frac{\beta \mu_s}{\alpha((\mu_i + \gamma)\theta + (1 - \theta)\beta)} \]
\[ R^* = \frac{\beta \gamma \Lambda}{\mu_3 (\mu_2 + \beta)(\mu_3 + \gamma)} - \frac{\beta \gamma \mu_i}{\alpha \mu_3 ((\mu_3 + \gamma) \theta + (1-\theta) \beta)} \]

Thus, the disease-endemic critical point obtained is \( E_1^*(S^*, E^*, I^*, R^*) \).

3.3. Stability Analysis of Disease-Free Critical Point

Based on the SEIR model, suppose the functions are determined as follows:

\[
\begin{align*}
  f_1(S, E, I, R) &= \Lambda - \alpha S (\theta E + (1-\theta) I) - \mu_1 S \\
  f_2(S, E, I, R) &= \alpha S (\theta E + (1-\theta) I) - (\mu_2 + \beta) E \\
  f_3(S, E, I, R) &= \beta E - (\mu_3 + \gamma) I \\
  f_4(S, E, I, R) &= \gamma I - \mu_4 R
\end{align*}
\]

so that the Jacobian matrix is obtained as follows:

\[
J = \begin{pmatrix}
\frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial E} & \frac{\partial f_1}{\partial I} & \frac{\partial f_1}{\partial R} \\
\frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial E} & \frac{\partial f_2}{\partial I} & \frac{\partial f_2}{\partial R} \\
\frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial E} & \frac{\partial f_3}{\partial I} & \frac{\partial f_3}{\partial R} \\
\frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial E} & \frac{\partial f_4}{\partial I} & \frac{\partial f_4}{\partial R}
\end{pmatrix}
\]

The Jacobian matrix at the free of virus critical point \( J(E_0) \) is as follows:

\[
J(E_0) = \begin{pmatrix}
-\mu_1 & -\frac{\alpha \Lambda \theta}{\mu_1} & -\frac{\alpha (1-\theta) \Lambda}{\mu_i} & 0 \\
0 & \frac{\alpha \Lambda \theta}{\mu_1} - (\mu_2 + \beta) & \frac{\alpha (1-\theta) \Lambda}{\mu_i} & 0 \\
0 & \beta & - (\mu_3 + \gamma) & 0 \\
0 & 0 & \gamma & -\mu_4 \\
\end{pmatrix}
\]

Next, we will look for the eigenvalues of the matrix \( J(E_0) \)

\[
\lambda I - J(E_0) = 0
\]

\[
\begin{pmatrix}
\lambda + \mu_1 & \frac{\alpha \Lambda \theta}{\mu_1} & \frac{\alpha (1-\theta) \Lambda}{\mu_i} & 0 \\
0 & \lambda - \frac{\alpha \Lambda \theta}{\mu_1} - (\mu_2 + \beta) & \frac{\alpha (1-\theta) \Lambda}{\mu_i} & 0 \\
0 & -\beta & \lambda + (\mu_3 + \gamma) & 0 \\
0 & 0 & -\gamma & \lambda + \mu_4 \\
\end{pmatrix} = 0
\]

can be written into a characteristic equation:

\[
(\lambda + \mu_1)(\lambda + \mu_4) r(\lambda) = 0 \quad \text{with} \quad r(\lambda) = a_2 \lambda^2 + a_1 \lambda + a_0
\]

where

\[
\begin{align*}
a_2 &= 1 \\
a_1 &= (\mu_3 + \gamma) + (\mu_2 + \beta) - \frac{\alpha \Lambda \theta}{\mu_1} \\
a_0 &= (\mu_2 + \beta)(\mu_3 + \gamma) - \frac{\alpha \Lambda \theta (\mu_3 + \gamma) + \alpha \beta \Lambda (1-\theta)}{\mu_1}
\end{align*}
\]
Further it is obtained \( \lambda_1 = -\mu_1 < 0 \) and \( \lambda_2 = -\mu_2 < 0 \) and the other eigen values contained in the polynomial of \( r(\lambda) \). Based on the theory of stability, the system will be stable if all eigen values are negative. According to the characteristic equation, the value of \( a_1 = 1 \) is positive, \( a_2 \) will be positive for 
\[
(\mu_1 + \gamma)(\mu_2 + \beta) > \frac{\alpha \Delta \theta}{\mu_1},
\]
and \( a_0 \) will be positive value \( (\mu_2 + \beta)(\mu_1 + \gamma) > \frac{\alpha \Delta \theta(\mu_1 + \gamma)(\mu_2 + \gamma)}{\mu_1} \)
Therefore it can be concluded that all characteristic roots are negative. Thus, the critical point \( E_0 \) is stable.

3.4. Stability Analysis of Disease-Endemic Critical Point

The point of \((S, E, I, R)\) is The stability analysis of the endemic critical point was carried out by looking for the equation of the Jacobian matrix \( J(E_1) \) as follows:

\[
J(E_1) = \begin{bmatrix}
-\frac{\alpha \Lambda(\theta(\mu_1 + \gamma) + \beta(1-\theta))}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{\theta(\mu_1 + \gamma)(\mu_1 + \beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{(1-\theta)(\mu_1 + \gamma)(\mu_2 + \beta)}{(1-\theta)(\mu_2 + \gamma)(\mu_1 + \beta)} & 0 \\
\frac{\alpha \Lambda(\theta(\mu_1 + \gamma)+(1-\theta)\beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{\theta(\mu_1 + \gamma)(\mu_1 + \beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{(1-\theta)(\mu_1 + \gamma)(\mu_2 + \beta)}{(1-\theta)(\mu_2 + \gamma)(\mu_1 + \beta)} & 0 \\
\frac{\alpha \Lambda(\theta(\mu_1 + \gamma)+(1-\theta)\beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{\theta(\mu_1 + \gamma)(\mu_1 + \beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{(1-\theta)(\mu_1 + \gamma)(\mu_2 + \beta)}{(1-\theta)(\mu_2 + \gamma)(\mu_1 + \beta)} & 0 \\
0 & 0 & 0 & \lambda + \mu_4
\end{bmatrix}
\]

Then the eigenvalues \( J(E_1) \) will be determined.

\[
|\lambda I - J(E_1)| = 0
\]

\[
\lambda + \frac{\alpha \Lambda(\theta(\mu_1 + \gamma) + \beta(1-\theta))}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{\theta(\mu_1 + \gamma)(\mu_1 + \beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{(1-\theta)(\mu_1 + \gamma)(\mu_2 + \beta)}{(1-\theta)(\mu_2 + \gamma)(\mu_1 + \beta)} & 0 \\
\frac{\alpha \Lambda(\theta(\mu_1 + \gamma)+(1-\theta)\beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{\theta(\mu_1 + \gamma)(\mu_1 + \beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{(1-\theta)(\mu_1 + \gamma)(\mu_2 + \beta)}{(1-\theta)(\mu_2 + \gamma)(\mu_1 + \beta)} & 0 \\
\frac{\alpha \Lambda(\theta(\mu_1 + \gamma)+(1-\theta)\beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{\theta(\mu_1 + \gamma)(\mu_1 + \beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)} & -\frac{(1-\theta)(\mu_1 + \gamma)(\mu_2 + \beta)}{(1-\theta)(\mu_2 + \gamma)(\mu_1 + \beta)} & 0 \\
0 & 0 & 0 & \lambda + \mu_4
\]

It can be written as a characteristic equation:

\[
(\lambda + \mu_4)s(\lambda) = 0 \text{ with } s(\lambda) = a_3 \lambda^3 + a_2 \lambda^2 + a_1 \lambda + a_0
\]

where

\[
a_3 = 1
\]

\[
a_2 = \frac{(\mu_2 + \beta)(1-\theta)\beta}{(\mu_2 + \gamma)(\mu_2 + \gamma)} + (\mu_1 + \gamma) + \frac{\alpha \Lambda(\theta(\mu_1 + \gamma) + (1-\theta)\beta)}{(\mu_1 + \gamma)(\mu_1 + \gamma)}
\]

\[
a_1 = \frac{\alpha \beta(1-\theta)}{(\mu_1 + \gamma)} + \frac{\alpha \Lambda(\theta(\mu_1 + \gamma) + (1-\theta)\beta)}{(\mu_1 + \gamma)} + \alpha \Lambda - \theta(\mu_1 + \beta)(\mu_1 + \gamma)
\]

\[
a_0 = \alpha \Lambda((\mu_1 + \gamma)\theta(1-\theta)\beta) - \theta(\mu_1 + \beta)(\mu_1 + \gamma)
\]

The eigen value \( \lambda_1 = \mu_1 < 0 \) and the other eigen values can be found on the polynomial of \( s(\lambda) \).

The value of \( a_3 = 1 \), and \( a_2 > 0 \), based on the parameter value. The values of \( a_1 \) and \( a_0 \) will be positive if it satisfies \( \alpha \Lambda((\mu_1 + \gamma)\theta + (1-\theta)\beta) > \theta(\mu_1 + \beta)(\mu_1 + \gamma) \). From the solution above, all characteristic roots are negative so that the critical point of \( E_0 \) is stable.

3.5. Numerical Simulation

The SEIR dynamics model of the corona virus will be simulated using covid-19 data in May-September, 2020 in Indonesia. The determination of the parameters in this simulation was carried out
based on data from the Indonesian Minister of Health regarding COVID-19 data and Statistics Indonesia on Demography.

Table 3. Data for COVID-19 in Indonesia

| Month | Suspect | Under Monitoring | Confirmed | Recovered | Died |
|-------|---------|------------------|-----------|-----------|------|
| May   | 216.769 | 47.714           | 25.773    | 7.015     | 1.573|
| June  | 465.683 | 41.605           | 55.092    | 23.800    | 2.805|
| July  | 856.003 | 53.723           | 106.336   | 62.138    | 5.058|
| August| 1.282.618| 77.951           | 172.053   | 124.185   | 7.343|
| September | 1.962.754 | 132.496 | 282.724 | 210.437 | 10.601 |

Table 4. Parameter Values

| Parameter | Value |
|-----------|-------|
| \( \Lambda \) | 0.352 |
| \( \alpha \) | 0.017 |
| \( \beta \) | 0.052 |
| \( \gamma \) | 0.041 |
| \( \mu_1 \) | 0.0001 |
| \( \mu_2 \) | 0.0001 |
| \( \mu_3 \) | 0.002 |
| \( \mu_4 \) | 0.0001 |

A numerical simulation can be obtained with the initial values of \( S = 217 \), \( E = 48 \), \( I = 26 \) and \( R = 7 \) based on the data in the Table 3 and Table 4 and assume that \( \theta = 0.6 \) as follows:

Figure 2 presents that the number of individuals \( S, E, I \) and \( R \) will be stable over a long time. If it is viewed based on graphs, the end of the spread of Covid-19 is expected to occur at the 800th time unit (month). The graph of Suspect will initially decrease and begin to increase due to the parameter \( \Lambda \) (rate of increase in the individual suspect).The graph of Exposed is known to have increased even though in the end it also decreased. In this case, the increase that occurs is caused by the \( \alpha \) parameter (or the rate at which \( S \) moves to \( E \)) while the decrease is caused by the \( \beta \) parameter (rate at which \( E \) moves to \( I \)).

The simulation of \( S \) value based on the \( \theta \) parameter is presented by Figure 3 below, so that the influence of \( \theta \) on \( S \) can be obtained.
Based on these Figure 3, it was found that if the $\theta$ parameters were higher, the graph of $S$ would also increase. Meanwhile, for the simulation of class $\text{Infected}$ value based on the $\theta$ parameter is as follows:

The following Figure 4 is a graph of the number of infected based on the assumed value of the theta parameter. Of course, the higher the value of the direct contact rate of the suspect group with the infected group will increase the spread of the virus. So, the theta parameter greatly affects the virus dynamics. Disciplined quarantine is needed to decrease the balance point.

### 4. Conclusions

The model for the spread of the Covid-19 virus has two critical points, the free of virus critical point $E_0$ and an endemic critical point $E_1$. The two critical points will be called asymptotically stable if they meet certain inequality of parameters. The dynamics of the corona virus in Indonesia will reach a stable point in the long term. The theta parameter, namely the rate of direct contact of the suspect groups to the exposed and infected groups plays an important role in the spread of the virus. Avoiding direct contact between individuals, disciplined quarantine of infected groups and vaccinations are needed to stop the spread of the virus.

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References

[1] Badan Pusat Statistik (Statistics Indonesia) 2010 Proyeksi penduduk Indonesia 2010-2035 [Accessed May 2020]

[2] Hou C, Chen J, Zhou Y, Hua L, Yuan J, He S, Guo Y, Zhang S, Jia Q, Zhao C, Zhang J, Xu G and Jia E 2020 The effectiveness of quarantine of Wuhan city against the Corona virus disease 2019 (COVID-19): A well-mixed SEIR model analysis J. Med. Vir. 92 841-48

[3] Iwata K and Miyakoshi C 2020 A simulation on potential secondary spread of Novel Coronavirus in an exported country using a stochastic epidemic SEIR model J. Clin. Med. 9 944

[4] Kementerian Kesehatan Republik Indonesia (Ministry of Health Republic of Indonesia) 2020 Available from: https://covid19.go.id/ [Accessed September 2020]

[5] Jonny, H.P., Rajagukguk, D. and Rajagukguk, J., 2020, January. Computational Modelling Based on Modellus to Improve Students’ Critical Thinking on Mechanical Energy. Journal of Physics: Conference Series. 1428, No. 1, p. 012042. IOP Publishing.

[6] Rajagukguk, J. and Sari, N.E., 2018, March. Detection system of sound noise level (SNL) based on condenser microphone sensor. J. Phys. Conf. Ser (Vol. 970, p. 012025).

[7] Li Y, Wang B, Peng R, Zhou C, Zhan Y, Liu Z, Jiang X and Zhao B 2020 Mathematical modeling and epidemic prediction of COVID-19 and its significance to epidemic prevention and control measures Ann. Infect. Dis. Epidemiol 5(1) 1052

[8] Mandal S, Bhatnagar T, Arinaminpathy N, Agarwal A, Chowdhury A, Murhekar M, Gangakhedkar R R and Sarkar S 2020 Prudent public health intervention strategies to control the coronavirus disease 2019 transmission in India: A mathematical model-based approach India. J. Med. Res. 151 190-9

[9] Rustan and Handayani I 2020 The outbreak’s modelling of Coronavirus (Covid-19) using The modified SEIR model in Indonesia Spek. 5(1) 61-8

[10] Pengpeng S, Shengli C and Peihua F 2020 SEIR transmission dynamics model of 2019nCov coronavirus with considering the weak infectious ability and changes in latency duration. medRxiv. Preprint doi: https://doi.org/10.1101/2020.02.16.20023655