CAUCHY –Jurnal Matematika Murni dan Aplikasi
Volume 8(2) (2023), Pages 125-141
p-ISSN: 2086-0382; e-ISSN: 2477-3344

Dynamic Analysis of the Susceptible-Exposed-Infected-Hospitalized-Critical-Recovered-Dead (SEIHCRD)

Juhari*, Silvi Kurnia

Mathematics Department, Universitas Islam Negeri Maulana Malik Ibrahim Malang, Indonesia

E-mail: juhari@uin-malang.ac.id

ABSTRACT

This study discusses the dynamic analysis of the *Susceptible–Exposed–Infected–Hospitalized–Critical–Recovered–Dead* (SEIHCRD) model using the fourth order Runge-Kutta method. The data used in this study is original data on *Infected*, *Hospitalized* and *Critical* cases in Indonesia from August to October 2021. Dynamic analysis of the model is carried out by determining disease-free and endemic equilibrium points, local stability analysis of disease-free and endemic equilibrium points, and determine the basic reproduction number. The result of this analysis is that the number of new infection cases in Indonesia will decrease over time and the COVID-19 outbreak will end. Then a numerical simulation was carried out using the fourth order Runge-Kutta method in dealing with COVID-19 cases in Indonesia. The simulations and calculations show that the rate of contact of susceptible individuals with infected individuals is 0.06 per day, the rate of movement of individuals in the Exposed class to the Infected class is 0.14 per day, the probability of infected individuals being hospitalized with a value of 0.95, the probability that COVID-19 patients become critical and enter the Intensive Care Unit (ICU) with a value of 0.485, and the probability of a critical patient dying with a value of 0.25 affects the slope of *Infected*, *Hospitalized* and *Critical* cases in Indonesia. Where *Infected* cases will be sloping with an absolute error value of 28%, *Hospitalized* cases with an absolute error value of 20% and *Critical* cases with an absolute error value of 33%. This research provides information that it is estimated that the daily infection cases of COVID-19 will decrease and be close to zero. So that infected patients who must be hospitalized and admitted to the Intensive Care Unit (ICU) are also decreasing, it is hoped that the COVID-19 pandemic will not happen again.

Keywords: Dynamic Analysis; Fourth Order Runge-Kutta Method; SEIHCRD Model; COVID-19

INTRODUCTION

Since the beginning of 2019, the world has been fighting together against COVID-19 which is a new virus. This virus spread very quickly, causing several countries to suffer from a shortage of inpatient beds and Intensive Care Unit (ICU) beds [1],[10], one of them in Indonesia. In June 2021 in Indonesia, every day the number of COVID-19 patients who die without receiving treatment is increasing. This is due to the increasing number of

Submitted: July 12, 2023 Reviewed: July 24, 2023 Accepted: August 20, 2023
DOI: http://dx.doi.org/10.18860/ca.v8i1.22812

COVID-19 cases and the decreasing availability of hospital beds. So, to overcome this condition, the Minister of Health asked hospitals in various regions to make the emergency room an additional isolation room. Meanwhile, emergency services were moved to emergency tents set up outside the hospital. Unfortunately, this solution has not been fully able to overcome the surge in COVID-19 cases, as a result, some patients with moderate and severe symptoms who do not receive an inpatient bed are forced to be placed in hospital halls, while several other patients die because they do not receive treatment. Therefore, a mathematical model is needed that can assist the government in understanding the scenario of the spread of COVID-19 in Indonesia and knowing how many inpatient beds and ICU beds are needed at any given time. In this case, the mathematical model that can be applied in Indonesia is the SEIHCRD model.

The SEIHCRD model is a modification of the Susceptible – Exposed – Infected - Recovered (SEIR) model [1]. This model added several additional compartments, including Hospitalized (H), Critical (C), and Dead (D). Where Hospitalized (H) itself is an individual infected with COVID-19 with moderate and severe symptoms or who has a congenital disease or is elderly who is hospitalized. Then Critical (C) is a COVID-19 patient who is hospitalized and then in a critical condition, so he is at high risk of experiencing complications and requires treatment in the Intensive Care Unit (ICU) room. Meanwhile, Dead (D) was a critical COVID-19 patient and had received treatment in the Intensive Care Unit (ICU), but eventually died. Each compartment in the model has a relationship with each other, that is, susceptible individuals in the Susceptible (S) class experience contact with infected individuals at a rate of β and do not keep their distance at a rate of η, so these susceptible individuals turn into exposed and enter the Exposed class. (E). Furthermore, individuals who have been exposed will turn into infected with a transfer rate of δ and enter the Infected (I) class. Then the infected individual will experience the development of COVID-19 symptoms with an average time of ψ, where if the symptoms are moderate or severe then the infected individual will enter the Hospitalized (H) class. Meanwhile, infected individuals with mild symptoms will carry out independent isolation until they recover with an average recovery time of γ and enter the Recovered (R) class.

Next, COVID-19 patients in the Hospitalized (H) class will recover and enter the Recovered (R) class after being hospitalized with an average length of stay of χ . Then COVID-19 patients in the Hospitalized (H) class can also experience a critical condition with a probability of θ and enter the Critical class (C). Where critical patients in the Critical (C) class will recover and enter the Recovered (R) class with an average recovery time from a critical condition of μ, critical patients can also die and enter the Dead (D) class with a probability of ω and the average Intensive Care Unit (ICU) admission time is φ.

In 2014, [2] study a VSEIR model for transmission of tuberculosis (tb) disease in north Sumatra, Indonesia. (V), Susceptible (S) Infected (I), and Recovered (R) (VSIR) model for transmission of Tuberculosis in North Sumatera is modified. [3] use a nonlinear susceptible, exposed, infectious and removed transmission model with added behavioral and government policy dynamics. Three models were used to fit and predict the epidemic situation in China: a modified SEIRD (Susceptible-Exposed-Infected-Recovered-Dead) dynamic model, a neural network method LSTM (Long Short-Term Memory), and a GWR (Geographically Weighted Regression) model reflecting spatial heterogeneity [4]. [5] aimed to analyze the situation of COVID-19 in Thailand and the challenging disease control by employing a dynamic model to determine prevention approaches. [6] propose a new model named Dynamic – Susceptible – Exposed – Infective -Quarantined (D-SEIQ), by making appropriate modifications of the Susceptible - Exposed – Infective - Recovered (SEIR) model and integrating machine learning based parameter optimization under

epidemiological rational constraints. [7] predict the long-term dynamic COVID-19 in Indonesia. 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 [8]. [9] propose a framework for stress testing and financial scenario generation of market indicators. [10] develop a dynamic transmission model to investigate the impact of social media, particularly tweets via the social networking platform, Twitter on the number of influenza and COVID-19 cases of infection and deaths. [11] propose a new seven compartmental model Susceptible – Exposed – Infected -Asymptomatic – Quarantined – Fatal - Recovered (SEIAQFR) which is based on classical Susceptible-Infected-Recovered (SIR) model dynamic of infectious disease and considered factors like asymptomatic transmission and quarantine of patients.

In 2020, [1] conducted an analysis of the SEIHCRD model using the Least-Square and Levenberg Marquadt methods in determining scenarios for the spread of COVID-19. Where this study considers the existence of a Case Fatality Rate based on age and comorbidity categories which will affect the spread scenario. In the following year [18] performed a dynamic analysis on the SEIHCRD model in the Kenyan population. The analysis was carried out to find out how sensitive the basic reproduction number analysis is to the parameters of physical distancing and mass testing, considering the presence of migration in the studied population. Then, the following year [11],[18], [19] also conducted a dynamic analysis of the SEIHCRD model on the spread of COVID-19 in Indonesia. Where the research aims to determine the sensitivity analysis of the parameters of physical distancing and mass testing of basic reproduction numbers. The flow of infection spread in this model includes, among others, susceptible individuals in the Susceptible class will be exposed and enter the Exposed class. Then the exposed individual will be infected and enter the Infectious or Hospitalized class. Furthermore, individuals in the Infectious and Hospitalized class have the possibility of recovering and dying. Where individuals in the Hospitalized class can also experience critical conditions and enter the Critical class. Then finally, the individual in this Critical class will die and enter the Dead class.

In contrast to these studies, in this study the proposed SEIHCRD model will be modified by adding the natural birth rate and natural death rate parameters which will then be analyzed using dynamic analysis. After that the model will be approached through a numerical method, namely the fourth order Runge-Kutta method to display the results of numerical calculations and their simulations. The data used in this study is original data in Indonesia from Infected, Hospitalized, Critical, Recovered and Dead cases from August to October, sourced from the website of the Ministry of Health and the Indonesian COVID-19 Task Force. Meanwhile, the original data from the Susceptible and Exposed cases are not available in Indonesia. Then this data will be used to find out whether the solution graph from the model can approach the solution graph from the original data. So, based on the background previously described, the author wants to apply the SEIHCRD model in solving the scenario of the spread of COVID-19 in Indonesia using the fourth order Runge-Kutta method.

METHODS

Data and Data Sources

In this study, the type of data used is secondary data from August to October 2021, in the form of daily COVID-19 cases on the website SATGAS COVID-19 and availability of hospital beds on the website KEMENKES [17]. This data was taken from August to October due to the complete data on daily cases of COVID-19 and the availability of hospital beds.

Research Steps

1. Dynamic analysis on the SEIHCRD model:
   a. Identify the initial values and parameters used.
   b. Determine the equilibrium point
   c. Determine the basic reproduction number (R_0)
   d. Define stability analysis
2. Numerical Simulation Using Fourth Order Runge-Kutta Method
   a. Specifies the set value.
   b. Perform the calculation of the first iteration using the fourth order Runge-Kutta formula by entering the obtained constant values.
   c. Perform calculations for the second to the 92nd iteration using the Octave software
3. Interpretation of Results
   a. Displays graphs obtained from Octave software.
   b. Analyze the results of the graph obtained
   c. Make conclusions from the results of the analysis.

RESULTS AND DISCUSSION

Seihcrd Model After Modification

The following is a modified SEIHCRD model:

$$\begin{aligned}
\frac{dS(t)}{dt} &= \xi N(t) - \frac{\eta\beta I(t)S(t)}{N(t)} - \tau S(t)\\
\frac{dE(t)}{dt} &= \frac{\eta\beta I(t)S(t)}{N(t)} - \delta E(t) - \tau E(t)\\
\frac{dI(t)}{dt} &= \delta E(t) - \psi\alpha I(t) - \gamma I(t) + \alpha\gamma I(t) - \tau I(t)\\
\frac{dH(t)}{dt} &= \psi\alpha I(t) - \sigma\theta H(t) - \chi H(t) + \chi\theta H(t)\\
&\quad -\tau H(t)\\
\frac{dC(t)}{dt} &= \sigma\theta H(t) - \varphi\omega C(t) - \mu C(t) + \mu\omega C(t) - \tau C(t)\\
\frac{dR(t)}{dt} &= \gamma I(t) - \alpha\gamma I(t) + \mu C(t) - \mu\omega C(t) + \chi H(t)\\
&\quad -\chi\theta H(t) - \tau R(t)\\
\frac{dD(t)}{dt} &= \varphi\omega C(t)
\end{aligned} \tag{1}$$

The compartment diagram of the SEIHCRD model is shown in the following figure:

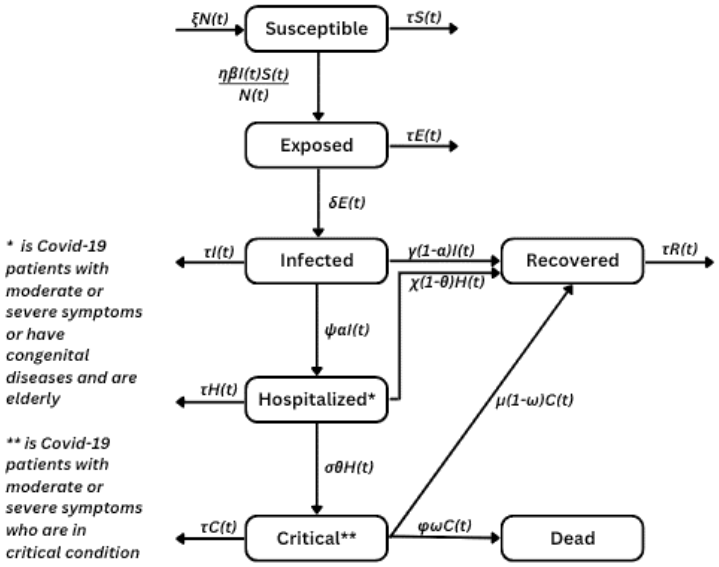

Figure 1. SEIHCRD Model Compartment Diagram

Identify Initial Values and Parameters Used

The following are the initial values and parameters in this study:

Table 1. The Initial Value of the SEIHCRD Model in Indonesia

Variabel	Definition	Value
(N_0)	The total number of people living in Indonesia	272.229.372
(S_0)	The number of individuals who are vulnerable to time	272.008.906
(E_0)	The number of individuals exposed to time	71.788
(I_0)	Number of infected individuals over time	30.738
(H_0)	Number of infected individuals hospitalized over time	70.568
(C_0)	The number of infected patients who are critical to time	7.926
(R_0)	The number of infected individuals who recover over time	39.446
(D_0)	The number of critically ill patients who died over time	1.604

Table 2. Parameter Value of SEIHCRD Model in Indonesia

Parameter	Definition	Value	Source
ξ	Natural birth rate	6.25×10^{-3}	[12]
τ	Natural death rate	6.25×10^{-3}	[12]
η	Social distancing factor	1	[1]
Parameter	Definition	Value	Source
δ	The rate of individual movement in the Exposed class to the Infected class	[0,1]	[13]
ψ	Average time to development of COVID-19 symptoms	$\frac{2}{14} = 0.142$	[14]
α	The probability of an infected individual being hospitalized	[0,1]	[1]
γ	The average recovery time for COVID-19 patients to recover	$\frac{14}{42} = 0.33$	[15]

σ	Average time from hospitalization to critical and ICU admission	$\frac{1}{5} = 0.2$	[16]
θ	Probability of a COVID-19 patient becoming critical and admitted to the ICU	[0,1]	[1]
ω	The probability that a critical patient will die	[0,1]	[1]
μ	Average recovery time of patients from critical condition	$\frac{12}{18} = 0.67$	[14]
χ	Average hospitalization time	$\frac{1}{14} = 0.07$	[16]

Determining the Equilibrium Point

The equilibrium points are divided into two, namely the disease-free equilibrium point and the endemic equilibrium point. In determining the two equilibrium points, each equation in the system of equations (1) must be zero, or $\frac{dS}{dt} = 0, \frac{dE}{dt} = 0, \frac{dI}{dt} = 0, \frac{dH}{dt} = 0, \frac{dC}{dt} = 0, \frac{dR}{dt} = 0, \frac{dD}{dt} = 0$. So that the equation in (1) becomes:

$$\xi N - \frac{\eta\beta I^* S^*}{N} - \tau S^* = 0 \quad (2)$$

$$\frac{\eta\beta I^* S^*}{N} - \delta E^* - \tau E^* = 0 \quad (3)$$

$$\delta E^* - \psi\alpha I^* - \gamma I^* + \alpha\gamma I^* - \tau I^* = 0 \quad (4)$$

$$\psi\alpha I^* - \sigma\theta H^* - \chi H^* + \chi\theta H^* - \tau H^* = 0 \quad (5)$$

$$\sigma\theta H^* - \varphi\omega C^* - \mu C^* + \mu\omega C^* - \tau C^* = 0 \quad (6)$$

$$\gamma I^* - \alpha\gamma I^* + \mu C^* - \mu\omega C^* + \chi H^* - \chi\theta H^* - \tau R^* = 0 \quad (7)$$

$$\varphi\omega C^* = 0 \quad (8)$$

Furthermore, equations $(5) - (8)$ are not included in the system (11) because equations $(2) - (4)$ do not depend explicitly on H^*, C^*, R^*, and D^*. Where H^* can be found by entering the obtained function $I(t)$ into equation (5), then C^* can be found by entering the obtained function $H(t)$ into equation (6), then R^* and D^* is not explicitly stated in the equation. The following is a system (9) for which we will find the disease-free equilibrium point and the endemic equilibrium point:

$$\begin{aligned} &\xi N - \frac{\eta\beta I^* S^*}{N} - \tau S^* = 0 \\ &\frac{\eta\beta I^* S^*}{N} - \delta E^* - \tau E^* = 0 \\ &\delta E^* - \psi\alpha I^* - \gamma I^* + \alpha\gamma I^* - \tau I^* = 0 \end{aligned} \quad (9)$$

The disease-free equilibrium point is the point at which there is no disease in the population. So that there are no infected individuals or $I^* = 0$, then the disease-free equilibrium point is obtained as follows:

$$E_0 = (S_0, E_0, I_0) = \left(\frac{\xi N}{\tau}, 0, 0\right) \quad (10)$$

The endemic equilibrium point is a point that indicates the conditions under which there is a spread of disease in the population. So that the endemic equilibrium point is obtained as follows:

$$E^* = (S^*, E^*, I^*) = \left(\frac{\rho N}{\eta\beta\delta}, \frac{-\rho\tau N + \eta\beta\delta\xi N}{\eta\beta\delta\,(\delta+\tau)}, \frac{\rho\tau N + \eta\beta\delta\xi N}{\rho\eta\beta}\right) \quad (11)$$

with

$$\rho = \psi\alpha\delta + \psi\alpha\tau - \alpha\delta\gamma - \alpha\gamma\tau + \delta\gamma + \delta\tau + \gamma\tau + \tau^2$$

Determining the Basic Reproduction Number ($\boldsymbol{R_0}$)

Based on the equation model of the infected subsystem, the Next-Generation matrix will be obtained. The steps in determining the basic reproduction number (R_0) are as follows:

1. Take an equation containing infected subsystems, where in this model the infected subsystems are E and I.
2. Linearization of the infected subsystem at the disease-free equilibrium point using the Jacobian matrix as follows:

$$J_{(E_1)} = \begin{bmatrix} \frac{dE}{dE} & \frac{dE}{dI} \\ \frac{dI}{dE} & \frac{dI}{dI} \end{bmatrix}$$

$$= \begin{bmatrix} -(\delta+\tau) & \frac{\eta\beta S}{N} \\ \delta & -(\psi\alpha+\gamma-\alpha\gamma+\tau) \end{bmatrix}$$

$$J_{(S,E,I)} = \begin{bmatrix} \frac{dE}{dE} & \frac{dE}{dI} \\ \frac{dI}{dE} & \frac{dI}{dI} \end{bmatrix}$$

$$= \begin{bmatrix} -(\delta+\tau) & \frac{\eta\beta\xi}{\tau} \\ \delta & -(\psi\alpha+\gamma-\alpha\gamma+\tau) \end{bmatrix}$$

3. Next, the decomposition of the Jacobian matrix (J) will be carried out. after that the basic reproduction number can be searched using the Next-Generation.

$$\boldsymbol{F} = \begin{pmatrix} 0 & \frac{\eta\beta S}{N} \\ 0 & 0 \end{pmatrix} = \begin{pmatrix} 0 & \frac{\eta\beta\xi}{\tau} \\ 0 & 0 \end{pmatrix}$$

$$\boldsymbol{V} = \begin{pmatrix} (\delta+\tau) & 0 \\ -\delta & (\psi\alpha+\gamma-\alpha\gamma+\tau) \end{pmatrix}$$

Where $\boldsymbol{F}$ is a transmission matrix that describes the rate of adding cases, while $\boldsymbol{V}$ is a transition matrix that describes the rate of case reduction. So, obtained:

$$\boldsymbol{V^{-1}} = \begin{pmatrix} \frac{1}{\delta+\tau} & 0 \\ \frac{-\delta}{\alpha\gamma\delta-\gamma\delta-\tau^2+\alpha\gamma\tau-\gamma\tau-\delta\tau-\alpha\delta\psi-\alpha\tau\psi} & \frac{-1}{\alpha\gamma-\gamma-\tau-\psi\alpha} \end{pmatrix}$$

4. Next calculate R_0 where $R_0 = \rho(\boldsymbol{FV^{-1}})$, where $\rho(\boldsymbol{FV^{-1}})$ is the dominant absolute eigenvalue (spectral radius) of $\boldsymbol{K}$ (Next-Generation Matrix).
   So that the basic reproduction number (R_0) is:
   $R_0 = \rho(\boldsymbol{K})$

$$= \frac{\eta\beta\delta\xi}{\tau^3-\alpha\gamma\tau^2+\gamma\tau^2+\delta\tau^2-\alpha\gamma\delta\tau+\gamma\delta\tau+\alpha\tau^2\psi+\alpha\delta\tau\psi}$$

Let

$$\phi = \psi\alpha+\gamma-\alpha\gamma+\tau$$

Then,

$$R_0 = \frac{\eta\beta\delta\xi}{\tau\phi(\delta+\tau)}$$

Define Local Stability Analysis

The mathematical model in equation (9) is a system of nonlinear differential equations. So, in looking for stability analysis, linearization will be carried out around the equilibrium point. Here is the jacobi matrix from the results of linearization on (9):

$$J = \begin{bmatrix} \frac{\partial S}{\partial S} & \frac{\partial S}{\partial E} & \frac{\partial S}{\partial I} \\ \frac{\partial E}{\partial S} & \frac{\partial E}{\partial E} & \frac{\partial E}{\partial I} \\ \frac{\partial I}{\partial S} & \frac{\partial I}{\partial E} & \frac{\partial I}{\partial I} \end{bmatrix} =$$

$$\begin{bmatrix} -\frac{\eta\beta I}{N} - \tau & 0 & -\frac{\eta\beta S}{N} \\ \frac{\eta\beta I}{N} & -\delta - \tau & \frac{\eta\beta S}{N} \\ 0 & \delta & -\psi\alpha - \gamma + \alpha\gamma - \tau \end{bmatrix}$$

1. Local Stability Analysis of Disease-Free Equilibrium Points

Based on the disease-free equilibrium point that has been obtained, namely $E_0 = \left(\frac{\xi N}{\tau}, 0,0\right)$, then the Jacobi matrix obtained from the linearization around the disease-free equilibrium point is:

$$\boldsymbol{J(E_0)} = \begin{bmatrix} -\tau & 0 & -\frac{\eta\beta\xi N}{\tau N} \\ 0 & -\delta - \tau & \frac{\eta\beta\xi N}{\tau N} \\ 0 & \delta & -\psi\alpha - \gamma + \alpha\gamma - \tau \end{bmatrix}$$

$$= \begin{bmatrix} -\tau & 0 & -\frac{\eta\beta\xi}{\tau} \\ 0 & -\delta - \tau & \frac{\eta\beta\xi}{\tau} \\ 0 & \delta & -\psi\alpha - \gamma + \alpha\gamma - \tau \end{bmatrix}$$

Furthermore, the eigenvalues of the matrix $\boldsymbol{J(E_0)}$ are obtained through the following equation:

$$det|\boldsymbol{J(E_0)} - \boldsymbol{\lambda I}| = 0$$

$$\begin{bmatrix} -\tau - \lambda & 0 & -\frac{\eta\beta\xi}{\tau} \\ 0 & -\delta - \tau - \lambda & \frac{\eta\beta\xi}{\tau} \\ 0 & \delta & -\psi\alpha - \gamma + \alpha\gamma - \tau - \lambda \end{bmatrix} \begin{matrix} -\tau - \lambda & 0 \\ 0 & -\delta - \tau - \lambda \\ 0 & \delta \end{matrix} = 0$$

So that the characteristic equation is obtained as follows

$$a_0\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0 \qquad (12)$$

With

$a_0 = \tau$

$a_1 = 3\tau^2 - \alpha\gamma\tau + \psi\alpha\tau + \gamma\tau + \delta\tau$
$a_2 = 3\tau^3 + 2\psi\alpha\tau^2 + 2\delta\tau^2 + 2\gamma\tau^2 - 2\alpha\gamma\tau^2 + \psi\alpha\delta\tau + \gamma\delta\tau - \alpha\gamma\delta\tau - \eta\beta\xi\delta$
$a_3 = \tau^4 - \alpha\gamma\tau^3 + \gamma\tau^3 + \delta\tau^3 + \gamma\delta\tau^2 - \eta\beta\xi\delta\tau + \psi\alpha\tau^3 + \psi\alpha\delta\tau^2 - \alpha\gamma\delta\tau^2$

Because the values of the roots in the characteristic equation (12) are difficult to obtain, using the Routh-Hurwitz criteria will determine the stability of the E_0 equilibrium point. So based on these criteria, the equilibrium point E_0 will be asymptotically stable if and only if it fulfills the following conditions:

a. $a_0 > 0$
b. $a_1 > 0$
c. $a_1 \cdot a_2 - a_0 \cdot a_3 > 0$
d. $a_3 > 0$

Then using the parameters in Table 2 is obtained

1) $a_0 = 0.00625 > 0$,
2) $a_1 = 0.0019384375 > 0$,
3) $a_1 \cdot a_2 - a_0 \cdot a_3 = 0{,}000000164269103 > 0$,
4) $a_3 = 0.000005809108887 > 0$

With

$$a_2 = 0.0001034730469$$

Based on the above calculations, it is found that conditions 1-4 are met and all eigenvalues in the characteristic equation for the disease-free equilibrium point are negative, which means that the disease-free equilibrium point in the locally asymptotically stable SEIHCRD model.

2. Local Stability Analysis of Endemic Equilibrium Points

Based on the disease-free equilibrium point that has been obtained, namely $E^* = \left(\frac{\rho N}{\eta\beta\delta}, \frac{-\rho\tau N + \eta\beta\delta\xi N}{(\delta+\tau)}, \frac{\rho\tau N + \eta\beta\delta\xi N}{\rho\eta\beta}\right)$, then the Jacobi matrix obtained from the results The linearization around the disease-free equilibrium point is:

$$\boldsymbol{J}(\boldsymbol{E_1}) = \begin{bmatrix} -\frac{\eta\beta(\rho\tau N + \eta\beta\delta\xi N)}{\rho\eta\beta N} - \tau & 0 & -\frac{\eta\beta\rho N}{\eta\beta\delta N} \\ \frac{\eta\beta(\rho\tau N + \eta\beta\delta\xi N)}{\rho\eta\beta N} & -\delta - \tau & \frac{\eta\beta\rho N}{\eta\beta\delta N} \\ 0 & \delta & -\psi\alpha - \gamma + \alpha\gamma - \tau \end{bmatrix}$$

$$= \begin{bmatrix} \frac{-2\rho\tau - \eta\beta\delta\xi}{\rho} & 0 & -\frac{\rho}{\delta} \\ \frac{\rho\tau + \eta\beta\delta\xi}{\rho} & -\delta - \tau & \frac{\rho}{\delta} \\ 0 & \delta & -\psi\alpha - \gamma + \alpha\gamma - \tau \end{bmatrix}$$

with

$\rho = \psi\alpha\delta + \psi\alpha\tau - \alpha\delta\gamma - \alpha\gamma\tau + \delta\gamma + \delta\tau + \gamma\tau + \tau^2$

Furthermore, the eigenvalues of the matrix $\boldsymbol{J}(\boldsymbol{E_1})$ are obtained through the following equation:

$$det|\boldsymbol{J}(\boldsymbol{E_1}) - \boldsymbol{\lambda I}| = 0$$

$$det\begin{bmatrix} \frac{-2\rho\tau-\eta\beta\delta\xi-\lambda\rho}{\rho} & 0 & -\frac{\rho}{\delta} \\ \frac{\rho\tau+\eta\beta\delta\xi}{\rho} & -\delta-\tau-\lambda & \frac{\rho}{\delta} \\ 0 & \delta & -\psi\alpha-\gamma+\alpha\gamma-\tau-\lambda \end{bmatrix} = 0$$

$$\begin{bmatrix} \frac{-2\rho\tau-\eta\beta\delta\xi-\lambda\rho}{\rho} & 0 & -\frac{\rho}{\delta} \\ \frac{\rho\tau+\eta\beta\delta\xi}{\rho} & -\delta-\tau-\lambda & \frac{\rho}{\delta} \\ 0 & \delta & -\psi\alpha-\gamma+\alpha\gamma-\tau-\lambda \end{bmatrix} \begin{matrix} \frac{-2\rho\tau-\eta\beta\delta\xi-\lambda\rho}{\rho} & 0 \\ \frac{\rho\tau+\eta\beta\delta\xi}{\rho} & -\delta-\tau-\lambda \\ 0 & \delta \end{matrix} = 0$$

So that the characteristic equation is obtained as follows

$$a_0\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0 \qquad (13)$$

with

$a_0 = \rho$

$a_1 = 4\rho\tau + \beta\delta\eta\xi - \alpha\gamma\rho + \gamma\rho - \delta\rho - \alpha\rho\psi$

$a_2 = 3\gamma\rho\tau + 3\delta\rho\tau - \rho^2 + 3\alpha\rho\tau\psi - 3\alpha\gamma\rho\tau - \alpha\gamma\delta\rho + \gamma\delta\rho + \beta\delta^2\eta\xi + \beta\gamma\delta\eta\xi + 2\beta\delta\eta\xi\tau - \alpha\beta\gamma\delta\eta\xi + \alpha\beta\delta\eta\xi\psi + \alpha\delta\rho\psi + 5\rho\tau^2$

$a_3 = \beta\gamma\delta^2\eta\xi - \alpha\beta\gamma\delta^2\eta\xi + 2\rho\tau^3 + \beta\delta\eta\xi\tau^2 - 2\alpha\gamma\rho\tau^2 + 2\gamma\rho\tau^2 + 2\delta\rho\tau^2 + \beta\delta^2\eta\xi\tau - \alpha\beta\gamma\delta\eta\xi\tau + \beta\gamma\delta\eta\xi\tau - \rho^2\tau - 2\alpha\gamma\delta\rho\tau + 2\gamma\delta\rho\tau + \alpha\beta\delta^2\eta\xi\psi + 2\alpha\rho\tau^2\psi + \alpha\beta\delta\eta\xi\tau\psi + 2\alpha\delta\rho\tau\psi$

Because the value of the roots of the characteristic equation (13) is difficult to obtain, then by using the Routh-Hurwitz criterion, the stability properties of the equilibrium point E^* will be known. So based on these criteria, the equilibrium point E^* will be asymptotically stable if and only if the following conditions are met:

a. $a_0 > 0$
b. $a_1 > 0$
c. $a_1 \cdot a_2 - a_0 \cdot a_3 > 0$
d. $a_3 > 0$

So, by using the parameters in Table 2, we get

a. $a_0 = 0.0230563125 > 0$,
b. $a_1 = -0.005328843338 < 0$,
c. $a_1 \cdot a_2 - a_0 \cdot a_3 = -0{,}0000005639381147 < 0$,
d. $a_3 = 0.000004532916074 > 0$

with

$$a_2 = 0.00008621491684$$

Based on the above calculations, it was found that conditions 2 and 3 were not fulfilled so that there were eigenvalues in the characteristic equation of the endemic equilibrium point with a positive value, which means that the endemic equilibrium point in the SEIHCRD model was unstable.

Define Global Stability Analysis

Based on the system (9) that S, E and I do not depend on H,C,R and D. hence dynamic analysis using S,E and I

$$\xi N - \frac{\eta\beta I^* S^*}{N} - \tau S^* = 0$$
$$\frac{\eta\beta I^* S^*}{N} - \delta E^* - \tau E^* = 0$$
$$\delta E^* - \psi\alpha I^* - \gamma I^* + \alpha\gamma I^* - \tau I^* = 0$$

Let

$$\phi = \psi\alpha + \gamma - \alpha\gamma + \tau$$

Then, the equilibrium points are:

$$E^0 = \left(\frac{\xi N}{\tau}, 0, 0\right)$$
$$E^* = \left(\frac{\rho N}{\eta\beta\delta}, \frac{\eta\beta\delta\xi N - \rho\tau N}{\eta\beta\delta(\delta+\tau)}, \frac{\eta\beta\delta\xi N + \rho\tau N}{\eta\beta\rho}\right)$$

And the Basic Reproduction Number (R_0) is:

$$R_0 = \frac{\eta\beta\delta\xi}{\tau\phi(\delta+\tau)}.$$

1. Theorem 1

Disease-free equilibrium points E^0 from a global asymptotic stable model if $R_0 \leq 1$ and unstable if $R_0 > 1$.

Proof:

Define the Lyapunov Function

$$\mathcal{L} = \left(S - S^0 - S^0 \ln\left(\frac{S}{S^0}\right)\right) + E + I$$

So that the derivative of the Lyapunov Function against time is as follows

$$\begin{aligned}
\frac{d\mathcal{L}}{dt} &= \left(1 - \frac{S^0}{S}\right)\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} \\
&= \frac{1}{S}(S - S^0)\left(\xi N - \frac{\eta\beta SI}{N} - \tau S\right) + \left(\frac{\eta\beta SI}{N} - (\delta+\tau)E\right) + (\delta E - \phi I) \\
&= \frac{1}{S}(S - S^0)(\xi N - \tau S) + \left(\frac{\eta\beta S^0 I}{N} - (\delta+\tau)E\right) + (\delta E - \phi I) \\
&= -\frac{\tau}{S}(S - S^0)^2 + \left(\frac{\eta\beta S^0}{N} - \phi\right) I - \tau E \\
&= -\frac{\tau}{S}(S - S^0)^2 - \tau\phi\left(1 - \frac{R_0}{\delta/(\delta+\tau)}\right) I - \tau E
\end{aligned}$$

If $R_0 \leq 1$ so $\mathcal{L}' < 0$ for each $(S, E, I) \neq (S^0, 0, 0)$. The singularity proved that $\{E^0\}$ is a set that satisfies the nature $\mathcal{L}' = 0$. Based on the principle of Invariant Lasalle equilibrium point E^0 globally asymptotic stable.

2. Theorem 2

Endemic equilibrium points E^* from a global asymptotic stable model if $R_0 > 1$.

Proof:

Define quadratic Lyapunov Function

$$\mathcal{V} = \frac{1}{2}[(S - S^*) + (E - E^*) + (I - I^*)]^2$$

So that the derivative of the Lyapunov Function against time is as follows

$$\frac{d\mathcal{V}}{dt} = [(S - S^*) + (E - E^*) + (I - I^*)]\frac{d(S + E + I)}{dt}$$
$$= [(S - S^*) + (E - E^*) + (I - I^*)](\xi N - \tau S - \tau E - \phi I)$$

Assume $\xi N = \tau S^* + \tau E^* - \phi I^*$ so that it is obtained

$$\frac{d\mathcal{V}}{dt} = [(S - S^*) + (E - E^*) + (I - I^*)][-\tau(S - S^*) - \tau(E - E^*) - \phi(I - I^*)]$$
$$= -\tau(S - S^*)^2 - \tau(E - E^*)^2 - \phi(I - I^*)^2 - \tau(S - S^*)[(E - E^*) + (I - I^*)]$$
$$-\tau(E - E^*)[(S - S^*) + (I - I^*)] - \phi(I - I^*)[(S - S^*) + (E - E^*)]$$

$\frac{d\mathcal{V}}{dt}$ negatively valued and $\frac{d\mathcal{V}}{dt} = 0$ if and only if $S = S^*, E = E^*$ and $I = I^*$. A set of solutions that do not contain any other solutions except E^* then for each solution towards the equilibrium point E^* when $t \longrightarrow \infty$. Based on the principle of Invariant Lasalle equilibrium point E^* global asymptotic stability.

Numerical Simulation Using the Fourth Order Runge-Kutta Method

Based on the fourth order runge-kutta formula, we get:

$$S_{i+1} = S_i + \frac{h}{6}(k_1 + 2k_2 + 2k_3 + k_4) \quad (14)$$

$$E_{i+1} = E_i + \frac{h}{6}(l_1 + 2l_2 + 2l_3 + l_4) \quad (15)$$

$$I_{i+1} = I_i + \frac{h}{6}(m_1 + 2m_2 + 2m_3 + m_4) \quad (16)$$

$$H_{i+1} = H_i + \frac{h}{6}(n_1 + 2n_2 + 2n_3 + n_4) \quad (17)$$

$$C_{i+1} = C_i + \frac{h}{6}(o_1 + 2o_2 + 2o_3 + o_4) \quad (18)$$

$$R_{i+1} = R_i + \frac{h}{6}(p_1 + 2p_2 + 2p_3 + p_4) \quad (19)$$

$$D_{i+1} = D_i + \frac{h}{6}(q_1 + 2q_2 + 2q_3 + q_4) \quad (20)$$

With the following set values

Table 3. SEIHCRD Model 1 and 2 Assignment Values

	1	2
k	951.1531962433364	951.1265181791969
l	−7.074192404409184	−7.072064874567189
m	−10.15790677056216	−10.15485173523335
n	−27.86872445688786	−27.86042234608118
o	−3.953709363652501	−3.952533386118616
p	−848.5151443955157	−848.5036030018114
q	4.009256058479258	4.008057590328402

Table 4. SEIHCRD Model 3 and 4 Assignment Values

	3	4
k	951.1265180970076	951.0998399513774
l	−7.072065514335547	−7.069938623983692
m	−10.15485265409406	−10.15179853707305
n	−27.86042479973261	−27.85212514114853
o	−3.952533732663641	−3.951358101474093
p	−848.5035989022803	−848.4920534119367
q	4.008057946796592	4.006859834903832

So that the value in the first iteration is obtained as follows:
$S = 272008906, E = 71788, I = 30738, H = 70568, C = 7926, R = 39446, D = 1604.$

NUMERICAL EXPERIMENT

Comparison of Graphs of Solutions I, H and C with Graphs of Original Data

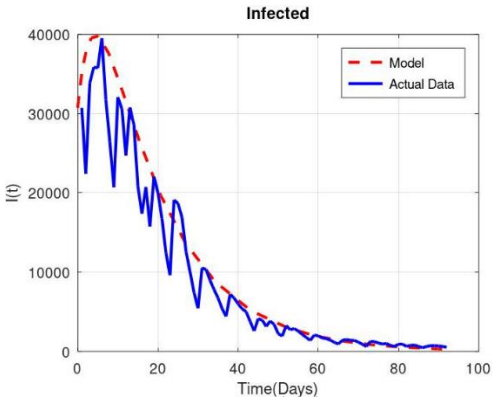

Figure 2. Infected Graphics on Model and Original Data

In Figure 2, we can see that there are 2 graphs of infection cases in the spread of COVID-19 in Indonesia. Where the graph with the blue line is a graph of the original data, while the graph with the dotted line in red is the result of a model simulation. Based on the results of the 2 graphs, it can be concluded that by using the parameters $\beta = 0.06, \delta = 0.14, \alpha = 0.95, \omega = 0.485,$ and $\theta = 0.25$, the SEIHCRD model can capture the peak of infection cases that occur in Indonesia even though an absolute error is obtained. by 28%. Where in the model, the peak of infection cases occurred earlier, namely on the 5th day, while in the original data it occurred on the 7th day. This is of course a good result, where the model can predict earlier when the peak of COVID-19 infection will occur. So that the government and all people in Indonesia can make earlier and more mature preparations

to deal with the peak of infection cases. Then based on the parameters used, cases of COVID-19 infection in Indonesia can decrease and subside over time, if the contact rate of susceptible individuals with infected individuals (β) is low, the rate of transfer of individuals in the Exposed class to the Infected class (δ) is low, the individual probability hospitalization (α) is high, the probability of a COVID-19 patient becoming critical and admitted to the Intensive Care Unit (ICU) (θ) is low, and the probability of a critical patient dying (ω) is low.

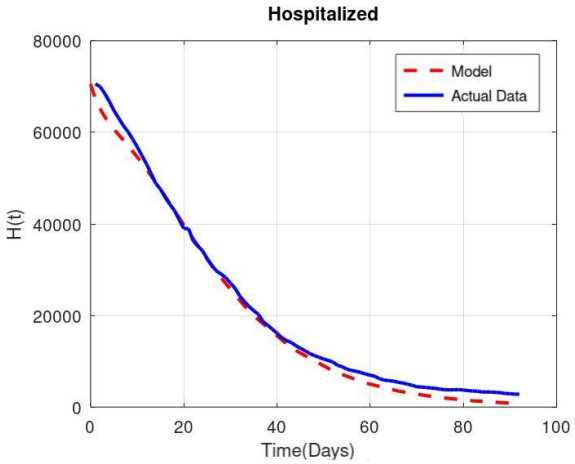

Figure 3. Hospitalized Graph on Model and Original Data

Next, in Figure 3, there are 2 graphs of hospitalization cases in the spread of COVID-19 in Indonesia. Where the graph with the blue line is a graph of the original data, while the graph with the dotted line in red is the result of a model simulation. Based on these 2 graphs, it can be seen that the graph of the model can approach the graph of the original data with an absolute error of 20% if $\beta = 0.06, \delta = 0.14, \alpha = 0.95, \omega = 0.485,$ and $\theta = 0.25$. This means that the number of hospitalized cases due to COVID-19 in Indonesia can be reduced and subsided, if the contact rate of susceptible individuals with infected individuals (β) is low, the rate of transfer of individuals in the Exposed class to the Infected class (δ) is low, the probability of infected individuals being hospitalized (α) is high, the probability of a COVID-19 patient becoming critical and admitted to the Intensive Care Unit (ICU) (θ) is low, and the probability of a critical patient dying (ω) is low. So, it can be concluded that the SEIHCRD model can capture the sloping trend of Hospitalized cases in Indonesia, where the peak of cases that occur in the model are the same as those that occurred in the original data, namely on the first day, with the number of cases being very close around the 10th day to the 30th day.

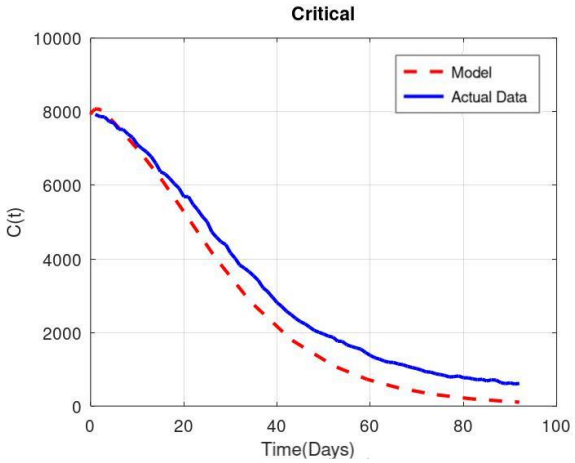

Figure 4. Critical Graph on Model and Original Data

Furthermore, in Figure 4 there are 2 graphs of critical cases in the spread of COVID-19 in Indonesia. Where the graph with the blue line is the original case data, while the graph with the red dotted line is the simulation result of the model. Based on the results of the 2 graphs, the graph of the model can approach the original data graph with an absolute error of 33%, if $\beta = 0.06$, $\delta = 0.14$, $\alpha = 0.95$, $\omega = 0.485$, and $\theta = 0.25$. That is, the number of critical cases can be reduced and further subsided if the contact rate of susceptible individuals with infected individuals (β) low, the rate of transfer of individuals in the Exposed class to the Infected class (δ) is low, the probability of an infected individual being hospitalized (α) is high, the probability of a patient being hospitalized is high. COVID-19 becomes critical and admission to the Intensive Care Unit (ICU) (θ) is low, and the probability of critical patients dying (ω) is low. So, it can be concluded that the SEIHCRD model can capture the sloping trend of Critical cases in Indonesia, where the peak cases that occur in the model are the same as those that occurred in the original data, namely on the first day, with the number of cases being very close in the first 20 days.

Based on the interpretation of the results in Susceptible, Exposed, and Infected cases above, COVID-19 will subside if the contact of vulnerable individuals with infected individuals is low, by implementing health protocols properly such as wearing masks, maintaining distance and doing vaccines. In addition, the existence of appropriate and fast medical treatment also affects the subsidence of COVID-19 cases.

CONCLUSIONS

Through the dynamic analysis that has been carried out on the SEIHCRD model, the result is that the number of cases will decrease with increasing time, so that the disease outbreak will end. Then, based on stability analysis at the equilibrium point, it is found that the disease-free equilibrium point is locally asymptotically stable, and the endemic equilibrium point is unstable. Furthermore, based on the results of numerical simulations using the Fourth Order Runge-Kutta method, the value obtained in the first iteration is $\beta = 0.06, \delta = 0.14, \alpha = 0.95, \omega = 0.485, \theta = 0.25$, namely $S = 272008906, E = 71788, I = 30738, H = 70568, C = 7926, R = 3.9446, D = 1.604$.

Then based on the solution graph obtained from the SEIHCRD model, it can be seen that by using $\beta = 0.06, \delta = 0.14, \alpha = 0.95, \omega = 0.485, \theta = 0.25$ and other parameters according to Table 2, the solution graph in cases of Infected, Hospitalized, and Critical can catch the sloping trend from the original data in Indonesia. Where the number of cases

will decrease and subside over time, if the following conditions are met: the rate of contact of susceptible individuals with infected individuals (β) is low, the rate of movement of individuals in the Exposed class to the Infected class (δ) is low, the probability of infected individuals being treated hospitalization (α) is high, the probability of a COVID-19 patient becoming critical and admitted to the Intensive Care Unit (ICU) (θ) is low and the probability of a critical patient dying (ω) is low. Then, the SEIHCRD model can describe the results of the solution graph in the exposed case well. Where the number of people exposed to it will also decrease along with the reduction in existing infection cases. While the solution graphs in the Susceptible, Recovered, and Dead cases cannot be described properly through the SEIHCRD model.

So based on the dynamic analysis that has been carried out, COVID-19 will subside if the contact of vulnerable individuals with infected individuals is low, by implementing health protocols properly such as wearing masks, maintaining distance, and doing vaccines. In addition, the existence of appropriate and fast medical treatment also affects the easing of covid-19 cases.

REFERENCES

[1] Singh A., Bajpai M K, "SEIHCRD Model For COVID-19 Spread Scenarios, Disease Predictions And Estimates The Basic Reproduction Number, Case Fatality Rate, Hospital, And ICU Beds Requirement", CMES - Computer Modeling in Engineering and Sciences, *125*(3), 991–1031, 2020. DOI: 10.32604/cmes.2020.012503, 2020

[2] Rangkuti Y M., Sinaga M S., Marpaung F, "A VSEIR Model for Transmission of Tuberculosis (TB) Disease in North Sumatera, Indonesia", AIP Conference Proceedings, 1635, 201, 2014. DOI: 10.1063/1.4903548

[3] Kwuimy C A K., Nazari F., Jiao X., Rohani P., Nataraj C, "Nonlinear Dynamic Analysis of An Epidemiological Model for COVID-19 Including Public Behavior and Government Action", Nonlinear Dynamics, 101, 1545-1559, 2020. DOI: 10.1O07/s11071-020-05815-z

[4] Tantrakarnapa K., Bhopdhornangkul B, "Challenging The Spread of COVID-19 in Thailand", ONE HEALTH, 11, 100173, 2020. DOI: 10.1016/j.onehlt.2020.100173

[5] Sun J., Chen X., Zhang Z., Lai S., Zhao B., Liu H., Wang S., Huan W., Zhao R., Ng M T A., Zheng Y, "Forecasting The Long-term Trend Of COVID-19 Epidemic Using A Dynamic Model", Scientific Reports, 10, 21122, 2020. DOI: 10.1038/s41598-020-78084-w

[6] Rifanti U M., Dewi A R., Hapsari ST, "COVID-19 Mathematical Epidemic Model for Impact Analysis of Large Scale Social Restriction: The Case Study of Indonesia", IOP Conference Series: Materials Science and Engineering, 115 012066, 2021. DOI: 10.1088/1757-899X/1115/1/012066

[7] Sinaga L P., Nasution H., Kartika D, "Stability Analysis of The Corona Virus (COVID-19) Dynamics SEIR Model in Indonesia", Journal of Physics: Conference Series, 2021. DOI: 10.1088/1742-6596/1819/1/012043

[8] Burmeister C., Kreinin A., Mendoza-Arriaga R., Rasouli H., Romanko O, "Analysis of Impact of Covid-19 Pandemic on Financial Markets", Infosys Science Foundation Series, 329-355, 2021. DOI: 10.1007/978-981-16-2450-6_1

[9] Kumar S., Xu C., Ghildayal N., Chandra C., Yang M, "Social Media Effectiveness As A Humanitarian Response to Mitigate Influenza Epidemic and COVID-19 Pandemic", Annals of Operations Research, 319(1), 823-851, 2022. DOI: 10.1007/s10479-021-03955-y

[10] Rakshit P., Kumar S., Noeiaghdam S., Fernandez-Gamiz U., Altanji M., Santra S S, "Modified SIR Model for COVID-19 Transmission Dynamics: Simulation with Case Study of UK, US and India", Results In Physics, 40, 105855, 2022. DOI: 10.1016/j.rinp.2022.105855

[11] Qur'ani F, "Analisis Dinamik Model Susceptible-Exposed-Infectious-Hospitalized-Critical-Recovered-Dead (SEIHCRD) Pada Penyebaran Covid-19, Etheses UIN MALANG, 2022. URL: http://etheses.uin-malang.ac.id/37095/1/18610060.pdf

[12] Ramadhani A, "Model Epidemi Susceptible-Exposed-Infected-Recovered (Seir) Menggunakan Metode Runge-Kutta Orde Empat Pada Penyebaran Covid-19 Di Indonesia", Etheses UIN MALANG, 2021. URL: http://etheses.uin-malang.ac.id/32520/1/17610098.pdf

[13] Rifanti U M., Dewi A. R., Nurlaili N., Hapsari S T, "Model Matematika COVID-19 dengan Sumber Daya Pengobatan yang Terbatas", Limits: Journal of Mathematics and Its Applications, 18(1), 23, 2021. DOI: 10.12962/limits.v18i1.8207

[14] Fadli R, "Butuh Berapa Lama Waktu Penyembuhan Corona", Halodoc, https://www.halodoc.com/artikel/butuh-berapa-lama-waktu-penyembuhan-corona (accessed Aug. 21, 2022)

[15] Manafe D, "Lama Pasien Covid-19 Dirawat Rata-rata Dua Minggu", Beritasatu.Com, https://www.beritasatu.com/nasional/651499/lama-pasien-covid19-dirawat-ratarata-dua-minggu (accessed Aug. 21, 2022)

[16] KEMENKES, "Data Ketersediaan Tempat Tidur RS COVID-19", https://www.kemkes.go.id/article/view/22040400001/Data-Ketersediaan-Tempat-Tidur-RS-COVID-19.html (accessed April. 11, 2022)

[17] KEMENKES, "Peta Sebaran COVID-19", https://covid19.go.id/peta-sebaran (accessed April. 11, 2022)

[18] Sofiah, "Analisa Penentuan Harga Gain Untuk Kestabilan Pada Sistem Pengendali Dengan Metode Routh-Hurwitz", Universitas Muhammadiyah Palembang, 3(2), 530–542, 2013.
URL: https://jurnal.um-palembang.ac.id/berkalateknik/article/view/358

[19] Mbogo R W., Orwa T O, "SARS-COV-2 outbreak and control in Kenya - Mathematical model analysis", Infectious Disease Modelling, 6, 370–380, 2021. DOI: 10.1016/j.idm.2021.01.009

[20] Vargas-De-León C, "On the global stability of SIS, SIR and SIRS epidemic models with standard incidence", Chaos, Solitons and Fractals, 44(12), 1106–1110, 2011. DOI:10.1016/j.chaos.2011.09.002