UNP JOURNAL MANAGEMENT CENTER

math.ppj.unp.ac.id
p-ISSN 2716-0726
e–ISSN 2716-0734

Indexed

Seaqir Covid -19 Mathematical Model

Fira Adila[1], Arnellis[2]

[1,2] Mathematics Study Program, Mathematics Department, Faculty of Mathematics and Natural Sciences, Universitas Negeri Padang,
Jl.Prof.Dr. Hamka, Air Tawar Barat, North Padang, Padang, 25171 Padang, West Sumatra

Rangkiang Mathematics Journal
Volume 2, No. 2, 2023

Subject Areas:
Mathematical Model, SEAQIR Model, Covid-19

Keywords:
Mathematical Model, SEAQIR Model, Covid-19

Author for correspondence:
Fira Adila
e-mail: fira.adilar@gmail.com

Abstract- This research discusses the mathematical model of Covid-19 disease. The model formed consists of 6 components, namely Susceptible (S), Exposed (E), Asymptotically Infected (A), Quarantined (Q), Symptomatic Infected (S), and Recovered (R). This research aims to determine the local stability analysis of the model formed. Apart from that, the R0 value of the model is also looked for. The model stability analysis was carried out in disease-free and endemic settings by showing asymptotic stability. Based on the analysis results obtained. The primary reproduction number for disease-free and endemic simulations is greater than 1. The interpretation of the COVID-19 mathematical model from the stability analysis shows that COVID-19 will still exist for a specific time and will not disappear.

1. Introduction

Coronaviruses are a group of viruses that can cause disease in animals or humans. Several types of coronavirus cause respiratory tract infections in humans, ranging from coughs and colds to more serious ones such as Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS). A new type of coronavirus was discovered that causes the disease COVID-19 (Pasaribu, 2020).

Coronavirus Disease 2019 (COVID-19), or also known as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), was first discovered in Wuhan in December 2019 (Sudarsa, 2020). Covid-19 then became a virus that shocked the world community when it became an epidemic in a short time and claimed thousands of lives in various countries. Coronaviruses can be transmitted from human to human (Resmawan, 2020).

As of February 3, 2022, 380,321,615 cases have been recorded, and 5,680,741 deaths have been confirmed. There are 227 approved countries, and one of them is Indonesia (WHO). In Indonesia, there were 4,353,370 cases, 4,140,454 people recovered, and 144,320 people died. Covid-19 then became a virus that shocked the world community when it became an

RANGKIANG MATHEMATICS JOURNAL
Journal of Mathematics and Mathematics Education

epidemic in a short time and claimed thousands of lives in various countries. Coronavirus can be transmitted from human to human (Susilo, 2020).

Patients with COVID-19 have symptoms such as fever, dry cough, and fatigue in the early stages. They can later develop acute respiratory distress (ARDS), respiratory failure, and shock, which may be fatal. The results showed that patients with mild symptoms took a week or more to recover, while severe cases gradually experienced respiratory failure that could lead to death. The high transmission level caused the WHO to declare this case a pandemic in early 2020. The transmission of COVID-19 is higher than SARS-CoV MERS-CoV (Resmawan, 2020). The high number of deaths and transmission rates of COVID-19 have caused various groups to become actively involved in contributing to finding the right solution to handling it.

Mathematical models are simple expressions of real-world problems into mathematical symbols. Mathematical models are used in many different scientific disciplines and fields of study, such as physics, biology, medicine, engineering, social and political sciences, economics, business and finance, and computer network problems (Widowati, 2007). Mathematical models can be used as one of the main tools used in epidemic planning to help solve the COVID-19 problem easier. The relationship between COVID-19 transmission and various epidemiological parameters can be identified through mathematical modeling, which can help in planning and considering appropriate control measures (Resmawan, 2020).

The measures used in control depend on the severity of the infection and the country dealing with the virus. Several Mathematical Models were formulated to investigate the dynamics of coronavirus disease worldwide by considering control measures. The discussion of COVID-19 from a mathematical modeling perspective is still being developed. Since the beginning of this case, various models have been constructed. A mathematical model that explains virus transmission by considering quarantine, lockdown, and vaccination: the system of equations presented includes ordinary SIR and SEIR models. Furthermore, the basic equation system is expanded to consider quarantine, isolation, partial and total lockdown, and vaccination (Fuso, 2020). Meanwhile, in this research, the mathematical model used is SEAQIR, with several epidemiological considerations not used in previous models.

The primary reproduction number is an essential parameter in epidemiological mathematics, which is the threshold for the spread of disease. This direct reproduction number is used as a measure to determine whether the population is endemic or not (Brauer, 2008).

Differential equations are mathematical equations that contain derivatives of one or more dependent variables relative to one or more independent variables (Simmon, 2007). Linear differential equations are differential equations that have linear forms of their derivatives (Holzner, 2008). If a system of differential equations is not included in a system of linear differential equations, then the system of equations is included in a system of non-linear differential equations (Perko, 2001)

For a scalar λ. The scalar λ is the eigenvalue of A, and x is said to be the eigenvector of A, which coincides with λ. To obtain the eigenvalues of a matrix A with size n×n, it can be rewritten together with $Ax=\lambda x$ as follows:

$(A-\lambda I)x=0$

Where I is the identity matrix and has a non-zero solution if and only if

$\det(\lambda I-A)=|A-\lambda I|=0$

Called the characteristic equation of matrix A, the scalars that satisfy this equation are the eigenvalues $A_{(n\times n)}$.
(Danang, 2010)

If all the eigenvalues of the Jacobian matrix are negative real, then the fixed points are stable. It happens only if all determinants of the Hurwitz matrix are positive, namely $\det \llbracket H_j>0 \rrbracket$, $j=1,2,3,\ldots,k$. For example, for $k=2,3,4$, the following criteria are obtained:

$k=2$ $a_1>0,\ a_2>0$

$k=3$ $a_1>0,\ a_3>0,\ a_1 a_2>a_3$
$k=4$ $a_1>0,\ a_3>0,\ a_4>0,\ a_1 a_2 a_3> \llbracket a_3 \rrbracket^2+ \llbracket a_1 \rrbracket^2 a_4$
(Rosha, 2013)

If A is a matrix of size n×n then the non-zero vector x in R^n is called an eigenvector of A if Ax is a scalar multiple of x, namely:
Ax=λx
(Anton, 2004).

2. Methods

This research began by conducting a library and literature study to build a mathematical model representing the dynamics of the spread of COVID-19. Several methods used to study the SEAQIR model are looking for disease-free and endemic equilibrium points, analyzing the stability of disease-free and endemic equilibrium points, basic reproduction numbers, and simulating the mathematical model.
The research steps carried out are as follows:

1. Identify, select, and formulate the problems to be discussed in the SEAQIR Covid-19 mathematical model
2. Collect and study theories and concepts relevant to the SEAQIR Covid-19 mathematical model problem
3. Make assumptions to determine variables and parameters, which can help form and analyze the SEAQIR Covid-19 mathematical model.
4. Form the SEAQIR Covid-19 mathematical model.
5. Analyze the SEAQIR Covid-19 mathematical model obtained by determining the equilibrium and stability of the model's fixed points.
6. Create a simulation for the fixed point SEAQIR Covid-19 mathematical model
7. Interpret the SEAQIR Covid-19 mathematical model analysis
8. Conclude.

3. Results and Discussion

(a) Establishment of the SEAQIR Covid-19 Mathematical Model Numbered Equations

For the distribution of the SEAQIR model, the total human population is denoted by$N(t)$ is divided into six classes, namely vulnerable humans$S(t)$, humans are exposed during the incubation period$E(t)$, humans are infected without clinical symptoms$A(t)$, infected humans accompanied by clinical symptoms$I(t)$, quarantined humans$Q(t)$ and humans recovering from COVID-19$R(t)$. In this research, there are several assumptions used to model Covid-19, namely:

1. The birth recruitment rate is only aimed at the population$S$, where every newborn individual will be included in the vulnerable human class.
2. The death rate consists of the natural death rate, which is aimed at all population classes, and the death rate caused by COVID-19, which is only aimed at the population$I$.
3. Transmission of COVID-19 occurs when there is contact between individuals in the population$S$with individuals in the population$E$, individuals in the population$A$, or individuals in the population$Q$.
4. A portion of the individuals in a population$E$will pass the incubation period and enter the population$A$or population$I$.
5. Quarantined individuals (Q) are individuals who come from the population$E$. In other words, the quarantine process is only applied to exposed human populations.
6. Some quarantined individuals can pass the incubation period and move into the population$I$.
7. A portion of the individuals in a population$A$, And$I$will experience recovery and move into the population$R$.
8. Individuals declared recovered from COVID-19 can return to their old age.

Based on the assumptions, the model can be described through the flow diagram in Figure 1.

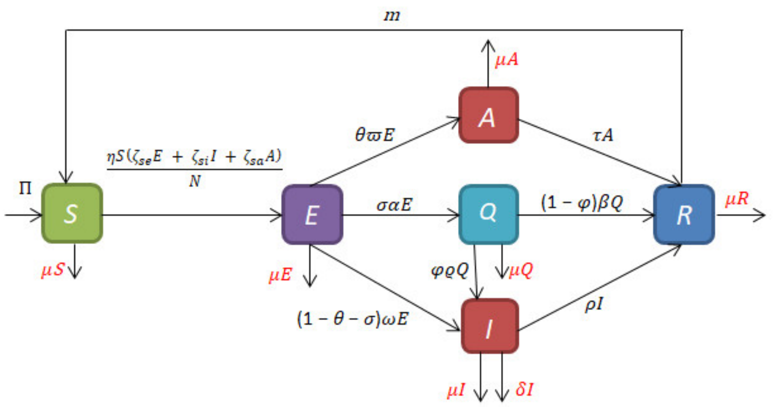

Figure 1. Compartmental Diagram of the Spread of Coronavirus Disease (COVID-19)

So that the SEAQIR Covid-19 mathematical model is obtained in the form of a system of differential equations as follows,

$$\frac{dS}{dt} = \Pi + m - \frac{\eta S(\zeta_{se}E + \zeta_{si}I + \zeta_{sa}A)}{N} - \mu S \tag{1}$$

$$\frac{dE}{dt} = \frac{\eta S(\zeta seE + \zeta siI + \zeta saA)}{N} - (\theta\varpi + \sigma\alpha + \mu + \omega - \theta\omega - \sigma\omega)$$

$$\frac{dA}{dt} = \theta\varpi E - (\tau + \mu)$$

$$\frac{dQ}{dt} = \sigma\alpha E - (\varphi\varrho + \beta - \beta\varphi + \mu)$$

$$\frac{dI}{dt} = (1 - \theta - \sigma) + \varphi\varrho Q - (\rho + \mu + \delta)$$

$$\frac{dR}{dt} = \tau A + (1 - \varphi) + \rho I - \mu R - m$$

SEAQIR COVID-19 Mathematical Model Variables

S(t): Number of people susceptible to COVID-19 at any time$t$.
E(t): The number of people exposed to COVID-19 at a time$t$.
A(t): Number of people infected with COVID-19 without clinical symptoms at any time$t$.
Q(t): Number of people exposed to COVID-19 who are quarantined at any time$t$.
I(t): Number of people infected with COVID-19 accompanied by clinical symptoms at any time$t$.
R(t): The number of people who have recovered from COVID-19 at a time$t$.

Parameters of the SEAQIR COVID-19 Mathematical Model

Π: Birth recruitment rate
η : Transmission probability when contact occurs Contact rate
ζse : susceptible individuals and exposed individuals
α : The rate of movement of exposed individuals to quarantine individuals
σ : Proportion of exposed individuals who are quarantined
ω : Transmission rate after completing the incubation period and moving to the infected class with clinical symptoms
ϖ : Transmission rate after completing the incubation period and moving to the infected class without clinical symptoms
μ : Natural death rate
ζsi : Contact rate of susceptible individuals with infected individuals with clinical symptoms
ρ : Recovery rate of infected individuals accompanied by clinical symptoms and moving to class R
φ : Proportion of quarantined individuals who are infected with clinical symptoms
ϱ : The rate of movement of quarantined individuals to infected individuals with clinical symptoms

β : Recovery rate of individuals who were quarantined and moved to class R
θ : The proportion of infected individuals without clinical symptoms
ζsa : Contact rate of susceptible individuals with infected individuals without clinical symptoms
τ : Recovery rate of infected individuals without clinical symptoms and moving to class R
δ : Death rate caused by COVID-19 in the class of infected individuals with clinical symptoms

(b) SEAQIR COVID-19 Mathematical Model Analysis

1. Equilibrium Point

The equilibrium point of equation (1) can be determined by satisfying the condition when. The system of equations (1) has two equilibrium points: the disease-free equilibrium point and the endemic equilibrium point. The disease-free equilibrium point can be obtained by assuming that it means there is no spread of infectious diseases in the population. Based on system (1), a disease-free equilibrium point is obtained. To find out the endemic equilibrium point of a condition, for example $(\left(\frac{dS}{dt},\frac{dE}{dt},\frac{dA}{dt},\frac{dQ}{dt},\frac{dI}{dt},\frac{dR}{dt}\right) = (0,0,0,0,0,0)T_0T_1E = 0I = 0T_0 = (S,E,A,Q,I,R) = (\frac{\Pi+m}{\mu}, 0,0,0,0,0)T_1S*, E*, A*, Q*, I*, R*)$, then it is assumed that $S*, E*, A*, Q*, I*, R* \neq 0$, so it is obtained $T1 = (S*, E*, A*, Q*, I*, R*)$

For example,$=S*, E=E*, A=A*, Q=Q*, I=I*, R=R*$,

$$S^* = \frac{\Pi}{\kappa_1 + \kappa_2 E^* + \mu} \qquad Q^* = \frac{\sigma\alpha E^*}{\varphi\varrho + \beta - \beta\varphi + \mu}$$

$$E^* = -\frac{\kappa_1}{\kappa_2 S^* - (\theta\varpi + \sigma\alpha + \mu + \omega - \theta\omega - \sigma\omega)} \qquad I^* = \frac{(1-\theta-\sigma)\omega E^* + \varphi\varrho Q^*}{\rho + \mu + \delta}$$

$$A^* = \frac{\theta\varpi E^*}{(\tau + \mu)} \qquad R^* = \frac{\tau A^* + (1-\varphi)\beta Q^* + \rho I^*}{\mu}$$

Where

$$\kappa_1 = \frac{\eta(\zeta_{si} I^* + \zeta_{sa} A^*)}{S^* + E^* + A^* + Q^* + I^* + R^*}$$

$$\kappa_2 = \frac{\eta\zeta_{se}}{S^* + E^* + A^* + Q^* + I^* + R^*}$$

2. Equilibrium Point Stability

Finding the stability of the equilibrium point can be determined by determining the eigenvalues of a Jacobi matrix from equation (1) so that the Jacobi matrix is obtained as follows:

$$J = \mathrm{J} = \begin{bmatrix} J_{11} & J_{12} & J_{13} & 0 & J_{15} & 0 \\ J_{21} & J_{22} & J_{23} & 0 & J_{25} & 0 \\ 0 & J_{32} & J_{33} & 0 & 0 & 0 \\ 0 & J_{42} & 0 & J_{44} & 0 & 0 \\ 0 & J_{52} & 0 & J_{54} & J_{55} & 0 \\ 0 & 0 & J_{63} & J_{64} & J_{65} & J_{66} \end{bmatrix} \tag{2}$$

a) Stability of the Disease-Free Equilibrium Point

Jacobi matrix of disease-free equilibrium point $T_0 = (\frac{\Pi+m}{\mu}, 0,0,0,0,0)$

To determine stability, look for the eigenvalues of the matrix by choosing where the eigenvalue is and the identity matrix. $T_0 J(T_0) \det(\lambda I - JT_0) = 0\lambda I$

The eigenvalue obtained is negative, so the disease-free equilibrium point is asymptotically stable. $\lambda_{1,2,3,4,5,6} T_0$

b) Stability of Endemic Equilibrium Points

The Jacobi matrix of the endemic equilibrium point is as follows: $T_1 = (S^*, E^*, A*, Q*, I^*, R^*)$

$$J = \begin{array}{l} J_{11} = \frac{\eta(\zeta_{se}E + \zeta_{si}I + \zeta_{sa}A)}{N} - \mu \quad J_{12} = \frac{\eta\zeta_{se}S}{N} \quad J_{13} = \frac{\eta\zeta_{sa}S}{N} \quad J_{15} = \frac{\eta\zeta_{si}S}{N} \\ J_{21} = \frac{\eta(\zeta_{se}E + \zeta_{si}I + \zeta_{sa}A)}{N} \quad J_{22} = \frac{\eta\zeta_{se}S}{N} - (\theta\varpi + \sigma\alpha + \mu + \omega - \theta\omega - \sigma\omega) \\ J_{23} = \frac{\eta\zeta_{sa}S}{N} \quad J_{25} = \frac{\eta\zeta_{si}S}{N} \quad J_{32} = \theta\varpi \quad J_{33} = -(\tau + \mu) \quad J_{42} = \sigma\alpha \\ J_{44} = -(\varphi\varrho + \beta - \beta\varphi + \mu) \quad J_{52} = (1 - \theta - \sigma)\omega \quad J_{54} = \varphi\varrho \\ J_{55} = -(\rho + \mu + \delta) \quad J_{63} = \tau \quad J_{64} = (1 - \varphi)\beta \quad J_{65} = \rho \quad J_{66} = -\mu \end{array}$$

To determine stability, look for the eigenvalues of the matrix by deciding where the eigenvalue is and the identity matrix. $T_1J(T_1)\det(\lambda I - JT_1) = 0\lambda I$
From the previous characteristic equation, six eigenvalues are obtained, 2 of which can be confirmed to be negative, namely
$\lambda1 = J11 = -\mu < 0$
$\lambda3 = J66 = -\mu < 0$
while the other four eigenvalues are obtained from fourth-order polynomial equations, viz
$A0\lambda4+A1\lambda3+A2\lambda2+A3\lambda+A4 = 0$
with
$A0 = 1$
$A1 = (\tau+\mu) + (\varphi\varrho+\beta-\beta\varphi+\mu) + (\rho+\mu+\delta) - (R1 - 1)$
$A2 = (\tau+\mu)(\varphi\varrho+\beta-\beta\varphi+\mu+\rho+\mu+\delta) + (\rho+\mu+\delta)(\varphi\varrho+\beta-\beta\varphi+\mu) - \eta\zeta sa\theta\varpi - (1 - \theta - \sigma) 2\omega2 - (\tau+\mu+\varphi\varrho+\beta-\beta\varphi+\mu+\rho+\mu+\delta)(R1 - 1)$
$A3 = (\tau+\mu)(\rho+\mu+\delta)(\varphi\varrho+\beta-\beta\varphi+\mu) - (R1 - 1)((\tau+\mu)(\mu+\beta-\beta\varphi+\varphi\varrho+\rho+\mu+\delta) + (\rho+\mu+\delta)(\mu+\beta-\beta\varphi+\varphi\varrho)) - (R2 - 1)$
$A4 = -(R1 - 1)(\rho+\mu+\delta)(\tau+\mu)(\varphi\varrho+\beta-\beta\varphi+\mu) - (R2 - 1)$
System stability is identified using the Ruth-Hurwitz criterion. The Ruth-Hurwitz criterion can be applied if the polynomial coefficient in the equation is positive.

System stability is identified using the Ruth-Hurwitz criterion. The Ruth-Hurwitz criterion can be applied if the polynomial coefficient in the equation is positive.

If $R0 > 1$, then $Ai < 0, = 1,2,3,4$, so the system is unstable. If $R0 < 1$, then $Ai > 0, = 0,1,2,3,4$. Next, the Ruth-Hurwitz criterion for fourth-order polynomials, viz $Ai > 0, = 0,1,2,3, A1A2 > A3$, and $A1A2A3 > A1A4 + A32$ can be shown using the coefficients of the equation. Thus, the disease-free equilibrium point ($E0$) of the system of equations (1) is locally asymptotically stable at time$R0 < 1$ and unstable at times$R0 > 1$.

Basic Reproduction Number

The primary reproduction number is denoted as determined to determine changes in the spread of disease. It is the average number of secondarily infected individuals from directly infected individuals who fall into the susceptible subpopulation. This can be determined using the Next Generation Matrix method. So, the primary reproduction number obtained from the SEAQIR Covid-19 mathematical model is $R_0R_0R_0$
Dalam bentuk sederhana, $R0$ dapat dinyatakan sebagai:

$$R0 = R1 + R2 \tag{3}$$

Dengan

$$R1 = (\eta\zeta se(\tau + \mu) + \eta\zeta sa\theta\varpi)/((\tau + \mu)(\mu + \omega + \theta\varpi + \alpha\sigma - \theta\omega - \sigma\omega))$$

$$R2 = \frac{\eta\zeta si\varphi\varrho\alpha\sigma + \eta\zeta si(\omega - \sigma\omega - \theta\omega)(\mu + \beta - \beta\varphi + \varphi\varrho)}{(\mu + \delta + \rho)(\mu + \beta - \beta\varphi + \varphi\varrho)(\mu + \omega + \theta\varpi + \alpha\sigma - \theta\omega - \sigma\omega)}$$

(c) Mathematical Model Simulation SEAQIR COVID-19

1. Disease-Free Equilibrium Point Simulation

The equilibrium point simulation can be determined by providing initial values and several parameter values in Table 1 $T_0 = (S, E, A, Q, I, R)$

Table 1. Parameter Values

Parameter	Mark
Π	3,947,567
μ	3.57×10-5
η	0.2
ζse	0.09
ζsa	0.07
ζsi	0.05
θ	0.12
σ	0.04
α	0.13266
ω	0.005
$\bar{\omega}$	0.00048
ϱ	0.1259
φ	0.05
τ	0.854302
β	0.11624
ρ	0.33029
δ	1.78×10-5
m	0.05

From the parameter values above, a value will be calculated $R0$ is obtained as Table 1
$R0 = 0.03288765794$
Obtained $R0 > 1$.
The interpretation of the COVID-19 mathematical model from the stability analysis shows that COVID-19 will still exist for a specific time and will not disappear.

4. Conclusion

Based on the results and discussions that have been carried out, the following conclusions can be made:

1. The SEAQIR Covid-19 mathematical model is as follows:

$$\frac{dS}{dt} = \Pi + m - \frac{\eta S(\zeta_{se}E + \zeta_{si}I + \zeta_{sa}A)}{N} - \mu S$$

$$\frac{dE}{dt} = \frac{\eta S(\zeta seE + \zeta siI + \zeta saA)}{N} - (\theta\varpi + \sigma\alpha + \mu + \omega - \theta\omega - \sigma\omega)$$

$$\frac{dA}{dt} = \theta\varpi E - (\tau + \mu)$$

$$\frac{dQ}{dt} = \sigma\alpha E - (\varphi\varrho + \beta - \beta\varphi + \mu)$$

$$\frac{dI}{dt} = (1 - \theta - \sigma) + \varphi\varrho Q - (\rho + \mu + \delta)$$

$$\frac{dR}{dt} = \tau A + (1 - \varphi) + \rho I - \mu R - m$$

With,
S(t) : Number of people susceptible to COVID-19 at any time$t$.
E(t) : The number of people exposed to COVID-19 at a time$t$.
A(t) : Number of people infected with COVID-19 without clinical symptoms at any time$t$.
Q(t) : Number of people exposed to COVID-19 who are quarantined at any time$t$.
I(t) : Number of people infected with COVID-19 accompanied by clinical symptoms at any time$t$.
R(t) : The number of people who have recovered from COVID-19 at a time$t$.
Π : Birth recruitment rate
η : Transmission probability when contact occurs Contact rate
ζse : susceptible individuals and exposed individuals
α : The rate of movement of exposed individuals to quarantine individuals
σ : Proportion of exposed individuals who are quarantined
ω : Transmission rate after completing the incubation period and moving to the infected class

with clinical symptoms

ϖ : Transmission rate after completing the incubation period and moving to the infected class without clinical symptoms

μ : Natural death rate

ζsi : Contact rate of susceptible individuals with infected individuals with clinical symptoms

ρ : Recovery rate of infected individuals accompanied by clinical symptoms and moving to class R

φ : Proportion of quarantined individuals who are infected with clinical symptoms

ϱ : The rate of movement of quarantined individuals to infected individuals with clinical symptoms

β : Recovery rate of individuals who were quarantined and moved to class R

θ : The proportion of infected individuals without clinical symptoms

ζsa : Contact rate of susceptible individuals with infected individuals without clinical symptoms

τ : Recovery rate of infected individuals without clinical symptoms and moving to class R

δ : Death rate caused by COVID-19 in the class of infected individuals with clinical symptoms

References

1. Anton, H & Rorres, C. 2004. Aljabar Linear Elementer Versi Aplikasi Edisi 8 Jilid 1. Jakarta: Erlangga.
2. Brauer, Fred, dkk. 2012. Mathematical Model in Biology, Mathematical Biosciences Suberies. Springer.
3. Danang, M. 2010. Aljabar Linear. Rekayasa Sains : Bandung.
4. Fosu, G.O., Opong, J.M., & Appati, J.K. (2020). Construction of compartmental models for COVID-19 with quarantine, lockdown, and vaccine interventions. Lockdown and Vaccine Interventions (April 12, 2020).
5. Holzner, S. 2008. Differential equations for dummies. Indiana: Wiley Publishing.
6. Pasaribu, RH, Harahap, ZIS, Putra, BA, & Siregar, SLA (2020). Mathematical modeling application in modeling the spread of the COVID-19 virus in Indonesia. SENATIK, 194-199.
7. Perko, Lawrence. 2001. Differential Equations and Dynamical Systems: Third Edition. New York.
8. Resmawan, LY SEAQIR Mathematical Model of Coronavirus Disease (COVID-19) Transmission.
9. Resmawan, R., Nuha, AR, & Yahya, L. (2021). Dynamic Analysis of COVID-19 Transmission Models Involving Quarantine Interventions. Jambura Journal of Mathematics, 3(1), 66-79.
10. Rosha, Media. 2013. Pemodelan Matematka. Jurusan Matematika : Universitas Negeri Padang.
11. Simmon, G.F. dan Steven G. Krantz. 2007. Differential Equations Theory, Technique, and Practice. McGraw-Hill International Edition.
12. Sudarsa, IW (2020). Cancer Surgery during the COVID-19 Pandemic. Jbn (National Surgical Journal), S1-S4.
13. Susilo, A., Rumende, CM, Pitoyo, CW, Santoso, WD, Yulianti, M., Herikurniawan, H., ... & Yunihastuti, E. (2020). Coronavirus disease 2019: A review of the current literature. Indonesian Journal of Internal Medicine, 7(1), 45-67.
14. Widowati, W., & Sutimin, S. (2007). Mathematical Modeling.
15. Wilandari, D. F., Hasanudin, H., Anggraeni, R. P., Susilawati, S., & Afandi, M. F. (2021). Sosialisasi Cara Pemakaian Masker Dan Hand Sanitizer Yang Baik Sebagai Upaya Memutus Mata Rantai Penyebaran Covid-19 Di Rumah Pintarkomplek Griya Asri Pamulang, Blok E 9 No. 7, Kecamatan Setu, Kelurahan Bhakti Jaya. Jurnal Lokabmas Kreatif: Loyalitas Kreatifitas Abdi Masyarakat Kreatif, 2(1), 20-28.