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SEIR Mathematical Model with the Use of Hand Sanitizers to Prevent the Spread of Covid-19 Disease

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ABSTRACT

The SARS-CoV-2 coronavirus can spread through contact with contaminated surfaces. The use of hand sanitizer is claimed to reduce the risk of transmission. For this reason, this study aims to develop a model of the spread of COVID-19 using the SEIR model with the use of hand sanitizer for infected individuals. The individual population is divided into six compartments, namely two compartments for susceptible individuals who using hand sanitizer and not, one compartment for exposed individuals, two compartments for infected individuals who using hand sanitizer and not, and one compartment for individuals died and recovered. The results obtained two equilibrium points: the disease-free and endemic equilibrium point, and also the basic reproduction number. The existence of a disease-free equilibrium point is unconditional, while the endemic there exist when the basic reproduction number is more than one. Stability analysis of the disease-free equilibrium point is locally asymptotic stable when the basic reproduction number is less than one. Numerical simulations carried out also strengthen them. Finally, the results of basic reproduction number sensitivity analysis show that the basic reproduction number is strongly influenced by contact of the susceptible individuals with exposed and infected individuals, neglecting of hand sanitizer use, mortality and cure rates.

Keywords: COVID-19; Hand sanitizer; SEIR Model; Basic Reproduction Number; Stability of Equilibrium Point

INTRODUCTION

In 2019, more precisely on December 31, we were shocked by a new disease that emerged from China. This disease is called the *Coronavirus disease* 2019 (COVID-19) caused by the coronavirus. COVID-19 is a respiratory syndrome disease caused by a type of corona virus, namely SARS-CoV-2. COVID-19 can cause mild, moderate and severe symptoms such as sneezing, coughing, respiratory problems, fever which can even be severe enough to cause death due to these symptoms [1]. In general, transmission of this disease is caused by droplets or body fluids or objects around 1-2 meters away when coughing and sneezing.

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The first case of the COVID-19 virus in Indonesia was confirmed on March 2 2020, two people who tested positive for the COVID-19 virus in the Depok area were Japanese citizens [2]. COVID-19 then increased to reach one million cases on January 26 2021 or 11 months when it was confirmed that this disease entered Indonesia. The government's efforts to prevent over transmission are by encouraging people to live clean, one of which is by using hand sanitizers. Hand sanitizers play an important role in the prevention of COVID-19. The SARS-CoV-2 coronavirus can spread through contact with contaminated surfaces. The use of hand sanitizers containing alcohol can kill the virus on the hands, helping to reduce the risk of transmission. Here are some ways in which hand sanitizers help in the prevention of COVID-19. For patients who experience symptoms such as flu, cough or respiratory problems, they can go directly to the nearest health center to do a swab test. Patients who do not have these symptoms can self-isolate so that the spread of COVID-19 can be controlled.

Mathematical modeling is one of the stages of solving mathematical problems by simulating or simplifying models of real phenomena in mathematical form so that a more precise understanding of a real problem can be obtained. Mathematical modeling can be an approach for the spread of COVID-19, so that the mathematical modeling of COVID-19 has begun to be developed since the pandemic occurred in early 2020. The SIR (Susceptible, infectious, Recovered) model is the basic model for the spread of a disease that was first introduced by Kernack & Mc Kendrick in 1927. This model was applied to COVID-19 disease by Mitra [3], Fosu et al. [4], Imran et al. [5], Ivanova & Dospatliev [6], Afwan et al. [7], Liao et al. [8] and Armita et al. [9]. Furthermore, the SIR model was developed by adding subpopulations exposed/ latent (E/L) obtained from the SIR model of the spread of COVID-19, as developed by Ala'raj et al. [10], Chinazzi et al. [11], Kai & Guy Philippe Goldstein [12], Kucharski et al. [13], Wang & Liu [14], Wu , Leung , & Leung [15], Yang et al. [16], and Zhao , Stone , & Gao [17].

This study developed an epidemic model of disease spread using the SEIR model on COVID-19 disease for hand sanitizer use cases. Based on the model, a balance point will be found in a disease-free and endemic state for each compartment. Furthermore, a model simulation will be carried out, with the values of the parameters used taken from several journals about the spread of COVID-19 disease [18, 19, 20, 21].

This study is different from previous studies, namely on the variable use of hand sanitizers because the current research discusses the use of health masks [22, 23, 1, 24], use of vaccinations [9, 4, 24, 25] and quarantine implementation [1, 25, 23, 18, 19]. This study was conducted to see its role in preventing the spread of COVID-19.

METHODS

This study used a mathematical modeling method used to determine the spread of Covid-19 disease with the SEIR model [26, 16, 11, 14, 13, 27, 28, 29, 30, 31].

Population is divided into six compartments, namely the compartment for susceptible individuals who do not use hand sanitizers (S_1), the compartment for susceptible individuals using hand sanitizers (S_2), the individual compartment who has contracted the disease but has not yet shown signs of having contracted the disease and cannot yet transmit disease (E), the infected individual compartment do not use a hand sanitizer (I_1), the infected individual compartment use a hand sanitizer (I_2), the individual compartment died and recovered (R).

The first step of development a mathematical model using the SEIR model is to collect information and data to determine assumptions and parameters. Then, defining a

flow chart based on predefined assumptions and parameters. Next, analyzing the stability of the SEIR model by determining the fixed point of the model. Stability analysis is performed at disease-free fixed points and disease-endemic fixed points based on eigenvalues obtained from the linearization method. The determination of the basic reproduction number is carried out for the analysis process. The last step observes the effect of using a hand sanitizer using simulations with previously obtained values.

RESULTS AND DISCUSSION

a. Model Assumptions

This research developed a mathematical model of the spread of COVID-19 disease using the SEIR model for hand sanitizer cases. The following present model assumptions.

1. The virus that causes COVID-19 disease is a coronavirus.
2. The population is assumed to be closed, which means that no individuals enter or leave the population (no migration). The total population is assumed to be constant.
3. The number of births and deaths in the population is assumed to be the same over time.
4. The population is assumed to be mixed homogeneously, meaning that each individual has the opportunity to contact other individuals.
5. Movement between regions in Indonesia does not include migration.
6. Susceptible individuals using hand sanitizer [S_2] cannot contract the virus
7. Susceptible individuals using hand sanitizer [S_2] will change back to susceptible individuals not using hand sanitizer [S_1] if these individuals stop using hand sanitizer
8. Infected individuals using hand sanitizer [I_2] will change back to the infected individual compartment not using hand sanitizer [I_1] if these individuals stop using hand sanitizer.
9. This virus can be transmitted if in direct contact with individuals infected with the corona virus
10. Individuals who are infected can recover and die from Covid-19.
11. Individuals who have recovered will have immunity to the corona virus.
12. Infected individuals wearing hand sanitizer [I_2]cannot transmit the disease.
13. Every subpopulation experience natural death.

b. Variables and parameters

The following is presented in table 1 and table 2 of the variables and models of the spread of the Covid-19 disease.

Table 1. List of variable models of the spread of covid-19 using hand sanitizers

No.	Variable	Definition	Condition	Unit
1.	*N(t)*	Total individual population at time t	N(t) ≥ 0	Individual
2.	S_1(t)	The number of individuals who are susceptible to infection do not use hand sanitizers at time t	$S_1(t) \geq 0$	Individual
3.	S_2(t)	Number of susceptible individuals using hand sanitizer at time t	S_2(t) ≥ 0	Individual
4.	E(t)	Amount individual *exposed* on time to -t	E(t) ≥ 0	Individual
5.	I_1(t)	Number of infected individuals not using hand sanitizer at time t	$I_1(t) \geq 0$	Individual
6.	$I_2(t)$	Number of infected individuals using hand sanitizer at time t	$I_2(t) \geq 0$	Individual
7.	R(t)	The number of individuals who died and recovered from the disease at time t	R(t) ≥ 0	individual

Table 2. List of Parameters for the Spread of Covid-19 with Hand Sanitizers

No.	Parameter	Definition	Condition	Unit
1.	μ	Birth and death rates experience population individual	$\mu \geq 0$	Individuals/ day
2.	u_1	Rate of use of hand sanitizer	$u_1 \geq 0$	Individuals/ day
3.	u_2	Hand sanitizer release rate	$u_2 \geq 0$	Individuals/ day
4.	β	The rate at which susceptible individuals become exposed individuals after interacting with infected individuals	$\beta \geq 0$	Individuals/ day
5.	ω	Individual transfer rate *exposed* to be individual infected	$\omega \geq 0$	Individuals/ day
6.	σ	The rate of death caused by disease	$\sigma \geq 0$	Individuals/ day
7.	θ	Cure rate each individual	$\theta \geq 0$	Individuals/ day

c. Spread Covid-19 disease

Based on the flowchart in the figure above, the individual population is divided into six compartments, namely the compartment for susceptible individuals who do not use hand sanitizers (S_1), the compartment for susceptible individuals using hand sanitizers (S_2), the individual compartment who has contracted the disease but has not yet shown signs of having contracted the disease and cannot yet transmit disease (E) [32], the infected individual compartment did not use a hand sanitizer (I_1), the infected individual compartment used a hand sanitizer (I_2), the individual compartment died and recovered (R). Any individual born at the birth rate (μ) will enter the compartment (S_1), susceptible individuals who use hand sanitizers are put into the compartment (S_2) at the rate u_1 but if they are stop wearing hand sanitizer, they will return to being susceptible individuals who do not use hand sanitizers (S_1) with a rate of u_2. The same process will also occur if the individual is infected. Individuals who do not use hand sanitizers can still be infected if they interact with infected individuals and will become *exposed* (E) individuals with a rate of β. The same process will also occur in the infected individual compartment. Individuals who are infected using hand sanitizer (I_2) will change back to infected individuals not using hand sanitizer (I_1) if they stop using hand sanitizer. Individuals who do not use hand sanitizers can still be infected if they interact with infected individuals and will become *exposed* (E) individuals with a rate of β. *Exposed* individuals become infected individuals at a rate ω. Infected individuals will die at a rate σ and will recover at a rate θ. In each compartment there is a natural birth with a rate μ.

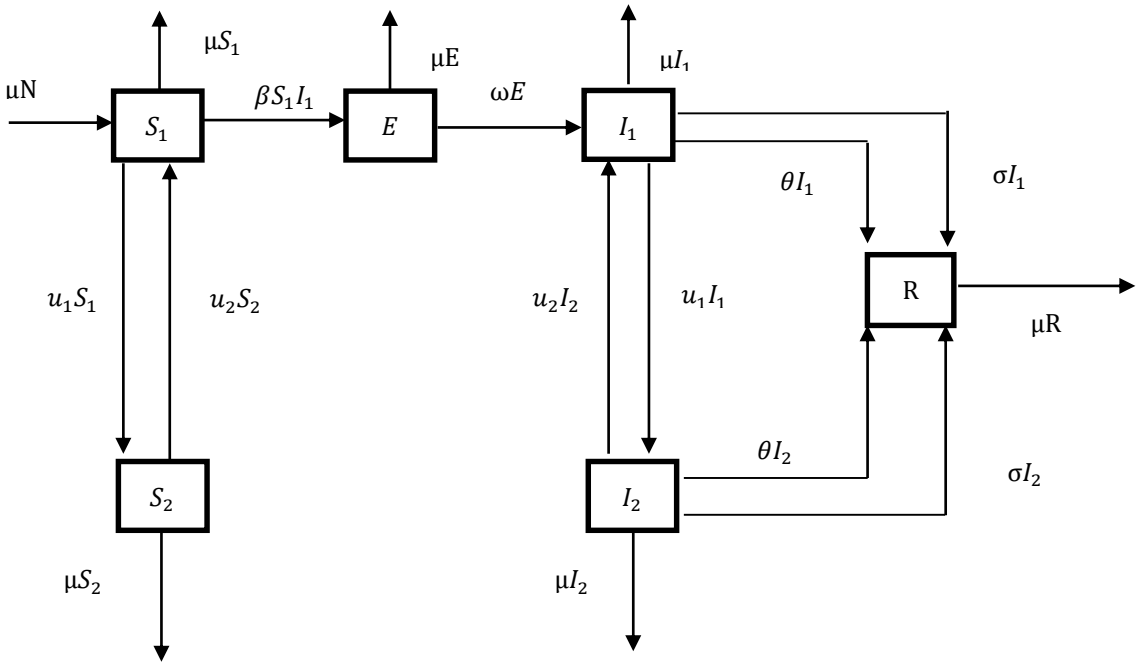


Figure 1. Flowchart of the Mathematical Model for the Spread of Covid-19 Disease Using Hand Sanitizer

Based on the flowchart of the spread of the Covid-19 disease on the use of hand sanitizers in Figure 1, a mathematical model can be formed in the form of a system of nonlinear ordinary differential equations as follows: systematically in the form of a nonlinear differential equation as follows

$$\begin{aligned}
\frac{(dS_1)}{dt} &= \mu N + u_2 S_2 - (\mu + u_1) S_1 - \beta S_1 I_1 \\
\frac{(dS_2)}{dt} &= u_1 S_1 - (\mu + u_2) S_2 \\
\frac{dE}{dt} &= \beta S_1 I_1 - (\mu + \omega) E \\
\frac{dI_1}{dt} &= \omega E + u_2 I_2 - (\mu + u_1 + \sigma + \theta) I_1 \\
\frac{dI_2}{dt} &= u_1 I_1 - (\mu + u_2 + \sigma + \theta) I_2 \\
\frac{dR}{dt} &= (\sigma + \theta) I_1 + (\sigma + \theta) I_2 - \mu R
\end{aligned} \tag{1}$$

where $N = S_1 + S_2 + E + I_1 + I_2 + R$.

In the system of equations (1) we can simplify it into a *non-dimensional model,* the proportion of the number of individuals in each compartment is as follows:

$$s_1 = \frac{S_1}{N}, s_2 = \frac{S_2}{N}, e = \frac{E}{N}, i_1 = \frac{I_1}{N}, i_2 = \frac{I_2}{N}, \text{ and } r = \frac{R}{N} \tag{2}$$

From equation (2) obtained $s_1 + s_2 + e + i_1 + i_2 + r = \frac{S_1}{N} + \frac{S_2}{N} + \frac{E}{N} + \frac{I_1}{N} + \frac{I_2}{N} + \frac{R}{N} = 1$ and non-dimensional model to become:

$$\begin{aligned}
\frac{(ds_1)}{dt} &= \mu + u_2 s_2 - (\mu + u_1)s_1 - \beta s_1 i_1 \\
\frac{(ds_2)}{dt} &= u_1 s_1 - (\mu + u_2)s_2 \\
\frac{de}{dt} &= \beta s_1 i_1 - (\mu + \omega)e \\
\frac{di_1}{dt} &= \omega e + u_2 i_2 - (\mu + u_1 + \sigma + \theta)i_1 \\
\frac{di_2}{dt} &= u_1 i_1 - (\mu + u_2 + \sigma + \theta)i_2 \\
\frac{dr}{dt} &= (\sigma + \theta)i_1 + (\sigma + \theta)i_2 - \mu r
\end{aligned} \tag{3}$$

Then system in (3), the compartment r will not appear in another equation because the number of compartments r does not affect the rate of change of any of the individual compartments, so compartment r is temporarily ignored from system. So, the system in (3) can be written as:

$$\begin{aligned}
\frac{(ds_1)}{dt} &= \mu + u_2 s_2 - (\mu + u_1)s_1 - \beta s_1 i_1 \\
\frac{(ds_2)}{dt} &= u_1 s_1 - (\mu + u_2)s_2 \\
\frac{de}{dt} &= \beta s_1 i_1 - (\mu + \omega)e \\
\frac{di_1}{dt} &= \omega e + u_2 i_2 - (\mu + u_1 + \sigma + \theta)i_1 \\
\frac{di_2}{dt} &= u_1 i_1 - (\mu + u_2 + \sigma + \theta)i_2
\end{aligned} \tag{4}$$

d. Equilibrium Point and Basic Reproductive Number

The equilibrium point occurs when $\left(\frac{(ds_1)}{dt}, \frac{(ds_2)}{dt}, \frac{de}{dt}, \frac{di_1}{dt}, \frac{di_2}{dt}\right) = (0, 0, 0, 0, 0)$. The system (4) has two equilibrium points, namely a disease-free equilibrium point and an endemic equilibrium point. Then the system can be written as:

$$\begin{aligned}
\mu + u_2 s_2 - (\mu + u_1)s_1 - \beta s_1 i_1 &= 0 \\
u_1 s_1 - (\mu + u_2)s_2 &= 0 \\
\beta s_1 i_1 - (\mu + \omega)e &= 0 \\
\omega e + u_2 i_2 - (\mu + u_1 + \sigma + \theta)i_1 &= 0 \\
u_1 i_1 - (\mu + u_2 + \sigma + \theta)i_2 &= 0
\end{aligned} \tag{5}$$

The disease-free equilibrium point is a condition where there are no infected individuals discussed in the population, so $e = 0$ and $i = 0$. By substituting them into the system of equation (5) we obtain a disease-free equilibrium point $E_1(s_1, s_2, e, i_1, i_2) = \left(\frac{(\mu + u_2)}{\mu + u_1 + u_2}, \frac{u_1}{\mu + u_1 + u_2}, 0, 0, 0\right)$.

The endemic equilibrium point is a condition where there are infected individuals in the population so that compartment I is at the endemic equilibrium point $s_1', s_2', e', i_1', i_2' \neq 0$. *The* endemic equilibrium point obtained from equation (5) is E_2 $(s_1', s_2', e', i_1', i_2')$

$$
\begin{aligned}
s_1' &= \frac{(\mu+\omega)(\mu+\theta+\sigma)(\mu+u_2+u_1+\theta+\sigma)}{\beta\omega\,(\mu+u_2+\theta+\sigma)} \\
s_2' &= \frac{u_1(\mu+\omega)(\mu+\theta+\sigma)(\mu+u_2+u_1+\theta+\sigma)}{\beta\omega\,(\mu+u_2)\,(\mu+u_2+\theta+\sigma)} \\
e' &= \frac{\beta s_1' i_1'}{(\mu+\omega)} \\
i_1' &= \frac{\mu}{\beta}\left(\frac{\beta\omega(c)(\mu+u_2)-a(\mu+\omega)(a+\theta+\sigma)(b)}{(\mu+\omega)(a+\theta+\sigma)(b)(\mu+u_2)}\right) \\
i_2' &= \frac{u_1 i_1'}{(\mu+u_2+\theta+\sigma)}
\end{aligned}
\tag{6}
$$

Next will be determined the basic reproduction number using NGM (*Next Generation Matrix*) developed by [32]. The basic reproduction number is the average number of secondary cases of a disease outbreak caused by one infected individual during the time the infection was still in the susceptible population. The basic reproduction number can be denoted as R_0. If the average infected individual is less than one individual in the area ($R_O < 1$), then the infection from the disease will not grow or spread widely. Conversely, if $R_0 > 1$, each infected individual can cause new individuals to become infected and the disease in the area will spread.

The first step is to linearize the infected subsystem (e, i) at the disease-free equilibrium point

$$
J = \begin{bmatrix} -(\mu+\omega) & \beta s_1 & 0 \\ \omega & -(\mu+u_1+\sigma+\theta) & u_2 \\ 0 & u_1 & -(\mu+u_2+\sigma+\theta) \end{bmatrix}
= \begin{bmatrix} -(\mu+\omega) & \beta\left(\frac{\mu+u_2}{\mu+u_1+u_2}\right) & 0 \\ \omega & -(\mu+u_1+\sigma+\theta) & u_2 \\ 0 & u_1 & -(\mu+u_2+\sigma+\theta) \end{bmatrix}
$$

substitute the disease-free equilibrium point $E_1(s_1, s_2, \mathrm{e}, i_1, i_2) = \left(\frac{\mu+u_2}{\mu+u_1+u_2}, \frac{u_1}{\mu+u_1+u_2}, 0,0,0\right)$ to matrix ***J***, then we get

$$
J = \begin{bmatrix} -(\mu+\omega) & \beta s_1 & 0 \\ \omega & -(\mu+u_1+\sigma+\theta) & u_2 \\ 0 & u_1 & -(\mu+u_2+\sigma+\theta) \end{bmatrix}
$$

Finally, decompose the Jacobi matrix J to $J = F - V$, where F is the transmission matrix and V is the transition matrix

$$
J = \begin{bmatrix} 0 & \beta s_1 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} - \begin{bmatrix} (\mu+\omega) & 0 & 0 \\ -\omega & (\mu+u_1+\sigma+\theta) & -u_2 \\ 0 & -u_1 & (\mu+u_2+\sigma+\theta) \end{bmatrix}
$$

Count $V^{-1} = \begin{bmatrix} \frac{1}{(\mu+\omega)} & 0 & 0 \\ \frac{\omega(\mu+u_2+\sigma+\theta)}{(\mu+\omega)L} & \frac{(\mu+u_2+\sigma+\theta)}{L} & \frac{u_2}{L} \\ \frac{\omega(u_1)}{(\mu+\omega)L} & \frac{u_1}{L} & \frac{(\mu+u_1+\sigma+\theta)}{L} \end{bmatrix}$ with $L = (\mu+\theta+\sigma)(\mu+u_2+u_1+\theta+\sigma)$. Next, count $R_0 = p(F\,V^{-1})$.

$$F\,V^{-1} = \begin{bmatrix} 0 & \beta s_1 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{(\mu+\omega)} & 0 & 0 \\ \frac{\omega(\mu+u_2+\sigma+\theta)}{(\mu+\omega)L} & \frac{(\mu+u_2+\sigma+\theta)}{L} & \frac{u_2}{L} \\ \frac{\omega(u_1)}{(\mu+\omega)L} & \frac{u_1}{L} & \frac{(\mu+u_1+\sigma+\theta)}{L} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{B\omega(\mu+u_2+\sigma+\theta)}{(\mu+u_1+u_2)(\mu+\omega)A} & \frac{B(\mu+u_2+\sigma+\theta)}{(\mu+u_1+u_2)A} & \frac{Bu_2}{(\mu+u_1+u_2)A} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

For A =(μ + θ + σ)(μ + u_2 + u_1 + θ + σ) and B = β(μ + u_2), the eigenvalues of the matrix (F V^{-1}) are obtained from the following equation

$$|\lambda I - F\,V^{-1}| = 0$$

$$\begin{vmatrix} \lambda - \frac{B\omega(\mu+u_2+\sigma+\theta)}{(\mu+u_1+u_2)(\mu+\omega)A} & \frac{B(\mu+u_2+\sigma+\theta)}{(\mu+u_1+u_2)A} & \frac{Bu_2}{(\mu+u_1+u_2)A} \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{vmatrix} = 0$$

So, it yields $\lambda_{1,2}$= 0 and λ_3= $\frac{\beta\omega(\mu+u_2)(\mu+u_2+\sigma+\theta)}{(\mu+u_1+u_2)(\mu+\omega)A}$ and hence

$$R_0 = \frac{\beta\omega(\mu+u_2)(\mu+u_2+\sigma+\theta)}{(\mu+u_1+u_2)(\mu+\omega)A} \quad (7)$$

e. Disease-free equilibrium point stability

In equation (4) it is possible to analyze the stability of the disease-free equilibrium point by forming a Jacobian matrix. After the Jacobian matrix is formed, we look for the eigenvalues by using linearization in equation (4) around the disease-free equilibrium point. Let E_1(s_1, s_2, e, i_1, i_2) be the disease-free equilibrium point of system (4). The Jacobian matrix resulting from the linearization of the Covid-19 disease distribution model around the disease-free equilibrium point can be expressed as follows.

$$J_{(E_1)} = \begin{bmatrix} -\mu-u_1-\beta i_1 & u_2 & 0 & -\beta s_1 & 0 \\ u_1 & -\mu-u_2 & 0 & 0 & 0 \\ \beta i_1 & 0 & -(\mu+\omega) & \beta s_1 & 0 \\ 0 & 0 & \omega & -(\mu+\theta+\sigma+u_1) & u_2 \\ 0 & 0 & 0 & u_1 & -(\mu+\theta+\sigma+u_2) \end{bmatrix}$$

The stability of the disease-free equilibrium point will be sought from the system of equation (4). Substitute the disease-free equilibrium point $E_1(s_1, s_2, e, i_1, i_2) = \left(\frac{(\mu+u_2)}{\mu+u_1+u_2}, \frac{u_1}{\mu+u_1+u_2}, 0,0,0\right)$ into the equation $J_{(E_1)}$ so that the following Jacobian matrix can be obtained

$$J_{(E_1)} = \begin{bmatrix} -\mu - u_1 & u_2 & 0 & -\beta\left(\frac{\mu + u_2}{\mu + u_1 + u_2}\right) & 0 \\ u_1 & -\mu - u_2 & 0 & 0 & 0 \\ 0 & 0 & -(\mu + \omega) & \beta\left(\frac{\mu + u_2}{\mu + u_1 + u_2}\right) & 0 \\ 0 & 0 & \omega & -(\mu + \theta + \sigma + u_1) & 0 \\ 0 & 0 & 0 & u_1 & -(\mu + \theta + \sigma + u_1) \end{bmatrix}$$

Theorem

If $R_0 < 1$ then equation (4) will be asymptotically stable locally at the disease-free equilibrium point $E_1(s_1, s_2, e, i_1, i_2) = \left(\frac{(\mu + u_2)}{\mu + u_1 + u_2}, \frac{u_1}{\mu + u_1 + u_2}, 0,0,0\right)$.

As proof, the eigenvalues of the matrix $J_{(E_1)}$ which has been substituted by a disease-free equilibrium point is obtained by the following equation

$$\left|\lambda I - J_{(E_1)}\right| = 0$$

$$\begin{vmatrix} \lambda + k & u_2 & 0 & -\beta(\frac{l}{q}) & 0 \\ u_1 & \lambda + l & 0 & 0 & 0 \\ 0 & 0 & \lambda + m & \beta(\frac{l}{q}) & 0 \\ 0 & 0 & \omega & \lambda + n & u_2 \\ 0 & 0 & 0 & u_1 & \lambda + p \end{vmatrix} = 0$$

where $k = \mu + u_1$, $l = \mu + u_2$, $m = \mu + \omega$, $n = k + \theta + \sigma$, $p = l + \theta + \sigma$, $q = \mu + u_1 + u_2$ *and* then the characteristic equation will be obtained from $J_{(E_1)}$is

$$(\lambda + \mu)(\lambda + \mu + u_1 + u_2)z = 0 \quad (9)$$

where $z = (\lambda + m)(\lambda + n)(\lambda + p) - (\lambda + m)(u_1 u_2) - \frac{\omega\beta l}{q}(\lambda + p)$

Then it is obtained $\lambda_1 = -\mu$, $\lambda_2 = -\mu - u_1 - u_2$, because μ, u_1, dan u_2 is positive then the real part of the two eigenvalues is negative. Obtained, $a_0 = 1$, $a_1 = n + p + m$, $a_2 = ((\mu + \theta + \sigma)(q + \theta + \sigma) + m(n + p) - R)$ and $a_3 = m(\mu + \theta + \sigma)(q + \theta + \sigma - Rp$, for $R = \frac{\omega\beta l}{q}$.

How to find out the eigenvalues of the equation will use the Routh-Hurwitz criteria [33], then we get

$$\frac{a_1}{a_0} = n + p + m$$

$$\frac{a_2}{a_0} = ((\mu + \theta + \sigma)(q + \theta + \sigma) + m(n + p) - R)$$

$$\frac{a_3}{a_0} = m(\mu + \theta + \sigma)(q + \theta + \sigma) - Rp$$

Condition the Routh-Hurwitz criterion is $\frac{a_1}{a_0} > 0, \frac{a_2}{a_0} > 0, \frac{a_3}{a_0} > 0$ of the Routh-Hurwtiz matrix is positive

$$\Delta_1 = |a_1|$$

$$\Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} = a_1.\ a_2 - a_3(1) = (n+p)\,[\mu + \theta + \sigma)(q + \theta + \sigma) + (n+p+m)\,m] - (n+m)R$$

$$\Delta_3 = \begin{bmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ 0 & 0 & a_3 \end{bmatrix} = a_3(\,a_1a_2 - a_3) = a_3(\,\Delta_2)$$

It is clear that $a_1 > 0$ so $\Delta_1 > 0$ next $\Delta_2 = a_1a_2 - a_3 > 0$, then $(n+p)[\mu + \theta + \sigma)(q + \theta + \sigma) + (n+p+m)\,m] > (\,n+m\,)R$ so that $\Delta_2 > 0$. Then to show $\Delta_3 > 0$, note that $a_3 > 0$ and $\Delta_2 > 0$, then it is certain $\Delta_3 = a_3(\Delta_2) > 0$. The determinant of the Routh-Hurwitz matrix Δ_1, Δ_2, Δ_3 is positive if $R_0 < 1$, it is concluded that the disease-free equilibrium point is locally asymptotically stable.

f. Model Simulation

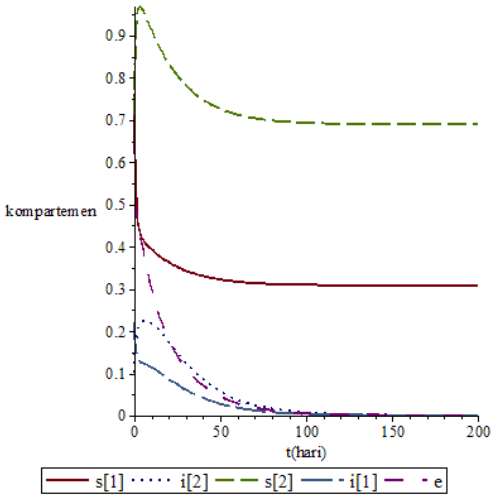
Model simulation of the spread of the Covid-19 disease on hand use Sanitizer is done using parameter values from several studies, presented in table form as follows.

Table 3. Parameter Values of the Spread of Covid-19 Disease Using Hands Sanitizer

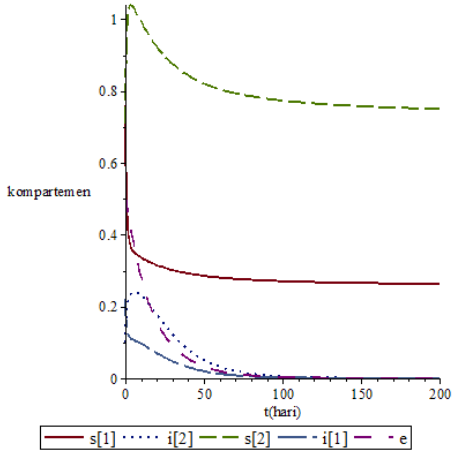
Parameter	Mark	Unit	Reference
N	10000	individual	[18]
μ	0.0125	Per day	[18]
B	0.2	$\frac{2}{individual\ per day}$	[19]
Ω	0.07142857143	$\frac{individual}{day}$	[20]
Σ	0.03333333333	$\frac{individual}{day}$	[21]
Θ	0.03333333333	$\frac{individual}{day}$	[21]

Based on the parameter values that have been presented, 5 possibilities are made using the disease-free equilibrium point with arbitrary initial values $s_1'(0) = 0.76, s_2'(0) = 0.71$, $i_1'(0) = 0.22$, $i_2'(0) = 0.1$ and $e(0) = 0.51$. Parameters $u_1$and u_2 are not included in the parameter table because in this study using 10 possibilities for u_1 and u_2.

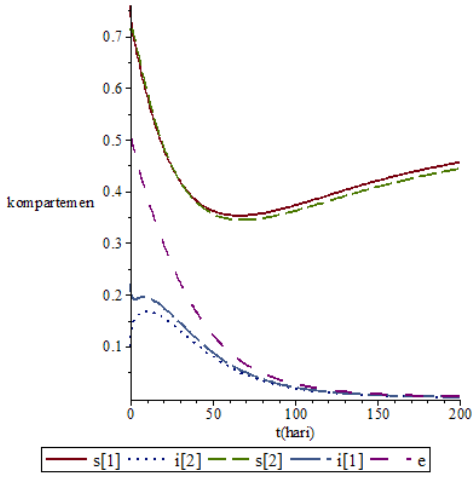
1. Simulation for parameter $u_1 = 1$ and $u_2 = 0$ obtained the basic reproduction number ($R_0 = 0.001947235991 < 1$) which means that the disease will not spread in the population. Can be presented in the image as follows.



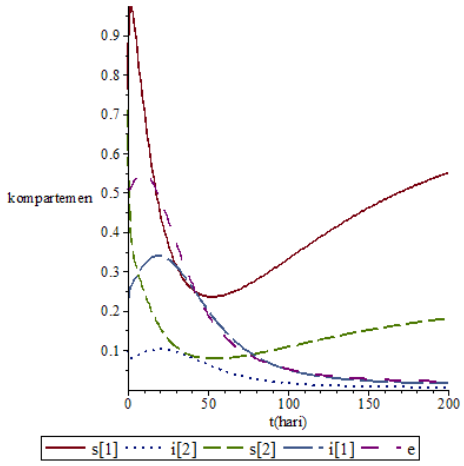
2. parameter $u_1 = 0.75$ and $u_2 = 0.25$ obtained the basic reproduction number ($R_0 = 0.1700244478 < 1$) which means that the disease will not spread in the population. Can be presented in the image as follows.



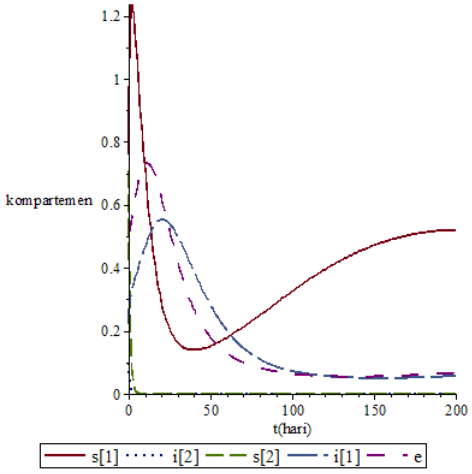
3. Simulations for values parameter $u_1 = 0.5$ and $u_2 = 0.5$ obtained the basic reproduction number ($R_0 = 0.5840683116 < 1$) which means that the disease will not spread in the population. Can be presented in the image as follows.



4. Simulations for values parameter $u_1 = 0.25$ and $u_2 = 0.75$ obtained the basic reproduction number ($R_0 = 1.244078827 > 1$) which means that the disease will spread in the population. Can be presented in the image as follows.

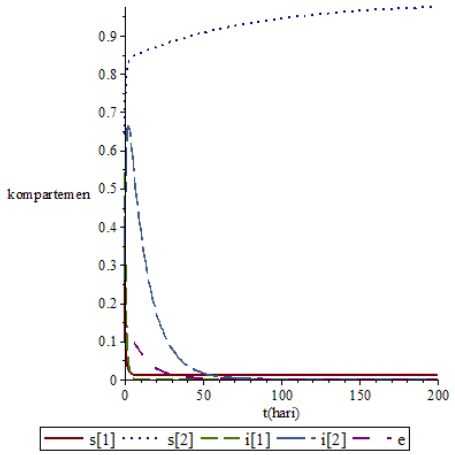


5. Simulation for values parameter $u_1 = 0$ and $u_2 = 1$ obtained the basic reproduction number ($R_0 = 2.150055994 > 1$) which means the disease will spread in the population. Can be presented in the image as follows.

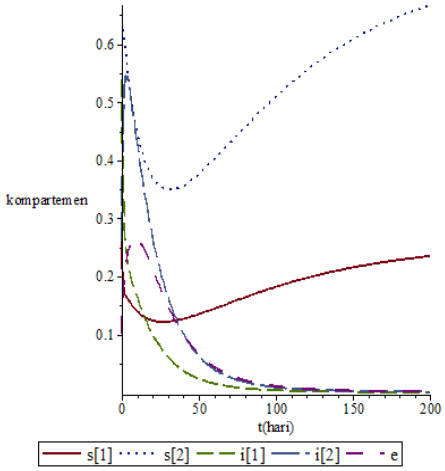


Furthermore, based on the parameter values that have been presented by increasing the value of β = 0.9, 5 possibilities will be made using an endemic equilibrium point with an arbitrary initial value. $s_1'(0) = 0.27, s_2'(0) = 0.64, i_1'(0) = 0.54, i_2'(0) = 0.26$ and $e(0) = 0.1$

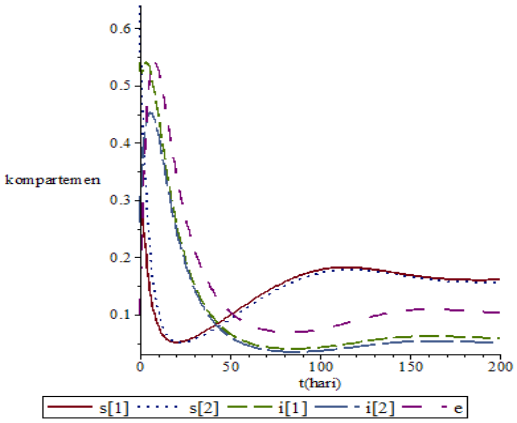
1. Simulation for values parameter $u_1 = 1$ and $u_2 = 0$ obtained the basic reproduction number ($R_0 = 0.001947235991 < 1$) which means that the disease will not spread in the population. Can be presented in the image as follows.



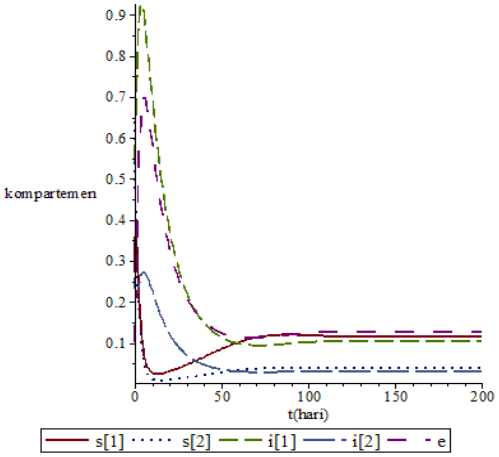
2. Simulations for parameter $u_1 = 0.75$ and $u_2 = 0.25$ obtained the basic reproduction number ($R_0 = 0.7651100155 < 1$) which means that the disease will not spread in the population. Can be presented in the image as follows.



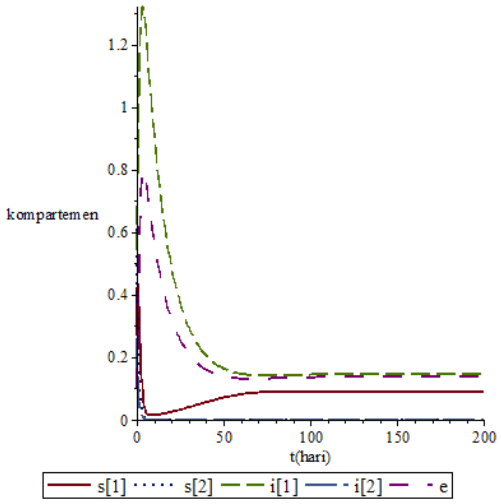
3. parameter $u_1 = 0.5$ and $u_2 = 0.5$ obtained the basic reproduction number ($R_0 = 2.628307399 > 1$), which means that the disease will not spread in the population. Can be presented in the image as follows.



4. Simulations for values parameter $u_1 = 0.25$ and $u_2 = 0.75$ obtained the basic reproduction number ($R_0 = 5.598354719 > 1$), which means that the disease will not spread in the population. Can be presented in the image as follows.



5. Simulation for values parameter $u_1 = 0$ and $u_2 = 1$ obtained the basic reproduction number ($R_0 = 9.675251969 > 1$) which means that the disease will not spread in the population. Can be presented in the image as follows.



From the results of the numerical simulation above, it was found that for numerical simulations at the disease-free equilibrium points at numbers 1, 2, and 3 and then at the endemic equilibrium points at numbers 1 and 2, the results of the basic reproduction number < 1, which means the disease will not spread. Then at the disease-free equilibrium points at numbers 4 and 5 and at the endemic equilibrium points at numbers 3, 4, and 5, the basic reproduction number > 1 was found which means that this covid disease will spread.

CONCLUSIONS

Based on the assumptions that have been made in this study, it is concluded that the SEIR mathematical model on the spread of Covid-19 disease in the case of using hand sanitizers by developing the susceptible compartment into two subpopulations, namely the subpopulation of vulnerable individuals not using hand sanitizers (S_1.) and vulnerable individuals using hand sanitizers (S_2.). Likewise, the *Infected compartment* is divided into two subpopulations that is individual infected No using hand sanitizer (I_1) and infected individuals using hand sanitizer (I_2). Then a system model of linear differential equations is obtained, namely:

$$\frac{(dS_1)}{dt} = \mu N + u_2 S_2 - (\mu + u_1) S_1 - \beta S_1 I_1$$
$$\frac{(dS_2)}{dt} = u_1 S_1 - (\mu + u_2) S_2$$
$$\frac{dE}{dt} = \beta S_1 I_1 - (\mu + \omega) E$$
$$\frac{dI_1}{dt} = \omega E + u_2 I_2 - (\mu + u_1 + \sigma + \theta) I_1$$
$$\frac{dI_2}{dt} = u_1 I_1 - (\mu + u_2 + \sigma + \theta) I_2$$
$$\frac{dR}{dt} = (\sigma + \theta) I_1 + (\sigma + \theta) I_2 - \mu R$$

with do analysis system equality differential into the *non-dimensional* model, two points are obtained equilibrium that is point equilibrium free disease and point equilibrium endemic. Point equilibrium free disease $E_1(s_1, s_2, e, i_1, i_2,) = (\frac{\mu + u_2}{\mu + u_1 + u_2}, \frac{u_1}{\mu + u_1 + u_2}, 0,0,0)$ which has a stable asimiotic local equilibrium point when $R_0 < 1$ and the endemic equilibrium point $E_2\ (s_1', s_2', e', i_1', i_2')$ exists if $R_0 > 1$ where

$$
\begin{aligned}
s_1' &= \frac{(\mu + \omega)(\mu + \theta + \sigma)(\mu + u_2 + u_1 + \theta + \sigma)}{\beta\omega\,(\mu + u_2 + \theta + \sigma)} \\
s_2' &= \frac{u_1(\mu + \omega)(\mu + \theta + \sigma)(\mu + u_2 + u_1 + \theta + \sigma)}{\beta\omega\,(\mu + u_2)\,(\mu + u_2 + \theta + \sigma)} \\
e' &= \frac{\beta s_1' i_1'}{(\mu + \omega)} \\
i_1' &= \frac{\mu}{\beta}\left(\frac{\beta\omega(c)(\mu + u_2) - a(\mu + \omega)(a + \theta + \sigma)(b)}{(\mu + \omega)(a + \theta + \sigma)(b)(\mu + u_2)}\right) \\
i_2' &= \frac{u_1 i_1'}{(\mu + u_2 + \theta + \sigma)}
\end{aligned}
$$

To find out whether an area is endemic or not, it can be seen from the basic reproduction number and the basic reproduction number is obtained

$$R_0 = \frac{\beta\omega(\mu + u_2)(\mu + u_2 + \sigma + \theta)}{(\mu + u_1 + u_2)(\mu + \omega)(\mu + \theta + \sigma)(\mu + u_2 + u_1 + \theta + \sigma)}$$

with the values of influential parameters such as the level of susceptible individuals to becoming infected individuals (β), the natural death of each individual (μ), the rate of using hand sanitizers (u_1), the rate of not using hand sanitizers (u_2), the rate of deaths caused by disease (σ), the recovery rate of each individual (θ), the rate of latent individuals becoming infected individuals (ω).

The mathematical model simulation is carried out using the Maple 18 application, and the parameter values used are taken from several journals and the results show that if $R_0 < 1$ then the disease will not spread because the factor of using hand sanitizer (u_1) is greater than those who do not use hand sanitizer (u_2), and vice versa if $R_0 > 1$ then the disease will spread if the factor of the rate of susceptible individuals becoming infected individuals (β) is enlarged and also the factor of the rate of using hand sanitizers (u_1) is smaller than those who do not use hand sanitizers (u_2). However, it can be prevented if susceptible individuals and infected individuals use hand sanitizers.

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