# Dynamics of SARS-CoV-2 Spread Model with Vaccine Administration and Use of Masks

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**Abstrak.** Penelitian ini bertujuan untuk mengonstruksi dan mengetahui dinamika model matematika penyebaran SARS-CoV-2 dengan adanya pemberian vaksin dan penggunaan masker. Pengonstruksian model dalam penelitian ini menggunakan model SEIR yang telah dimodifikasi dengan beberapa tahapan yaitu melakukan studi literatur mengenai pemodelan matematika pada virus SARS-CoV-2, menyusun asumsi awal, membuat diagram kompartemen, mengonstruksi model matematika, menentukan titik kesetimbangan, menentukan bilangan reproduksi dasar, melakukan analisis kestabilan dan sinkronisasi hasil analisa dengan melakukan simulasi numerik. Didapatkan 2 titik kesetimbangan yaitu titik kesetimbangan bebas penyakit dan titik kesetimbangan endemik. Dengan menggunakan bilangan reproduksi dasar, didapatkan syarat kestabilan untuk titik bebas penyakit dan juga titik endemik. Ketika titik bebas penyakit stabil maka SARS-CoV-2 akan hilang dari populasi, sedangkan ketika titik bebas penyakit tidak stabil maka SARS-CoV-2 akan terus ada didalam populasi.

**Abstract.** The purpose of this study was to construct and determine the dynamics of the mathematical model of the reach of SARS-CoV-2 with the provision of vaccines and the use of masks. In this study, the modified SEIR model was used with the stages of conducting a literature study on mathematical modeling of the SARS-CoV-2 virus, compiling initial assumptions, making compartment diagrams, constructing mathematical models, determining equilibrium points, determining basic reproduction numbers, conducting stability analysis and synchronization of analysis results by performing numerical simulations. In this study, two equilibrium points were obtained the disease-free equilibrium point and the endemic equilibrium point. Using the basic reproduction number, we get the stability conditions for the disease-free point and the endemic point. When the disease-free point is stable, SARS-CoV-2 will disappear from the population, while when the disease-free point unstable, SARS-CoV-2 will be exist's in the population.

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## 1. Introduction

Coronaviruses are a group of viruses that infect animals and can attack the human respiratory system. In 2002 and 2012, respectively, the coronavirus named Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) emerged with bats as natural hosts [1] and the Middle East Respiratory Syndrome Coronavirus (MERS-CoV), which were transmitted from camels to humans [2]. This has become a new health problem in the 21st century [3]. At the end of 2019, the coronavirus called Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) was detected in Wuhan City, China. The SARS-CoV-2 virus is the virus that causes the Covid-19 disease outbreak and has spread rapidly throughout the world [4].

Coronavirus is an infectious disease and can spread quickly [5]. According to WHO, the spread of the SARS-CoV-2 virus occurs when interaction or contact with people with Covid-19. When a person with COVID-19 coughs, talks, sneezes, sings, or breathes, the virus spreads from the mouth and nose in the form of small particles or liquids. This virus can also spread in places with poor ventilation and also crowded. This can happen due to the aerosol can be suspended in the air. In addition, the transmission of Covid-19 can also occur when someone touches the surface of an object that has been contaminated by the virus [6].

The use of masks in the community is one of the practical efforts in preventing the spread of the SARS-CoV-2. This is because masks work in 2 ways. The first is to prevent people infected with Covid-19 from transmitting the virus by blocking breathing containing the virus into the air. Second, masks protect people who are not infected by Covid-19 by being a barrier for liquids or small particles containing the virus from sticking to an open nose and mouth. Masks can also filter particulate matter from inhaled air [7]. Based on a systematic review of 172 studies conducted by [8], the use of masks can protect a person from infection with the SARS-CoV-2.

Vaccination is another form of the government effort to suppress the spread of the SARS-CoV-2. Vaccines contain antigens that can stimulate the body's immune system to produce an immune response [9]. According to [10], through clinical trials, the Covid-19 vaccine has shown good immunogenicity with different levels of effectiveness in each vaccine variant. So that it can help suppress the spread of the SARS-CoV-2.

According to [11] the SEIR model is the most commonly used mathematical algorithm to describe the diffusion of epidemic diseases, for example to characterize the COVID-19 epidemic[12]. The SEIR model is applied to cases of disease that have a long incubation period, so that the effect of incubation on the spread of disease can be analyzed[13]. In various other research articles, many discuss the mathematical model of the spread of disease using the SEIR Model. An article entitled Mathematical Model for MERS-CoV Disease Transmission with Medical Mask Usage and Vaccination by [14]. This article discusses the model for spreading the MERS-CoV virus using masks and vaccinations using the SEIR model. In addition, an article entitled Stability Analysis and Numerical Simulation of SEIR Model for Pandemic COVID-19 Spread in Indonesia by [15]. Therefore, in this article, the author discusses the spread of Covid-19 in Indonesia using the SEIR model. Based on this description, the authors are interested in discussing the model for the space of SARS-CoV-2 with masks and vaccinations and adding the assumption of re-infection. Re-infection is possible when recovered individuals ignore the use of masks even though they have been vaccinated.

The purpose of this study was to construct and determine the mathematical model of the spread of SARS-CoV-2 by administering vaccines and using masks.

## 2. Method

This research article refers to a research article conducted by [14] with the following research design are :

a. Literature study on mathematical modeling of the SARS-CoV-2 virus using masks and vaccines.
b. Preparation of initial assumptions.
c. Compile a compartment diagram based on assumptions.
d. Construct mathematical models based on compartment diagrams.
e. Determine the equilibrium point.
f. An equilibrium point is a point that will not change with time. In other words, when time $t$ goes to infinity, the value of that point will not change. Systematically the definition can be written as follows:
g. Definition : $\bar{x} \in \mathbb{R}^n$ point is said to be the equilibrium point of $\dot{x}(t) = f(x,t)$ if it satisfies $f(\bar{x}) = 0$. [16]
h. Determine the basic reproduction number ($R_0$).

   The basic reproduction number ($R_0$) is used to measure the potential for disease transmission[17]. By determining the stability conditions, $R_0$ can analyze the equilibrium point. When $R_0 < 1$, then the number of infected populations is decreasing. This means that the disease will disappear from the population. But when $R_0 > 1$, the number of infected individuals is increasing. This means that the disease will be exist in the population[18].

   In order to get $R_0$ we have to look at the dominant eigenvalues from the next generation matrix [19], as follows:

$$K = FV^{-1}$$

$F$ and $V$ is the $nxn$ matrix with

$$F = \left[\frac{\partial F_i(x_1)}{\partial y_j}\right] \text{ dan } V = \left[\frac{\partial V_i(x_2)}{\partial y_j}\right]$$

   $x_1$ : laten population

   $x_2$ : infected population

i. Perform stability analysis.
j. Numerical simulation using MATLAB program.

## 3. Results and Discussion

### 3.1 Mathematical Model

This study uses the SEIR model (Susceptible, Exposed, Infected, Recovered), modified into five subpopulations. A subpopulation of susceptible individuals not wearing a mask ($S_1$), a subpopulation of susceptible individuals using a mask ($S_2$), a subpopulation of latent individuals (E) where the individual has been infected but cannot transmit the virus because in the case of Covid-19 there is an incubation period, a subpopulation of infected individuals (I) and the cured subpopulation (R). The initial assumptions used in the model are as follows:

a. The population is assumed to be closed.
b. The number of births and the number of deaths is assumed to be the same per unit of time at the rate $\mu$. This means that the population is constant.
c. Death due to the disease is negligible. Death that occurs in each population is natural death.
d. The population is homogeneous. This means that each individual has the same possibility to make contact with other individuals.
e. Vulnerable individuals will be vaccinated with a vaccination proportion is $\rho$.
f. Unvaccinated newborn will enter $S_1$(t) at rate $(1 - \rho)\mu$.

g.  The virus cannot infect vulnerable individuals who wear masks at the awareness rate of wearing masks $u$.

h.  Individuals in compartment $S_2$ will be placed into compartment $S_1$ if they are no longer wearing the mask at a rate of $(1 - u)$.

i.  Transmission of the virus occurs when susceptible individuals contact infected individuals, either directly or indirectly at a rate of $\beta$.

j.  Individuals infected with the virus in the latent subpopulation (E) will enter the infected individual (I) at a rate of $\delta$.

k.  Individuals infected with the virus can recover from the disease at a rapid rate $\sigma$.

l.  Individuals who have recovered from the disease but have a low awareness of using masks can be re-infected when they encounter infected individuals at a rate of $\frac{\beta RI}{N}(1 - u)$.

Based on these assumptions, a compartment diagram can be formed, as follows:
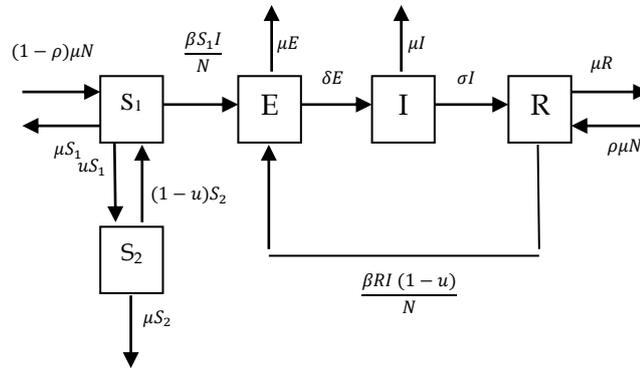


**Figure 1.** Compartment Diagram of the SARS-CoV-2 SEIR Model with Vaccine Administration and Use of Masks

Then based on the compartment diagram obtained a system of differential equations, as follows:

$$\frac{dS_1}{dt} = (1 - \rho)\mu N + (1 - u)S_2 - (\mu + u)S_1 - \frac{\beta S_1 I}{N} \tag{1}$$

$$\frac{dS_2}{dt} = uS_1 - (\mu + (1 - u))S_2 \tag{2}$$

$$\frac{dE}{dt} = \frac{\beta S_1 I}{N} + \frac{\beta RI(1-u)}{N} - (\mu + \delta)E \tag{3}$$

$$\frac{dI}{dt} = \delta E - (\mu + \sigma)I \tag{4}$$

$$\frac{dR}{dt} = \sigma I + \rho\mu N - \mu R - \frac{\beta RI(1-u)}{N} \tag{5}$$

**Table 1.** Variable Description

| Variable | Description |
|---|---|
| $S_1$ | Number of vulnerable individuals not wearing masks |
| $S_2$ | Number of vulnerable individuals wearing masks |
| E | Number of latent individuals |
| I | Number of infected individuals |
| R | Number of recovered individuals |

Since N is constant, it is possible to do scaling on each subpopulation to the total population in order to simplify the system. The proportion of the number of individuals in each subpopulation is stated as follows:

$$s_1 = \frac{S_1}{N}, s_2 = \frac{S_2}{N}, e = \frac{E}{N}, i = \frac{I}{N}, r = \frac{R}{N}$$

Then the system can be changed to the following:

$$\frac{ds_1}{dt} = (1-\rho)\mu + (1-u)s_2 - (\mu+u)s_1 - \beta s_1 i \qquad (6)$$

$$\frac{ds_2}{dt} = us_1 - (\mu + (1-u))s_2 \qquad (7)$$

$$\frac{de}{dt} = \beta s_1 i + \beta r i(1-u) - (\mu+\delta)e \qquad (8)$$

$$\frac{di}{dt} = \delta e - (\mu+\sigma)i \qquad (9)$$

$$\frac{dr}{dt} = \sigma i + \rho\mu - \mu r - \beta r i(1-u) \qquad (10)$$

**Table 2.** Parameter Description

| Parameter | Description |
|---|---|
| $\mu$ | Birth and death rates |
| $\rho$ | Coverage rate of vaccination |
| $u$ | The rate of awareness of the use of masks |
| $\beta$ | The rate of transmission when in contact with an infected individual |
| $\delta$ | Transmission rate from compartment E to I |
| $\sigma$ | Cure rate |

### 3.2 Equilibrium Point

Equating to zero in equation (4) – (8), the equilibrium point is found [16]. We get two equilibrium points from the model, namely the disease-free equilibrium points and the endemic equilibrium point.

a.  Disease-Free Equilibrium Point
    The disease-free state is fulfilled when no individual is infected with the virus or it can be said i = 0.
    If $E_0$ is a disease-free equilibrium point, then

$$E_0 = \left\{ s_1 = \frac{(1-\rho)(\mu+1-u)}{\mu+1}, s_2 = \frac{(1-\rho)u}{\mu+1}, e = 0, i = 0, r = \rho \right\}$$

b.  Endemic Equilibrium Point
    If $E_1$ is an endemic equilibrium point, then

$$E_1 = \{s_1 = s_1^*, s_2 = s_2^*, e = e^*, i = i^*, r = r^*\}$$

    Because the shape of the endemic equilibrium point is complex, it cannot be written in the article

### 3.3 Basic Reproduction Number

The basic reproduction number ($R_0$) is obtained using the next generation matrix [17][19].
Known:

$$\frac{de}{dt} = \beta s_1 i + \beta r i(1-u) - (\mu+\delta)e$$

$$\frac{di}{dt} = \delta e - (\mu+\sigma)i$$

so that

$$f = \begin{pmatrix} \beta s_1 i + \beta r i(1-u) \\ 0 \end{pmatrix} \text{ and } v = \begin{pmatrix} (\mu + \delta)e \\ -\delta e + (\mu + \sigma)i \end{pmatrix}$$

Then the Jacobian matrix is

$$F = \begin{bmatrix} 0 & \beta s_1 + \beta r(1-u) \\ 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \mu + \delta & 0 \\ -\delta & \mu + \sigma \end{bmatrix}$$

$$V^{-1} = \frac{1}{(\mu+\delta)(\mu+\sigma)} \begin{bmatrix} \mu + \sigma & 0 \\ \delta & \mu + \delta \end{bmatrix} = \begin{bmatrix} \dfrac{1}{\mu+\delta} & 0 \\ \dfrac{\delta}{(\mu+\delta)(\mu+\sigma)} & \dfrac{1}{\mu+\sigma} \end{bmatrix}$$

So that it is obtained
$$K = F \cdot V^{-1}$$

$$= \begin{bmatrix} 0 & \beta s_1 + \beta r(1-u) \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{\mu+\delta} & 0 \\ \dfrac{\delta}{(\mu+\delta)(\mu+\sigma)} & \dfrac{1}{\mu+\sigma} \end{bmatrix}$$

$$= \begin{bmatrix} \dfrac{\delta(\beta s_1 + \beta r(1-u))}{(\mu+\delta)(\mu+\sigma)} & \dfrac{\beta s_1 + \beta r(1-u)}{\mu+\sigma} \\ 0 & 0 \end{bmatrix}$$

The substitution of the disease-free equilibrium point is $s_1 = \frac{(1-\rho)(\mu+1-u)}{\mu+1}$ and $r = \rho$,
we get:

$$K = \begin{bmatrix} \dfrac{\delta(\beta\frac{(1-\rho)(\mu+1-u)}{\mu+1}+\beta\rho(1-u))}{(\mu+\delta)(\mu+\sigma)} & \dfrac{\left(\beta\frac{(1-\rho)(\mu+1-u)}{\mu+1}+\beta\rho(1-u)\right)}{(\mu+\sigma)} \\ 0 & 0 \end{bmatrix}$$

The eigenvalues of K are obtained, namely
1. $\lambda_1 = \frac{\delta\beta((1-\rho)(\mu+1-u)+\rho(1-u)(\mu+1))}{(\mu+1)(\mu+\delta)(\mu+\sigma)}$
2. $\lambda_2 = 0$

Then the basic reproduction number is obtained as follows:
$$R_0 = \frac{\delta\beta((1-\rho)(\mu+1-u)+\rho(1-u)(\mu+1))}{(\mu+1)(\mu+\delta)(\mu+\sigma)}$$

## 3.4 Stability Analysis

Based on the theory presented by [18] when $R_0 < 1$ will cause the virus to disappear from the population or go to the point of being free of disease. Therefore, the stability analysis is carried out using the basic reproduction number, and $R_0 < 1$ will be used to determine the condition for the stability of the disease-free equilibrium point:

$$R_0 = \frac{\delta\beta((1-\rho)(\mu+1-u)+\rho(1-u)(\mu+1))}{(\mu+1)(\mu+\delta)(\mu+\sigma)} < 1$$

so that it is obtained

$$\frac{\delta\beta((1-\rho)(\mu+1-u)+\rho(1-u)(\mu+1))}{(\mu+1)(\mu+\delta)(\mu+\sigma)} < 1$$
$$\Leftrightarrow \delta\beta\big((1-\rho)(\mu+1-u)+\rho(1-u)(\mu+1)\big) < (\mu+1)(\mu+\delta)(\mu+\sigma)$$
$$\Leftrightarrow \delta\beta(\mu-\rho\mu+1-\rho-u+u\rho+\rho\mu+\rho-u\rho\mu-u\rho) < (\mu+1)(\mu+\delta)(\mu+\sigma)$$
$$\Leftrightarrow \delta\beta(\mu+1-u-u\rho\mu) < (\mu+1)(\mu+\delta)(\mu+\sigma)$$
$$\Leftrightarrow \delta\beta(\mu+1+u(-1-\rho\mu)) < (\mu+1)(\mu+\delta)(\mu+\sigma)$$
$$\Leftrightarrow \delta\beta(\mu+1)+\delta\beta u(-1-\rho\mu) < (\mu+1)(\mu+\delta)(\mu+\sigma)$$

$\Leftrightarrow \delta\beta u(-1 - \rho\mu) < (\mu + 1)(\mu + \delta)(\mu + \sigma) - \delta\beta(\mu + 1)$

$\Leftrightarrow u > \frac{(\mu+1)(\mu+\delta)(\mu+\sigma)-\delta\beta(\mu+1)}{\delta\beta(-1-\rho\mu)}$ , because $-1 - \rho\mu < 0$ .

So, when the value of $\boldsymbol{u} > \frac{(\boldsymbol{\mu}+\boldsymbol{1})(\boldsymbol{\mu}+\boldsymbol{\delta})(\boldsymbol{\mu}+\boldsymbol{\sigma})-\boldsymbol{\delta}\boldsymbol{\beta}(\boldsymbol{\mu}+\boldsymbol{1})}{\boldsymbol{\delta}\boldsymbol{\beta}(-\boldsymbol{1}-\boldsymbol{\rho}\boldsymbol{\mu})}$, $R_0 < 1$ is obtained. This means that the disease-free point is stable so that the SARS-CoV virus will disappear from the population. When we take the value of $\boldsymbol{u} < \frac{(\boldsymbol{\mu}+\boldsymbol{1})(\boldsymbol{\mu}+\boldsymbol{\delta})(\boldsymbol{\mu}+\boldsymbol{\sigma})-\boldsymbol{\delta}\boldsymbol{\beta}(\boldsymbol{\mu}+\boldsymbol{1})}{\boldsymbol{\delta}\boldsymbol{\beta}(-\boldsymbol{1}-\boldsymbol{\rho}\boldsymbol{\mu})}$, $R_0 > 1$ is obtained. This means that the disease-free point is unstable, so the SARS-CoV-2 virus will be exist in the population.

### 3.5  Numerical Simulation

The simulation of the dynamics of the SARS-CoV-2 distribution model with the provision of vaccines and masks was carried out using the MATLAB program. Simulations were carried out at disease-free points and endemic points, as follows:

**Table 3.** Parameter Value and Source

| Parameter | Parameter Value | Source |
|-----------|-----------------|--------|
| $\mu$ | 0.0125000 | [20] |
| $\rho$ | 0.6000000 | Assumption |
| $\beta$ | 0.0400000 | Assumption |
| $\delta$ | 0.0714258 | [15] |
| $\sigma$ | 0.0000667 | [15] |

With the initial value used is
$S_1(0) = 0.20$, $S_2(0) = 0.25$, $E(0) = 0.12$ , $I(0) = 0.25$ , $R(0) = 0.18$ .

a. Disease-Free Equilibrium Point
The disease-free equilibrium point will be stable when the value of $u > \frac{(\mu+1)(\mu+\delta)(\mu+\sigma)-\delta\beta(\mu+1)}{\delta\beta(-1-\rho\mu)} = 0.62$. So here will be compared three parameter values as follows

**Table 4.** Assumptions Parameter Values of u at the Disease-Free Equilibrium Point

|  | $u_1$ | $u_2$ | $u_3$ |
|---|-------|-------|-------|
| Parameter Value | 0.65 | 0.75 | 0.85 |
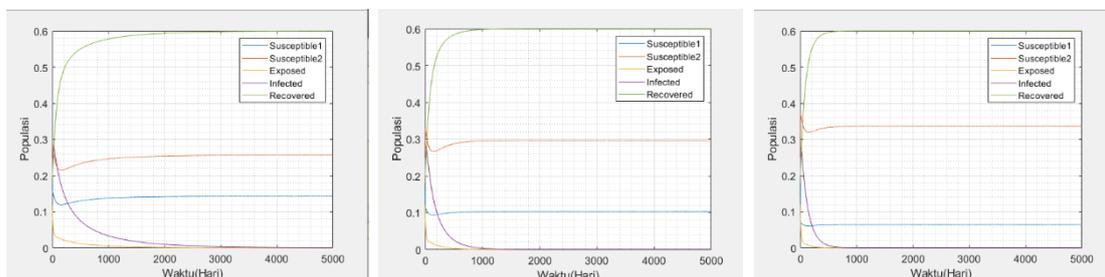


**Figure 2.** Graph of Disease-Free Equilibrium Point with Parameter Values $u_1, u_2, u_3$.
(In order from left)

Based on Figures 2, it can be seen that the population of infected individuals is closer to zero when the value $u_3$ or $u = 0.85$ is taken. This means that the greater the value of u taken, the faster the population of infected individuals will be exhausted.

When given the values of $u_1 = 0.65$, $u_2 = 0.75$, and $u_3 = 0.85$ in the simulation of disease-free equilibrium point, we get $R_0$ are 0.913, 0.656, and 0.399 respectively, the three results meet $R_0 < 1$.

b. Endemic Equilibrium point

The endemic point will be stable when the value of $u < \frac{(\mu+1)(\mu+\delta)(\mu+\sigma)-\delta\beta(\mu+1)}{\delta\beta(-1-\rho\mu)} = 0.62$. So here will be compared three parameter values as follows:

**Table 5.** Assumptions Parameter Values of u at the Endemic Equilibrium Point

|  | $u_1$ | $u_2$ | $u_3$ |
|---|---|---|---|
| Parameter Value | 0.55 | 0.40 | 0.20 |
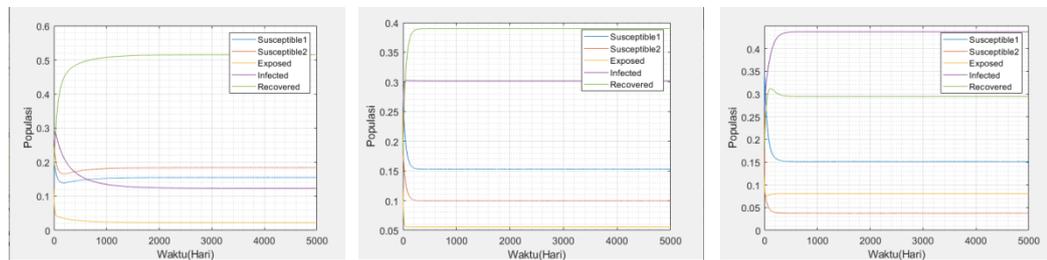


**Figure 3**. Graph of the Endemic Equilibrium Point with parameter values $u_1, u_2, u_3$. (In order from left)

Based on Figure 3, in order from left it can be seen that by taking the value of $u_1 = 0.55$ obtained stable at the number of infected subpopulations of 0.1230, $u_1 = 0.40$ obtained stable at the number of infected subpopulations of 0.3018 and $u_1 = 0.20$ obtained stable at the number of infected subpopulations of 0.4366. This shows that by taking a smaller value, the value of the infected individual or population will be even greater.

When given the values of $u_1 = 0.55$, $u_2 = 0.40$, dan $u_3 = 0.20$ in the simulation of endemic equilibrium point, we get $R_0$ are 1.170, 1.556, and 2.071 respectively, the three results meet $R_0 > 1$.

On the results of [14], the value of $\beta, \delta, u_1, u_2$ and $\rho$ has changed to obtain the $R_0 > 1$. However, in this article researchers have considered only one parameter namely $u$ or the awareness rate of using a mask with a threshold $u < \frac{(\mu+1)(\mu+\delta)(\mu+\sigma)-\delta\beta(\mu+1)}{\delta\beta(\rho\mu-1)}$ so that the resulting mathematical model will be easier to use in determining SARS-CoV-2 virus control policies.

## 4. Conclusions

Based on the initial assumptions and the compartment diagram that has been compiled, a mathematical model of the spread of SARS-CoV-2 in the presence of vaccines and the use of masks is obtained as follows:

$$\frac{dS_1}{dt} = (1-\rho)\mu N + (1-u)S_2 - (\mu + u)S_1 - \frac{\beta S_1 I}{N}$$

$$\frac{dS_2}{dt} = uS_1 - (\mu + (1-u))S_2$$

$$\frac{dE}{dt} = \frac{\beta S_1 I}{N} + \frac{\beta RI(1-u)}{N} - (\mu + \delta)E$$

$$\frac{dI}{dt} = \delta E - (\mu + \sigma)I$$

$$\frac{dR}{dt} = \sigma I + \rho\mu N - \mu R - \frac{\beta RI(1-u)}{N}$$

The basic reproduction number ($R_0$) is used to perform stability analysis and the basic reproduction number is $R_0 = \frac{\delta\beta((\mu+1-u)(1-\rho)+\rho(1-u)(\mu+1))}{(\mu+1)(\mu+\delta)(\mu+\sigma)}$. When the value $u > \frac{\delta\beta((\mu+1-u)(1-\rho)+\rho(1-u)(\mu+1))}{(\mu+1)(\mu+\delta)(\mu+\sigma)}$ taken, $R_0 < 1$ is obtained. This means that the disease-free point is stable so that the SARS-CoV-2 virus will disappear from the population. When the value $u < \frac{\delta\beta((\mu+1-u)(1-\rho)+\rho(1-u)(\mu+1))}{(\mu+1)(\mu+\delta)(\mu+\sigma)}$ taken, $R_0 < 1$ is obtained. This means that the disease-free point is unstable so that the SARS-CoV-2 virus will continue to exist in the population

The decreasing awareness of using masks will cause the number of infected individuals to become higher. Thus, awareness of the use of masks significantly affects the control of the SARS-CoV-2 virus.

For further researchers, it is recommended to add the assumption of death due to disease because in the case of Covid-19, death caused by the disease will probably occur. Researchers can also use new parameter values to simulate the model.

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