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Education and Mathematics Models (A Case Study of Epidemiology of Virus Spread)

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Abstract

Viruses are the cause of diseases that affect the human body and can lead to pandemics and epidemics in various countries. No new content has been added beyond the original text. Viruses are the cause of diseases that affect the human body and can lead to pandemics and epidemics in various countries. The language used is clear, objective, and value-neutral, with a formal register and precise word choice. The text adheres to conventional structure and format, with consistent citation and footnote style. The text is free from grammatical errors, spelling mistakes, and punctuation errors. The purpose of this research is to determine the SIS model for the spread of viral diseases, such as Covid-19 and bird flu, and their resolution behavior. The model is formed by creating a flow diagram of the disease spread using the SIS (Susceptible, Infected, Susceptible) model. The sentences and paragraphs create a logical flow of information with causal connections between statements. The study revealed two equilibrium points: the disease-free equilibrium point and the endemic equilibrium point. To analyze the stability of the disease-free equilibrium point, linearization around the equilibrium point was used. The disease-free equilibrium point is asymptotically stable if the basic reproduction number is less than one, indicating that the disease will disappear after a certain period of time. Numerical simulations were conducted to analyze the behavior of the disease model.

Keywords: Education Models, Mathematics Models, SIS (Susceptible, Infected, Susceptible)

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INTRODUCTION

Viruses are microorganisms that are too small to see with a normal microscope. They cannot be cultured outside of their host. Although viruses have been known to cause disease for centuries, they were not well understood until the 20th century. Aristotle, for example, described rabies in 400 B.C.. Rabies is a viral disease that affects animals.

Epidemiological investigations are required for revealing disease causes or disease prevention and eradication programs that require expertise such as physiology, biochemistry, pathology, microbiology, and genetics. Epidemiology is a discipline of health science that studies the nature and spread of various health issues and diseases in a specific population in order to prevent and control them. Epidemiology is derived from the Greek words Epi (on/about), Demos (population), and Logos (knowledge). Thus, epidemiology is the study of populations. In this situation, the essential essence of epidemiology is to focus on specific demographic groups or communities and quantify events in society (using rate values, ratios, proportions, and the like).

An epidemic is an event where a disease spreads over a large area and affects many people. Epidemiologists consider the term 'plague' to be synonymous with 'epidemic'. The term 'epidemic' comes from the Greek words 'epi', meaning 'above', and 'demos', meaning 'people'. It is an extraordinary occurrence when a disease affects the people of a certain area in greater numbers than normal estimates of occurrence within a short period of time. The Hebrew term for epidemic is Magefa, which appears in the book of Numbers (B'midbar) describing the depiction of Jews in the Sinai desert. This caused the death of 14,700 people. The term 'magefa' describes an outbreak with the connotation of a dangerous and infectious disease. Examples of epidemic outbreaks include the bubonic plague, also known as the Black Death, which occurred in medieval Europe, the Ebola virus outbreak in the Democratic Republic of Congo in 2019, bird flu (H5N1) outbreak in Indonesia in 2012, and the SARS outbreak in 2003.

One of the newest viruses is the Corona Virus Disease 2019, commonly known as Covid-19, which causes respiratory tract infections in animals and humans. In humans, it can cause mild symptoms such as the common cold, as well as more severe diseases such as Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS). Coronavirus Disease (COVID-19) is a virus that can spread to various animals, such as camels, cats, and bats. It is important to note that this information is objective and based on scientific evidence. Although rare, it can also infect humans, as evidenced by the case in China in December 2019. . The Covid-19 virus is highly contagious and poses a significant risk to people of all ages. It cannot survive outside of a host organism for extended periods of time. As of June 30, 2020, the Ministry of Health of the Republic of Indonesia Indonesia has confirmed 56,385 cases of Covid-19, with deaths reported in 34 provinces (case fatality rate 5.1%). Men accounted for 51.5% of cases, and patients aged 55-64 had the highest death rate compared to other age groups.

The execution of measures to combat Covid-19 is dependent on the intensity of the infection and the countries' ability to handle the virus. Several population dynamics models were developed to explore the global dynamics of the Covid-19 disease by calculating various control approaches. The models account for virus transmission by include the usage of medical masks and isolation.

Previous research by Nining (2013) has extensively used mathematical models to study the distribution of diseases, including influenza, HIV co-infection, hepatitis, malaria, and others. Mathematical methods aid in predicting future disease progression and identifying developing diseases, allowing for anticipation and preventive measures. Most mathematical models used to study diseases are SIR (Susceptible, Infected, and Recovered) models. The SIR model represents the number of people who are susceptible to the disease (S), the number of people who have contracted the disease (I), and the number who have recovered or died (R). The SIR model is widely used by researchers around the world, including in Indonesia, to predict when Covid-19 will end.

The SIS model is an epidemiological model that describes the transmission rates of infectious diseases. It represents a person's lack of immunity after being infected by a disease, causing the individual to become susceptible again after recovering from the disease. This model was derived from the SIR model created by Kermack and McKendrick in 1927. The SIS (Susceptible, Infected, Susceptible) model is a disease spread model where individuals are vulnerable to infection and may recover with medical treatment or natural processes. However, recovery does not guarantee immunity, meaning individuals can be reinfected at any time. This model does not account for immunity after recovery.

The SIS (Susceptible, Infected, Susceptible) model has been used for researching malaria disease, as well as for qualitative analysis of the SIS epidemic model with treatment. No changes in content have been made.

Mathematical modeling is the creation of a description of some real-world behavior (natural phenomena) in the world of mathematics. There are two kinds of mathematical models: deterministic models and empirical models. A deterministic model is a mathematical model that is created around the system's laws or attributes. Meanwhile, empirical models typically concentrate on facts offered by systems or data.

When building a model, it is necessary to follow several stages to produce a variable model. These stages include: 1) Identifying the problem to understand the issue that needs to be formulated; 2) Building necessary assumptions because the model is a simplification of complex reality. The complexity of the problem can be simplified by assuming simple relationships between variables. The assumptions are divided into two categories: a). In step 1, variables that influence observation behavior are classified as either independent or dependent. This classification allows for the exclusion of certain variables if necessary. The model will explain the relationship between the dependent and independent variables. B). Determining the interrelationships between selected study variables before hypothesizing about their relationships generally requires additional simplification. Complex problems may obscure variable relationships, requiring the creation of a submodel.

Model construction can be accomplished through functional relationships, flow diagrams, mathematical equations, or software. Model analysis is performed to find solutions to questions developed during the identification stage. Analysis can be conducted through optimization or simulation. Interpretation is crucial to assess the rationality of the model results, and validation is necessary to test the model's accuracy in predicting real-world events. Optimization is used to determine the optimal solution, while simulation is used to predict the outcome. Interpretation is crucial to assess the rationality of the model results, and validation is necessary to test the model's accuracy in predicting real-world events. A valid model adheres to sound theoretical principles and provides an interpretation of the results that is consistent with reality. If the majority of verification standards are met, the model can be implemented. If not, the model construction must be redesigned. Only then can the results be accepted and the model can be implemented.Implementation is only carried out if the validation results meet the requirements and are rational.

Differential equations are classified into two types based on the number of independent variables involved: ordinary differential equations and partial differential equations. A differential equation is an equation that involves one or more derivatives of an unknown function. There are two types of differential equations: ordinary differential equations and partial differential equations, depending on the derivative of the independent variables involved in the equation. The second ordinary differential equation involves the derivative of one more dependent variable with respect to one independent variable. A partial differential equation involves the derivative of one or more dependent variables on two or more independent variables

METHOD

This research method involves using the library or literature study to identify problems related to the spread of viruses such as Covid-19. The assumptions for mathematical modeling of the virus spread are formulated using a modified SIS model that includes controls such as health masks or isolation. A mathematical model of the virus spread is then created using the formulated assumptions. To complete the stability analysis, first find the equilibrium point. Then, linearize the model using the Jacobi matrix and identify the stability properties of the obtained equilibrium point. Next, search for numerical solutions of the SIS epidemic model simulated with Maple 13. Finally, interpret the results obtained.

RESULT & DISCUSSION

The SIS model is used to describe the spread of the virus. It was developed by adding factors for the use of health masks and isolation. The population is divided into four subpopulations: Susceptible (S), which includes individuals who are susceptible to the disease. This compartment is further divided into two subpopulations: susceptible individuals who do not use health masks (S1) and susceptible individuals who use health masks (S2). The 'Infected' (I) compartment refers to individuals who are infected and capable of transmitting the disease. This compartment is further divided into two subpopulations: 'I1' for individuals who are infected but asymptomatic, and 'I2' for individuals who are infected and either symptomatic or isolated. To model the spread of the virus while taking into account the use of masks and isolation, certain assumptions must be made, such as:

1. The disease is assumed to be non-fatal, meaning it does not cause death.
2. The virus that causes Covid-19 is the corona virus.
3. The population is assumed to be closed, meaning that no individuals enter the population or leave the population (no migration). The total population is assumed to be constant.
4. Natural birth and death rates are assumed to be the same so that the total population is always constant.
5. The population is assumed to be homogeneous, meaning that each individual has the same opportunity to make contact with other individuals.
6. Vulnerable individuals who use health masks $S2$ cannot be infected by the virus.
7. Vulnerable individuals using health masks ($S2$) will return to the vulnerable compartment not using health masks ($S1$) if they stop using health masks.
8. Susceptible individuals who do not use a health mask ($S1$) will go to the infected individual compartment and are not yet sick ($I1$) if infected by the virus because they do not use a health mask.
9. Infected individuals who are not yet sick ($I1$) will go to the compartment for vulnerable individuals who do not use health masks ($S1$) if they recover naturally but are still susceptible to infection.
10. Individuals who are infected and not yet sick ($I1$) will go to the infected and sick individual compartment or be isolated ($I2$) if they are infected and sick because they are not wearing a health mask.
11. Individuals who are infected and sick or isolated ($I2$) will return to the infected and not yet sick individual compartment ($I1$) if they are still infected but no longer sick.
12. Individuals who are infected and sick or isolated ($I2$) will return to the compartment of susceptible individuals who do not wear masks health ($S1$) if you have recovered and are not wearing a mask.
13. Susceptible individuals who do not wear health masks ($S1$) cannot be in the compartment of infected and sick individuals or isolated ($I2$) because they are infected but not sick.
14. The disease is transmitted through direct contact with individuals infected with the corona virus.
15. Every infected individual will definitely go through an isolation process if they are sick.
16. Susceptible and infected individuals may die from natural death.
17. Individuals who are infected but not sick can recover but remain susceptible to infection.

18. Individuals who are isolated can recover from the disease but remain susceptible to infection

The variables and parameters used in the Covid-19 spread model using health and isolation masks are presented in the following table.

Table 1. List of model variables for the spread of Covid-19 disease using health masks and isolation

Variable	Indicator	Unit
$S1(t)$	The amount of people who are susceptible to infection and do not utilize health masks at the time t	Individu
$S2(t)$	Number of people exposed to illness while wearing medical masks at time t	Individu
$I1(t)$	Number of infected and uninfected people at time t	Individu
$I2(t)$	Number of people infected, unwell, or isolated at time t	Individu

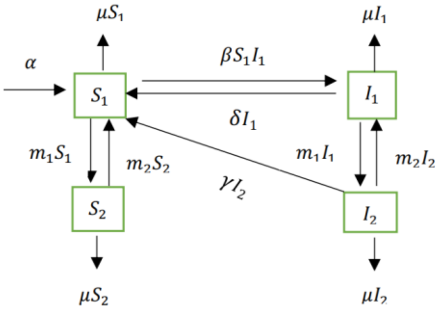
In Table 1, compartment S is separated into two parts: those sensitive to infection without using a health mask (S1) and those susceptible to infection while using a health mask (S2). Compartment I is separated into two sections: one for infected but not sick people (I1) and another for infected and sick or isolated people (I2).

Table 2. List of model parameters for Covid-19 disease propagation employing health masks and isolation

Parameter	Indicator	Unit
α	The birth rate of an individual population	Per day
μ	Individual population death rates	Per day
β	Population change rate $S1$ becomes population $I1$.	Individu / day
δ	The rate of change of population $I1$ to population $S1$ per unit time	Individu / day
γ	The rate of change of population $I2$ to population $S1$ per unit time	Individu / day
$m1$	Level of use of medical masks	Per day
$m2$	Level without using a health mask	Per day

Schematically, the process of spreading disease with the use of health masks and isolation in a population can be presented in the transfer diagram in Figure 1 below.

Figure 1. Transfer diagram



Based on the transfer diagram above, the individual population is divided into four compartments, namely the compartment for individuals susceptible to infection without using a health mask ($S1$), the compartment for individuals susceptible to infection using a health mask ($S2$), the compartment for individuals infected but not sick ($I1$), and the individual compartment infected and sick or isolated($I2$). Every individual born (α) enters compartment ($S1$), individuals who use health masks are grouped into the individual compartment using health masks ($S2$) and will be moved back to ($S1$) if the individual stops using a health mask and is assumed to be an individual in compartment ($S2$) are individuals without symptoms (OTG).

The same process occurs in the infected individual compartment, infected individuals without illness ($I1$) are grouped into the infected and sick individual compartment or isolated ($I2$) if the individual stops using a health mask they will be placed back into ($I1$). Susceptible individuals who can become infected due to direct interaction with infected individuals at a daily cost of per individual. Individuals who are infected but do not become ill can recover spontaneously and return to being vulnerable without wearing a health mask at a rate of per individual each day. persons who are ill, sick, or secluded can recover spontaneously and return to being vulnerable persons at a rate of per individual per day without utilizing health masks.

The following are the factors that influence variations in the number of people in each compartment of the population.

a. Change in subpopulation $S1$ with time (t)

The population of susceptible individuals (S1) increases due to the birth rate at a rate of α, the release rate of health masks from the susceptible population (S2) at a rate of $m2$, the transition rate of the infected but not sick population (I1) to the susceptible population without using a health mask (S1) at a rate of δ, and the transition rate of the isolated infected and sick population (I2) to the susceptible population without using a health mask (S1) at a rate of γ. The Susceptible 1 (S1) population decreases due to natural mortality (μ), interaction with the Infected 1 (I1) population (β), and transition to the Susceptible 2 (S2) population (m1). The mathematical model is as follows:

$$\frac{dS_1}{dt} = \alpha + m_2 S_2 + \delta I_1 + \gamma I_2 - \mu S_1 - \beta S_1 I_1 - m_1 S_1$$

b. Change in $S2$ subpopulation over time (t)

Class $S2$ increases due to the addition of Suscepted 1 ($S1$) with a mask wearing rate of $m1$. The population of Suscepted 1 ($S1$) is reduced because the mask removal rate is $m2$ and natural deaths by population $S2$ are μ. The mathematical model is

$$\frac{dS_2}{dt} = m_1S_1 - m_2S_2 - \mu S_2$$

c. Time (t) variation in subpopulation I1.

Class I1 grows as the Suscepted 1 (S1) population becomes infected but not sick by and the infected and sick (isolated) population (I2) transitions to the infected but not sick population (I1) by m2. The population of Infected 1 (I1) decreases due to the rate of change from an infected but not sick population (I1) to a population susceptible to infection without using a health mask (S1) of m1, as well as natural deaths in the population I1. The mathematical model is as follows:

$$\frac{dI_1}{dt} = \beta S_1I_1 + m_2I_2 - \delta I_1 - m_1I_1 - \mu I_1$$

d. Time (t) variation in subgroup I2.

The population of susceptible individuals (S1) increases due to the birth rate at a rate of α, the release rate of health masks from the susceptible population (S2) at a rate of $m2$, the transition rate of the infected but not sick population (I1) to the susceptible population without using a health mask (S1) at a rate of δ, and the transition rate of the isolated infected and sick population (I2) to the susceptible population without using a health mask (S1) at a rate of γ. The Susceptible 1 (S1) population decreases due to natural mortality (μ), interaction with the Infected 1 (I1) population (β), and transition to the Susceptible 2 (S2) population (m1). The mathematical model is as follows:

$$\frac{dI_2}{dt} = m_1I_1 - m_2I_2 - \gamma I_2 - \mu I_2$$

Based on the description above, the spread of viral diseases can be modeled mathematically in the form of a system of first order nonlinear differential equations, namely as follows:

$$\frac{dS_1(t)}{dt} = \alpha + m_2S_2 + \delta I_1 + \gamma I_2 - \mu S_1 - \beta S_1I_1 - m_1S_1$$
$$\frac{dS_2(t)}{dt} = m_1S_1 - m_2S_2 - \mu S_2$$
$$\frac{dI_1(t)}{dt} = \beta S_1I_1 + m_2I_2 - \delta I_1 - m_1I_1 - \mu I_1$$
$$\frac{dI_2(t)}{dt} = m_1I_1 - m_2I_2 - \gamma I_2 - \mu I_2$$

The equilibrium point of the above system will then be found, and stability analysis will be presented in relation to this equilibrium point.

The spread of Covid-19 can be modeled using a system of nonlinear differential equations that incorporate health masks and isolation. The system has two equilibrium points: the disease-free equilibrium point and the endemic equilibrium point. The equilibrium point of System (3.3.1), obtained by solving for ($S1$, $S2$, $I1$, $I2$), is also included.

$$\frac{dS_1}{dt} = \frac{dS_2}{dt} = \frac{dI_1}{dt} = \frac{dI_2}{dt} = 0$$

(Equation 1)

The equation is then expressed as follows:

$$\begin{aligned}
\alpha + m_2S_2 + \delta I_1 + \gamma I_2 - \mu S_1 - \beta S_1 I_1 \\ - m_1 S_1 &= 0\\
m_1S_1 - m_2S_2 - \mu S_2 &= 0\\
\beta S_1 I_1 + m_2 I_2 - \delta I_1 - m_1 I_1 - \mu I_1 &= 0\\
m_1 I_1 - m_2 I_2 - \gamma I_2 - \mu I_2 &= 0
\end{aligned}$$

The disease-free equilibrium point (E_0) is the point at which there is no disease in the population and I1 = I2 = 0. Then we have:

$$\begin{aligned}
E_0 &= (S_1, S_2 . I_1, I_2)\\
&= \left(\frac{\alpha(\mu + m_2)}{\mu(\mu + m_1 + m_2)}, \frac{m_1\alpha}{\mu(\mu + m_1 + m_2)}, 0,0\right)
\end{aligned}$$

The Endemic Equilibrium Point (E1) is the point at which the infected class is not equal to zero or when the disease has spread throughout the population. Endemic sickness means that there are always infected individuals in the population, hence I1 > 0 and I2 > 0. As a result,

$$\begin{aligned}
S_1^* &= \frac{BC - G}{\beta C}\\
S_2^* &= \frac{m_1(BC - m_2 m_1)}{\beta CF}
\end{aligned}$$

$$\begin{aligned}
I_1^* &= \frac{CF\alpha\beta - FH(BC - G) + m_2(m_1(BC - G))}{\beta F\big((B - \delta)C - m_1\gamma - G\big)}\\
I_2^* &= \frac{m_1 I_1}{(\mu + m_2 + \gamma)}
\end{aligned}$$

$B = (\mu + m1 + \delta)$, $C = (\mu + m2 + \gamma)$, $F = (\mu + m2)$, $G = m2m1$, dan $H = (\mu + m1)$.

The Basic Reproduction Number (R0) is used to determine whether or not an endemic will emerge in a given location.

$$R_0 = \beta\left(\frac{\mu + m_2}{\mu + m_1 + m_2}\right)\frac{m_2 + \gamma + \mu}{BC - m_1 m_2}$$

$B = (\mu + m1 + \delta)$ dan $C = (\mu + m2 + \gamma)$

The mathematical model for the spread of the virus illness is a nonlinear system. The stability of the model's equilibrium point is examined by first constructing a Jacobian matrix and then determining the eigenvalues of the Jacobian matrix acquired through the system linearization model around the equilibrium or equilibrium point. The linearized system will be as follows.

$$\begin{aligned}
f_1(S_1, S_2, I_1, I_2 &= \alpha + m_2S_2 + \delta I_1 + \gamma I_2 - \mu S_1 - \beta S_1 I_1 - m_1 S_1 \\
f_2(S_1, S_2, I_1, I_2 &= m_1S_1 - m_2S_2 - \mu S_2 \\
f_3(S_1, S_2, I_1, I_2 &= \beta S_1 I_1 + m_2 I_2 - \delta I_1 - m_1 I_1 - \mu I_1 \\
f_4(S_1, S_2, I_1, I_2 &= m_1 I_1 - m_2 I_2 - \gamma I_2 - \mu I_2
\end{aligned}$$

The Taylor series is then applied around the equilibrium point to obtain a linear approximation. The linear approximation derived from the preceding set of equations is as follows:

$$\frac{dx}{dt} = \mathrm{Ax}$$

$\boldsymbol{x} = (S1, S2, I1, I2)$ and A is the Jacobian matrix or $A = J$.

$$\begin{aligned}
J &= \begin{bmatrix} \frac{\partial f_1}{\partial S_1} & \frac{\partial f_1}{\partial S_2} & \frac{\partial f_1}{\partial I_1} & \frac{\partial f_1}{\partial I_2} \\ \frac{\partial f_2}{\partial S_1} & \frac{\partial f_2}{\partial S_2} & \frac{\partial f_2}{\partial I_1} & \frac{\partial f_2}{\partial I_2} \\ \frac{\partial f_3}{\partial S_1} & \frac{\partial f_3}{\partial S_2} & \frac{\partial f_3}{\partial I_1} & \frac{\partial f_3}{\partial I_2} \\ \frac{\partial f_4}{\partial S_1} & \frac{\partial f_4}{\partial S_2} & \frac{\partial f_4}{\partial I_1} & \frac{\partial f_4}{\partial I_2} \end{bmatrix} \\
&= \begin{bmatrix} -B & m_2 & \delta - \beta S_1 & \gamma \\ m_1 & -(\mu + m_2) & 0 & 0 \\ \beta I_1 & 0 & \beta S_1 - B & m_2 \\ 0 & 0 & m_1 & -C \end{bmatrix}
\end{aligned}$$

$B = \delta + m1 + \mu$ dan $C = m2 + \gamma + \mu$

The disease-free equilibrium point of System (3.3.1) is denoted as $E0 = (S1, S2.\ I1, I2)$. The Jacobian matrix resulting from the linearization of the Covid-19 disease spread model around this point can be expressed as follows:

$$J(E_0) = \begin{bmatrix} -(\mu + m_1) & m_2 & \delta - \beta\left(\frac{\alpha(\mu + m_2)}{\mu A}\right) & \gamma \\ m_1 & -(\mu + m_2) & 0 & 0 \\ 0 & 0 & \beta\left(\frac{\alpha(\mu + m_2)}{\mu A}\right) - B & m_2 \\ 0 & 0 & m_1 & -C \end{bmatrix}$$

$A = \mu + m1{+}m2$, $B = \delta + m1 + \mu$, dan $C = m2 + \gamma + \mu$

The next step for the proof writer is to look for the eigenvalues of the Jacobian matrix $J(E0)$. The characteristic equation can be obtained by using the matrix equation $J(E0)$.

$$\begin{aligned}
\frac{1}{\mu A}\big((-\beta\alpha\mu C - \beta\alpha\mu\lambda - \beta\alpha m_2 C - \beta\alpha m_2\lambda + B\mu AC + B\mu A\lambda \\
+ \lambda\mu AC - \lambda^2\mu A - m_1 m_2 \mu A)(\mu^2 + \mu m_2 \\
+ 2\lambda\mu + m_1\mu + m_1\lambda + \lambda m_2 - \lambda^2)\big) = 0
\end{aligned}$$

Then, using Maple 13, we obtain the eigenvalues of the following matrix $J(E0)$.

$$
\begin{aligned}
\lambda_1 &= -\frac{1}{2}\frac{1}{\mu A}\left(P-\sqrt{Q}\right)\\
\lambda_2 &= -\frac{1}{2}\frac{1}{\mu A}\left(P+\sqrt{Q}\right)\\
\lambda_3 &= -\mu\\
\lambda_4 &= -(\mu+m_1+m_2)
\end{aligned}
$$

$A = \mu + m1+m2$, $B = \delta + m1 + \mu$, dan $C = m2 + \gamma + \mu$, $P = -\beta\alpha\mu - \beta\alpha m2 + B\mu A + \mu AC$, $Q = \beta 2\alpha 2\mu 2 + 2\beta 2\alpha 2\mu m2 - 2\beta\alpha\mu 2BA + 2\beta\alpha\mu 2AC + \beta 2\alpha 2m22 - 2\beta\alpha m2B\mu A + 2\beta\alpha m2\mu AC + B2\mu 2A2 - 2\mu 2A2C + \mu 2A2C2 + 4\mu 2A2m1m2$

Because the parameter values α, β, μ, , δ, γ, $m1$, $m2 > 0$, the eigenvalues obtained from the disease-free equilibrium point are $\lambda 1 < 0$, $\lambda 2 < 0$, $\lambda 3 < 0$, and $\lambda 4 < 0$, so the property The stability of the eigenvalue is stable.

Endemic equilibrium point $E1(S1*, S2*, I1*, I2*)$

$$E_1\left(\frac{BC-G}{\beta C}, \frac{m_1(BC-G)}{\beta CF}, \frac{CF\alpha\beta-FH(BC-G)+m_2(m_1(BC-G))}{\beta F\big((B-\delta)C-m_1\gamma-G\big)}, \frac{m_1 I_1}{(\mu+m_2+\gamma)}\right)$$

$B = (\mu + m1 + \delta)$, $C = (\mu + m2 + \gamma)$,
$F = (\mu + m2)$, $G = m2m1$, dan $H = (\mu + m1)$

Inserted into the Jacobian matrix (3.5.2) to produce the following

$$J(E_1)=\begin{bmatrix} -(\mu+m_1+\beta I_1) & m_2 & \delta-\beta S_1 & \gamma\\ m_1 & -(\mu+m_2) & 0 & 0\\ \beta I_1 & 0 & \beta S_1-B & m_2\\ 0 & 0 & m_1 & -C \end{bmatrix}$$

The eigenvalue of the Jacobian matrix J(E1) at the endemic equilibrium point will then be computed numerically.

DISCUSSION SECTION

The parameters and total population used were taken from several studies of the Corona virus and the author's assumptions. The parameter values used are

Tabel 3. Parameter & Total Population

No	Parameter	Indicator	Score
1.	α	Natural birth rate	$\frac{10.000}{75 \times 365}$
2.	μ	Natural death rate	$\frac{10.000}{75 \times 365}$

3.	$m1$	Rate of mask use	70%
4.	$m2$	Mask removal rate	30%
5.	β	The rate of change of $S1$ becomes $I1$	1
6.	δ	The rate of change of $I1$ to $S1$	1 14
7.	γ	The rate of change of $I2$ becomes $S1$	1 14

Based on the above parameter values, the basic reproduction number of the system (3.3.1) is $R0 = 0.5251283124$. Since $R0 < 1$, the disease will not spread, which will cause the Covid-19 disease to disappear, and after a certain period of time, the population will be disease-free. The simulation results at the disease-free equilibrium point $E0$ are presented in Appendix 1 using the Maple 13 program based on the parameter values in Table 3.6.1 and with the initial value distribution $S1(0) = 0.75, S2(0) = 0.35, I1(0) = 0.25, I2(0) = 0.11$

It can be seen that the population of susceptible individuals who do not use health masks ($S1$) decreases until day 5, then increases until day 10, reaching the point 0.4872909698 and is stable at that point. The population of susceptible individuals using respirators ($S2$) decreases until day 10, then increases until day 15, reaches the point 0.5127090300 and is stable at this point. The population of infected but not sick individuals ($I1$) decreases until the 20th day toward the point 0 and stabilizes at that point. The population of infected and sick or isolated individuals ($I2$) decreases toward point 0 by day 20 and stabilizes at that point.

For conditions $R0 < 1$, the disease-free equilibrium point is asymptotically stable, meaning that over a long period of time the population of infected individuals will become smaller or the system will become disease-free faster.

Next, a numerical simulation of the endemic equilibrium point $E1$ is performed for $R0 > 1$. If the values of the parameters $m2$ and β are increased to $m2 = 0.8$ and the parameter $m1$ is decreased to $m1 = 0.2$, the basic reproduction number of the system (3.3.1) is $R0 = 1.574842019$. Since $R0 > 1$, the disease will spread, in other words, it will become endemic. Simulation results by providing any initial value, it is found that the solution will always go towards the endemic equilibrium point ($E1$) and away from the disease-free equilibrium point ($E0$).

This research used SIS model was developed by adding the factors of health mask use and isolating the spread of Corona Virus Disease 2019 (Covid-19) by dividing the individual population into four subpopulations, namely Susceptible (S), namely individuals who are susceptible to the disease, which in this compartment is divided into two subpopulations, namely susceptible individuals not using health masks ($S1$) and susceptible individuals using health masks ($S2$), infected (I), namely individuals who are infected and can transmit the disease, divided in this compartment into two subpopulations, namely infected and not ill individuals ($I1$) and infected and ill or isolated individuals ($I2$).

Tabel 4. State of Art from another research

Author	Years	Title	Purpose of Research
Abdullahi, et al	2020	Mathematical modeling for infectious viral disease: The COVID-19 perspective	examined various forms of mathematical models relevant to containment, risk analysis, and the characteristics of COVID-19. Special emphasis was placed on the extension of Susceptible-Infectious-Recovered (SIR) models for policy relevance in the COVID-19 era.
Ali Yousef, et al	2023	A mathematical model of COVID-19 and the multi fears of the community during the epidemiological stage	In this paper, they present the existence and unambiguousness of the initial value problem, and analyze the local stability of the two equilibria, namely the disease-free and the positive equilibrium. Finally, with the help of a suitable Lyapunov function, it shows that global asymptotic stability holds under certain conditions. It conclude by simulating and summarizing our theoretical results.
Alemzewde Ayalew,Yezbalem Molla,Tenaw Tilahun,and Tadele Tesfa	2022	Mathematical Model and Analysis on the Impacts of Vaccination and Treatment in the Control of the COVID-19 Pandemic with Optimal Control	By introducing two time-dependent variables representing the educational campaign for susceptible individuals and the continuous treatment for

			quarantined individuals, they extended the considered model to an optimal control problem system. Using MATLAB ode45, numerical results were presented to complement the analytical results of the model.
B. Ivorra, et al	2020	Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections	This is a mathematical model for the spread of COVID-19. It is a new θ-SEIHRD model that considers the disease's unique characteristics, such as the presence of undetected cases and varying levels of infectiousness and sanitation in hospitals.
Harraq, et al.	2020	Epidemiological models in high school mathematics education	to introduce the basic concepts and notions of mathematical modeling of infectious diseases, we propose that these models be taught and learned in high school mathematics education
Hamou, A.A., et al.	2022	Analysis and dynamics of a mathematical model to predict unreported cases of COVID-19 epidemic in Morocco.	A Matlab tool was used to demonstrate the progress of unexplored cases in Morocco and to verify predicted results.
Pinky Lubna, Dobrovolny Hana M	2022	Epidemiological Consequences	The model was used to simulate co-

		of Viral Interference: A Mathematical Modeling Study of Two Interacting Viruses	circulating epidemics of SARS-CoV-2 and other respiratory viruses, including influenza, respiratory syncytial virus (RSV), and rhinovirus. The results showed that co-circulation of SARS-CoV-2 and RSV caused the greatest suppression of SARS-CoV-2. However, co-circulating SARS-CoV-2 with influenza or rhinovirus resulted in little change in SARS-CoV-2 emergence, but shifted the timing of influenza and rhinovirus emergence.
Salihu, et al.	2021	Mathematical modeling of COVID-19 epidemic with effect of awareness programs.	awareness programs and hospitalization strategies for mild and severe cases to evaluate the impact of public awareness on the spread of COVID-19. The model was fitted to the cumulative number of confirmed COVID-19 cases
Vytla, et al.	2020	Mathematical Models for Predicting Covid-19 Pandemic: A Review	focuses on popular techniques in use for the predictive modeling of the Covid-19 epidemic. The paper covers the Gaussian model, SIRD, SEIRD, and the latest θ-SEIHRD techniques used for predictive modeling of epidemics.
Zakharov, Victor,	2022	Forecasting a	This research aims

Yulia Balykina, Igor Ilin, and Andrea Tick		New Type of Virus Spread: A Case Study of COVID-19 with Stochastic Parameters	to solve the problem of predicting the future dynamics of stochastic model parameters. These parameters are used to define the future values of the total number of cases (C), recovered and deceased individuals (R), and active cases (I). Intelligent heuristic algorithms are proposed to calculate future trajectories of stochastic parameters, including the percentage increase in the total number of confirmed cases of the disease and the dynamic characteristics of epidemiological processes.

The spread of Covid-19 can become an epidemic if infected and infectious individuals remain in the population by removing more masks than using them. However, the use of medical masks for susceptible and infected individuals and the isolation of infected individuals can prevent this outbreak. By incorporating the use of health masks and isolating the spread of the virus, an SIS model was developed in this research. By incorporating vaccination, lockdown, and quarantine factors, the mathematical modeling of virus spread can be further developed. In addition, open population assumptions The Next Generation Approach can be utilized.

CONCLUSION

The discussion above leads to the following conclusions.. The SIS model was developed by adding the factors of using health masks and isolating the spread of Corona Virus Disease 2019 (Covid-19) by dividing the individual population into four subpopulations, namely: Susceptible (S), namely individuals who are susceptible to disease, which in this compartment is divided into two subpopulations, namely susceptible individuals not using health masks ($S1$) and susceptible individuals using health masks ($S2$), Infected (I) namely individuals who are infected and can transmit the disease, where in this compartment it is divided into two subpopulations, namely individuals who are infected and not sick ($I1$) and infected and sick or isolated individuals ($I2$) are as follows. By studying the system of differential equations in a non-dimensional model, two equilibrium points are derived from the SIS model, which was built by adding parameters for the usage of health masks and virus isolation. The parameters that affect the basic reproduction number (R0) are the level of susceptible individuals who do not wear masks when in contact with infected individuals who are not sick (β), the level of mask usage (m1), and the level of mask removal (m2). the rate of natural death (μ), the rate of infected individuals without illness becoming susceptible individuals not using health masks (δ), and the rate of infected and sick or isolated individuals becoming susceptible individuals not using health masks (γ).

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