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Analysis of Stability Covid19 Spread Mathematical Model Type *SV_1V_2EIR* Regarding Both Vaccinated and Not Vaccinated Human Population

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ABSTRACT

The Covid19 case dated 11 November 2021 recorded that the human population died from Covid19 (143,595 people) with confirmed cases (4,249,323 cases) and active cases (9,537 cases). Based on these data, it can be concluded that COVID-19 is an acute and deadly disease. In addition to deaths, due to Covid-19, namely the increase in divorce cases, decreased income in the economy and tourism. In this study, the author made a mathematical modeling of Covid19 type SV_1V_2EIR as an effort to prevent the spread of Covid19. In the modeling there are human populations susceptible to Covid19 (S), human populations have been vaccinated (V_1), human populations have not been vaccinated (V_2), human populations are *exposed* (E), human populations are infected with Covid19 (I), and human populations recovered from Covid19 (R). The research objectives are 1) to build a mathematical model of Covid19, 2) to determine the fixed point and basic reproduction numbers, and 3) to analyze the stability of the fixed point. This type of research includes applied science research. The research procedure is 1) observing real phenomena, 2) searching literature, 3) determining variables, parameters, and assumptions in mathematical modeling, 4) building a mathematical model of Covid19, 5) analyzing the Covid19 mathematical model in the form of fixed points, basic reproduction numbers, and fixed point stability. The results of the analysis 1) the mathematical model type SV_1V_2EIR has a fixed point without disease and an endemic fixed point, 2) a fixed point without disease is stable for the condition, and the endemic fixed point is stable for the condition.

I. Introduction

In March 2020, Indonesia was hit by an infectious disease known as Covid19. The latest update of Covid19 cases on November 11, 2021, it was recorded that the human population who died from Covid19 (143,595 people) with confirmed cases (4,249,323 cases) and active cases (9,537 cases) [1]. Based on these data, it can be concluded that Covid-19 is an acute and deadly disease. In addition to death, due to Covid19, it causes several problems in the life of the human population, including increasing divorce cases [2], declining income in the economy and tourism

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[3][4]. Based on the data of Covid19 and the impact that occurs in human life, it can be said that Covid19 is a serious threat and a real problem faced by humans. The government and the public have taken several solutions to prevent the spread of Covid-19. Actions taken include implementing health protocols, health education, vaccinations [5][6].

Real events that occur in everyday life can be modeled mathematically. Real events modeled in Mathematical Language have been carried out by [7]–[9]. In the research that was developed, real events were created in a mathematical language called mathematical modeling.

Mathematical modeling was first developed by Rose and MacDonald who are known as the Ross and Ross-MacDonald models, respectively [10]. Mathematical modeling can be used to describe problems that occur in the fields of health, social, education, economics, and other fields [11]–[14].

In this paper, the authors develop a mathematical model of Covid19 type SV_1V_2EIR by considering the human population that has been vaccinated and has not been vaccinated. In the modeling developed, there are 6 (six) populations, including the human population susceptible to Covid19 (S), the human population having been vaccinated (V_1), the human population not being vaccinated (V_2), the human population *exposed* (E), the human population being infected with Covid19 (I), and the human population recovering from Covid19 (R).

The objectives of this research are 1) to build a mathematical model of Covid19 type SV_1V_2EIR, 2) to determine the fixed point and basic reproduction number, analyze the stability of the fixed point, and 4) numerical simulation to see the behavior of the population in the model.

II. Method

A. Type of Research

Research being developed is applied science research on Covid19 cases. The data used in the simulation is secondary data taken from journals and the official website of the Ministry of Health of the Republic of Indonesia.

B. Procedure

Procedures carried out to achieve the goals set in this study include:

1) Observing real phenomena that occur in daily life related to Covid19 through print media, electronic media, and social media,
2) Looking for literature or related references with Covid19 sourced from journals, books, proceedings, and *websites* official,
3) Determine the variables, parameters, and assumptions in the mathematical model that is built,
4) Build a mathematical model of Covid19 type SV_1V_2EIR,
5) Analyze the mathematical model of Covid19 type SV_1V_2EIR,
   a) Determine fixed point
   b) Determining the basic reproduction number [11], [15], [16],
   c) Determining the stability of the fixed point [7], [9],
6) Conclusions and suggestions

The research procedure carried out is presented in a flow chart as shown in Figure 1.

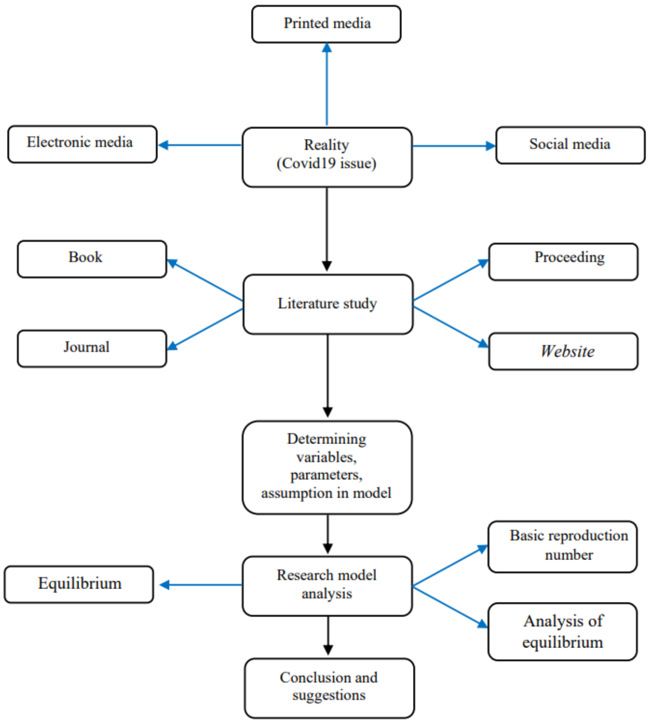

Figure 1. Research flowchart

III. Results and Discussion

A. Real Phenomenon and Literature Studies

The results of observations made showed that a real phenomenon that has occurred in Indonesia since March 2020 is the spread of Covid19. This phenomenon is interesting to research mathematically by making a mathematical modeling related to Covid19 and supported by literature or references related to the disease. Some of the literature related to Covid19, among others [17]–[21].

B. Mathematical model Type SV_1V_2EIR

Mathematical model Type SV_1V_2EIR consists of 6 (six) populations, including the human population susceptible to Covid19 (S), the human population having been vaccinated (V_1), human population having not vaccinated (V_2), *exposed* group (E), Covid19 infected population (I), and Covid19 recovered (R). The model SV_1V_2EIR is shown as the following figure 2.

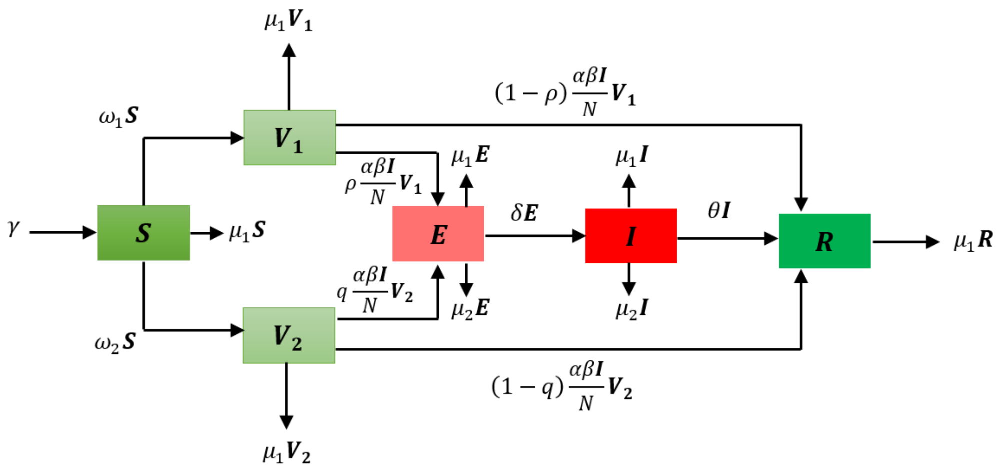

Figure 2. Type of SV_1V_2EIR Model

Based on that model, obtained a system of differential equations for each population, namely;

$$
\begin{aligned}
\frac{ds}{dt} &= \gamma - (\omega_1 + \omega_2 + \mu_1)S \\
\frac{dV_1}{dt} &= \omega_1 S - \left(\mu_1 + \rho\frac{\alpha\beta I}{N}\right)V_1 \\
\frac{dV_2}{dt} &= \omega_2 S - \left(\mu_1 + q\frac{\alpha\beta I}{N}\right)V_2 \\
\frac{dE}{dt} &= (\rho V_1 + qV_2)\left(\frac{\alpha\beta I}{N}\right) - (\mu_1 + \mu_2 + \delta)E \\
\frac{dI}{dt} &= \delta E - (\mu_1 + \mu_2 + \theta)I \\
\frac{dR}{dt} &= \left((1-\rho)V_1 + (1-q)V_2\right)\left(\frac{\alpha\beta I}{N}\right) + \theta I - \mu_1 R
\end{aligned}
\tag{1}
$$

with

$$S + V_1 + V_2 + E + I + R = N \tag{2}$$

In the model SV_1V_2EIR, the rate of the human population that has been and has not been vaccinated into an exposed population of $\rho\frac{\alpha\beta I}{N}V_1$ dan $q\frac{\alpha\beta I}{N}V_2$. Proportion of the rate of the human population having been vaccinated to the exposed population (ρ) and the rate of the unvaccinated human population being the exposed population (q). The average contact that occurs between the human populations has and has not been vaccinated with the human population infected with Covid19 (α). Covid-19 transmission rate per one contact (β).

The mathematical modeling of the spread of Covid19 that was built in this study consisted of 6 populations with the following assumptions:

a) The vulnerable population increases due to the birth rate,
b) Birth rate equals natural death rate,
c) The natural death rate is present in every human population,
d) The proportion of the vaccinated human population being exposed is greater than the unvaccinated human population,
e) The death rate due to disease is only found in the exposed population and the population infected with Covid19,
f) The recovered population is a population that has recovered from Covid19 and is permanent.

The parameters contained in the mathematical model of type SV_1V_2EIR contained in Table 1.

Table 1. Parameters in a Mathematical Model of type SV_1V_2EIR

Parameters	Description
γ	Human birth rate
μ_1	Morbidity rate
μ_2	Covid19 Caused Morbidity Rate
α	Average contact
β	Covid-19 transmission rate per one contact
ω_1	The rate of movement of the susceptible human population into the vaccinated human population
ω_2	The rate of movement of the susceptible human population to the unvaccinated human population
δ	The rate of movement of the exposed human population to the infected human population
ψ	The rate of movement of the infected human population to the recovered human population

To simplify the analysis of the system of differential equations (1), it is converted into a non-dimensional system of differential equations. The system of non-dimensional differential equations is obtained by making a comparison of each population to the total population, namely:

$$s=\frac{S}{N};v_1=\frac{V_1}{N};v_2=\frac{V_2}{N};\ e=\frac{E}{N};i=\frac{I}{N};\text{dan } r=\frac{R}{N} \tag{3}$$

Then system (3) is substituted into system (1) so that a system of differential equations is obtained, namely:

$$\begin{aligned}
\frac{ds}{dt}&=\frac{\gamma}{N}-(\omega_1+\omega_2+\mu_1)s\\
\frac{dv_1}{dt}&=\omega_1 s-(\mu_1+\rho\alpha\beta i)v_1\\
\frac{dv_2}{dt}&=\omega_2 s-(\mu_1+q\alpha\beta i)v_2\\
\frac{de}{dt}&=(\rho v_1+qv_2)(\alpha\beta i)-(\mu_1+\mu_2+\delta)e\\
\frac{di}{dt}&=\delta e-(\mu_1+\mu_2+\theta)i\\
\frac{dr}{dt}&=\big((1-\rho)v_1+(1-q)v_2\big)(\alpha\beta i)+\theta i-\mu_1 r
\end{aligned} \tag{4}$$

with

$$s+v_1+v_2+e+i+r=\frac{S}{N}+\frac{V_1}{N}+\frac{V_2}{N}+\frac{E}{N}+\frac{I}{N}+\frac{R}{N}=1 \tag{5}$$

And the set of positive invariants

$$P=\{(s,v_1,v_2,e,i,r)\geq 0|s+v_1+v_2+e+i+r=1\} \tag{6}$$

As the origin (domain) of the system of equations (4). Furthermore, from the system of equations (4), the variable r only exists in the recovered population and has no effect on other populations in the model, so that to perform the analysis, the recovered population can be ignored. The system of differential equations analyzed is as follows.

$$\begin{aligned}
\frac{ds}{dt}&=\frac{\gamma}{N}-(\omega_1+\omega_2+\mu_1)s\\
\frac{dv_1}{dt}&=\omega_1 s-(\mu_1+\rho\alpha\beta i)v_1\\
\frac{dv_2}{dt}&=\omega_2 s-(\mu_1+q\alpha\beta i)v_2\\
\frac{de}{dt}&=(\rho v_1+qv_2)(\alpha\beta i)-(\mu_1+\mu_2+\delta)e\\
\frac{di}{dt}&=\delta e-(\mu_1+\mu_2+\theta)i
\end{aligned} \tag{7}$$

C. Mathematical Model Analysis Type SV_1V_2EIR

C.1 Fixed Point

The system of differential equations (7) is used to determine the fixed point. The fixed point is determined by making each differential equation in (7) equal to 0 (zero) [14].

$$\frac{ds}{dt}=0,\ \frac{dv_1}{dt}=0,\ \frac{dv_2}{dt}=0,\ \frac{de}{dt}=0 \text{ dan } \frac{di}{dt}=0.$$

The disease-free fixed point (disease-free equilibrium) contains, $e=0$, and $i=0$, while *endemic equilibrium has* $e\neq 0$, and $i\neq 0$. The fixed point of the system (7) is as follows.

C.1.1 Fixed Point Without Disease

$$T_0(s,v_1,v_2,e,i)=\left(\frac{\gamma}{(\omega_1+\omega_2+\mu_1)\mathrm{N}},\frac{\gamma\omega_1}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1},\frac{\gamma\omega_2}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1},0,0\right)$$

C.1.2 Fixed Point With Disease

$T_1(s^*, v_1^*, v_2^*, e^*, i^*)$, where

$$s^* = \frac{\gamma}{AN}$$

$$v_1^* = \frac{ABHN\alpha\beta\mu_1(q-\rho) + q\alpha^2\beta^2\gamma\delta\rho(\omega_1+\omega_2)}{2AN\alpha^2\beta^2\delta\mu_1\rho(q-\rho)} + \frac{\sqrt{\alpha^2\beta^2\left(\left(ABHN\mu_1(q+\rho) - q\alpha\beta\gamma\delta\rho(\omega_1+\omega_2)\right)^2 - 4ABHNq\mu_1\rho\left(ABHN\mu_1 - \alpha\beta\gamma\delta(\rho\omega_1+q\omega_2)\right)\right)}}{2AN\alpha^2\beta^2\delta\mu_1\rho(q-\rho)}$$

$$v_2^* = \frac{ABHN\alpha\beta\mu_1(-q+\rho) + q\alpha^2\beta^2\gamma\delta\rho(\omega_1+\omega_2)}{2ANq\alpha^2\beta^2\delta\mu_1(\rho-q)} + \frac{\sqrt{\alpha^2\beta^2\left(\left(ABHN\mu_1(q+\rho) - q\alpha\beta\gamma\delta\rho(\omega_1+\omega_2)\right)^2 - 4ABHNq\mu_1\rho\left(ABHN\mu_1 - \alpha\beta\gamma\delta(\rho\omega_1+q\omega_2)\right)\right)}}{2ANq\alpha^2\beta^2\delta\mu_1(\rho-q)},$$

$$e^* = \frac{q\alpha^2\beta^2\gamma\delta\rho(\omega_1+\omega_2) - ABHN\alpha\beta\mu_1(q+\rho)}{2ABNq\alpha^2\beta^2\delta\rho} - \frac{\sqrt{\alpha^2\beta^2\left(\left(ABHN\mu_1(q+\rho) - q\alpha\beta\gamma\delta\rho(\omega_1+\omega_2)\right)^2 - 4ABHNq\mu_1\rho\left(ABHN\mu_1 - \alpha\beta\gamma\delta(\rho\omega_1+q\omega_2)\right)\right)}}{2ABNq\alpha^2\beta^2\delta\rho},$$

$$i^* = \frac{Aq\alpha^2\beta^2\gamma\delta\rho(\omega_1+\omega_2) - BHN\alpha\beta\mu_1(q+\rho)}{2ABHNq\alpha^2\beta^2\rho} - \frac{\sqrt{\alpha^2\beta^2((ABHN\mu_1(q+\rho) - q\alpha\beta\gamma\delta\rho(\omega_1+\omega_2))^2 - 4ABHNq\mu_1\rho(ABHN\mu_1 - \alpha\beta\gamma\delta(\rho\omega_1+q\omega_2)))}}{2ABHNq\alpha^2\beta^2\rho}$$

with

$$A = (\omega_1 + \omega_2 + \mu_1)$$
$$B = (\mu_1 + \mu_2 + \delta)$$
$$H = (\mu_1 + \mu_2 + \theta)$$

D. Basic Reproductive Number

Basic Reproductive Number $(\mathcal{R}_0)$ is the expected number of susceptible populations to become infected during the course of infection [22], [23]. The basic reproduction number is determined using the next generation matrix G [11]. The equation used is only the infected equation, i.e

$$\frac{de}{dt} = (\rho v_1 + q v_2)(\alpha\beta i) - (\mu_1 + \mu_2 + \delta)e$$
$$\frac{di}{dt} = \delta e - (\mu_1 + \mu_2 + \theta)i \quad (8)$$

with

$$F_i = \begin{pmatrix} (\rho v_1 + q v_2)(\alpha\beta i) \\ \delta e \end{pmatrix}$$

$$F = \begin{pmatrix} 0 & \left(\frac{\rho\gamma\omega_1}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1} + \frac{q\gamma\omega_2}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1}\right)(\alpha\beta) \\ \delta & 0 \end{pmatrix} \quad (9)$$

and

$$V_i = \begin{pmatrix} (\mu_1 + \mu_2 + \delta)e \\ (\mu_1 + \mu_2 + \theta)i \end{pmatrix} \quad (10)$$

$$V = \begin{pmatrix} (\mu_1 + \mu_2 + \delta) & 0 \\ 0 & (\mu_1 + \mu_2 + \theta) \end{pmatrix} \quad (11)$$

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu_1+\mu_2+\delta} & 0 \\ 0 & \frac{1}{\mu_1+\mu_2+\theta} \end{pmatrix} \quad (12)$$

So that :

$$G = FV^{-1} = \begin{pmatrix} 0 & \left(\frac{\rho\gamma\omega_1}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1} + \frac{q\gamma\omega_2}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1}\right)\left(\frac{\alpha\beta}{\mu_1+\mu_2+\theta}\right) \\ \frac{\delta}{\mu_1+\mu_2+\delta} & 0 \end{pmatrix}$$

Based on the analysis conducted, the dominant eigenvalue of the G matrix is obtained, namely:

$$\mathcal{R}_0 = \sqrt{\frac{\alpha\beta\delta(\mu_1+\omega_2+\omega_1)q\gamma\omega_2 + (\mu_2+\omega_2+\omega_1)\rho\gamma\omega_1}{N\mu_1(\mu_1+\mu_2+\delta)(\mu_1+\mu_2+\theta)(\mu_1+\omega_2+\omega_1)(\mu_2+\omega_2+\omega_1)}}$$

The next step is to analyze the stability of the fixed point without disease and the endemic fixed point.

E. Fixed Point Stability Without Disease

Let the system of equations (7) be written in the form,

$$\begin{aligned} f_1(s,v_1,v_2,e,i) &= \frac{\gamma}{N} - (\omega_1+\omega_2+\mu_1)s \\ f_2(s,v_1,v_2,e,i) &= \omega_1 s - (\mu_1+\rho\alpha\beta i)v_1 \\ f_3(s,v_1,v_2,e,i) &= \omega_2 s - (\mu_1+q\alpha\beta i)v_2 \\ f_4(s,v_1,v_2,e,i) &= (\rho v_1+qv_2)(\alpha\beta i) - (\mu_1+\mu_2+\delta)e \\ f_5(s,v_1,v_2,e,i) &= \delta e - (\mu_1+\mu_2+\theta)i \end{aligned} \tag{13}$$

To determine stability around a fixed point without disease T_0, First, the linearization of equation (13) is carried out, by means of

$$J = \begin{pmatrix} \frac{\partial f_1}{\partial s} & \frac{\partial f_1}{\partial v_1} & \frac{\partial f_1}{\partial v_2} & \frac{\partial f_1}{\partial e} & \frac{\partial f_1}{\partial i} \\ \frac{\partial f_2}{\partial s} & \frac{\partial f_2}{\partial v_1} & \frac{\partial f_2}{\partial v_2} & \frac{\partial f_2}{\partial e} & \frac{\partial f_2}{\partial i} \\ \frac{\partial f_3}{\partial s} & \frac{\partial f_3}{\partial v_1} & \frac{\partial f_3}{\partial v_2} & \frac{\partial f_3}{\partial e} & \frac{\partial f_3}{\partial i} \\ \frac{\partial f_4}{\partial s} & \frac{\partial f_4}{\partial v_1} & \frac{\partial f_4}{\partial v_2} & \frac{\partial f_4}{\partial e} & \frac{\partial f_4}{\partial i} \\ \frac{\partial f_5}{\partial s} & \frac{\partial f_5}{\partial v_1} & \frac{\partial f_5}{\partial v_2} & \frac{\partial f_5}{\partial e} & \frac{\partial f_5}{\partial i} \end{pmatrix} \tag{14}$$

$$J = \begin{pmatrix} -(\omega_1+\omega_2+\mu_1) & 0 & 0 & 0 & 0 \\ \omega_1 & -(\mu_1+\rho\alpha\beta i) & 0 & 0 & -\rho\alpha\beta v_1 \\ \omega_2 & 0 & -(\mu_1+q\alpha\beta i) & 0 & -q\alpha\beta v_2 \\ 0 & \rho\alpha\beta i & q\alpha\beta i & -(\mu_1+\mu_2+\delta) & (\rho v_1+qv_2)(\alpha\beta) \\ 0 & 0 & 0 & \delta & -(\mu_1+\mu_2+\theta) \end{pmatrix}$$

so that the Jacobi matrix is obtained, then the fixed point T_0 substituting into the Jacobi matrix, the result of the substitution is a matrix:

$$J = \begin{pmatrix} -(\omega_1+\omega_2+\mu_1) & 0 & 0 & 0 & 0 \\ \omega_1 & -\mu_1 & 0 & 0 & -\frac{\rho\alpha\beta\gamma\omega_1}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1} \\ \omega_2 & 0 & -\mu_1 & 0 & -\frac{q\alpha\beta\gamma\omega_2}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1} \\ 0 & 0 & 0 & -(\mu_1+\mu_2+\delta) & \left(\frac{\alpha\beta\gamma(\rho\omega_1+q\omega_2)}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1}\right) \\ 0 & 0 & 0 & \delta & -(\mu_1+\mu_2+\theta) \end{pmatrix}$$

To determine the eigenvalues used the equation:

$$\left|J_{T_0} - \lambda I\right| = 0 \tag{15}$$

or

$$\begin{vmatrix} -(\omega_1+\omega_2+\mu_1)-\lambda & 0 & 0 & 0 & 0 \\ \omega_1 & -\mu_1-\lambda & 0 & 0 & -\dfrac{\rho\alpha\beta\gamma\omega_1}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1} \\ \omega_2 & 0 & -\mu_1-\lambda & 0 & -\dfrac{q\alpha\beta\gamma\omega_2}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1} \\ 0 & 0 & 0 & -(\mu_1+\mu_2+\delta)-\lambda & \left(\dfrac{\alpha\beta\gamma(\rho\omega_1+q\omega_2)}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1}\right) \\ 0 & 0 & 0 & \delta & -(\mu_1+\mu_2+\theta)-\lambda \end{vmatrix} = 0$$

Based on the analysis carried out, five eigenvalues were obtained, namely:

$\lambda_1 = -\mu_1 < 0$

$\lambda_2 - \mu_1 < 0$

$\lambda_3 - (\omega_1+\omega_2+\mu_1) < 0$

$$\lambda_4 = \frac{1}{2}\left(-(2\mu_1+2\mu_2+\theta+\delta) - \sqrt{\left((\mu_1+\mu_2+\theta)-(\mu_1+\mu_2+\delta)\right)^2 + \frac{4\alpha\beta\gamma\delta(\rho\omega_1+q\omega_2)}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1}}\right) < 0$$

$$\lambda_5 = \frac{1}{2}(-(2\mu_1+2\mu_2+\theta+\delta) + \sqrt{\left((\mu_1+\mu_2+\theta)-(\mu_1+\mu_2+\delta)\right)^2 + \frac{4\alpha\beta\gamma\delta(\rho\omega_1+q\omega_2)}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1}} < 0$$

To make $\lambda_5 < 0$ so

$$(2\mu_1+2\mu_2+\theta+\delta) > \sqrt{\left((\mu_1+\mu_2+\theta)-(\mu_1+\mu_2+\delta)\right)^2 + \frac{4\alpha\beta\gamma\delta(\rho\omega_1+q\omega_2)}{(\omega_1+\omega_2+\mu_1)\mathrm{N}\mu_1}}$$

According to [16], the stability of the fixed point can be seen from its eigenvalues, namely stable, if

a) Every real eigenvalue is negative: $\lambda_i < 0$ for each *i*, or
b) Part complex eigenvalues $Re(\lambda_i) < 0$ for each *i*.

Based on the analysis it can be concluded that it can be concluded that the system (7) is stable around a fixed point without disease.

The stability of the endemic fixed point is determined by linearizing equation (13), in order to obtain the Jacobi matrix (14). Next, the endemic fixed point T_1 is substituted into equation (14)

$$J = \begin{pmatrix} -(\omega_1+\omega_2+\mu_1) & 0 & 0 & 0 & 0 \\ \omega_1 & -(\mu_1+\rho\alpha\beta i^*) & 0 & 0 & -\rho\alpha\beta {v_1}^* \\ \omega_2 & 0 & -(\mu_1+q\alpha\beta i^*) & 0 & -q\alpha\beta {v_2}^* \\ 0 & \rho\alpha\beta i^* & q\alpha\beta i^* & -(\mu_1+\mu_2+\delta) & (\rho {v_1}^* + q {v_2}^*)(\alpha\beta) \\ 0 & 0 & 0 & \delta & -(\mu_1+\mu_2+\theta) \end{pmatrix}$$

and determine the eigenvalues using the equation (15).

$$J = \begin{pmatrix} -(\omega_1+\omega_2+\mu_1)-\lambda & 0 & 0 & 0 & 0 \\ \omega_1 & -(\mu_1+\rho\alpha\beta i^*)-\lambda & 0 & 0 & -\rho\alpha\beta {v_1}^* \\ \omega_2 & 0 & -(\mu_1+q\alpha\beta i^*)-\lambda & 0 & -q\alpha\beta {v_2}^* \\ 0 & \rho\alpha\beta i^* & q\alpha\beta i^* & -(\mu_1+\mu_2+\delta)-\lambda & (\rho {v_1}^* + q {v_2}^*)(\alpha\beta) \\ 0 & 0 & 0 & \delta & -(\mu_1+\mu_2+\theta)-\lambda \end{pmatrix}$$

The results of the analysis obtained 5 (five) eigenvalues, namely. First eigenvalue $-(\omega_1+\omega_2+\mu_1)$ and the next four eigenvalues are the roots of the characteristic equation

$$b_0\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4 = 0 \tag{16}$$

where i^*, ${v_1}^*$, ${v_2}^*$ can be gained at T_1 and value for b_0, b_1, b_2, b_3 and b_4 as followed.

$b_0 = 1$

$b_1 = (\mu_1+\mu_2+\theta) + (\mu_1+\mu_2+\delta) + (\mu_1+\rho\alpha\beta i^*) + (\mu_1+q\alpha\beta i^*)$

$$\begin{aligned} b_2 = {} & (\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + (\mu_1+\mu_2+\theta)\left((\mu_1+\mu_2+\delta)+(\mu_1+q\alpha\beta i^*)\right) \\ & + (\mu_1+\rho\alpha\beta i^*)\left((\mu_1+\mu_2+\theta)+(\mu_1+\mu_2+\delta)+(\mu_1+q\alpha\beta i^*)\right) - (\rho {v_1}^* + q {v_2}^*)(\alpha\beta)\delta \end{aligned}$$

$$b_3 = (\mu_1+\mu_2+\theta)(\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + (\mu_1+\rho\alpha\beta i^*)((\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + (\mu_1+\mu_2+\theta)((\mu_1+\mu_2+\delta)+(\mu_1+q\alpha\beta i^*)) - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)\delta) + \delta(q\alpha\beta v_2{}^* q\alpha\beta i^* - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)(\mu_1+q\alpha\beta i^*) + \rho\alpha\beta v_1{}^* \rho\alpha\beta i^*)$$

$$b_4 = (\mu_1+\rho\alpha\beta i^*)((\mu_1+\mu_2+\theta)(\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + q\alpha\beta v_2{}^* q\alpha\beta i^*\delta - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)(\mu_1+q\alpha\beta i^*)\delta) + \rho\alpha\beta v_1{}^*(\mu_1+q\alpha\beta i^*)\delta\rho\alpha\beta i^*$$

According to the Routh-Hurwitz criteria [16], for a characteristic equation of degree 4, the stability condition must meet the property,

$$b_1 > 0, b_3 > 0, b_4 > 0 \text{ dan } b_1 b_2 b_3 > b_3^2 + b_1^2 b_4$$

By analyzing the value of b_0, b_1, b_2, b_3 and b_4 gained :

$$b_1 = (\mu_1+\mu_2+\theta) + (\mu_1+\mu_2+\delta) + (\mu_1+\rho\alpha\beta i^*) + (\mu_1+q\alpha\beta i^*) > 0$$

Value for $b_3 > 0$ if :

$$(\mu_1+\rho\alpha\beta i^*)\Big((\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + (\mu_1+\mu_2+\theta)\big((\mu_1+\mu_2+\delta)+(\mu_1+q\alpha\beta i^*)\big) - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)\delta\Big) > 0$$

$$\delta(q\alpha\beta v_2{}^* q\alpha\beta i^* - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)(\mu_1+q\alpha\beta i^*) + \rho\alpha\beta v_1{}^* \rho\alpha\beta i^*) > 0$$

so that it is obtained

$$b_3 = (\mu_1+\mu_2+\theta)(\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + (\mu_1+\rho\alpha\beta i^*)\Big((\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + (\mu_1+\mu_2+\theta)\big((\mu_1+\mu_2+\delta)+(\mu_1+q\alpha\beta i^*)\big) - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)\delta\Big) + \delta(q\alpha\beta v_2{}^* q\alpha\beta i^* - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)(\mu_1+q\alpha\beta i^*) + \rho\alpha\beta v_1{}^* \rho\alpha\beta i^*) > 0$$

Value for $b_4 > 0$ jika :

$$\big((\mu_1+\mu_2+\theta)(\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + q\alpha\beta v_2{}^* q\alpha\beta i^*\delta - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)(\mu_1+q\alpha\beta i^*)\delta\big) > 0$$

so that it is obtained

$$b_4 = (\mu_1+\rho\alpha\beta i^*)\big((\mu_1+\mu_2+\theta)(\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + q\alpha\beta v_2{}^* q\alpha\beta i^*\delta - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)(\mu_1+q\alpha\beta i^*)\delta\big) + \rho\alpha\beta v_1{}^*(\mu_1+q\alpha\beta i^*)\delta\rho\alpha\beta i^* > 0$$

Value for $b_1 b_2 b_3 > b_3^2 + b_1^2 b_4$ fulfilled if:

$$\big((\mu_1+\mu_2+\theta)(\mu_1+\mu_2+\delta)(\mu_1+q\alpha\beta i^*) + q\alpha\beta v_2{}^* q\alpha\beta i^*\delta - (\rho v_1{}^* + q v_2{}^*)(\alpha\beta)(\mu_1+q\alpha\beta i^*)\delta\big) < 0$$

Based on the analysis, it can be concluded that system (7) is stable around the endemic fixed point. The stability properties of the system (7) around the disease-free and endemic fixed points are summarized in Table 2.

Table 2 Fixed point stability properties

Condition	Fixed point without disease T_0	Endemic fixed point T_1
$\mathcal{R}_0 < 1$	Stable	Unstable
$\mathcal{R}_0 > 1$	Unstable	Stable

IV. Conclusion

The results of the analysis and discussion that have been described, it can be concluded that:

1) The type mathematical model SV_1V_2EIR has 2 (two) fixed points, namely a fixed point without disease and an endemic fixed point.
2) A fixed point without stable disease for conditions where the basic reproduction number is more than zero or $\mathcal{R}_0 < 1$, and a stable endemic fixed point for conditions where the basic reproduction number is more than zero or $\mathcal{R}_0 > 1$.

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