JOURNAL OF FUNDAMENTAL MATHEMATICS
AND APPLICATIONS (JFMA) VOL. 6 NO. 2 (NOV 2023)
Available online at www.jfma.math.fsm.undip.ac.id

MATHEMATICAL MODEL OF MEASLES DISEASE SPREAD WITH TWO-DOSE VACCINATION AND TREATMENT

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Abstract. This study developed a model for the spread of measles based on the SEIR model by adding the factors of using the first dose of vaccination, the second dose of vaccination, and treatment. Making this model begins with making a compartment diagram of the spread of the disease, which consists of seven subpopulations, namely susceptible subpopulations, subpopulations that have received the first dose of vaccination, subpopulations that have received the second dose vaccination, exposed subpopulations, infected subpopulations, subpopulations that have received treatment, and subpopulations healed. After the model is formed, the disease-free equilibrium point, endemic equilibrium point, and basic reproduction number (R_0) are obtained. Analysis of the stability of the disease-for equilibrium point was locally asymptotically stable when $(R_0) < 1$. The backward bifurcation analysis occurs when (R_c) is present and $R_c < R_0$. Numerical simulations of disease-free and endemic equilibrium points are carried out to provide an overview of the results analyzed with parameter values from several sources. The results of the numerical simulation are in line with the analysis carried out. From the model analysis, the disease will disappear more quickly when the level of vaccine used and individuals who carry out treatment are enlarged.

Keywords: Measles, SEIR model, Equilibrium Point, Basic Reproduction Number, Bifurcation

I. INTRODUCTION

Measles is an acute infectious disease caused by the measles virus from the paramyxovirus group [1]. A person who interacts closely with a person infected with measles can become infected if they do not yet have immunity. People previously vaccinated or infected with the measles virus may be immune to measles [2]. Meanwhile, people exposed to the measles virus are characterized by red spots on the skin, followed by early symptoms of fever, watery eyes, cough, and runny nose. Usually, the rash appears first on the face and upper neck. Then, the rash will spread to the hands and feet after three days [3]. Measles is very dangerous because it can cause brain and organ damage, complications, and paralysis, and the most dangerous is death [4].

Measles surged worldwide in 2019, reaching the highest number of cases reported in 23 years. Highlighted in WHO and United States Centers for Disease Control and Prevention (CDC) publications, the global number of measles cases rose to 869,770 in 2019, the highest number reported since 1996, with increases in all World Health Organization (WHO) regions. Deaths from global measles have increased by almost 50% since 2016, with an estimated

207,500 deaths in 2019 [5]. Until 2018, there were 89,127 cases of measles in Indonesia, with 22 of them ending in death [6]. The incidence of measles outbreak transmission in a population can be modeled mathematically. Many studies are on modeling this measles disease. Jaharuddin and Toni Bakhtiar [7], who developed the SVEITR model. In this model, there are six populations, namely S susceptible human population (Susceptible), V vaccinated population (Vaccinated), E exposed human population (Exposed), I infected human population (Infected), T human population undergoing treatment (Treated), and R human population recovered (Recovered). Furthermore, Abdul Kudus, Mohiuddin, and Rahman [8] developed the SVEIR model. In this model, there are six populations, namely S susceptible human population (Susceptible), V vaccinated population (Vaccinated), where the vaccine is divided into two, namely, first dose vaccination and second dose vaccination, E human population exposed (Exposed), I human population infected (Infected), and the human population R recovered (Recovered).

This research will develop a mathematical model for the spread of measles by integrating the models presented in [7] and [8], incorporating the administration of vaccines and treatment. The model in this study assumes that individuals who are given up to two stages, individuals who have been vaccinated, can still be infected with measles. However, individuals who have been vaccinated will have optimal immunity. Thus, the measles infection that occurs will not be too severe.

II. MATHEMATICAL MODEL

The model used in the spread of Measles is SV_1V_2EITR (*Susceptible, Vaccination dose 1, Vaccination dose 2, Exposed, Infected, Treatment, Recovered*), which was developed by dividing the individual population into seven compartments: *Susceptible* (S), which is individuals who are susceptible to infection, first dose vaccination (V_1) namely disease-prone individuals who carry out the first dose of vaccination, second dose vaccination (V_2) namely disease-prone individuals who have vaccinated the first dose and then take the second dose, exposed (E) is individuals who have contracted the disease but have not shows signs of disease and cannot transmit the disease, Infected (I) is an individual who is infected with measles, treatment (T) is an infected individual who is receiving treatment, recovered (R) is an individual who has recovered from measles. Assuming the total population (N) is constant, with $N = S + V_1 + V_2 + E + I + T + R$. In forming the model, we use the following assumptions: (1) The population is assumed to be homogeneous, meaning that each individual has the same opportunity to make contact with other individuals; (2) the population is assumed to be closed, meaning that no individual enters the population or leaves the population (no migration) total population is assumed to be constant, (3) every individual born is susceptible to contracting the disease, (4) natural birth and death rates are assumed to be the same per unit of time, (5) vaccination is carried out in two stages. It is assumed that individuals who carry out the first dose of vaccination can still be infected, while those who have received the second dose of vaccination are immune to the disease, (6) infected individuals will undergo treatment or recover naturally, (7) individuals who receive treatment will recover from disease, (8) recovered individuals have immunity to disease, (9) death from disease is negligible. Schematically spreading Measles by vaccination and treatment can be presented in the transfer diagram in Figure 1 and the list of parameters in Table 1.

Table 1. List of Parameters for the Measles Disease Spread Model with Two-Dose Vaccination and Treatment

NO	Parameter	Definition	Requirement	*Unit*
1	μ	Birth and natural death rate.	$0 < \mu \leq 1$	$\frac{1}{day}$
2	ρ	Rate of development of susceptible individuals who have just received the first vaccination.	$0 < \rho \leq 1$	$\frac{1}{day}$
3	β	Transition rate from susceptible individuals to exposed individuals through contact with infected individuals.	$0 < \beta \leq 1$	$\frac{1}{day}$
4	α	Transition rate from exposed individuals to infected individuals.	$0 < \alpha \leq 1$	$\frac{1}{day}$
5	ϵ	Transition rate from infected individuals to individuals undergoing treatment.	$0 \leq \epsilon \leq 1$	$\frac{1}{day}$
6	η	Transition rate from susceptible individuals to individuals receiving the first dose of vaccination.	$0 < \eta \leq 1$	$\frac{1}{day}$
7	σ	Transition rate from individuals receiving the first vaccination dose to receiving the second dose.	$0 \leq \sigma \leq 1$	$\frac{1}{day}$
8	ω	The recovery rate of individuals who have received the second dose of vaccination.	$0 \leq \omega \leq 1$	$\frac{1}{day}$
9	γ_1	The recovery rate of exposed individuals.	$0 \leq \gamma_1 \leq 1$	$\frac{1}{day}$
10	γ_2	The recovery rate of infected individuals (natural recovery).	$0 \leq \gamma_2 \leq 1$	$\frac{1}{day}$
11	γ_3	The recovery rate of individuals undergoing treatment for measles.	$0 \leq \gamma_3 \leq 1$	$\frac{1}{day}$

The mathematical model above transfer diagram can be expressed as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \mu N + \rho V_1 - S(\mu + \eta) - \frac{\beta SI}{N} \\
\frac{dV_1}{dt} &= \eta S - V_1(\rho + \sigma + \mu) \\
\frac{dV_2}{dt} &= \sigma V_1 - V_2(\mu + \omega) \\
\frac{dE}{dt} &= \frac{\beta SI}{N} - E(\mu + \alpha + \gamma_1) \\
\frac{dI}{dt} &= \alpha E - I(\mu + \gamma_2 + \epsilon) \\
\frac{dT}{dt} &= \epsilon I - T(\mu + \gamma_3) \\
\frac{dR}{dt} &= \gamma_1 E + \gamma_2 I + \gamma_3 T + \omega V_2 - \mu R
\end{aligned} \tag{1}$$

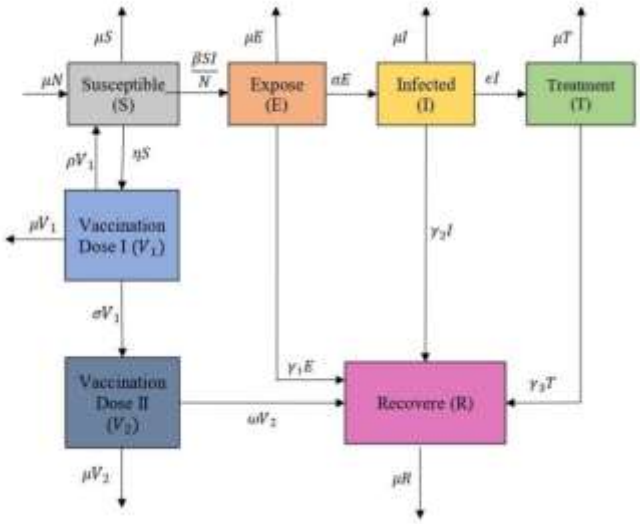


Figure 1. The diagram of transfer model of spread disease Measles

From the system (1) obtained $N = S + V_1 + V_2 + E + I + T + R$, $\frac{dN}{dt} = 0$, so $N(t) = k$, to k the real number positive, therefore proved $N(t)$ is constant. The system (1) is formed in a non-dimensional model to simplify the system (1). The proportion of the number of individual compartments can be expressed as follows:

$$s = \frac{dS}{dN}, v_1 = \frac{dV_1}{dN}, v_2 = \frac{dV_2}{dN}, e = \frac{dE}{dN}, i = \frac{dI}{dN}, t = \frac{dT}{dN}, r = \frac{dR}{dN} \tag{2}$$

Furthermore, the system (2) variable r does not appear in other equations, then the equation r for a while can be ignored from the system. So, the system (2) can be written into:

$$\begin{aligned}
\frac{ds}{dt} &= \mu + \rho v_1 - s(\mu + \eta + \beta i) \\
\frac{dv_1}{dt} &= \eta s - v_1(\rho + \sigma + \mu) \\
\frac{dv_2}{dt} &= \sigma v_1 - v_2(\mu + \omega) \\
\frac{de}{dt} &= \beta s i - e(\mu + \alpha + \gamma_1) \\
\frac{di}{dt} &= \alpha e - i(\mu + \gamma_2 + \epsilon) \\
\frac{dt}{dt} &= \epsilon i - t(\mu + \gamma_3)
\end{aligned} \tag{3}$$

III. MODEL ANALYSIS

The stability of the equilibrium point of the model carries out the analysis model. The equilibrium point is obtained by creating an equation on the system (3) equal to zero. First, to find the equilibrium-free disease that is the point of equilibrium when there is no infected in the population so that $i = 0$. It obtained free of the disease equilibrium point.

$$E_1(s, v_1, v_2, e, i, t) = \left(\frac{\mu(\rho\mu+(\sigma+\mu)(\mu+\eta))+\rho\eta\mu}{[\rho\mu+(\sigma+\mu)(\mu+\eta)](\mu+\eta)}, \frac{\eta\mu}{[\rho\mu+(\sigma+\mu)(\mu+\eta)]}, \frac{\sigma\eta\mu}{[\rho\mu+(\sigma+\mu)(\mu+\eta)](\mu+\omega)}, 0,0,0\right).$$

To simplify the next writing, suppose $A = (\sigma + \mu)$, $B = (\mu + \eta), C = (\mu + \gamma_2 + \epsilon), D = (\mu + \alpha + \gamma_1)$, $E = (\mu + \eta), F = (\rho + \sigma + \mu), G = (\mu + \alpha\gamma_1)$, and $H = (\mu + \gamma_2 + \epsilon), I = (\mu + \omega), J = (\mu + \gamma_3)$.

Then, determine the basic reproduction number of (R_0) from the system (3) by finding the maximum eigenvalues obtained from the next-generation matrix. The system Determination steps R_0 system (3) as [9]:

1. Take the equations that describe the case of new infections and changes in the infection compartment of the system. Furthermore, this system is called an infected subsystem.
2. Do linearization against infected subsystems at the disease-free equilibrium point. This linear system is represented by the Jacobi matrix (**J**) as follows:
$$J_{(e,i,t)} = \begin{bmatrix} -(\mu+\alpha+\gamma_1) & \beta s & 0 \\ \alpha & -(\mu+\gamma_2+\epsilon) & 0 \\ 0 & \epsilon & -(\mu+\gamma_3) \end{bmatrix}$$
3. The Jacobi matrix (**J**) decomposition becomes $\boldsymbol{J = F - V}$, with $\boldsymbol{F}$ being the transmission matrix and $\boldsymbol{V}$ being the transmission matrix.
$$\boldsymbol{F} = \begin{bmatrix} 0 & \left(\frac{\beta\mu[\rho\mu+(\sigma+\mu)(\mu+\eta)]+\beta\rho\eta\mu}{[\rho\mu+(\sigma+\mu)(\mu+\eta)](\mu+\eta)}\right) & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, \boldsymbol{V} \begin{bmatrix} (\mu+\alpha+\gamma_1) & 0 & 0 \\ -\alpha & (\mu+\gamma_2+\epsilon) & 0 \\ 0 & -\epsilon & (\mu+\gamma_3) \end{bmatrix}$$
4. Find R_0 with $R_0 = \rho(FV^{-1})$
By completing the equation $\det(\lambda I - FV^{-1}) = 0$ or $\left(\lambda - \frac{\alpha\beta\mu(z+xy)+\alpha\beta\rho\eta\mu}{(z+xy)yuh}\right)\lambda^2 = 0$, obtained $\lambda_{1,2} = 0$ and $\lambda_3 = \frac{\alpha\beta\mu(z+xy)+\alpha\beta\rho\eta\mu}{(z+xy)yuh}$. As R_0 obtained from spectral radius or the greatest value of the eigenvalues, then obtained:
$$R_0 = \frac{\alpha\beta\mu\left(\rho\mu+(\sigma+\mu)(\mu+\eta)\right)+\alpha\beta\rho\eta\mu}{[\rho\mu+(\sigma+\mu)(\mu+\eta)](\mu+\eta)(\mu+\alpha+\gamma_1)(\mu+\gamma_2+\epsilon)}$$

Next, we will look for the endemic equilibrium point when the infected class is not zero or when the disease spreads or becomes epidemic in the population. Endemic equilibrium point means that in a population there are always individuals with disease, obtained I at the disease endemic equilibrium point $I^* > 0$. So, disease endemic equilibrium point system (3) is $E_2 = (s^*, v_1^*, v_2^*, e^*, i^*, t^*)$ with

$$\begin{aligned} s^* &= \frac{\mu[\rho(\mu+\beta i^*)+(\sigma+\mu)(\mu+\eta+\beta i^*)]+\rho\eta\mu}{[\rho(\mu+\beta i^*)+(\sigma+\mu)(\mu+\eta+\beta i^*)](\mu+\eta+\beta i^*)} \\ v_1^* &= \frac{\eta\mu}{[\rho(\mu+\beta i^*)+(\sigma+\mu)(\mu+\eta+\beta i^*)]} \\ v_2^* &= \frac{\sigma\eta\mu}{[\rho(\mu+\beta i^*)+(\sigma+\mu)(\mu+\eta+\beta i^*)](\mu+\omega)} \\ e^* &= \frac{\beta i^*\mu[\rho(\mu+\beta i^*)+(\sigma+\mu)(\mu+\eta+\beta i^*)]+\rho\eta\mu}{[\rho(\mu+\beta i^*)+(\sigma+\mu)(\mu+\eta+\beta i^*)](\mu+\eta+\beta i^*)(\mu+\alpha+\gamma_1)} \\ i^* &= \frac{-b\pm\sqrt{b^2-4ac}}{2a} \\ t &= \frac{\epsilon i^*}{\mu+\gamma_3} \end{aligned} \quad (4)$$

with
$a = C\rho\beta^2 D + CA\beta^2 D$
$b = C\rho\mu D\beta + C\rho\beta DB + CABD\beta + CA\beta DB - \alpha\beta^2\rho\mu - \alpha\beta^2\mu A$
$c = C\rho\mu DB + CAB^2 D - \alpha\beta\rho\mu^2 - \alpha\beta\mu AB - \alpha\beta\rho\eta\mu$
$A = (\sigma+\mu), B = (\mu+\eta), C = (\mu+\gamma_2+\epsilon)$, dan $D = (\mu+\alpha+\gamma_1)$.

Theorem 1 *If $R_0 > 1$, the system (3) has two equilibrium points: the free equilibrium point of this disease, E1, and the equilibrium endemic to E_2.*

Proof: To prove theorem 1 needs to be demonstrated if $R_0 > 1$ then the equilibrium point E_2 exists. The existence of an equilibrium point is indicated by each of its positive elements then i at the equivalence point of $E_2 = (s^*, {v_1}^*, {v_2}^*, e^*, i^*, t^*)$ the equation (4) clearly positive $s^*, {v_1}^*, {v_2}^*, e^*, i^*, t^*$ and positive, so it needs to be demonstrated $i^* > 0$.

$$\begin{aligned} c &= (\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)\\ &\quad (\mu+\eta)^2(\mu+\alpha+\gamma_1)-\alpha\beta\rho\mu^2-\alpha\beta\mu(\sigma+\mu)(\mu+\eta)-\alpha\beta\rho\eta\mu\\ &= \frac{(\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2(\mu+\alpha+\gamma_1)}{(\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2(\mu+\alpha+\gamma_1)}\\ &\quad \big((\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2\\ &\quad (\mu+\alpha+\gamma_1)-(\alpha\beta\rho\mu^2+\alpha\beta\mu(\sigma+\mu)(\mu+\eta)+\alpha\beta\rho\eta\mu)\big)\\ &= (\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2\\ &\quad (\mu+\alpha+\gamma_1)\Big(\frac{(\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2(\mu+\alpha+\gamma_1)}{(\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2(\mu+\alpha+\gamma_1)}-\\ &\quad \Big(\frac{\alpha\beta\rho\mu^2+\alpha\beta\mu(\sigma+\mu)(\mu+\eta)+\alpha\beta\rho\eta\mu}{(\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2(\mu+\alpha+\gamma_1)}\Big)\Big)\\ &= \big((\mu+\gamma_2+\epsilon)\rho\mu(\mu+\alpha+\gamma_1)(\mu+\eta)+(\mu+\gamma_2+\epsilon)(\sigma+\mu)(\mu+\eta)^2\\ &\quad (\mu+\alpha+\gamma_1)\big)(1-R_0)\\ &= (H(\rho\mu)GE+H(\sigma+\mu)E^2G)(1-R_0) \end{aligned} \tag{5}$$

with $E = (\mu+\eta), G = (\mu+\alpha+\gamma_1)$, and $H = (\mu+\gamma_2+\epsilon)$.
With $R_0 >$ obtained the value $c < 0$, the equation has at least one positive root. Then obtained $i^* > 0$ if and only if $R_0 > 1$.

Theorem 2*: If $R_0 < 1$, then E_1 disease-free Equilibrium point stable asymptotic local.*
Bukti: The value of Eigen matrix Jacobi from the system (3) at the E_1 disease-free equilibrium point is obtained from the following dispute

$$J_{(E_1)} = \begin{bmatrix} -(E+\beta i) & \rho & 0 & 0 & -\beta s & 0\\ \eta & -F & 0 & 0 & 0 & 0\\ 0 & \sigma & -I & 0 & 0 & 0\\ \beta i & 0 & 0 & -G & \beta s & 0\\ 0 & 0 & 0 & \alpha & -H & 0\\ 0 & 0 & 0 & 0 & \epsilon & -J \end{bmatrix}$$

$$\det\big(\lambda I - J_{(E1)}\big) = 0$$

$$\Leftrightarrow \begin{vmatrix} \lambda+E & -\rho & 0 & 0 & \beta s & 0\\ -\eta & \lambda+F & 0 & 0 & 0 & 0\\ 0 & -\sigma & \lambda+I & 0 & 0 & 0\\ 0 & 0 & 0 & \lambda+G & -\beta s & 0\\ 0 & 0 & 0 & -\alpha & \lambda+H & 0\\ 0 & 0 & 0 & 0 & -\epsilon & \lambda+J \end{vmatrix} = 0$$

So, the characteristic equation for $J_{(E1)}$ is
$\Leftrightarrow (\lambda+J)(\lambda+I)[\lambda^2+(H+G)\lambda+GH-\beta s\alpha][\lambda^2+(F+E)\lambda+FE-\eta\rho] = 0$
Obtained $\lambda_1 = -(\mu+\gamma_3)$ and $\lambda_2 = -(\mu+\omega)$, because μ, γ_3, and ω positive value, then the real part of both Eigenvalues are, negative. The other Eigenvalues are the polynomial roots as follow. Let $P = [\lambda^2+(H+G)\lambda+GH-\beta s\alpha]$
Obatined $a_{P0} = 1, a_{P1} = H+G, a_{P2} = GH-\beta s\alpha$, with $G = (\mu+\alpha+\gamma_1)$, and $H = (\mu+\gamma_2+\epsilon)$.

$$a_{P1} = H + G$$
$$= (\mu + \gamma_2 + \epsilon) + (\mu + \alpha + \gamma_1)$$
$$= 2\mu + \gamma_2 + \epsilon + \alpha + \gamma_1 > 0 \quad (6)$$

$$a_{P2} = GH - \beta s\alpha = GH(1 - R_0) \quad (7)$$

Based on the equation (8) because $R_0 < 1$ then $a_{P2} > 0$.

Let $Q = [\lambda^2 + (F + E)\lambda + FE - \eta\rho]$

Obatined $a_{Q0} = 1, a_{Q1} = F + E, a_{Q2} = FE - \eta\rho$, with $E = (\mu + \eta)$, and $F = (\rho + \sigma + \mu)$.

$$a_{Q1} = F + E = (\rho + \sigma + \mu) + (\mu + \eta) = 2\mu + \rho + \sigma + \eta > 0 \quad (8)$$

$$a_{Q2} = FE - \eta\rho = (\rho + \sigma + \mu)(\mu + \eta) - \eta\rho = (\rho + \sigma + \mu)\mu + (\sigma + \mu)\eta > 0 \quad (9)$$

Because of $a_{P1}, a_{P2}, a_{Q1}$and a_{Q2} are positive, so based on the Lienard-Chipart criteria [10], the equation (6) has negative. So, it can be concluded that the disease-free equilibrium E_1 point is a local asymptotic stable.

3.1 Bifurcation Analysis

In this case, we use the endemic equilibrium point to find the optimum R_0 equation to create a bifurcation curve, so that for the R_0 alue which is smaller than the optimum value, there is no spread of infectious diseases. [11].

know the equation as follows:

$$g(I) = a(i^*)^2 + b(i^*) + c = 0 \quad (10)$$

with

$$a = (\mu + \gamma_2 + \epsilon)\rho\beta^2(\mu + \alpha + \gamma_1) + (\mu + \gamma_2 + \epsilon)(\sigma + \mu)\beta^2(\mu + \alpha + \gamma_1)$$
$$b = (\mu + \gamma_2 + \epsilon)\rho\mu(\mu + \alpha + \gamma_1)\beta + (\mu + \gamma_2 + \epsilon)\rho\beta(\mu + \alpha + \gamma_1)(\mu + \eta) + (\mu + \gamma_2 + \epsilon)(\sigma + \mu)(\mu + \eta)(\mu + \alpha + \gamma_1)\beta + (\mu + \gamma_2 + \epsilon)(\sigma + \mu)\beta(\mu + \alpha + \gamma_1)(\mu + \eta) - \alpha\beta^2\rho\mu - \alpha\beta^2\mu(\sigma + \mu)$$
$$c = (\mathrm{H}(\rho\mu)\mathrm{GE} + \mathrm{H}(\sigma + \mu)\,\mathrm{E}^2\mathrm{G})(1 - R_0)$$

and $R_0 = \left(\frac{\alpha\beta\mu(\rho\mu + (\sigma+\mu)(\mu+\eta)) + \alpha\beta\rho\eta\mu}{[\rho\mu + (\sigma+\mu)(\mu+\eta)](\mu+\eta)(\mu+\alpha+\gamma_1)(\mu+\gamma_2+\epsilon)}\right)$

where,

$E = (\mu + \eta), F = (\rho + \sigma + \mu), G = (\mu + \alpha + \gamma_1)$, and $H = (\mu + \gamma_2 + \epsilon)$.

Next, the backward bifurcation equation will be searched by finding the optimum point Equation $g(I)$ then, substitute the result into the equation $g(I) = 0$ to get value R_c.

$$R_0^c = 1 - \frac{b^2}{4a(H(\rho\mu)GE + H(\sigma+\mu)\,E^2G)}$$

So, the backward bifurcation is true for the value of $R_0 < 1$, so the backward bifurcation equation is $R_0^c < R_0 < 1$. This means that the disease will remain in the population when $R_0 > 1$ and $R_0^c < R_0 < 1$, disease disappears from the population when $R_0 < 1$.

3.2 Model Simulation

This section contains a numerical simulation of a mathematical model of the spread of measles with the first dose of vaccination, second dose of vaccination, and treatment. Simulations are carried out to see the stability of the disease-free equilibrium point and the

endemic equilibrium point. Simulation using *Maple 2020* and the function DETools with the parameters obtained from previous studies and measles-related assumptions.

Table 2. The parameter and unit are used in the simulation

No	Parameter	Value	Unit	Reference
1	μ	0,02	$\frac{1}{day}$	[12]
2	ρ	0,6	$\frac{1}{day}$	[8]
3	β	0,33	$\frac{1}{day}$	[13]
4	α	0,018	$\frac{1}{day}$	[8]
5	ϵ	0,050	$\frac{1}{day}$	[7]
6	η	0,94	$\frac{1}{day}$	[8]
7	σ	0,93	$\frac{1}{day}$	[8]
8	ω	0,8	$\frac{1}{day}$	[8]
9	γ_1	0,08	$\frac{1}{day}$	[7]
10	γ_2	0,6	$\frac{1}{day}$	[8]
11	γ_3	0,136	$\frac{1}{day}$	[7]

Based on Figure 2, it can be interpreted as follows: the vulnerable individual population declines, reaching a point and stabilizing on that point by day 20. The population of individuals who have received the first vaccination dose decreases, reaching a point and stabilizing on that point by day 20. The population of individuals who have received the second vaccination dose decreases, reaching a point and stabilizing on that point by day 20. The exposed individual population decreases, reaching 0 by day 70 and stabilizing. The infected individual population decreases, reaching 0 by day 15 and stabilizing. The population of individuals undergoing treatment decreases, reaching 0 by day 60 and stabilizing. The recovered individual population increases, reaching a point and stabilizing on that point by day 50.

Next, a numerical simulation will be performed for $R_0 > 1$. Based on Table 1, if the value of the parameter β is enlarged from the previous value to $\beta = 0.94$, the value of the parameter α is enlarged from the previous value to $\alpha = 0.3$, the value of the parameter η is reduced from the previous value to $\eta = 0.00015$, and the value of the parameter γ_2 is reduced from the previous value to $\gamma_2 = 0.2$. Based on these parameters' values, the system's basic reproduction number (3) is $R_0 = 2.887959271 > 1$. Because $R_0 > 1$, the disease will spread, or in other words, it will be endemic. Then, the simulation results are obtained as follows:

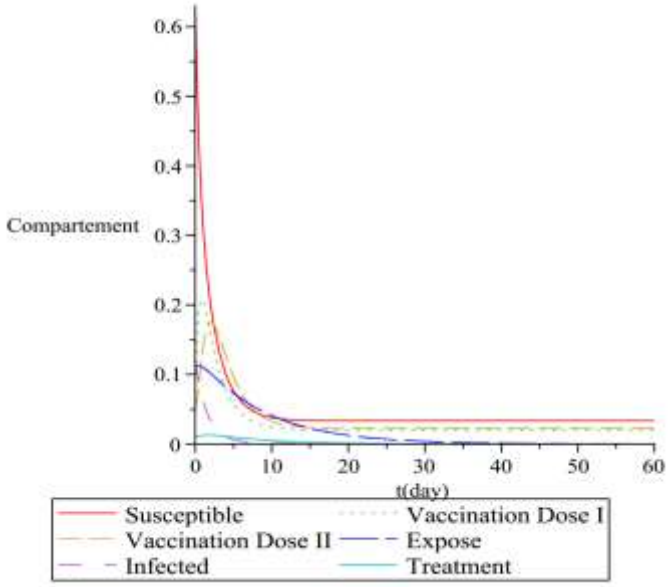


Figure 2. Simulation System (3) to a disease free equilibrium point.

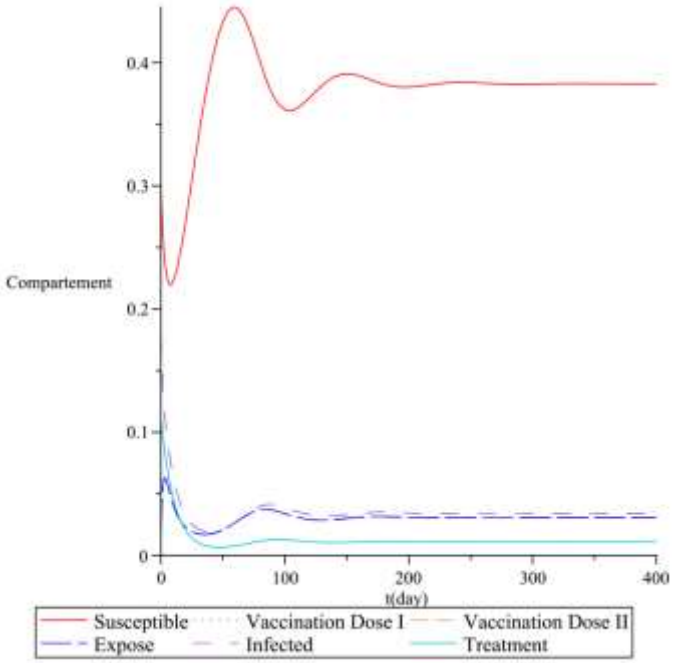


Figure 4. Simulation System (3) to an endemic equilibrium

Based on the results of numerical simulations, it can be concluded that the disease will disappear if $R_0 < 1$ and remain in the population if $R_0 > 1$.

3.3 Sensitivity Analysis

Sensitivity analysis is used to identify which parameter significantly influences the value of R_0, which is then used as an intervention. Parameters with the highest impact on R_0 indicate that these parameters have the most dominant influence on the epidemic or the spread of measles. Using the parameter values in Table 1, the sensitivity index of each parameter in the

basic reproduction number R_0 is shown in Table 2 below as an example of finding the sensitivity index value of R_0 to the parameter β.

$$C_\beta^{R_0} = \frac{\partial R_0}{\partial \beta} \times \frac{\beta}{R_0}$$

$$= \frac{\alpha\mu\big(\rho\mu + (\sigma+\mu)(\mu+\eta)\big) + \alpha\rho\eta\mu}{[\rho\mu + (\sigma+\mu)(\mu+\eta)](\mu+\eta)(\mu+\alpha+\gamma_1)(\mu+\gamma_2+\epsilon)} \times \frac{\beta}{R_0}$$

$$= \frac{\beta\alpha\mu\big(\rho\mu + (\sigma+\mu)(\mu+\eta)\big) + \beta\alpha\rho\eta\mu}{[\rho\mu + (\sigma+\mu)(\mu+\eta)](\mu+\eta)(\mu+\alpha+\gamma_1)(\mu+\gamma_2+\epsilon)R_0}$$

$$= 1.000000000$$

Table 3. Parameter Sensitivity Index

No	Parameter	Sensitivity Index
1	β	+1,000000000
2	η	−0,9664502161
3	γ_2	−0,8955223883
4	α	+0,8474576273
5	μ	+0,7592319496
6	γ_1	−0,6779661013
7	ρ	+0,3741097612
8	σ	−0,3662337660
9	ϵ	−0,07462686566

Table 3 shows the sensitivity index of each parameter used in this model. The sensitivity index is ordered by how much influence the parameter has on the value of R_0. The parameter index with a positive value indicates that if the index is enlarged while the other indexes are constant, it will affect the value of R_0, which also increases. In contrast, if the index is decreased, the value of R_0 will also decrease. Parameter index with a negative value indicates that if the index is increased, the value of R_0 will decrease, whereas if the index is decreased, the value of R_0 will increase.

The sensitivity index shows that the parameter β (the rate of transmission from susceptible individuals to exposed individuals after infection from infected individuals) is the parameter that has the most influence (positive) on measles transmission if the sensitivity index value level β is 1.00 when the parameter β is increased (or reduced) by 10%, the value of R_0 will increase or decrease by 10%. If the value is 10%, then the value of R_0 will increase (or decrease) by 10%. The sensitivity index η (the rate of transfer from susceptible individuals to individuals vaccinated with the first dose) is the most influential (negative) parameter on the transmission of Measles when the sensitivity index η value is 0,966 when the parameter η enlarged (or reduced) by 10%, and the R_0 value will increase or decrease. reduced by 10%, then the value of R_0 will decrease (or increase) by 9,66%.

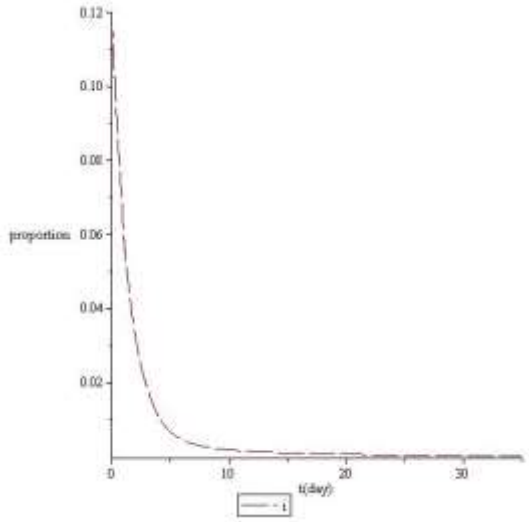
Next, a numerical simulation will be carried out to see the effectiveness of using the first dose of vaccine by changing the parameter value of the proportion of the first dose of vaccine

(η) with other parameter values constant according to Table 2 and presented in the following table:

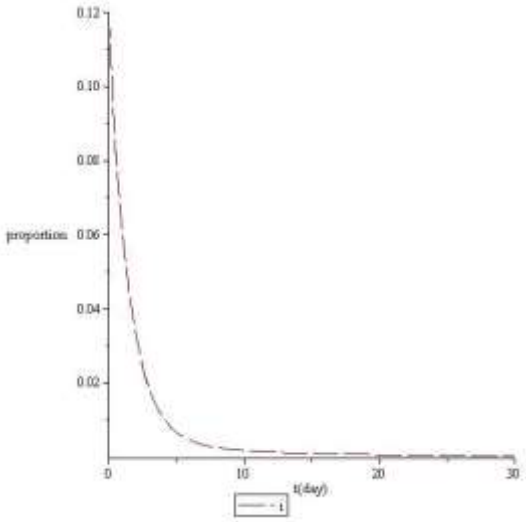
Table 4. Effectiveness of Using the First Dose of Vaccine

$\boldsymbol{\eta}$	$\boldsymbol{R_0}$	The disease disappeared day -
0	0,07513281052	35
0, 3	0,007370623818	30
0, 6	0,003875402873	25
1	0,002374227449	13

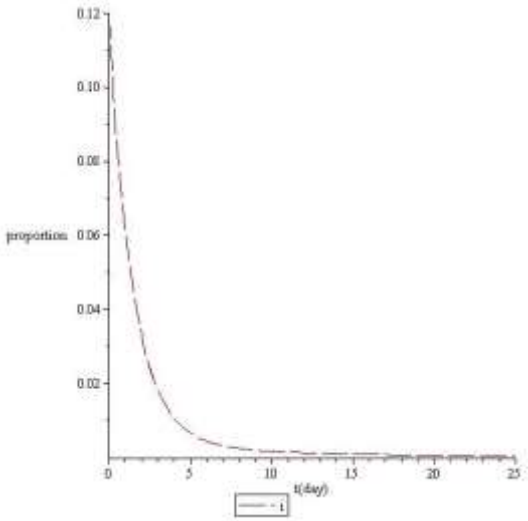
The following is a graph for simulating the effectiveness of using the first dose of the vaccine:



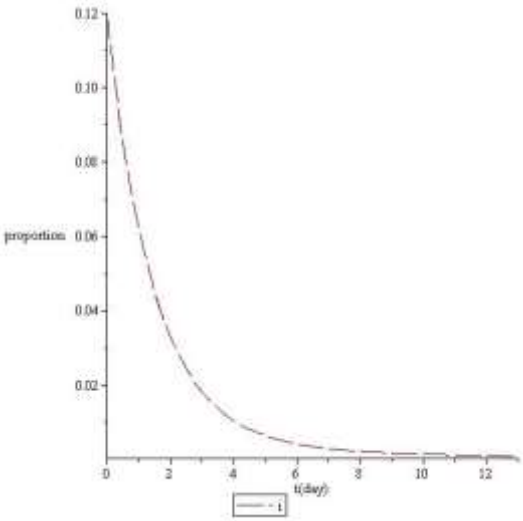
a. simulation of point i when $\eta = 0$



b. simulation of point i when $\eta = 0{,}3$



c. simulation of point i when $\eta = 0{,}6$



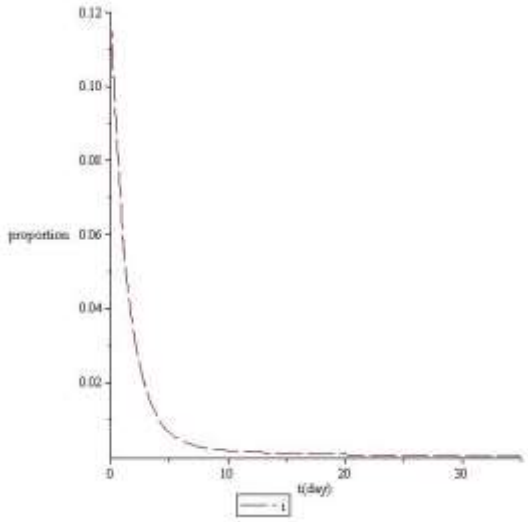
d. simulation of point i when $\eta = 1$

Figure 5. (a) simulation of point i when $\eta = 0$; (b) simulation of point i when $\eta = 0{,}3$; (c) simulation of point i when $\eta = 0{,}6$; (d) simulation of point i when $\eta = 1$

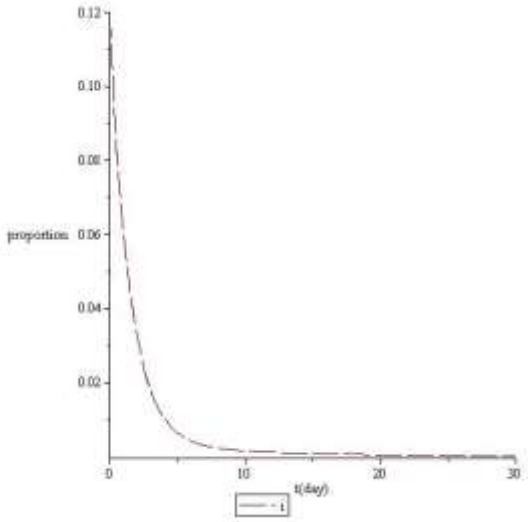
Next, a numerical simulation will be carried out to see the effectiveness of using the second dose of vaccine by changing the parameter value of the second vaccine dose proportion (σ) with the other parameter values constant according to Table 1 and presented in the following table:

Table 4. Effectiveness of Using Second Dose of Vaccine

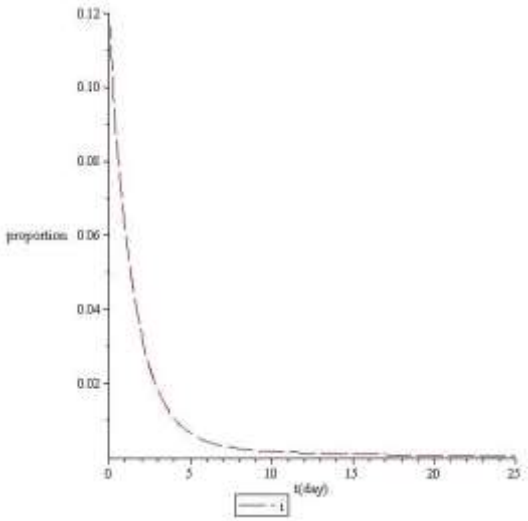
σ	R_0	The disease disappeared day -
0	0,02986047598	35
0,3	0,004330964015	30
0,6	0,003019170910	25
1	0,002455915115	13



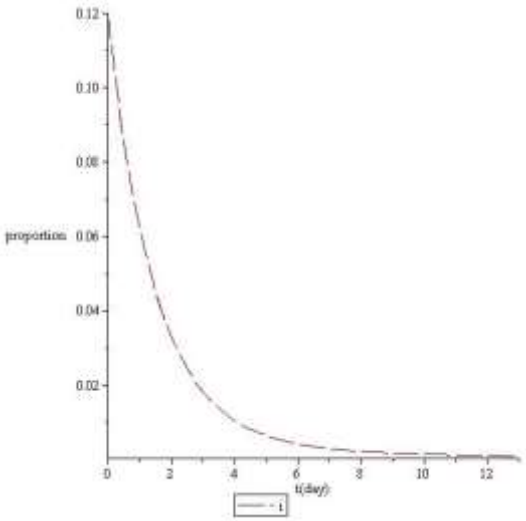
a. simulation of point i when $\sigma = 0$



b. simulation of point i when $\sigma = 0{,}3$



c. simulation of point i when $\sigma = 0{,}6$



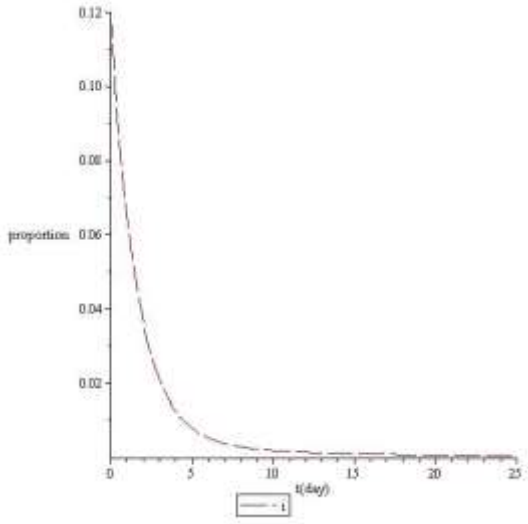
d. simulation of point i when $\sigma = 1$

Figure 6. (a) simulation of point i when $\sigma = 0$; (b) simulation of point i when $\sigma = 0{,}3$; (c) simulation of point i when $\sigma = 0{,}6$; (d) simulation of point i when $\sigma = 1$

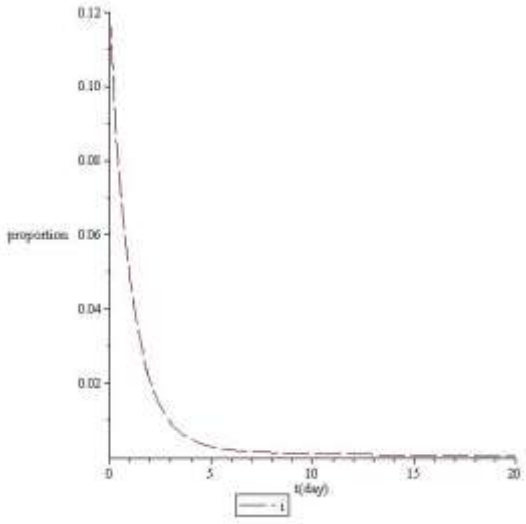
Next, a numerical simulation will be carried out to see the effectiveness of individuals undergoing treatment by changing the value of the treatment proportion parameter (ϵ) with the other parameter values constant according to Table 1 and presented in the following table:

Table 1. Effectiveness of Individuals Performing Treatment

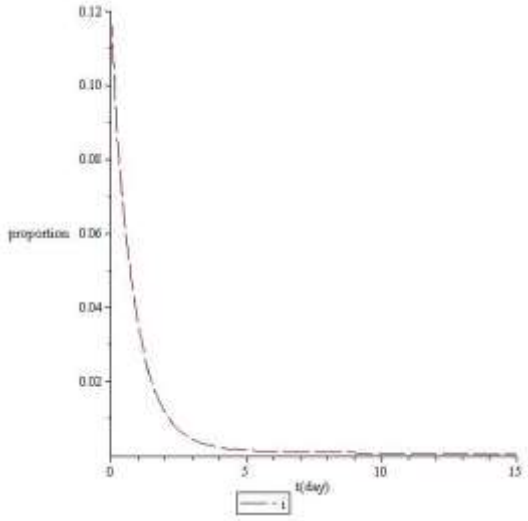
ϵ	R_0	The disease disappeared day -
0	0,002723970945	25
0,3	0,001835719550	20
0,6	0,001384313103	15
1	0,001042507399	10



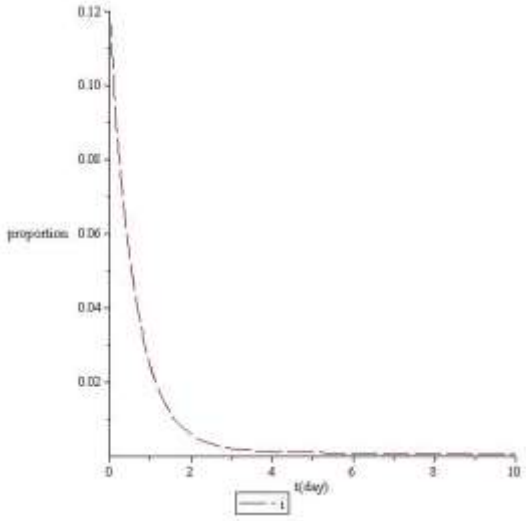
a. simulation of point i when $\epsilon = 0$



b. simulation of point i when $\epsilon = 0{,}3$



c. simulation of point i when $\epsilon = 0{,}6$



d. simulation of point i when $\epsilon = 1$

Figure 7. (a) simulation of point i when $\epsilon = 0$; (b) simulation of point i when $\epsilon = 0{,}3$; (c) simulation of point i when $\epsilon = 0{,}6$; (d) simulation of point i when $\epsilon = 1$

Based on the simulation results of the effectiveness of the use of the first dose of vaccine, second dose of vaccine, and treatment, the disease will disappear more quickly when the level of use of the vaccine and the individual undergoing treatment is increased, which means that the use of vaccine and treatment is quite effective.

Research implications were further detailed before conclusions were drawn. For instance, recommendations to mitigate the spread rate and actions stakeholders can take to decrease the number of infected individuals have been included. In light of the simulation results regarding the effectiveness of the first dose of the vaccine, the second dose of the vaccine, and treatment, it has been emphasized that the disease will dissipate more rapidly with increased vaccine utilization and greater numbers of individuals undergoing treatment. This underscores the effectiveness of both vaccination and treatment.

IV. CONCLUSIONS

This research obtained a mathematical model for the spread of Measles SV_1V_2EITR where Suspectible (S), First Dose Vaccination (V_1), Second Dose Vaccination (V_2), Exposed (E), Infected (I), Treatment (T), Recovery (R). It has a disease-free equilibrium point $E_1 = (s, v_1, v_2, e, i, t)$ which has a local asymptotically stable equilibrium point when $R_0 < 1$ and an endemic equilibrium point $E_2 = (s^*, {v_1}^*, {v_2}^*, e^*, i^*, t^*)$ which exists if the value of $R_0 > 1$. The basic reproduction number of the model that has been obtained. Based on the stability analysis of the equilibrium point and numerical simulations, it is concluded that the disease will disappear if $R_0 < 1$ and remain in the population or become epidemic if $R_0 > 1$. Based on the simulation results of the effectiveness of the use of the first dose of vaccine, second dose of vaccine, and treatment, the disease will disappear more quickly when the level of use of the vaccine and the individual undergoing treatment is increased, which means that the use of vaccine and treatment is quite effective.

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