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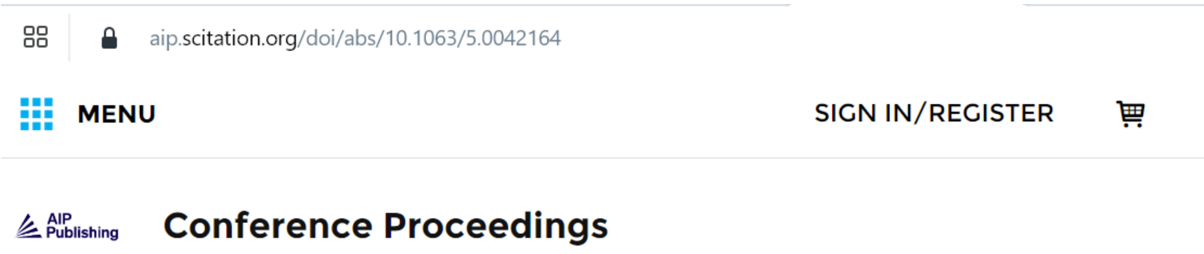

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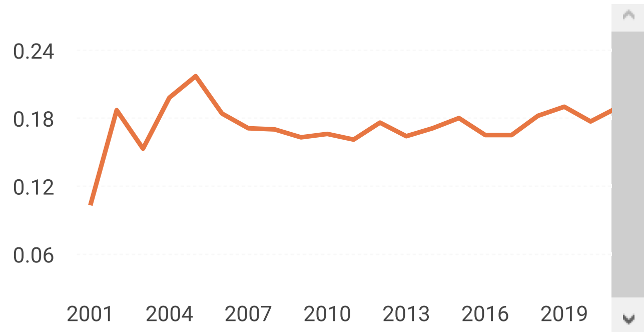

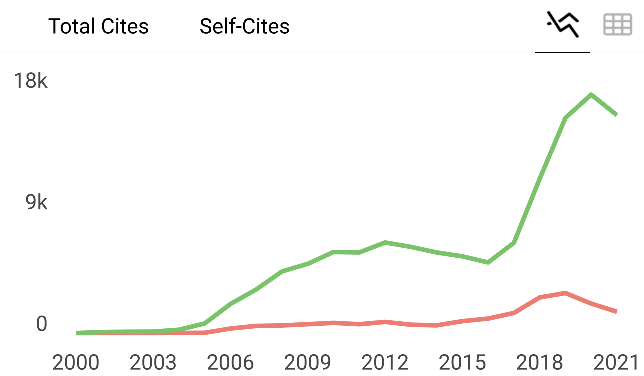

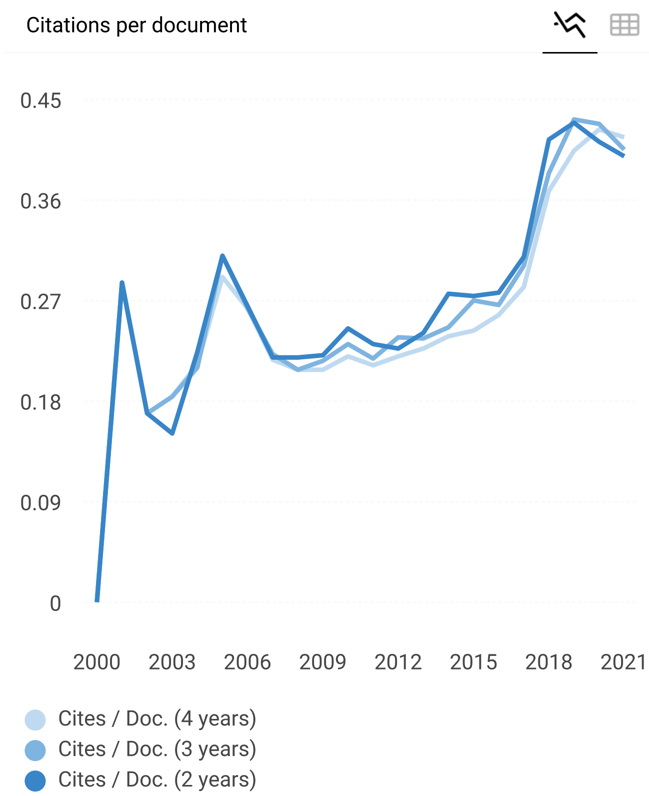

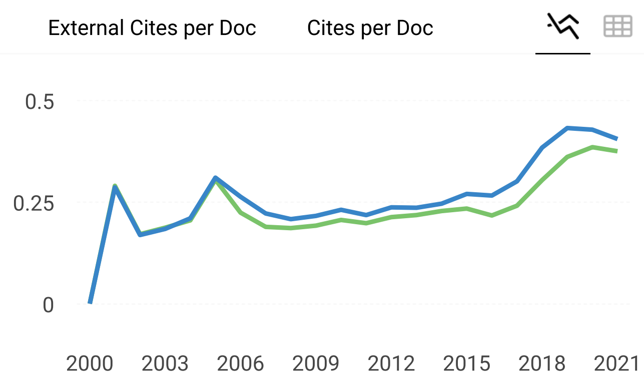

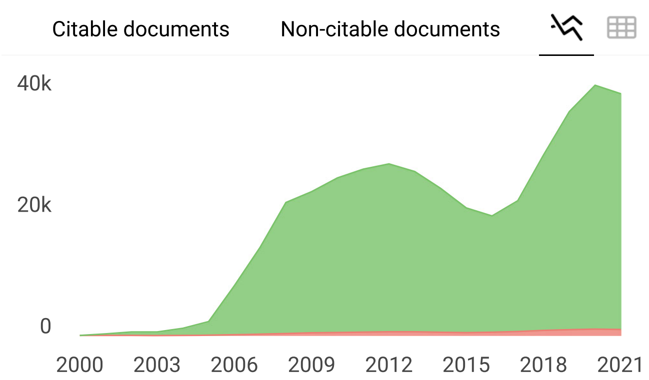

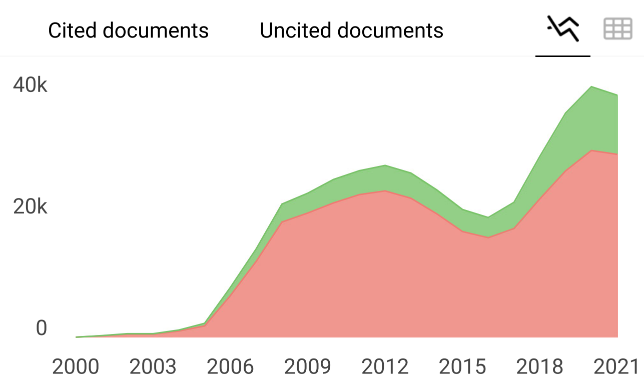

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Preface: International Conference on Mathematics, Computational Sciences and Statistics 2020

On behalf of the Program Committee, we would like to thank all participants of "The International Conference on Mathematics, Computational Sciences and Statistics (ICoMCoS) 2020" hosted by Department of Mathematics, Universitas Airlangga.

2020 has been a very challenging year due to Covid-19 pandemic, in which for the sake of safety and well-being of all participants, our initial plan to held ICoMCoS 2020 in Surabaya, Indonesia, has been converted to be fully delivered virtually. Nevertheless, while we may all be physically distant, we hope we can still connect intellectually.

The theme of ICoMCoS 2020 is "Mathematics, Computational Sciences and Statistics for a Better Future". With increasing complexities of our world today, Mathematics, Computational Sciences and Statistics have become powerful tools to elucidate all the complexities as well as provide the solution. ICoMCoS 2020, in a more detail outfit, is designed to provide a multidisciplinary forum for promoting and fostering interactions between mathematics (Analysis and Geometry, Algebra and Combinatoric, Applied Mathematics), computational sciences (algorithm analysis, network security and cryptography, artificial intelligence and machine learning, knowledge discovery and data mining, machine translation, image processing), and statistics (statistical theory, statistics modeling, forecasting methods, multivariate methods, econometrics, biostatistics, actuarial sciences) as well as related methodologies in studying various phenomena in the area.

We would like to say thanks to all authors who have submitted the paper to our proceedings. We also thank the scientific committee members and all of the reviewers for all supports during the conference and the preparation of the proceedings. As the scientific manuscripts of the conference, we provide the AIP Proceedings which contains the high-quality paper selected by a blind review process. We apologize to the authors if this process creates inconvenience.

Last but not least, there have been enormous collective efforts being put to run ICoMCoS 2020, in one form or another, so, on behalf of the Program Committee, let me take this opportunity to express my high appreciation to all of those that have contributed.

Cicik Alfiniyah, PhD
ICOMCOS 2020 Program Committee Chair

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Stability analysis of SIVS epidemic model with vaccine ineffectiveness

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Rosita Yuliana, Cicik Alfiniyah, and Windarto

Stability Analysis of SIVS Epidemic Model with Vaccine Ineffectiveness

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Abstract. Vaccination is the act of getting a vaccine to help the immune system develop protection from a disease. Vaccination is a good and efficient step to protect population from epidemic. However, vaccines do not necessarily provide perfect immunity to body because not all type of vaccines have 100% effectiveness. The ineffectiveness of a vaccine affects the dynamics of the spread of an infectious disease. The dynamics of the spread of infectious diseases with vaccine ineffectiveness can be approached by mathematical models. This paper aims to analyze the stability of SIVS epidemic model with vaccine ineffectiveness. Based on model analysis result, the model obtained two equilibrium points namely, the disease free-equilibrium point (E_0) and endemic equilibrium point (E_1). In addition, the basic reproduction number (R_0) also obtained, which determines the existence and stability of equilibrium point. Disease free-equilibrium point (E_0) local asymptotically stable if $R_0 < 1$, then through phase plane simulation it conclude that endemic equilibrium point (E_1) local asymptotically stable if $R_0 > 1$. Based on numerical simulation results, it shows that vaccine ineffectiveness affects the high spread of disease.

INTRODUCTION

Any slow prevention of infectious disease would lead to outbreak and panic attack to everyone [1]. The spread of infectious disease can cause damage to health, economic and other sectors for a country [2, 3]. As example, when cholera became plague in Peru (1991) that cause lost to 770 million dollar; it is impact of a decrease in tourist numbers and an embargo on food trade. Then, on 2006 Somalia lost of 300 million dollar because *Rift Valley* Fever became epidemic on that country. Furthermore, Mexico lost 2,8 million dollar in tourism sector (2009), that is the impact of influenza H1N1 epidemic [3]. That several cases show that the spread of infectious disease is a serious problem.

Vaccination becomes innovation to prevent the spread of infectious disease. Vaccination help the immune system develop protection from a disease [4, 5]. Vaccination has a significant positive impact in the health sector. However according to [6], vaccines do not necessarily provide perfect immunity to body because not all type of vaccines have 100% effectiveness. The vaccine-based protection is dependent on the immune status of the recipient [7, 8]. As example, *varicella* vaccine is effective in preventing chickenpox by 85%, people who receive this vaccine remain at risk of developing chickenpox by 15% [9]. Also, diphtheria vaccine research in North Sumatra shows that giving vaccines to children aged 6-14 years has an effectiveness of 89.5% which means they still have the potential to be infected with diphtheria by 9.5% [10].

There are some works on SIVS epidemic model in which a vaccination program has been included [11, 12, 13, 14]. In previous research, the development of epidemic model is assumed that vaccine 100% effective, so that, the vaccinated individuals could not get infected. Vaccine ineffectiveness has not count as factor of infectious diseases spread.

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Research on the spread of infectious diseases in the presence of vaccination can also be done through mathematical models. Mathematical models are representations of real-world problems into mathematical formulas [15]. The susceptible-infectious-vaccinated-susceptible (SIVS) model is a mathematical model consisting of three compartments, namely the population of susceptible individuals (S), populations of infected individuals (I), and populations of vaccinated individuals (V) [16]. The SIVS model can be applied to diseases that have been found in vaccines such as chickenpox, polio, and measles [17]. Vaccination in the SIVS model plays a role in providing immunity for vulnerable individuals

There are several researchers who have developed models of the spread of infectious diseases by vaccination. Gumel and Moghadas [12] present a mathematical model of the spread of infectious diseases with the assumption that vaccinated individuals do not experience a decrease in vaccine effectiveness so they cannot return to being vulnerable. Yang, et al [6] developed the Susceptible-Infectious-Recovered-Vaccination (SIRV) model with vaccination carried out in susceptible individuals. Sun et al [14] present a model for the spread of cholera by vaccination carried out in susceptible individuals. Then, Farnoosh and Parsamanesh [11] developed the Susceptible-Infectious-Susceptible (SIS) model with the assumption that the vaccine is 100% effective so that vaccinated individuals cannot be infected. Then, Parsamanesh and Erfanian [13] developed a model of the spread of infectious diseases and assumed that no vaccinated individual could be infected because the vaccine was considered to be very effective.

Based on the description above, we are interested in studying the model of the spread of infectious diseases with assumption that vaccine is not 100% effective so the vaccinated individual can become infected. The basic model used in this paper refers to [13].

The paper is organized as follows: the mathematical model of SVIS is presented in second section. The stability analysis is given in third section, then we conduct a numerical exploration of both types model in fourth section. We conclude by discussing our finding and suggesting future work in the last section.

MATHEMATICAL MODEL

The mathematical model in this research is development of the model used in journal written by [13] which consists of 3 compartment that is, population of susceptible individuals at time t notated with $S(t)$, population of infected individuals at time t notated with $I(t)$, population of vaccinated individuals at time t notated with $V(t)$. The model's transmission diagram can be seen in Fig. 1. The following is assumption that used on SIVS epidemic model with vaccine ineffectiveness:

1. Vaccination is given to new individuals and susceptible individuals.
2. Not every new individual receive vaccine, then the new individuals who do not receive vaccine become susceptible.
3. Vaccination has temporary immunity that will lose as time pass, vaccinated individuals have potential to become susceptible again.
4. Vaccine does not 100% effective, consequently vaccinated individuals can get infected.

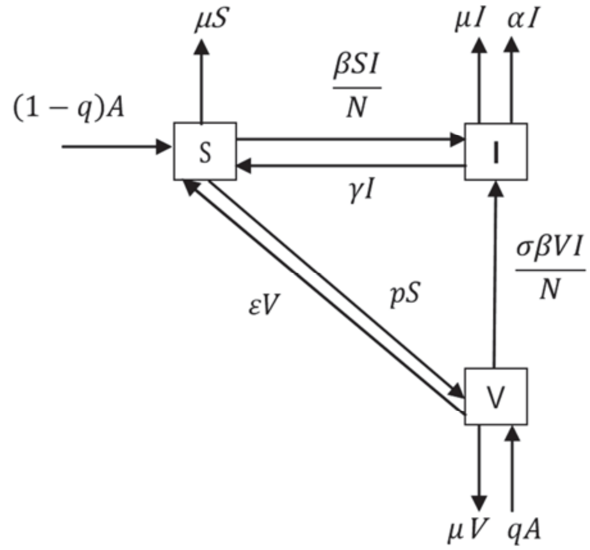

FIGURE 1. Transmission Diagram of SIVS Epidemic Model with Vaccine Ineffectiveness

Based on previous assumption, then the SIVS epidemic model with vaccine ineffectiveness can be formed as follows:

$$\frac{dS}{dt} = (1-q)A + \gamma I + \varepsilon V - \frac{\beta SI}{N} - (\mu + p)S \quad (1)$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} + \frac{\sigma \beta VI}{N} - (\mu + \gamma + \alpha)I \quad (2)$$

$$\frac{dV}{dt} = q\text{A} + \text{pS} - \frac{\sigma \beta SI}{N} - (\mu + \varepsilon)V \quad (3)$$

where assumptions are the parameter values $\text{A}, \beta, \gamma, \mu, \alpha, \varepsilon > 0$, and $0 \le p \le 1$, $0 \le q \le 1$, $0 \le \sigma \le 1$. The definition of variables and parameters are presented in Table 1 and Table 2 as follow,

TABLE 1. Variable in SIVS epidemic model with vaccine ineffectiveness

Variable	Description	Unit
$S(t)$	Population of susceptible individuals at time t	Individual
$V(t)$	Population of vaccinated individuals at time t	Individual
$I(t)$	Population of infected individuals at time t	Individual
$N(t)$	Total population at time t	Individual

TABLE 2. Parameter in SIVS epidemic model with vaccine ineffectiveness

Parameter	Description	Unit
A	Number of new individuals input to the population per unit time	Individual/unit time
q	Proportion of new individuals who are vaccinated	-
β	Rate of disease transmission	1/unit time
γ	Rate of recovery	1/unit time
μ	Rate of natural death	1/unit time
α	Rate of disease-related death	1/unit time
p	Rate of susceptible individuals who are vaccinated	1/unit time
ε	Rate of losing vaccine immunity	1/unit time
σ	Vaccine ineffectiveness	-

From equation (1)-(3), it is clear that rate of total population is not constant and fulfill the following equation,

$$\frac{dN}{dt} = A - \mu N - \alpha I \cdot$$

Substituting $S = N - I - V$ into (1)-(3), and we get the following system,

$$\frac{dI}{dt} = I\left[\frac{\beta(N - I - V + \sigma V)}{N} - (\mu + \gamma + \alpha)\right] \tag{4}$$

$$\frac{dV}{dt} = qA + p(N - I) - \left[\mu + p + \varepsilon + \frac{\sigma\beta I}{N}\right]V \tag{5}$$

$$\frac{dN}{dt} = A - \mu N - \alpha I \tag{6}$$

Furthermore, an analysis is performed on (4)-(6).

STABILITY OF EQUILIBRIUM

The SIVS epidemic model with vaccine ineffectiveness have two equilbrium points namely, the disease free-endemic equilibrium point (E_0) and endemic equilibrium point (E_1). Then, stability of equilibrium point will be analyzed.

Equilibrium Points

By assuming $\frac{dI}{dt} = 0$, $\frac{dV}{dt} = 0$, and $\frac{dN}{dt} = 0$, the model obtain two equilbrium points namely, the disease free-endemic equilibrium point (E_0) and endemic equilibrium point (E_1). Equilibrium point E_0 show as follows.

$$E_0 = \left(0, \frac{A(\mu q + p)}{\mu(\mu + p + \varepsilon)}, \frac{A}{\mu}\right)$$

Then, the *basic reproduction number* (R_0) are obtained to determine the level of the spread of infectious disease in a population with Next-Generation Matrix (NGM) method through the [18] approach. Equation (4) can be written as follows,

$$\frac{dI}{dt} = F(I) - Z(I)$$

with,

$$F(I) = \left(\frac{\beta I(N - I - V)}{N} + \frac{\beta IV}{N}\right),$$

$$Z(I) = (\mu + \gamma + \alpha)I.$$

So that $\frac{dI}{dt} = \left(\frac{\beta I(N - I - V)}{N} + \frac{\beta IV}{N}\right) - (\mu + \gamma + \alpha)I.$

Let $\mathbb{F}$ and $\mathbb{Z}$ is Jacobian matrix of $F(I)$ and $Z(I)$ respectively so that obtained,

$$\mathbb{F} = \left(\frac{\beta I(N - I - V)}{N} + \frac{\beta IV}{N}\right),$$

$$\mathbb{Z} = (\mu + \gamma + \alpha) \text{ and}$$

$$\mathbb{Z}^{-1} = \frac{1}{(\mu+\gamma+\alpha)}$$

Suppose $\mathcal{L} = \mathbb{F}\mathbb{Z}^{-1}$, R_0 are obtained by determining the biggest eigenvalue of the matrix $\mathcal{L}$, so that it can be obtained,

$$\mathcal{L} = \left(\frac{\beta I(N - I - V)}{N} + \frac{\beta IV}{N}\right)\frac{1}{(\mu+\gamma+\alpha)}$$

Subtituting disease free-equilibrium $E_0 = \left(0, \frac{A(\mu q + p)}{\mu(\mu + p + \varepsilon)}, \frac{A}{\mu}\right)$ to matrix $\mathcal{L}$ so that,

$$\mathcal{L} = \left(\frac{\beta(\mu(1 - q + \sigma q) + \sigma p + \varepsilon)}{(\mu + p + \varepsilon)(\mu + \gamma + \alpha)}\right)$$

Then determining the eigenvalue of matrix $\mathcal{L}$,

$$\det(\lambda I - \mathcal{L}) = 0$$

$$\Leftrightarrow \lambda = \left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)(\mu+\gamma+\alpha)}\right).$$

R_0 are the biggest eigenvalue of matrix $\mathcal{L}$, then R_0 are obtained as follows,

$$R_0 = \left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)(\mu+\gamma+\alpha)}\right),$$

and E_1 show as follows.

$$E_1 = \left(I^*, \frac{(A-\alpha I^*)(\mu q A + p(A-\alpha I^* - \mu I^*)}{\mu((A-\alpha I^*)(\mu+\varepsilon+p)+\mu\sigma\beta I^*)}, \frac{(A-\alpha I^*)}{\mu}\right).$$

Endemic equilibrium point E_1 exists if,

i. $A > A - \mu I^* > \alpha I^*$,

ii. $\left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)(\mu+\gamma+\alpha)}\right) > 1$ or $R_0 > 1$

iii. $\frac{\mu\sigma\beta\alpha(\mu+\gamma+\alpha)+\alpha\beta(\alpha+\gamma)(\mu+\varepsilon+p)+\sigma p\alpha\beta(\mu+\alpha)}{\beta^2\mu\sigma(\alpha+\mu)+\alpha^2(\mu+\varepsilon+p)+(\mu+\gamma+\alpha)+\alpha\beta p(\mu+\alpha)} < 1.$

Stability Analysis of the Equilibrium Points

In analyzing the model localy asymptotically stable is by linearization using Jacobian matrix. The Jacobian matrix of equation (4)-(6) is,

$$J = \begin{pmatrix} G_I - (\mu+\gamma+\alpha) & G_V & G_N \\ -\left(p+\frac{\sigma\beta V}{N}\right) & -\left(\mu+p+\varepsilon+\frac{\sigma\beta I}{N}\right) & \left(p+\frac{\sigma\beta IV}{N^2}\right) \\ -\alpha & 0 & -\mu \end{pmatrix} \tag{7}$$

where,

$$G = \frac{\beta I(N-I-V+\sigma V)}{N}, \quad G_I = \frac{\partial G}{\partial I} = \frac{\beta I(N-I-V+\sigma V)}{N} - \frac{\beta I}{N},$$

$$G_V = \frac{\partial G}{\partial V} = -\frac{\beta I}{N} + \frac{\sigma\beta I}{N}, \quad G_N = \frac{\beta I}{N}\left(\frac{I+V-\sigma V}{N}\right).$$

Stability analysis of disease free-equilbrium point is done by substituting the disease free-equilibrium point to (7). The eigenvalues can be obtained from the Jacobian matrix, as follows.

$$J(E_0) = \begin{pmatrix} \frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)} - (\mu+\gamma+\alpha) & 0 & 0 \\ -\left(p - \frac{\sigma\beta(\mu q+p)}{(\mu+p+\varepsilon)}\right) & -(\mu+p+\varepsilon) & p \\ -\alpha & 0 & -\mu \end{pmatrix}. \tag{8}$$

From the equation 8, then can be obtained the eigenvalue of matrix $J(E_0)$,

$$\det(\lambda I - J) = 0$$

It obtained the following characteristic equation,

$$(\lambda - b_1)(\lambda+\mu)(\lambda+b_2) = 0 \tag{9}$$

in which,

$$b_1 = \left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)} - (\mu+\gamma+\alpha)\right),$$

$$b_2 = (\mu+p+\varepsilon)$$

and the eigenvalues are obtained,

$$\lambda_1 = \left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)} - (\mu+\gamma+\alpha)\right),$$

$$\lambda_2 = -\mu,$$

$$\lambda_3 = -(\mu+p+\varepsilon).$$

It is clear $\lambda_2, \lambda_3 < 0$ because every parameter value is positive. Then the conditions for λ_1 will be determined so that the system (4)-(6) is stable. Suppose $\lambda_1 < 0$ if,

$$\Leftrightarrow \left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)} - (\mu+\gamma+\alpha) \right) < 0$$

$$\Leftrightarrow \left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)(\mu+\gamma+\alpha)} \right) < 1$$

$$\Leftrightarrow R_0 < 1$$

Based on description above, the disease free-equilbirum point $E_0 = \left(0, \frac{A(\mu q+p)}{\mu(\mu+p+\varepsilon)}, \frac{A}{\mu}\right)$ is locally asymptotically stable if $R_0 < 1$.

The similar steps are also applied to determine the stability of the endemic equilibrium point. The initial step is determining the characteristic equation of the second equilibrium point by determining the formula,

$$J(E_1) = \begin{pmatrix} G_{I^*} - (\mu+\gamma+\alpha) & G_{V^*} & G_{N^*} \\ -\left(p + \frac{\sigma\beta V^*}{N^*}\right) & -\left(\mu+p+\varepsilon+\frac{\sigma\beta I^*}{N^*}\right) & \left(p + \frac{\sigma\beta I^* V^*}{(N^*)^2}\right) \\ -\alpha & 0 & -\mu \end{pmatrix}$$

$$\det(\lambda I - J) = 0.$$

It is obtained the following characteristic equation,

$$\lambda^3 + c_1\lambda^2 + c_2\lambda + c_3 = 0, \qquad (10)$$

where

$$c_1 = 2\mu + p + \varepsilon + \frac{\sigma\beta I^*}{N^*} + \frac{\beta I^*}{N^*},$$

$$c_2 = \mu(\mu+p+\varepsilon) + \frac{\beta I^*}{N^*}\left[\left(\mu\frac{\sigma\beta I^*}{N^*} + \mu + p + \varepsilon + \sigma p + \frac{\sigma^2\beta V^*}{N^*} + \alpha\right) - \left(p + \frac{\sigma\beta V^*}{N^*} + \frac{\alpha(\mu+\gamma+\alpha)}{\beta}\right)\right],$$

$$c_3 = \frac{\beta I^*}{N^*}\left[\begin{array}{l}\left(\mu(\mu+p+\varepsilon) + \mu\frac{\sigma\beta I^*}{N^*} + \sigma(\mu p+\alpha p) + \sigma\left(\mu\frac{\sigma\beta V^*}{N^*} + \frac{\sigma\beta\alpha V^* I^*}{(N^*)^2}\right) + \alpha\left(\mu+p+\varepsilon+\frac{\sigma\beta I^*}{N^*}\right)\right) - \\ \left((\mu p+\alpha p) + \left(\mu\frac{\sigma\beta V^*}{N^*} + \frac{\sigma\beta\alpha V^* I^*}{(N^*)^2}\right) + \frac{\alpha(\mu+\gamma+\alpha)}{\beta}\left(\mu+p+\varepsilon+\frac{\sigma\beta I^*}{N^*}\right)\right)\end{array}\right].$$

Because every c_1, c_2, c_3 contain parameters that are difficult to simplify so it is difficult to determine the root of characteristic equation analytically. Then a phase plane simulation is performed to analyze the stability of endemic equilibrium point E_1.

This simulation is carried out on equations (4.4)-(4.6) by giving three different initial values for $(I(0), V(0), N(0))$ and parameter values, which are presented in Table 3 and Table 4 respectively. It aims to determine the convergence of the solution of each initial value and given parameters.

TABLE 3. Initial Values of Endemic Equilibrium Phase Plane

Initial Value	$\boldsymbol{I(0)}$	$\boldsymbol{V(0)}$	$\boldsymbol{N(0)}$
1	100	80	2800
2	70	50	2600
3	40	30	2400

TABLE 4. Parameter values of Endemic Equilibrium Point E_1 Phase Plane

Parameter	Parameter Values	Source
A	10	[13]
q	0.1	[13]
β	0.8	[13]
γ	0.01	Assumed
μ	0.2	[13]
α	0.02	Assumed
p	0.1	[13]
ε	0.2	[13]
σ	0.4	Assumed

The following is an endemic equilibrium point E_1 phase plane.

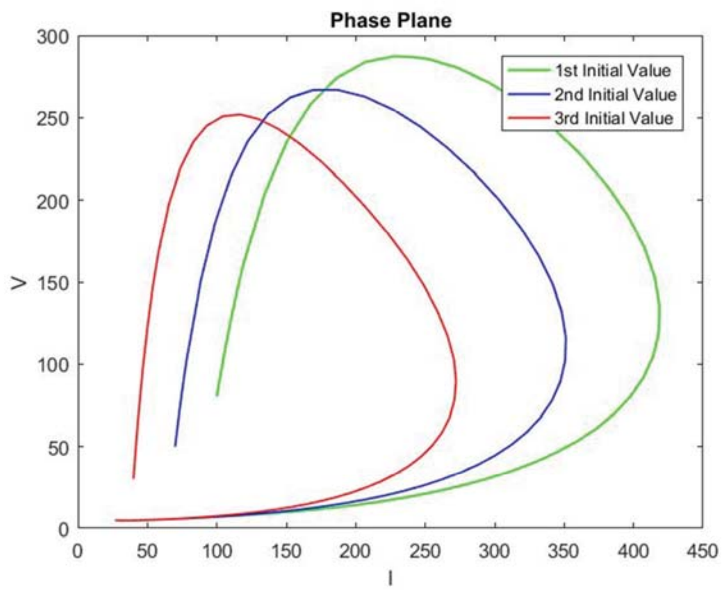

FIGURE 2. Phase Plane Graphic of Infected Individual Population (I) and Vaccinated Individual Population (V)

Based on Fig. 2 shows that the greater t, values of I and V tend to go to the same point respectively 33 and 3. This means that the dynamics of each population of SIVS epidemic model with vaccine ineffectiveness overall will towards to endemic equilbrium point $E_1 = (I, V, N) = (33,3,49)$. Then, it is also obtained that $R_0 = 2.97 > 1$.

Then it can be concluded if the endemic equilibrium point tend to asymptotically stable if $R_0 > 1$. This means the population of infected individuals can transmit disease to susceptible (vaccinated) individuals so that there will be a spread of infectious disease in the population.

SENSITIVITY ANALYSIS OF PARAMETER

Parameter sensitivity analysis aims to determine which parameters have the most affect to R_0. According to [19], sensitivity index of parameters can be formulated as follows,

$$e_m = \left(\frac{\partial R_0}{\partial m}\right)\frac{m}{R_0},$$

where,

$m =$ parameters to be analyzed

$e_m =$ sensitivity index of parameter m.

The basic reproduction number that used on this research is below,

$$R_0 = \left(\frac{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)(\mu+\gamma+\alpha)}\right).$$

From R_0, there are 8 parameters to which the sensitivity index will determined, including, $\beta, \mu, q, p, \sigma, \varepsilon, \gamma, \alpha.$ As example, the following is the calculation of the sensitivity index for β parameter.

$$e_\beta = \left(\frac{\partial R_0}{\partial \beta}\right)\frac{\beta}{R_0} = \frac{(\mu(1-q+\sigma q)+\sigma p+\varepsilon)}{(\mu+p+\varepsilon)(\mu+\gamma+\alpha)}\frac{\beta(\mu+p+\varepsilon)(\mu+\gamma+\alpha)}{\beta(\mu(1-q+\sigma q)+\sigma p+\varepsilon)} = 1.$$

Then, Table 5 is the result of sensitivity index of parameters on the model. Furthermore, the affect of parameters value changes to R_0 changes is presented in Table 6.

TABLE 5. Sensitivity Index of Parameters

Parameter	**Nilai**	**Indeks Sensitivitas**
q	0.1	-0.028
β	0.8	1
γ	0.1	-0.25
μ	0.2	-0.46
α	0.1	-0.25
p	0.1	-0.10
ε	0.2	0.06
σ	0.4	0.11

TABLE 6. The Affect of Parameters Value Changes to R_0 Changes

Parameter (p)	**Nilai**	***R₀*** $p-10\%$	$p-15\%$	$p+10\%$	$p+15\%$
q	0.1	1.716	1.719	1.707	1.671
β	0.8	1.540	1.455	1.883	1.968
γ	0.1	1.755	1.778	1.670	1.411
μ	0.2	1.794	1.839	1.636	1.601
α	0.1	1.712	1.733	1.670	1.411
p	0.1	1.688	1.697	1.694	1.579
ε	0.2	1.526	1.518	1.554	1.560
σ	0.4	1.692	1.683	1.731	1.740

Based on Table 6, a positive sensitivity index indicates that if the value of a parameter increases, the R_0 value will increase. Conversely, if the sensitivity index is negative, it indicates that if the value of a parameter increases, it will cause R_0 to decrease. For example, when (β) increases by 10%, that is 0.88, the R_0 value will increase by 10% from the initial R_0 value to 1.883 and vice versa. The analysis also applies to the parameters ε and σ. However, when p increases by 10%, namely 0.11, the R_0 value will decrease by 0.01% from the initial R_0 value to become 1,694 and vice versa. The analysis will also apply to the parameters q, μ, γ, α. Based on this description, it can be concluded that the parameters that have a significant influence on the model are $\beta, \mu, \sigma, \mathrm{p}, \gamma, \alpha$.

Next, we will simulate the sensitivity of the parameters (β) and σ to R_0, which are the rate of disease transmission and vaccine ineffectiveness, respectively. In this simulation, three different σ values were selected, namely, $\sigma = 0.004$, $\sigma = 0.04$, and $\sigma = 0.4$, while β is in the $0.1 \le \beta \le 1$ interval. The following Fig. 3 shows the simulation results of the graph of sensitivity β to R_0.

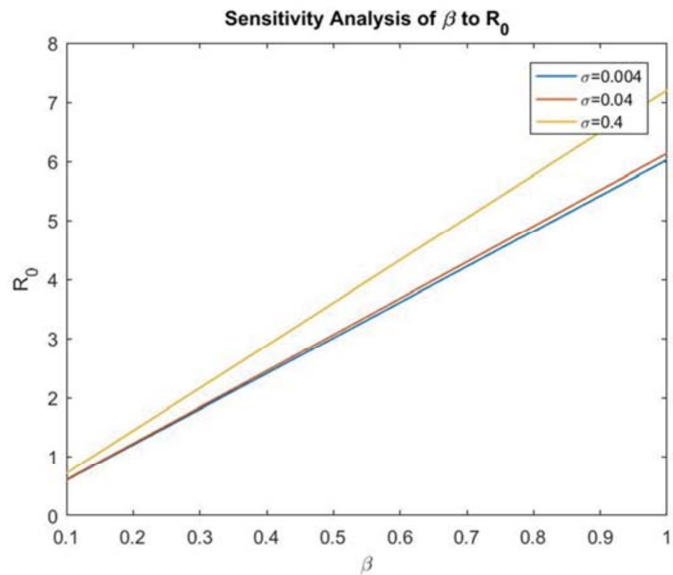

FIGURE 3. Sensitivity Analysis of β to R_0

In the calculation of the sensitivity index for the parameters β and σ, it can be seen that each of them is positive, so from Fig. 3 it shows that when $\beta = 0$ causes the value of $R_0 < 1$, while when $\beta = 1$ causes the value of $R_0 > 1$. Then it can also be noted in the initial conditions, when the value of $\sigma = 0.004$ causes the value of $R_0 = 0.60$, while when $\sigma = 0.4$ causes the value of $R_0 = 0.72$. .

Based on the explanation above, it can be concluded that the greater the rate of disease transmission (β) and the ineffectiveness of the vaccine (σ), the greater the R_0 value, which means that the disease has the potential to become endemic.

NUMERICAL SIMULATION

Model (1)-(3) simulations are carried out in two conditions namely disease free and endemic conditions, with initial values for each condition are same, $\left(S(0), I(0), V(0)\right) = (500,300,50)$. The model solved by Runge Kutta method.

Disease free conditions occur when there is no spread of infectious diseases, so the population of infected individuals is zero $I = 0$. With $t = 0$ to $t = 50$ year and the values parameter are presented in Table 7.

TABLE 7. Parameter Value for Simulation of Disease Free Conditions

Parameter	Parameter Values	Source
A	10	[13]
q	0.1	[13]
β	0.3	[6]
γ	0.3	Assumed
μ	0.01	Assumed
α	0.1	[13]
p	0.05	Assumed
ε	0.2	[13]
σ	0.01	[6]

Based on the parameter values given, $R_0 = 0.58 < 1$. The following are simulation results for disease free conditions,

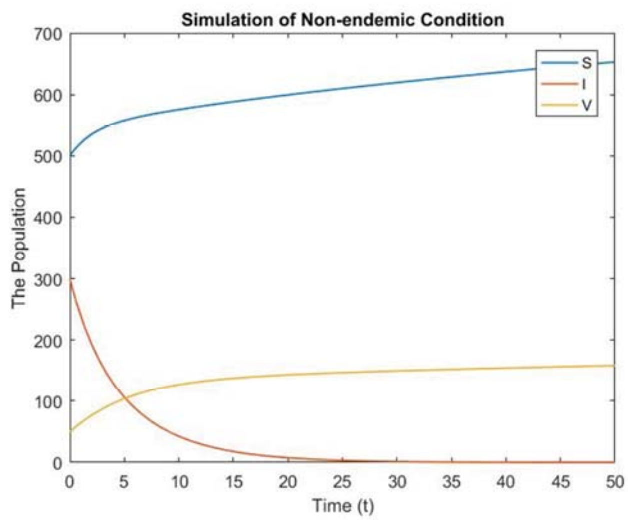

FIGURE 4. The Dynamics of Spread Infectious Disease when $R_0 < 1$.

Based on Fig. 4 it shows that susceptible individual population (S) is increased. Vaccinated individuals population (V) keep increasing. Meanwhile, infected individuals population (I) is decreased then at $t = 25$ tends to be constant towards zero.

Endemic conditions occur when there is a spread of infectious diseases, so there is a population of infected individuals $(I \neq 0)$, susceptible individuals $(S \neq 0)$, and vaccinared individuals $(V \neq 0)$ with $t = 0$ to $t = 50$ year. The parameter values are presented in Table 8.

TABLE 8. Parameter Value for Simulation of Endemic Conditions

Parameter	Parameter Value	Source
A	10	[13]
q	0.1	[13]
β	0.8	[13]
γ	0.1	[13]
μ	0.01	Assumed
α	0.001	Assumed
p	0.1	[13]
ε	0.2	[13]
σ	0.4	Assumed

Based on the parameter values given, $R_0 = 5.7 > 1.$. The following are simulation results for disease free conditions,

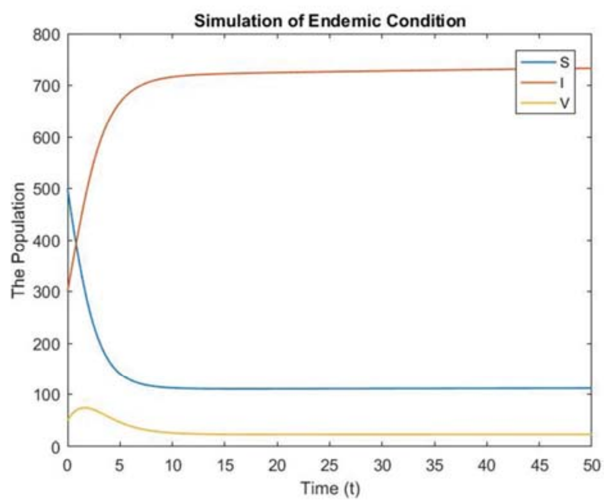

FIGURE 5. The Dynamics of Spread Infectious Diseasi when $R_0 > 1$.

Based on Fig. 5**,** it shows that at $t = 0$, susceptible individuals population (S) is decreased and tends to be constant at $t = 0$ onwards. Vaccinated individuals population (V) is increased then decreased and become constant at $t = 10$ onwards. Meanwhile, infected individuals population (I) is increased and tends to be constant at $t = 40$ onwards.

Next, observing vaccine ineffectiveness can be done by simulation of endemic condition of V and I with different value of σ. The following is simulation of V and time with intial value $(V(0) = 50)$,

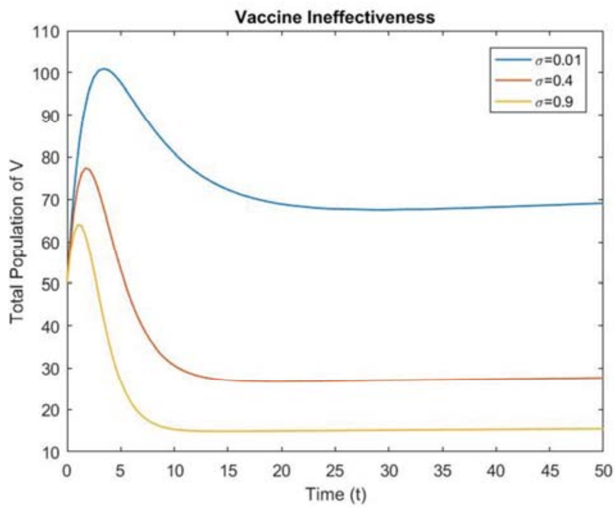

FIGURE 6. Simulation of V to time when $\sigma = 0.1$, $\sigma = 0.4$, $\sigma = 0.9$.

Based on Fig. 6 it shows that number of vaccinated individuals has increased then tends to decreases, when $\sigma = 0.9$ vaccinated individual population decreases with the lowest population number compared to when $\sigma = 0.4$ or $\sigma = 0.1$.

The following is simulation of I and time with intial value $(I(0) = 300)$,

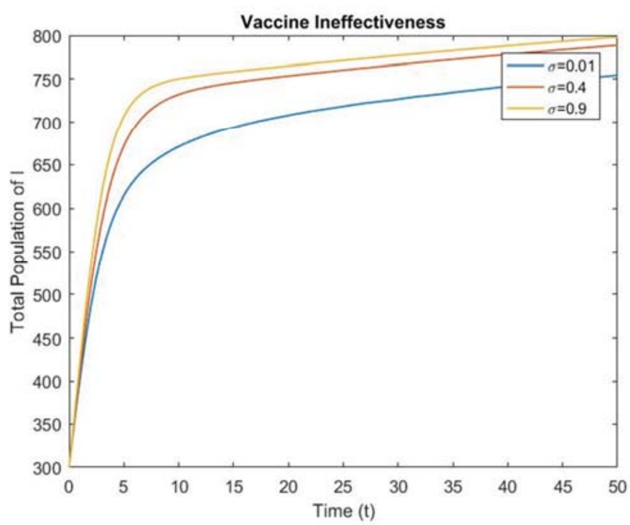

FIGURE 7. Simulation of I to time when $\sigma = 0.1$, $\sigma = 0.4$, $\sigma = 0.9$.

Based on Fig. 7 it shows when $\sigma = 0.9$ population of infected individual decreases then tends to be constant with the highest number of population, than compared to when $\sigma = 0.4$ or $\sigma = 0.1$.

From explanation above, it conclude that vaccine ineffectiveness (σ) affects the high spread of disease, as vaccine more ineffective then number of infected individuals population (I) become higher.

CONCLUSION

Based on model analysis result, the model obtained two equilibrium points namely, the disease free-equilibrium point (E_0) and endemic equilibrium point (E_1). In addition, the basic reproduction number (R_0) also obtained, which determines the existence and stability of equilibrium point. disease free-equilibrium point (E_0) local asymptotically stable if $R_0 < 1$, then through phase plane simulation it conclude that endemic equilibrium point (E_1) local asymptotically stable if $R_0 > 1$.

Based on the sensitivity analysis of parameter, it can be concluded that the parameters that have a significant influence on the model are $\beta, \mu, \sigma, \mathrm{p}, \gamma, \alpha$. Also, it can be concluded that the greater the rate of β, σ, the greater the R_0 value. Conversly, the greater the rate of μ, p, γ, α, then the lower the R_0 value. So, the less the rate of disease transmission (β) and the more effective a vaccine then the lower the spread of infectious diseases $(R_0 < 1)$. This applies to the more vaccinated individuals (p) and the more recovery individuals (γ), the lower the spread of infectious diseases. The opposite applies. This means that the parameters that cause the high spread of infectious diseases must be suppressed, thus the parameters that cause the decrease in the spread of infectious diseases must be increased. Furthermore, based on numerical simulation result, it shows that vaccine ineffectiveness affects the high spread of disease.

On this research, we only discuss about the stability of SIVS epidemic model with vaccine ineffectiveness. Then, there is chance for the next researchers to add optimal control on SIVS epidemic model with vaccine ineffectiveness.

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