Stability Analysis of the SIRS Epidemic Model using the Fifth-order Runge Kutta Method

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Abstract: Transmission of the disease occurs through interactions in the infection chain both directly and indirectly. There are several causes of a disease that can enter endemic conditions, namely the condition of a disease outbreak in an area for a long time. This condition can be modeled mathematically using certain assumptions that will then be solved by analytical and numerical solutions. In this study, an analysis of the stability of disease spread will be carried out by constructing a mathematical model of the SIRS epidemic in infectious diseases. The results obtained are based on numerical solutions obtained through the Runge-Kutta 5th Order Method. After that, analysis and simulation are done with the MATLAB program. In the simulation results, it can be seen that the greater the rate of disease transmission or the low recovery rate and natural death causes endemic conditions.

1 INTRODUCTION

The epidemic model studies the dynamics of the spread or transmission of a disease in a population. The SIRS epidemic model is an outgrowth of the SIR epidemic model. The SIRS epidemic model differs from the previous model when individuals who have recovered can return to the susceptible class (Adda & Bichara, 2012).

The numerical method is also called an alternative to the analytic method, which is a method of solving mathematical problems with standard or common algebraic formulas. So, called, because sometimes math problems are difficult to solve or even cannot be solved analytically so it can be said that the mathematical problem has no analytical solution. Alternatively, the mathematical problem is solved by numerical method, for which the Runge-Kutta method of order 5 is used with a high degree of accuracy (Xiaobin et al., 2018).

2 RUNGE-KUTTA ORDER 5

The fifth-order Runge-Kutta method is the most meticulous method in terms of second, third and fourth order (Sinuhaji, 2015). The fifth-order Runge-Kutta order is derived and equates to the terms of the taylor series for the value of n = 5 (Tulus, 2012).

The fifth-order Runge-Kutta can be done by following the steps below:

$$
\begin{aligned}
k_1 &= hf(t_i, x_i)\\
k_2 &= hf\left(t_i + \frac{h}{2}, x_i + \frac{k_1}{2}\right)\\
k_3 &= hf\left(t_i + \frac{h}{4}, x_i + \frac{3k_1 + k_2}{16}\right)\\
k_4 &= hf\left(t_i + \frac{h}{2}, x_i + \frac{k_3}{2}\right)\\
k_5 &= hf\left(t_i + \frac{3h}{4}, x_i + \frac{-3k_2 + 6k_3 + 9k_4}{16}\right)\\
k_6 &= hf\left(t_i + h, x_i + \frac{k_1 + 4k_2 + 6k_3 - 12k_4 + 8k_5}{7}\right)
\end{aligned}
\tag{1}
$$

$$x_{i+1} = x_i + 1 / 90(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6)$$

3 MODEL FORMULATION

Let $S(t)$, $I(t)$ dan $R(t)$ successive states subpopulation density of susceptible individuals is infected and recovered, with number at time t (Steven, 2017). In this model it is assumed that the total population density at all times is constant, that is

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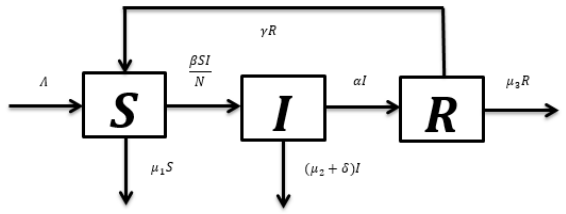
$N = S(t) + I(t) + R(t)$. SIRS models discussed in this paper compartment illustrated in the following diagram:



Obtained system of ordinary differential equations with three dependent variables were respectively declared rate of change in density of susceptible, infected and recovered:

$$\begin{aligned}\frac{dS}{dt} &= \Lambda - \frac{\beta SI}{N} - \mu_1 S + \gamma R \\ \frac{dI}{dt} &= \frac{\beta SI}{N} - (\mu_2 + \delta + \alpha)I \\ \frac{dR}{dt} &= \alpha I - (\mu_3 + \gamma)R\end{aligned} \quad (2)$$

Since the total population rate is equal to the rate of death, then $\Lambda = \mu_1 S + (\mu_2 + \delta)I + \mu_3 R$, and $S + I + R = N$ so the system becomes

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta SI}{N} + (\mu_2 + \delta - \mu_3 - \gamma)I + \\ &\quad (\mu_3 + \gamma)N - (\mu_3 + \gamma)S \\ \frac{dI}{dt} &= \frac{\beta SI}{N} - (\mu_2 + \delta + \alpha)I \\ \frac{dR}{dt} &= \alpha I - (\mu_3 + \gamma)R.\end{aligned} \quad (3)$$

If $S = \frac{S}{N}$, $I = \frac{I}{N}$ and $R = \frac{R}{N}$, then system (3.2) with the first two equations can be simplified into:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI + (\mu_2 + \delta - \mu_3 - \gamma)I \\ &\quad -(\mu_3 + \gamma)S + (\mu_3 + \gamma) \\ \frac{dI}{dt} &= \beta SI - (\mu_2 + \delta + \alpha)I \\ \frac{dr}{dt} &= \alpha I - (\mu_3 + \gamma)R\end{aligned} \quad (4)$$

Note that the first two equations in the system (3.3) do not contain the variable R (t) so that for the next reason enough to be discussed the system with two equations. If the value of $S(t)$ and $I(t)$ has been obtained, then the value of $R(t)$ will be obtained by using the relationship $S + I + R = N$.

4 RESULT

4.1 Disease Free Equilibrium Point

The equilibrium point is reached when the variable that originally changes with time becomes constant. Thus, the equilibrium point is obtained when $\frac{dS}{dt}$ and $\frac{dI}{dt}$ in equation (4) are zero.

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI + (\mu_2 + \delta - \mu_3 - \gamma)I - (\mu_3 + \gamma)S \\ &\quad +(\mu_3 + \gamma) = 0\end{aligned}$$

$$\frac{dI}{dt} = \beta SI - (\mu_2 + \delta + \alpha)I = 0$$

Based on equation (6) two possibilities are obtained, namely $I = 0$ or $S = \frac{\mu_2 + \delta + \alpha}{\beta}$. If $I = 0$ is substituted in equation (5)

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI + (\mu_2 + \delta - \mu_3 - \gamma)I - (\mu_3 + \gamma)S \\ &\quad +(\mu_3 + \gamma) = 0 \\ &= -\beta S(0) + (\mu_2 + \delta - \mu_3 - \gamma)(0) \\ &\quad -(\mu_3 + \gamma)S + (\mu_3 + \gamma) = 0 \\ &= -(\mu_3 + \gamma)S + (\mu_3 + \gamma) = 0 \\ S &= \frac{(\mu_3 + \gamma)}{(\mu_3 + \gamma)} = 1\end{aligned}$$

obtained $S = 1$, so that obtained the disease-free equilibrium point $E_0 = (1,0)$.

4.2 The Endemic Equilibrium Point

The endemic equilibrium point is a point that indicates the possibility of spreading the disease in the population. In equation (6) if $S = \frac{\mu_2 + \delta + \alpha}{\beta}$, obtained equilibrium point is a second, which is the point of equilibrium endemics $E^* = (S^*, I^*)$, with $S^* = \frac{\mu_2 + \delta + \alpha}{\beta}$, then if the substitution of the equation (5)

$$\begin{aligned}\frac{ds}{dt} &= -\beta\left(\frac{\mu_2 + \delta + \alpha}{\beta}\right)I^* + (\mu_2 + \delta - \mu_3 - \gamma)I^* \\ &\quad -(\mu_3 + \gamma)\left(\frac{\mu_2 + \delta + \alpha}{\beta}\right) + (\mu_3 + \gamma) = 0\end{aligned}$$

is obtained $I^* = \frac{\mu_3 + \gamma}{\mu_3 + \gamma + \alpha} - \frac{(\mu_3 + \gamma)\mu_2 + \delta + \alpha}{\beta(\mu_3 + \gamma + \alpha)}$ or $I^* = \frac{\mu_3 + \gamma}{\mu_3 + \gamma + \alpha}(1 - \frac{1}{R_0})$ with $R_0 = \frac{\beta}{\mu_2 + \delta + \alpha}$ is the basic reproduction number. Note that the endemic

equilibrium point $E^* = (S^*, I^*)$ will exist when $R_0 > 1$.

4.3 Analysis of Local Stability on E_0

The nature of local stability at equilibrium point E_0 is determined by linearizing the system of equation (4) around the equilibrium point.

Suppose:

$$f(S,I) = -\beta SI + (\mu_2 + \delta - \mu_3 - \gamma)I - (\mu_3 + \gamma)S + (\mu_3 + \gamma)$$
$$g(S,I) = \beta SI - (\mu_2 + \delta + \alpha)I$$

Then each function is derived partially to the variable on the function, so that Jacobi matrix is obtained

$$J(S,I) = \begin{pmatrix} -\beta I - (\mu_3 + \gamma) & -\beta S + (\mu_2 + \delta - \mu_3 - \gamma) \\ \beta I & \beta S - (\mu_2 + \delta + \alpha) \end{pmatrix}$$

The system linearization of equation (4) around the equilibrium point $E_0 = (1,0)$ gives the Jacobi matrix

$$J(1,0) = \begin{pmatrix} -(\mu_3 + \gamma) & -\beta + (\mu_2 + \delta - \mu_3 - \gamma) \\ 0 & \beta - (\mu_2 + \delta + \alpha) \end{pmatrix},$$

which has an eigen value $\lambda_1 = -(\mu_3 + \gamma) < 0$ and $\lambda_2 = \beta - (\mu_2 + \delta + \alpha)$ or $\lambda_2 = (R_0 - 1)(\mu_2 + \delta + \alpha)$. If $R_0 < 1$ then $\lambda_2 < 0$ so the equilibrium point E_0 is stable. Conversely, if $R_0 > 1$ then the equilibrium point E_0 is unstable.

4.4 Analysis of Local Stability on E^*

To obtain local stability properties in E^*, the linearization around the endemic equilibrium point $E^* = (S^*, I^*)$ resulted in Jacobi matrix

$$J(S^*, I^*) = \begin{pmatrix} -(\mu_2 + \delta + \alpha)\frac{\mu_3+\gamma}{\mu_3+\gamma+\alpha}(R_0 - 1) - (\mu_3 + \gamma) & -(\alpha + \mu_3 + \gamma) \\ (\mu_2 + \delta + \alpha)\frac{\mu_3+\gamma}{\mu_3+\gamma+\alpha}(R_0 - 1) & 0 \end{pmatrix}$$

.

obtained a complex eigen value $\lambda_{1,2} = a + ib$, with $a < 0$. Therefore, the equilibrium point E^* is asymptotically stable.

4.5 Model Solution with 5th Order Runge-Kutta Method

Numerical analysis illustrates more clearly the model of disease spread by using certain predefined parameters and values. The system of equation (4) will be solved by simulating the Runge-Kutta method of order 5. The simulation of the SIRS epidemic model solved by the 5th order runge-kutta method is performed by giving the initial value of the susceptible (S), infected (I), recovered (R) individual size, and varying the parameters that influence the model interaction so that there will be 2 possibilities that is $R_0 < 1$ and $R_0 > 1$. The initial values given for the SIRS epidemic model for HSV disease are:

Table 1: The initial value of each subpopulation.

Subpopulation	Initial value (million souls)
S	400
I	200
R	100

4.5.1 Simulation $R_0 < 1$

For $R_0 < 1$, given the parameter values to qualify $R_0 < 1$, earned value $R_0 = 0{,}6$. The value of the given value as follows:

Table 2: The parameter values $R_0 < 1$.

Parameter	Value
α	0,013
β	0,014
γ	0,007
δ	0,009
μ_1	0,001
μ_2	0,0013
μ_3	0,00115

From the initial value and the given parameter values obtained simulation $R_0 < 1$ shown in Figure 1 & 2. Population S, I, R experience changes with time, indicating that the behavior of the solution will be towards the point E_0 or it can be said that when $R_0 < 1$ the longer the epidemic disease will disappear from the population.

Graphs do not reflect system behavior over time $h = 0.09$. So, it can be concluded at the time range $h = 0.09$ unstable system. The following is given a table that describes the stability of the system depends on the value of h.

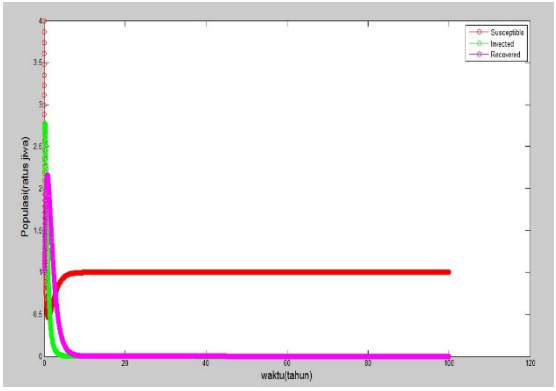


Figure 1: Simulation SIRS Model $R_0 < 1$ with h $= 0.01$.

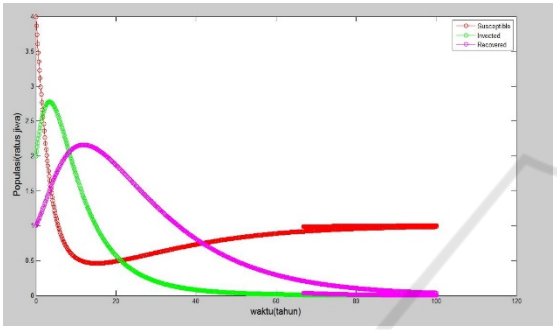


Figure 2: Simulation SIRS Model $R_0 < 1$ with h $= 0.09$.

Table 3: The behavior of the system is based on the value of h on the disease-free SIRS model.

Step time (h)	System behavior
0,01	Stable
0,02	Stable
0,03	Stable
0,05	Stable
0,07	Stable
0,08	Stable
0,09	Unstable

The graph does not show stability in the population because h is so large, the graph will be stable if the h value is less than 0,09.

4.5.2 Simulation $R_0 > 1$

For $R_0 > 1$, given the parameter values to qualify $R_0 > 1$, from the values obtained value $R_0 = 1{,}34$. The value of the given value as follows:

Table 4: The parameter values simulation 1 $R_0 > 1$.

Parameter	Value
α	0,012
β	0,026
γ	0,008
δ	0,006
μ_1	0,002
μ_2	0,0014
μ_3	0,0017

From the initial values and given parameter values $R_0 > 1$ simulation is shown in Figure 3 & 4. The change in each population S.I,R against time, population S has decreased even close to zero. When $t > 5$ years, population S has increased while population I and R continue to decrease but not to zero. This indicates that the epidemic disease will become endemic.

The graph does not reflect system behavior over time $h = 0.07$ as shown in Figure 4.6. So, it can be concluded that the system is not stable at the time range $h = 0.07$. The following is given a table that describes the stability of the system depends on the value of h.

Table 5: The behavior of the system is based on the value of h on the endemic SIRS model.

Step time (h)	System behavior
0,01	Stable
0,02	Stable
0,03	Stable
0,04	Stable
0,05	Stable
0,06	Stable
0,07	Unstable

The graph does not show stability in the population because h is large, the graph will be stable if the h value is less than 0,07.

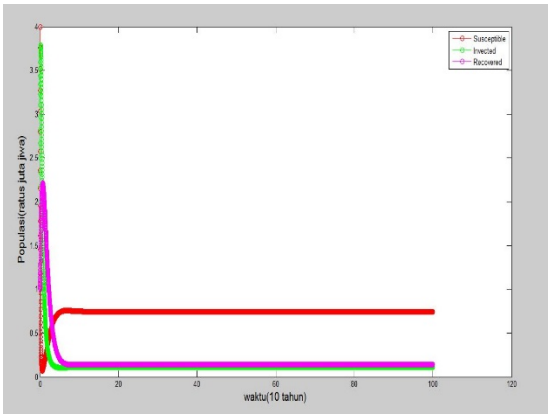


Figure 3: Simulation 1 SIRS Model $R_0 > 1$ with h $= 0{,}01$.

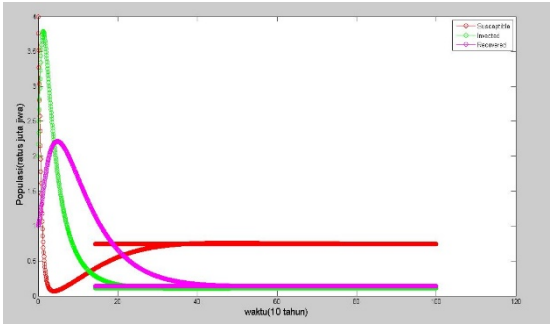


Figure 4: Simulation 1 SIRS Model $R_0 > 1$ with h = 0,07.

Then given the values for simulation $R_0 > 1$ with different parameter values, the values given are as follows:

Table 6: The parameter values simulation 2 $R_0 > 1$.

Parameter	Value
α	0,008
β	0,076
γ	0,008
δ	0,004
μ_1	0,0016
μ_2	0,0012
μ_3	0,0017

From the initial value and the given parameter values obtained simulation $R_0 > 1$ shown in Figure 5 and 6. The population change of S and I is very significant, population S is at critical point while population I increases dramatically, population R also increase, but it does not affect population S because population I increases very fast. When $t >$ 10 years population I and R decreased while population S increased but did not exceed population I as in figure 5.

The graph does not reflect the behavior of the system at a time range $h = 0.08$ as in figure 6. The following is given a table that describes the stability of the system depends on the value of h.

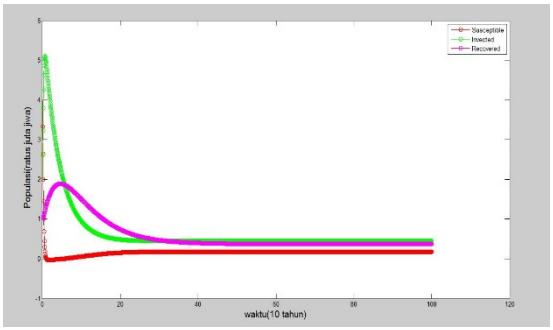


Figure 5: Simulation 2 SIRS Model $R_0 > 1$ with h = 0,01.

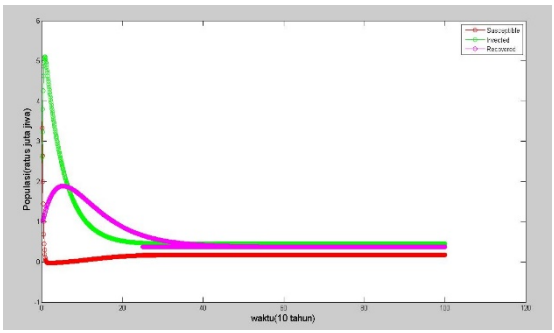


Figure 6: Simulation 2 SIRS Model $R_0 > 1$ with h = 0,07.

The graph does not show stability in the population because h is so large, the graph will be stable if the h value is less than 0.08. So, the 5th order Runge-Kutta numerical scheme satisfies the stability properties of the SIRS model with $R_0 > 1$ when the time step size(h) is not greater than 0,07.

SIRS epidemic model simulation using Runge-Kutta method of order 5 is influenced by time step (h). The time step (h) affects the time needed to approach the equilibrium point, the greater the time step (h) is used the shorter the time needed to approach the equilibrium point.

5 CONCLUSIONS

1) At condition $R_0 < 1$ indicates that the behavior of the solution will be longer to point E_0, which means the longer the disease will be lost from the population.
2) Under condition $R_0 > 1$ there will be an endemic condition, where the *Infected* population is still in the population, in other words the greater the rate of transmission of the disease (β) or the smaller the cure rate (α) and natural death (μ) cause endemic conditions.
3) Time step (h) affects the time required to approach the equilibrium point in the SIRS epidemic model using the Runge-Kutta method of order 5, the greater the time step (h) used the shorter the time it takes to approach the equilibrium point.

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