

Stability Analisis of SEIR Epidemiological Models with Nonlinear Incidence: Case Study in the Central Java Province, Indonesia

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ABSTRACT

SEIR epidemic models that are described as the system of ordinary differential equations with nonlinear incidence rates are proposed. In the SEIR model, the total population is divided into four classes, i.e., susceptible, exposed, infective, and recovered. The model has two equilibrium states; an infection-free equilibrium and an endemic equilibrium state. Local stability of each equilibrium point is determined by Lyapunov first method. It is found that the infection-free equilibrium is unstable and the endemic equilibrium state is asymptotically stable. Global stability of the endemic equilibrium state is analyzed by Lyapunov second method. Numerical simulations with case study of measles disease are presented. The measles disease data is taken from the Central Java Health Office, Indonesia.

Key words : *SEIR, nonlinear incidence, equilibrium, Lyapunov method, stability.*

1. INTRODUCTION

Infectious diseases is a major cause of suffering and death in developing countries. Measles, polio, malaria, rabies, herpes, and HIV are a serious public health problem in several countries. The disease is caused by a virus that can spread through direct contact with patients.

These diseases can be represented into a mathematical model of SIR (Susceptible-Infectious-Recovered). In some diseases [1] such as measles, influenza, malaria and tuberculosis, there is the latent period, i.e., these who are already infected but are not yet infectious. Therefore, with compartmental approach, then the infected susceptible individuals will first enter to the exposed class and then entered the infective class. Further, recovered infective individuals will enter to the recovered class. This model is called by SEIR (Susceptible–Exposed-Infectious-Recovered) model. Some researchers [5, 7] have proposed the concavity of the incidence rate with respect to the number of infective individuals is sufficient conditions for stability of SIR and SEIR models.

Global stability properties and stability analysis by using Lyapunov function for SIR and SEIR epidemiological with non linear transmission have been published by Korobeinikov and Wake [3, 6]. Furthermore, some researchers [4, 9, 10] has studied about basic reproduction number and equilibrium point for compartmental mathematical models of disease transmission. Mathematical modeling for designing programs to control spreading infection of avian influenza diseases and spreading of malaria which depend on human and mosquito populations have been presented by Kartono, et.al, Renny and Widowati [2, 8].

In this paper, we propose mathematical model for susceptible, exposed, infectious, recovered dynamics model of measles disease with data from the Central Java Health Office, Indonesia. Numerical analysis to check equilibrium states stability of the systems by using Lyapunov method are discussed. Then, simulation results are given to show the trajectories and behaviour of SEIR subpopulations dynamics.

The paper is organized as follows. Section 2 describes the mathematical modeling of SEIR dynamics. Numerical results corresponding to stability analysis of equilibrium points are presented in Section 3. In Section 4, the simulations results of measles diseases dynamics are demonstrated. Finally, concluding remarks are given in Section 5.

2. SEIR DYNAMICS MODEL

In the model of the spread of infectious diseases, the epidemic model population was divided into several classes of the epidemic and the mixture was homogeneous. In the class division of the epidemic, the population (N) is assumed constant. In the compartmental model SEIR, the population is divided into four classes, susceptible(S), exposure(E), Infectious(I), Recovered (R), so that $S + E + I + R = N$.

Total population is assumed constant, each newly born individuals to the S-class as susceptible individuals, disease transmission occurs horizontally, spread of disease occur in closed populations and recovered individuals will have permanent immunity. SEIR model discussed has the incidence rate function in the form $f(S, I) = \beta I^p S^q$, with parameter β, p, q are positive constants. This model leads to global stability if this function satisfies the conditions feasible of biological incidence rate and a concave function [5]. To be biologically feasible, the function $f(S, I)$ must satisfy the following conditions,

$$f(0, 0) = f(0, I) = 0 \quad (2.1)$$

and

$$\frac{\partial f(S, I)}{\partial I} > 0, \quad \frac{\partial f(S, I)}{\partial S} > 0, \text{ for all } S, I > 0. \quad (2.2)$$

Function $f(S, I)$ is concave function with respect to variables I , if satisfy

$$\frac{\partial^2 f(S, I)}{\partial I^2} \leq 0 \text{ for all } S, I > 0. \quad (2.3)$$

The function $f(S, I) = \beta I^p S^q$ satisfy the condition (2.1), (2.2) and (2.3). Condition (2.3) is satisfied with $0 < p < 1$. If the incident function is a convex function then equilibrium states and dynamics of the model becomes very complex. The incidence concave function implies that the probability of a single infective individual to transmit the disease will increase with population growth infective [5]. With the incidence rate in the form of $f(S, I) = \beta I^p S^q$, SEIR dynamic models are given by systems differential as follows.

$$\begin{aligned} \frac{dS}{dt} &= b - \beta I^p S^q - \mu S \\ \frac{dE}{dt} &= \beta I^p S^q - \sigma E \\ \frac{dI}{dt} &= \theta E - \delta I \\ \frac{dR}{dt} &= \alpha I - \mu R \end{aligned} \quad (2.4)$$

with μ is the sum of mortality rates and rate of exposure to infective, and δ is the number of infective deaths and healing. Feasible region T for the system (2.4) is $T = \{(S, E, I, R) \mid S, E, I, R \geq 0, S + E + I + R = N\}$.

Individuals in the R-class does not affect the rate of change in the number of individuals in S-class and I-class, so that equation (2.4) can be reduced to

$$\begin{aligned} \frac{dS}{dt} &= b - \beta I^p S^q - \mu S \\ \frac{dE}{dt} &= \beta I^p S^q - \sigma E \\ \frac{dI}{dt} &= \theta E - \delta I \end{aligned} \quad (2.5)$$

where $\mu = \mu_1 + \mu_2$. If $0 < p < 1$, then the system (2.5) has two equilibrium points are infection-free equilibrium point $E_1 = (S_1, E_1, I_1) = (b/\mu, 0, 0)$ and the endemic equilibrium point $E_2 = (S_2, E_2, I_2)$, such that

$$S_2 = \left(\frac{\beta \theta}{\sigma \delta}\right)^{\frac{1}{1-p}}, \quad E_2 = \frac{\sigma S_2^q}{\theta} \quad \text{and} \quad I_2 = \left(\frac{\beta \theta}{\sigma \delta}\right)^{\frac{1}{1-p}} \quad (2.6)$$

To determine the endemic equilibrium state on the system consider the following lemma.

Lemma 2.5 [5]

If the conditions (2.1), (2.2) and (2.3) hold, and if (S^*, I^*) is the endemic equilibrium state, then $\frac{\partial f(S^*, I^*)}{\partial I} = 0$.

The strict equality holds only if $\frac{\partial^2 f(S^*, I^*)}{\partial I^2} < 0$, for all $(S, I) = (S^*, I^*)$.

Basic reproductive number of SEIR on the system (2.5) model is

$$R_0 = \frac{\theta}{\delta\sigma} \frac{\partial f(S_0, I_0)}{\partial I} \tag{2.7}$$

Value of the basic reproduction number can be to determine the existence and uniqueness of equilibrium points on the model of disease transmission. This can be investigated by the following lemma.

Lemma 2.6 [5]

If conditions (2.1) - (2.3) are satisfied, and if $R_0 > 1$, then the system (2.5) has a unique infection-free equilibrium state Q_0 and the unique positive endemic equilibrium state Q . If $R_0 < 1$, then the system (2.5) has no endemic equilibrium state. In this case the only non-negative equilibrium in the system is the infection-free equilibrium state Q_0 .

Theorem 2.7 [4]

If $0 < R_0 < 1$ then the endemic equilibrium state from the system (2.4) and (2.5) is globally asymptotically stable. Equilibrium does not depend on the parameters θ, δ, σ .

3. NUMERICAL RESULTS

In this section, we propose a case study about measles. Measles is a highly infectious disease caused by a virus. Measles is the leading cause of child mortality in developing countries including Indonesia. Measles transmission from person to person through saliva spray and transfer by air through coughing or sneezing. Delivery time 4 days before the rash (red spots) to 4 days after the appearance of the rash, the average incubation period of 10 days and the average period of healing within 2 weeks. Most people with measles will recover. Mortality from measles is typically caused by complications such as bronchial pneumonia and malnutrition.

For the application of the model is used data measles in Central Java in 2009 obtained from the Central Java provincial health office. The data obtained are data measles clinical case that is not blood specimens and there is no epidemiological connection with certain cases. In other words, the number of cases detected there are a number of individuals who suffer from measles with fever, rash shaped, cough / runny nose or red eyes (conjunctivitis) or diagnosed by doctors as measles cases and laboratory have not confirmed whether it is a particular case of measles or rubella (measles Germany). According to the data, we have the average incubation period is 10 days, then $\theta = 1/10 = 0,1$. The average period of infection is the average delivery time is 6 days, so $\sigma = 1/6 = 0,1667$, and $\delta = 0,0011$. Birth rate, $\lambda = 0,1282132$, death rate, $\mu = 1,4757 \times 10^{-5}$. Based on the data and with the least-squares method, we find the parameters $\beta = 0,2$ and $\gamma = 1,4$.

Further, by substituting the parameter values to the system, we obtain the dynamic model as follows.

$$\begin{aligned} \dot{S} &= 0,1282132 - (0,0011) \cdot S \cdot I - (1,4757 \times 10^{-5}) \cdot S \\ \dot{E} &= (0,0011) \cdot S \cdot I - (0,1014757) \cdot E \\ \dot{I} &= (0,1) \cdot E - (0,1681757) \cdot I \\ \dot{R} &= (0,1667) \cdot I - (1,4757 \times 10^{-5}) \cdot R \end{aligned} \tag{3.1}$$

The number of individuals in the R-class does not affect the rate of change in the S, E, I-class and with the assumption that N is constant, then the above equations can be reduced to R-class with $\dot{S} = 1 - (S + E + I)$. Hence, the above systems can be written by

$$\begin{aligned}
 \dot{I} &= 0,1282132 - (0,0011) \cdot I \cdot S - (1,4757 \times 10^{-5}) \cdot I \cdot E \\
 \dot{E} &= (0,0011) \cdot I \cdot S - (0,1014757) \cdot E \\
 \dot{I} &= (0,1) \cdot I - (0,1681757) \cdot I
 \end{aligned}
 \tag{3.2}$$

Furthermore, can be found two equilibrium points of the systems, i.e., infection-free equilibrium state, $(S, E, I) = (86,88297079; 0; 0)$ and endemic equilibrium state, $(S, E, I) = (25,55131602; 0,8919093237; 0,5303437558)$

This means that at some time in a population where individuals are infected with measles disease (there are individuals in the exposed and infective classes).

From the equation (2.7) known that the basic reproduction number of SEIR model is

$$R_0 = \frac{\beta \cdot I \cdot S}{\gamma}$$

The rate of incidence on the system (3.2) can be written in $(S, E, I) = (0,0011) \cdot I \cdot S$, so the first derivative of (S, E, I) to I is

$$\frac{\partial}{\partial I} (0,0011) \cdot I \cdot S = 0,0011 \cdot S$$

Hence, we have basic reproduction number,

$$\begin{aligned}
 R_0 &= \frac{0,1 \cdot 2,2 \times 10^{-5}}{(0,1681757)(0,1014757)} \\
 &= 0,01706574688 \frac{2,2 \times 10^{-5} (86,88297079)}{(0)} \\
 &=
 \end{aligned}$$

Basic reproductive number system (3.2) is $R_0 > 1$, which means $R_0 > 1$ so that each infected individual produces an average of more than one new infection, and disease can develop. And the equilibrium point is unstable. Further, we use Lyapunov method to analyze the stability of each equilibrium state.

3.1. Stability Analysis with First Lyapunov Method

Incidence rate functions of (3.2) system can be written in the form

$$\begin{aligned}
 \dot{I} &= (0,0011) \cdot I \cdot S, \text{ so that} \\
 \frac{\partial}{\partial I} &= 1,54 \times 10^{-5}
 \end{aligned}$$

and

$$\frac{\partial}{\partial I} (0,0011) \cdot I \cdot S = 0,0011 \cdot S$$

Jacobian matrix of the system (3.2) has form,

$$\begin{aligned}
 J &= \begin{pmatrix} -\frac{\partial}{\partial I} (0,0011) \cdot I \cdot S - 1,4757 \times 10^{-5} & 0 & -\frac{\partial}{\partial I} (0,0011) \cdot I \cdot S \\ \frac{\partial}{\partial I} (0,0011) \cdot I \cdot S & -0,1014757 & \frac{\partial}{\partial I} (0,0011) \cdot I \cdot S \\ 0 & 0,1 & -0,1681757 \end{pmatrix}
 \end{aligned}$$

The eigen values of the matrix can be obtained by determining the roots of the characteristic equation by the formula $|J - \lambda I| = 0$, so we have

$$\begin{aligned}
 \begin{vmatrix} 0 & 0 & -\frac{\partial}{\partial I} (0,0011) \cdot I \cdot S - 1,4757 \times 10^{-5} & 0 & -\frac{\partial}{\partial I} (0,0011) \cdot I \cdot S \\ 0 & 0 & \frac{\partial}{\partial I} (0,0011) \cdot I \cdot S & -0,1014757 & \frac{\partial}{\partial I} (0,0011) \cdot I \cdot S \\ 0 & 0 & 0 & 0,1 & -0,1681757 \end{vmatrix} &= 0 \\
 + 0,2711271 + \dots + 0,017065746 - 0,1 \dots + 0,2696514 \dots &
 \end{aligned}$$

$$+ 0,017065746 - + 2,5183921 \times 10^{-6} - 1,4757.10^{-6} = 0 \quad (3.3)$$

In the first Lyapunov method, the equilibrium point is said asymptotically stable if $\text{Re}(\lambda) < 0$. To determine the sign of the real part of the equation (3.3) were used Routh-Hurwitz criterion. By using Routh-Hurwitz criterion, the condition $\text{Re}(\lambda) < 0$ hold if

$$a_1 > 0, \quad a_2 > 0 \text{ and } \Delta = a_1 a_2 - a_3 > 0, \text{ where}$$

$$a_1 = 0,2711271 + \dots$$

$$a_2 = 0,017065746 - 0,1 \dots + 0,2696514 \dots$$

$$\Delta = 0,017065746 \dots + 2,5183921 \times 10^{-6} - 1,4757.10^{-6} \dots$$

Next, by some algebra manipulation we found that the real part eigen values of equation (3.3) for Q_0 are not negative. Therefore, it can be concluded that the infection-free equilibrium point (Q_0) is unstable. Further, we will check the stability of endemic equilibrium state. We have

$$Q_0 = (S_0, I_0, R_0) = (25,55131602; 0,8919093237; 0,5303437558), \text{ so that}$$

$$\lambda_1 = 1,54 \times 10^{-6} \dots$$

$$\lambda_2 = 1,54 \times 10^{-6} (0,5303437558) \cdot (25,55131602) \cdot \dots$$

$$= 0,00495903898$$

and

$$\lambda_3 = 2,2 \times 10^{-6} \dots$$

$$\lambda_4 = \frac{2,2 \times 10^{-6} (25,55131602) \cdot \dots}{(0,5303437558) \cdot \dots}$$

$$= 0,03413149377$$

From the equation (3.2), for λ_1 , we obtain

$$a_1 = 0,2711271 + \frac{\lambda_1}{\dots}$$

$$= 0,2711271 + 0,00495903898$$

$$= 0,2760861390 > 0$$

$$a_2 = 0,017065746 - 0,1 \frac{\lambda_1}{\dots} + 0,2696514 \frac{\lambda_1}{\dots}$$

$$= 0,017065746 - 0,1(0,03413149377) + 0,2696514(0,00495903898)$$

$$= 0,01498980842 > 0$$

$$\Delta = 0,017065746 \frac{\lambda_1}{\dots} + 2,5183921 \times 10^{-6} - 1,4757.10^{-6} \frac{\lambda_1}{\dots}$$

$$= 0,017065746(0,00495903898) + 2,5183921 \times 10^{-6}$$

$$- 1,4757.10^{-6} (0,03413149377)$$

$$= 0,0001047768361 > 0$$

and

$$a_1 a_2 - a_3 = 0,2760861390 (0,01498980842) - 0,0001047768361$$

$$= 0,004033701495 > 0$$

Because $a_1 > 0$, $a_2 > 0$ and $\Delta > 0$, then all of the real eigen values are negative, then the endemic equilibrium point Q^* is asymptotically stable. This means that in a long time, there will always be measles disease in the population and there are always individuals who enter the exposed and infective class.

3.2. Stability Analysis by Using Second Lyapunov Method

In this subsection, global stability of the endemic equilibrium point will be analyzed by using the second Lyapunov method. Because the value of $p, q > 1$ with $p = 0.2$ and $q = 1.4$, we have the Lyapunov function for system (3.2) is

$$V(S, E, I) = 1 + \frac{5}{2} S - \frac{1}{2} S^2 + -1 - \frac{5}{4} E - \frac{1}{4} E^2 + (I - \ln I), \quad (3.4)$$

where $(S^*, E^*, I^*) = (25,55131602 ; 0,8919093237; 0,5303437558)$ dan $\frac{\sigma}{\theta} = 1,014757$. This function is defined and continuous for each $S, E, I > 0$.

Next, we find Hess matrix of the function V as follows.

$$H = \begin{pmatrix} 1,4 & 0 & 0 \\ 0 & - & 0 \\ 0 & 0 & 0,2 - \end{pmatrix}$$

Determinant of the Hess sub matrix above is

$$|H_{11}| = 1,4 > 0$$

$$|H_{11, 22}| = \begin{vmatrix} 1,4 & 0 \\ 0 & - \end{vmatrix} = 1,4 > 0$$

$$|H_{11, 22, 33}| = \begin{vmatrix} 1,4 & 0 & 0 \\ 0 & - & 0 \\ 0 & 0 & 0,2 - \end{vmatrix} = 1,4 \cdot - \cdot 0 - 0 - 0 + 0 = 1,4 \cdot - \cdot 0,2 - > 0$$

Since $|H_{11}| > 0, |H_{11, 22}| > 0,$ dan $|H_{11, 22, 33}| > 0$ then Q^* is a local minimum point of the function V, so $(S^*, E^*, I^*) = (25,55131602 ; 0,8919093237; 0,5303437558)$. Since Q^* is the only stationary point then the Q^* is the global minimum. So that V is a Lyapunov function. Further, the derivative function $V(S, E, I)$ with respect to t is

$$\begin{aligned} \dot{V} &= \dot{S} + \dot{E} + \dot{I} \\ &= 1 - \frac{1}{2} (0,1282132 - (0,0011) \cdot \cdot - (1,4757 \times 10^{-5})) \\ &\quad + 1 - \frac{1}{4} (0,0011) \cdot \cdot - (0,1014757) \\ &\quad + -1 - \frac{1}{4} (0,1) - (0,1681757) \\ &= 0,1282132 - (0,0011) \cdot \cdot - (1,4757 \times 10^{-5}) - 0,1282132 - \end{aligned}$$

$$\begin{aligned}
& + (0,0011) \cdot \cdot + 1,4757 \cdot 10 \quad - \quad + (0,0011) \cdot \cdot \\
& - (0,1014757) - (0,0011) \cdot \cdot - + 0,1014757 \\
& + - 0,1 - 0,1681757 - 0,1 - \quad + 0,1681757 - \\
& = 0,1282132 - 1,4757 \cdot 10 \quad - 0,1282132 - \\
& + (0,0011) \cdot \cdot + 1,4757 \cdot 10 \quad - \quad - (0,0011) \cdot \cdot - \\
& + 0,1014757 \quad + - - 0,1681757 - 0,1 - \quad + 0,1681757 - \quad (3.5)
\end{aligned}$$

From the equation $\dots = \dots$, $\dots = - \dots$ dan $\dots - \dots + \dots = \dots$,
let $(0,0011) \cdot \cdot = (\dots / \dots)$ and $0,1014757 = (\dots / \dots)$ so the equation (3.5), can be written by

$$\begin{aligned}
& - = 0,1282132 - 1,4757 \cdot 10 \quad - 0,1282132 - \\
& + - \quad - \quad + 1,4757 \cdot 10 \quad - \quad - - \quad - - \quad - \quad - \quad + - \\
& + - - 0,1681757 - 0,1 - \quad + 0,1681757 - \\
& - = - \quad 1 + - \quad - - - \quad - - - - - \quad - \quad + - \\
& + 1,4757 \cdot 10 \quad - - + - \quad + 0,1282132 \quad 1 - -
\end{aligned}$$

By substituting the value of \dots and $\frac{\sigma}{\theta} \delta = 0,170657468$ to the above equation, we obtain

$$\begin{aligned}
& - = 0,09050712253 + 0,1027475005 \cdot \cdot - \frac{0,09164145364 \cdot \cdot}{\cdot \cdot} \\
& - 0,170657468 - \frac{0,0009811002511 \cdot \cdot}{\cdot \cdot} + 0,1503269305 \cdot \cdot \\
& - 0,0014757 + \frac{0,1378404429}{\cdot \cdot} + 0,1282132 - \frac{11,97598718}{\cdot \cdot}
\end{aligned}$$

$$\frac{dV}{dt} \leq 0 \text{ for all } \cdot \cdot, \cdot \cdot > 0.$$

Because the value of $\frac{dV}{dt} \leq 0$, for all $S, E, I > 0$ with equality only applies at the equilibrium state, then the endemic equilibrium state Q^* is globally asymptotically stable. This means that asymptotic stability holds for all conditions (all points in state space) trajectories starting point.

4. SIMULATION RESULTS

In this section, simulation results are presented to check the behavior of the susceptible, exposed, infected, and recovered subpopulations dynamics. These behavior and the trajectories are given in Figure 1 and Figure 2. From Figure 1, it can be seen that the red curve shows the changes of reducing the number of susceptible people class over time. This is because the disease infected and susceptible people enter exposed class, and can also be caused by natural death of susceptible people. However, at certain times of the number of susceptible subpopulations have not changed. In such circumstances, the system achieve steady state.

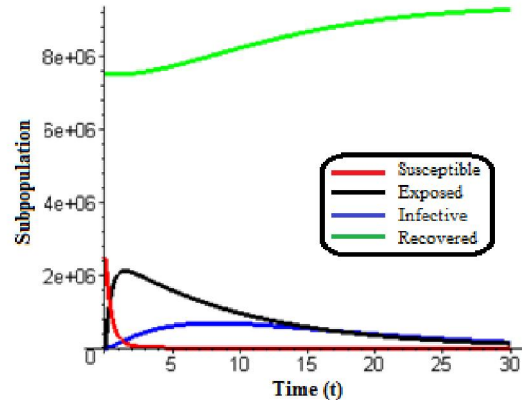


Figure 1. The behavior of sub population dynamic

The proportion of exposed subpopulation indicated by the black curve. The curve shows that the sub-populations exposed to increased from the initial state. This is because the addition of susceptible individuals infected with the disease. At any given time the number of this population has decreased, because the number of infective subpopulation incoming class. Blue curve shows the proportion of infective individuals. Increase due to infective subpopulation of exposed individuals to enter this class. At any given time and the proportion of individuals exposed to infection has not changed so the system is at equilibrium, which in this condition until the disease will always be there for a long time. Therefore, the disease is endemic.

The proportion of recovered individuals is shown by the green curve. Recovered class increases from time to time. This is due to an infective individual recovers from the disease so that individuals entering this class. At any given time this class has not changed so that the system is at equilibrium conditions.

The stability of the system can be described by the trajectories in a phase plane. The trajectories of the systems are depicted as follows.

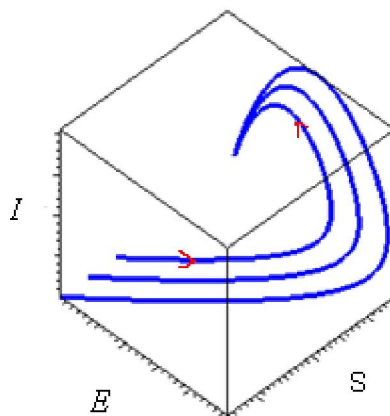


Figure 2. Trajectories of the systems

Trajectories in phase plane shows that for a very long time, for any initial value terms will lead to a certain point, which indicate the global stability.

5. CONCLUDING REMARKS

Global stability of the spread measles diseases associated with the incidence rate concave function has been proposed. For the SEIR model with the incidence rate βI , this condition is satisfied with $0 < \beta < 1$. For $0 < \beta < 1$, the model has two equilibrium states, i.e., infection-free equilibrium state $E_1 = (N, 0, 0)$ and the endemic equilibrium state $E_2 = (N, I, R)$.

In the case studies used SEIR model for measles with data obtained from the Central Java Provincial Health Office. From the numerical results using these data, it is found that stability analysis by first Lyapunov method at infection-free equilibrium state is unstable. Whereas, the endemic equilibrium state is asymptotically stable. By using the second Lyapunov method is found that the endemic equilibrium state achieve globally asymptotically stable. From the simulation results also are obtained that endemic equilibrium point is globally asymptotically stable. it is indicate that in a long time then the measles diseases will always exist in the population of Central Java and there are always individuals who enter the infective class.

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