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Global Stability Analysis of Susceptible, Infected, Recovered (S, I, R) Model Measles Vaccination Based on Age

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Abstract

This study discusses the behavioral analysis model of the Susceptible-Infected-Recovered (SIR) epidemic of the spread of measles based on age structure. The total population of measles is grouped into four age groups, namely the first age group (0-4 years), the second age group (5-9 years), the third age group (10-14 years) and the fourth age group (> 15 years). The steps in modeling behavior can be done by determining the equilibrium point, and the basic reproduction number and performing a global stability analysis by building the Lyapunov function. This research contributes to providing information both to the government and the community.
Keywords: Epidemic Model; SIR; Lyapunov function; Measles.

Abstrak

Penelitian ini membahas model analisis perilaku epidemi Susceptible-Infected-Recovered (SIR) penyebaran campak berdasarkan struktur umur. Jumlah penduduk yang terkena campak dikelompokkan menjadi empat kelompok umur, yaitu kelompok umur pertama (0-4 tahun), kelompok umur kedua (5-9 tahun), kelompok umur ketiga (10-14 tahun) dan kelompok umur keempat. (> 15 tahun). Langkah-langkah dalam pemodelan perilaku dapat dilakukan dengan menentukan titik ekuilibrium, bilangan reproduksi dasar dan melakukan analisis stabilitas global dengan membangun fungsi Lyapunov. Penelitian ini memberikan kontribusi untuk memberikan informasi baik kepada pemerintah maupun masyarakat.
Kata Kunci: *Model Epidemi; PAK; fungsi Lyapunov; Campak.*

2020MSC: 00A71.

1. INTRODUCTION

The SIR (*Susceptible-Infected-Recovered)* Epidemic Model was first introduced by Kermack & McKendrick in 1927. The model was developed to describe the rate of spread and extinction of disease in an area in a closed population. This model is one of the mathematical models that can be described in a differential equation [1], which includes linear differential equations [2] and nonlinear equations [3]. This epidemic model contains three subclasses in an equation system, namely *Susceptible* which is a subclass of susceptible individuals in a group, *infected* which is a subclass of individuals who have been infected in a group, and *Recovered* is a subclass of individuals who have recovered in a group.

The SIR distribution model can be used to describe the current phenomenon, one of which is the spread of measles. Measles is a disease caused by a virus belonging to the family *Paramyxviridae,* genus Morbillivirus. The measles virus can be spread through air contaminated with secretions from an infected person, [4], [5], [6]. This disease is a disease that causes the main death that attacks toddlers

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and children. In the spread of measles, age distribution is one of the factors that can accelerate the rate of spread of the disease where individuals of different ages have different levels of immunity to infectious diseases. These differences can affect the age-specific mortality rate and the individual's recovery rate from infection. According to the Agency for Disease Control and Prevention [7], ninety percent of people who have interacted or made direct contact with sufferers can be infected if each individual does not have an immune system against measles. Preferably, an individual will be immune if they have been vaccinated or have been infected with the virus before. In a disease spread in a population, vaccination is an effective effort to prevent and reduce the spread of measles.

In previous studies, models of the spread of measles have been constructed with different problem constraints using various approaches [8], [9], [10], [11]. The World is in a vulnerable state in disease spreading, facing a great loss of lives and socioeconomic aspects also. That is why ([12] propose a potential mathematical model with data analysis to predict and control the outcome of this pandemic. [13] construct quadratic and logarithmic Lyapunov functions to establish the global asymptotic stability of the two steady states. [14] Develop a stochastic model of measles transmission dynamics with double-dose vaccination. The qualitative behavior of the model, like conditions for positivity of solutions, invariant region of the solution, the existence of equilibrium points of the model and their stability, and also sensitivity analysis of the model were analyzed. This model is expressed in the form of a 6th order differential equation with state variables as follows susceptible, exposed, infected, quarantine, recovered, and vaccination. The analysis shows that varicella dynamic behavior depends on the basic reproduction number (R_0) [15]. The effect of vaccination on the dengue fever epidemic described by an age-structured modified SIR (Susceptible-Infected-Retired) model is studied using standard stability analysis. [16] Analyze the mathematical dynamics SIR transmission model of the epidemic. To prevent this viral disease, children must receive an MMR (measles, mumps, and rubella) vaccine twice. Based on the biological behavior of rubella disease, the SVPEIRS (susceptible, vaccinated, protected, exposed, infected, recovered) deterministic mathematical model of rubella disease dynamics is proposed [14]. Other influential work includes [17]. In this study, the researchers completed research [11] that constructed a measles distribution model based on the age structure, the researchers divided into four age groups as follows: (1) Group 1 (0-4 years); (2) Group 2 (5-9 years); (3) Group 3 (10-14 years); (4) Group 4 (above 15 years). The mathematical model of the spread of the measles virus explains the process of infection of an individual due to direct interaction with individuals infected with the measles virus who will then be given treatment so that a population has a good immune system or recovers. Parameters used in the model include vaccination effectiveness (θ_k), average vaccination coverage (σ_k), birth rate (Λ_k), natural death rate (d_k), death rate due to disease (μ_k), as well as the rate of change in susceptible individuals becoming an infected individual due to interactions with previously infected individuals with the rate (β_k), and the rate of change of infected individuals into recovered individuals (γ_k). with $k = 1,2,3,4$. In this study, the researcher focuses on analyzing the global stability of the SIR epidemic model by building the Lyapunov function. In search of global stability analysis described in [18].

2. METHOD

The research methods are

1. Analysis of the Global Stability of Equilibrium on the Dynamics of the Spread of Measles by Age. This section will explain the global dynamic behavior analysis of the mathematical model, namely:

a. Analyzed the SIR model of the spread of measles using equilibrium points. Analyze the SIR model of measles spread using equilibrium points. Two equilibrium points were obtained, namely the disease-free equilibrium point and the endemic equilibrium point. The disease-free equilibrium point can be obtained by assuming $I = 0$, while the endemic equilibrium point can be obtained by assuming $I \neq 0$.
b. Conduct model sensitivity analysis of the basic reproduction number. The basic reproduction number (R_0) can be determined using the next-generation matrix method
c. Analyzing the global stability of the equilibrium points of the model for the spread of measles based on age in measles vaccination. Stability analysis can be done by constructing the Lyapunov Function. To find out the value of the basic reproduction number (R_0) in the first, second, third, and fourth groups, you can linearize the infected subsystem at the disease-free equilibrium point, in the model the infected subsystem is I_1, I_2, I_3, I_4. Due to the absence of interaction between each group, the basic reproduction number from groups I-IV is the product of the basic reproduction number of each group.

2. Numerical simulation of behavior analysis/global stability using ODE45.

3. RESULTS AND DISCUSSION

3.1. Model Solution Limit

3.1.1. Age Group Model Solution Limit I

The dynamics model of the spread of measles group I will determine the solution limit, because $N_1 = S_1 + I_1 + R_1$, so

$$\frac{dN_1}{dt} = \frac{dS_1}{dt} + \frac{dI_1}{dt} + \frac{dR_1}{dt} = \Lambda - d_1 N_1 - \mu_1 I_1 - \alpha_1 S_1. \quad (1)$$

Then, from equation (1), if the population is free from disease then

$$\frac{dN_1}{dt} + d_1 N_1 + \alpha_1 S_1 = \Lambda. \quad (2)$$

The solution to the equation (2) is $N_1(t) = \frac{\Lambda}{d_1+\alpha_1 S_1} + Ce^{-(d_1+\alpha_1 S_1)t}$. If we substitute the initial conditions, $N(0) = N_0$we get a special solution

$$N_1(t) = N_0 e^{-(d_1+\alpha_1 S_1)t} + \frac{\Lambda}{d_1 + \alpha_1 S_1}(1 - e^{-(d_1+\alpha_1 S_1)t}).$$

If t it enlarges then it gets $\lim_{t\to\infty} N_1(t) = \frac{\Lambda}{d_1+\alpha_1 S_1}$. So it can be explained the number of human populations in the long term towards the limit capacity, namely $\frac{\Lambda}{d_1+\alpha_1 S_1}$. Furthermore, it is assumed that the number of human population in the age group I (0-4 years), $N_1 \leq \frac{\Lambda}{d_1+\alpha_1 S_1}$, for each $t \geq 0$. So model solution (1) can be defined in the area Γ_1 with

$$\Gamma_1 = \{(S_1, I_1, R_1)\} \in \mathbb{R}_+^3 : S_1 \geq 0; I_1 \geq 0; R_1 \geq 0; S_1 + I_1 + R_1 \leq \frac{\Lambda}{d_1 + \alpha_1 S_1}.$$

3.1.2. Age Group II Model Solution Limit

The dynamics model of the spread of measles group II will determine the solution limit, because $N_2 = S_2 + I_2 + R_2$, so

$$\frac{dN_2}{dt} = \frac{dS_2}{dt} + \frac{dI_2}{dt} + \frac{dR_2}{dt} = \alpha_1 S_1 - d_2 N_2 - \mu_2 I_2 - \alpha_2 S_2. \quad (3)$$

Then, from equation (3), if the population is free from disease then

$$\frac{dN_2}{dt} + d_2 N_2 + \alpha_2 S_2 = \alpha_1 S_1. \quad (4)$$

The solution to the equation (4) is $N_2(t) = \frac{\alpha_1 S_1}{d_2 + \alpha_2 S_2} + Ce^{-(d_2 + \alpha_2 S_2)t}$. If we substitute the initial conditions, $N(0) = N_0$ we get a special solution

$$N_2(t) = N_0 e^{-(d_2 + \alpha_2 S_2)t} + \frac{\alpha_1 S_1}{d_2 + \alpha_2 S_2}(1 - e^{-(d_2 + \alpha_2 S_2)t}).$$

If t it enlarges then it gets $\lim_{t \to \infty} N_2(t) = \frac{\alpha_1 S_1}{d_2 + \alpha_2 S_2}$. So it can be explained the number of human populations in the long term towards the limit capacity, namely $\frac{\Lambda}{d_2 + \alpha_2 S_2}$. Furthermore, it is assumed that the number of human population in age group II $N_2 \leq \frac{\alpha_1 S_1}{d_2 + \alpha_2 S_2}$, for each $t \geq 0$. So model solution (2) can be defined in the area Γ_2 with

$$\Gamma_2 = \{(S_2, I_2, R_2)\} \in \mathbb{R}_+^3 : S_2 \geq 0; I_2 \geq 0; R_2 \geq 0; S_2 + I_2 + R_2 \leq \frac{\alpha_1 S_1}{d_2 + \alpha_2 S_2}.$$

3.1.3. Age Group Model Solution Limit III

The dynamics model of the spread of group III measles will determine the limit of the solution, because $N_3 = S_3 + I_3 + R_3$, so:

$$\frac{dN_3}{dt} = \frac{dS_3}{dt} + \frac{dI_3}{dt} + \frac{dR_3}{dt} = \alpha_2 S_2 - d_3 N_3 - \mu_3 I_3 - \alpha_3 S_3. \quad (5)$$

Then, from equation (5), if the population is free from the disease then

$$\frac{dN_3}{dt} + d_3 N_3 + \alpha_3 S_3 = \alpha_2 S_2. \quad (6)$$

The solution to the equation (6) is $N_3(t) = \frac{\alpha_2 S_2}{d_3 + \alpha_3 S_3} + Ce^{-(d_3 + \alpha_3 S_3)t}$. If we substitute the initial conditions $N(0) = N_0$, we get a special solution

$$N_3(t) = N_0 e^{-(d_3 + \alpha_3 S_3)t} + \frac{\alpha_2 S_2}{d_3 + \alpha_3 S_3}\left(1 - e^{-(d_3 + \alpha_3 S_3)t}\right).$$

If t it enlarges then it gets $\lim_{t \to \infty} N_3(t) = \frac{\alpha_2 S_2}{d_3 + \alpha_3 S_3}$. So it can be explained the number of human populations in the long term towards the limit capacity, namely $\frac{\alpha_2 S_2}{d_3 + \alpha_3 S_3}$. Furthermore, it is assumed

that the number of human population in age group III, $N_3 \leq \frac{\alpha_2 S_2}{d_3+\alpha_3 S_3}$, for each $t \geq 0$. So model solution (3) can be defined in the area Γ_3 with

$$\Gamma_3 = \{(S_3, I_3, R_3)\} \in \mathbb{R}^3_+ : S_3 \geq 0; I_3 \geq 0; R_3 \geq 0; S_3 + I_3 + R_3 \leq \frac{\alpha_2 S_2}{d_3 + \alpha_3 S_3}.$$

3.1.4. Age Group Model Solution Limit IV

The dynamics model of the spread of measles group IV will determine the solution limit, because $N_4 = S_4 + I_4 + R_4$, so

$$\frac{dN_4}{dt} = \frac{dS_4}{dt} + \frac{dI_4}{dt} + \frac{dR_4}{dt} = \alpha_3 S_3 - d_4 N_4 - \mu_4 I_4. \quad (7)$$

Then, from equation (7), if the population is free from the disease then

$$\frac{dN_4}{dt} + d_4 N_4 = \alpha_3 S_3. \quad (8)$$

The solution to the equation (8) is $N_4(t) = \frac{\alpha_3 S_3}{d_4} + Ce^{-d_4 t}$. If we substitute the initial conditions, $N(0) = N_0$ we get a special solution

$$N_4(t) = N_0 e^{-d_4 t} + \frac{\alpha_3 S_3}{d_4}(1 - e^{-d_4 t}).$$

If t it enlarges then it gets $\lim_{t\to\infty} N_4(t) = \frac{\alpha_3 S_3}{d_4}$. So it can be explained the number of human populations in the long term towards the limit capacity, namely $\frac{\alpha_3 S_3}{d_4}$. Furthermore, it is assumed that the number of human population in age group IV, $N_4 \leq \frac{\alpha_3 S_3}{d_4}$., for each $t \geq 0$. So model solution (4) can be defined in the area Γ_4 with

$$\Gamma_4 = \{(S_4, I_4, R_4)\} \in \mathbb{R}^3_+ : S_4 \geq 0; I_4 \geq 0; R_4 \geq 0; S_4 + I_4 + R_4 \leq \frac{\alpha_3 S_3}{d_4}.$$

3.2. Global Stability Analysis

To simplify the calculation of the stability analysis, a stability analysis of each group will be sought because there is no interaction between each group and other groups that can transmit the disease. In analyzing the global stability of the disease-free equilibrium point and the endemic equilibrium point, we can construct the Lyapunov function. Where the disease-free equilibrium point, the endemic equilibrium point, and the basic reproduction number are referred to [11].

Theorem 5 [Global stability of the disease-free equilibrium point] The disease-free equilibrium point is E^0globally asymptotically stable if $R_0 < 1$ and vice versa [19].

Theorem 6 [Global stability of the endemic equilibrium point] The global asymptotically stable $R_0 > 1$ disease-free equilibrium point if $E^*$and vice versa [19]

3.2.1. Group I Global Stability Analysis

A. Disease-free Global Stability Analysis

Theorem 5 The disease-free equilibrium point in group I (E_1^0) of the globally asymptotically stable SIR model if $R_0^1 < 1$.

Proof:

Defined $V_1 : \Gamma_1 \subset \mathbb{R}^3 \to \mathbb{R}$ and

$$V_1(S_1, I_1, R_1) = I_1. \tag{9}$$

The function V_1 can be called a Lyapunov function with the condition that [20]

1. The function V_1 is continuous and the first partial derivative is continuous on Γ_1.
2. The first derivative of the function V_1 with respect to time is obtained

$$\begin{aligned}\frac{dV_1}{dt} &= \frac{dI_1}{dt}\\ &= (\beta_1 S_1^0 - (d_1 + \mu_1 + \gamma_1) I_1)\\ &= \left(\beta_1 \left(\frac{\Lambda(1-\theta_1\sigma_1)}{d_1+\alpha_1}\right) - (d_1 + \mu_1 + \gamma_1)\right) I_1\\ &= \left(\frac{\beta_1\Lambda(1-\theta_1\sigma_1)}{d_1+\alpha_1} - (d_1 + \mu_1 + \gamma_1)\right) I_1\\ &= (d_1 + \mu_1 + \gamma_1)\left(\frac{\beta_1\Lambda(1-\theta_1\sigma_1)}{(d_1+\alpha_1)\,(d_1+\mu_1+\gamma_1)} - 1\right) I_1\\ &= (d_1 + \mu_1 + \gamma_1)(R_0^1 - 1) I_1.\end{aligned}$$

When $R_0^1 < 1$, it causes $\frac{dV_1}{dt} = (d_1 + \mu_1 + \gamma_1)(R_0^1 - 1) I_1 < 0$. So, $\frac{dV_1}{dt} < 0$, provided that $R_0^1 < 1$.

3. $S = \left\{I_1 \in \Gamma_1 \,\middle|\, \frac{dV_1}{dt} = 0\right\} \Leftrightarrow S = \{I_1 \in \Gamma_1 \,|I_0 = I_1\}$, the set S contains only equilibrium points E_0^1.

$$\begin{aligned}\frac{dV_1}{dt} &= \frac{dI_1}{dt}\\ &= (\beta_1 S_1^0 - (d_1 + \mu_1 + \gamma_1) I_1)\\ &= \left(\beta_1 \left(\frac{\Lambda(1-\theta_1\sigma_1)}{d_1+\alpha_1}\right) - (d_1 + \mu_1 + \gamma_1)\right) I_1\\ &= \left(\frac{\beta_1\Lambda(1-\theta_1\sigma_1}{d_1+\alpha_1} - (d_1 + \mu_1 + \gamma_1)\right) I_1\\ &= (d_1 + \mu_1 + \gamma_1)\left(\frac{\beta_1\Lambda(1-\theta_1\sigma_1}{(d_1+\alpha_1)\,(d_1+\mu_1+\gamma_1)} - 1\right) I_1\\ &= (d_1 + \mu_1 + \gamma_1)(R_0^1 - 1)\,(0)\\ &= 0\end{aligned}$$

Because the set S does not contain any other solutions.

Then based on the principle of Invariant La Salle [21] the disease-free equilibrium point in age group I E_1^0 is globally asymptotically stable.

B. Endemic Global Stability Analysis

In determining the global stability analysis, the left-hand endemic equilibrium point is made equal to zero, so it can be written as follows:

$$0 = (1-\theta_1\sigma_1)\Lambda - \beta_1 S_1^* I_1^* - d_1 S_1^* - \alpha_1 S_1^* \quad (10)$$
$$0 = \beta_1 S_1^* I_1^* - (d_1+\mu_1+\gamma_1) I_1^* \quad (11)$$
$$0 = \theta_1\sigma_1\Lambda + \gamma_1\ I_1^* - d_1 R_1^* \quad (12)$$

Theorem 6 The endemic equilibrium point in group I E_1^* is globally asymptotically stable if $R_0^1 \geq 1$.

Proof:

Defined $V_1^*: \Gamma_1 \subset \mathbb{R}^3 \to \mathbb{R}$ and

$$V_1^*(S_1, I_1) = c_1\left[S_1 - S_1^* \ln\left(\frac{S_1}{S_1^*}\right)\right] + c_2\left[I_1 - I_1^* \ln\left(\frac{I_1}{I_1^*}\right)\right], \quad (13)$$

where c_1 and c_2 are positive constants and $\Gamma_1 = \{(S_1, I_1) \in \Gamma_1 / S_1 > 0, I_1 > 0\}$.

The function V_1 can be called a Lyapunov function with the condition that [20]

1. The function V_1^* is continuous and the first partial derivative is continuous at Γ_1.
2. The first derivative of the function V_1^* with respect to time is obtained

$$\begin{aligned} V_1^*(S_1, I_1) &= c_1\left[S_1 - S_1^* \ln\left(\frac{S_1}{S_1^*}\right)\right] + c_2\left[I_1 - I_1^* \ln\left(\frac{I_1}{I_1^*}\right)\right], \\ \frac{dV_1^*(S_1, I_1)}{dt} &= \frac{dV_1}{dS_1}\cdot\frac{dS_1}{dt} + \frac{dV_1}{dI_1}\cdot\frac{dI_1}{dt} \\ &= c_1\left[1 - \frac{S_1^*}{S_1}\right][(1-\theta_1\sigma_1)\Lambda - \beta_1 S_1 I_1 - d_1 S_1 - \alpha_1 S_1] \\ &\quad + c_2\left[1 - \frac{I_1^*}{I_1}\right][\beta_1 S_1 I_1 - d_1 I_1 - \mu_1 I_1 - \gamma_1 I_1] \end{aligned} \quad (14)$$

Based on equations (14) and (15), we get

$$\begin{aligned} 0 &= (1-\theta_1\sigma_1)\Lambda - \beta_1 S_1^* I_1^* - d_1 S_1^* - \alpha_1 S_1^*, \\ \frac{(1-\theta_1\sigma_1)\Lambda}{S_1^*} &- \beta_1 I_1^* - \alpha_1 = d_1, \end{aligned} \quad (15)$$

and

$$\begin{aligned} 0 &= \beta_1 S_1^* I_1^* - d_1 I_1^* - \mu_1 I_1^* - \gamma_1 I_1^*, \\ \beta_1 S_1^* &- \mu_1 - \gamma_1 = d_1. \end{aligned} \quad (16)$$

Then equations (15) and (16) can be substituted into partial derivatives (14) so we get

$$\frac{dV_1^*}{dt} = c_1\left[1 - \frac{S_1^*}{S_1}\right][(1-\theta_1\sigma_1)\Lambda - \beta_1 S_1 I_1 - \alpha_1 S_1 - d_1 S_1]$$

$$
\begin{aligned}
&+c_2\left[1-\frac{I_1^*}{I_1}\right][\beta_1 S_1 I_1-\mu_1 I_1-\gamma_1 I_1-d_1 I_1]\\
&=c_1\left[1-\frac{S_1^*}{S_1}\right]\left[(1-\theta_1\sigma_1)\Lambda-\beta_1 S_1 I_1-\alpha_1 S_1-\left(\left(\frac{(1-\theta_1\sigma_1)\Lambda}{S_1^*}\right)-\beta_1 I_1^*-\alpha_1\right)S_1\right]\\
&\quad+c_2\left[1-\frac{I_1^*}{I_1}\right][\beta_1 S_1 I_1-\mu_1 I_1-\gamma_1 I_1-(\beta_1 S_1^*-\mu_1-\gamma_1)I_1]\\
&=c_1\left[-(1-\theta_1\sigma_1)\Lambda\left(-1+\frac{S_1}{S_1^*}+\frac{S_1^*}{S_1}-1\right)-\beta_1 S_1 I_1+\beta_1 S_1 I_1^*-\beta_1 S_1^* I_1^*\right]\\
&\quad+c_2[\beta_1 S_1 I_1-\beta_1 S_1^* I_1-\beta_1 S_1 I_1^*+\beta_1 S_1^* I_1^*]\\
&=c_1\left[-(1-\theta_1\sigma_1)\Lambda\left(\frac{-S_1 S_1^*+S_1^2+(S_1^*)^2-S_1 S_1^*}{S_1 S_1^*}\right)-\beta_1 S_1 I_1+\beta_1 S_1 I_1^*-\beta_1 S_1^* I_1^*\right]\\
&\quad+c_2[\beta_1 S_1 I_1-\beta_1 S_1^* I_1-\beta_1 S_1 I_1^*+\beta_1 S_1^* I_1^*]\\
&=c_1\left[-(1-\theta_1\sigma_1)\Lambda\frac{[S_1-S_1^*]^2}{S_1 S_1^*}-\beta_1 S_1 I_1+\beta_1 S_1 I_1^*-\beta_1 S_1^* I_1^*\right]\\
&\quad+c_2[\beta_1 S_1 I_1-\beta_1 S_1^* I_1-\beta_1 S_1 I_1^*+\beta_1 S_1^* I_1^*]\\
&=-(1-\theta_1\sigma_1)\Lambda\, c_1\,\frac{[S_1-S_1^*]^2}{S_1 S_1^*}+\beta_1(c_2-c_1)[S_1-S_1^*][I_1-I_1^*]
\end{aligned}
$$

For $c_1 = c_2 = 1$, so we get

$$\frac{dV_1^*(S_1,I_1)}{dt} = -(1-\theta_1\sigma_1)\Lambda\,\frac{[S_1-S_1^*]^2}{S_1 S_1^*} < 0$$

3. $S = \left\{S_1, I_1 \in \Gamma_1 \left| \frac{dV^*(S_1,I_1)}{dt} = 0\right.\right\} \Leftrightarrow S = \{S_1 \in \Gamma_1 | S_1 = S_1^*\}$.
   Because the set S does not contain other solutions or only contains equilibrium points E_1^*.

So based on the La Salle Invariant principle, [21] the endemic equilibrium point in Group I is globally asymptotically stable in the interior Γ_1.

3.2.2. Group II Global Stability Analysis

A. Disease-free Global Stability Analysis

Theorem 5 The disease-free equilibrium point in group II (E_2^0) of the globally asymptotically stable SIR model if $R_0^2 < 1$. In the same way as the previous group, it can be proven as follows

Proof:

Defined $V_2 : \Gamma_2 \subset \mathbb{R}^3 \to \mathbb{R}$ and

$$V_2(S_2, I_2, R_2) = I_2. \tag{17}$$

The function V_2 can be called a Lyapunov function with the condition that [20]

1. The function V_2 is continuous and the first partial derivative is continuous on Γ_2.
2. The first derivative of the function V_2 with respect to time is obtained

$$\begin{aligned}\frac{dV_2}{dt} &= \frac{dI_2}{dt}\\ &= (\beta_2 S_2^0 - (d_2+\mu_2+\gamma_2)I_2)\\ &= (d_2+\mu_2+\gamma_2)\left(\frac{\beta_2\alpha_1 S_1(1-\theta_2\sigma_2)}{(d_2+\alpha_2)\,(d_2+\mu_2+\gamma_2)}-1\right)I_2\\ &= (d_2+\mu_2+\gamma_2)(R_0^2-1)I_2\end{aligned}$$

When $R_0^2 < 1$, it causes $\frac{dV_2}{dt} = (d_2+\mu_2+\gamma_2)(R_0^2-1)I_2 < 0$. So, $\frac{dV_2}{dt} < 0$, provided that $R_0^2 < 1$.

3. $S = \left\{I_2 \in \Gamma_2 \left| \frac{dV_2}{dt} = 0\right.\right\} \Leftrightarrow S = \{I_2 \in \Gamma_1 \,|I_0 = I_2\}$, the set S contains only equilibrium points E_0^2.

$$\begin{aligned}\frac{dV_2}{dt} &= \frac{dI_2}{dt}\\ &= (\beta_2 S_2^0 - (d_2+\mu_2+\gamma_2)I_2)\\ &= (d_2+\mu_2+\gamma_2)(R_0^2-1)(0)\\ &= 0\end{aligned}$$

Because the set S does not contain any other solutions.

Salle Invariant principle [21], the disease-free equilibrium point in age group II E_2^0 is globally asymptotically stable.

B. Endemic Global Stability Analysis

In determining the global stability analysis, the left-hand endemic equilibrium point is made equal to zero, so it can be written as follows:

$$0 = (1-\theta_2\sigma_2)\alpha_1 S_1 - \beta_2 S_2^* I_2^* - d_2 S_2^* - \alpha_2 S_2^* \quad (18)$$

$$0 = \beta_2 S_2^* I_2^* - (d_2+\mu_2+\gamma_2)I_2^* \quad (19)$$

$$0 = (\theta_2\sigma_2)\alpha_1 S_1 + \gamma_2 I_2^* - d_2 R_2^* \quad (20)$$

Theorem 6 The endemic equilibrium point in group II E_2^* is globally asymptotically stable if $R_0^2 \geq 1$.

Proof:

Defined $V_2^*: \Gamma_2 \subset \mathbb{R}^3 \to \mathbb{R}$, and

$$V_2^*(S_2, I_2) = c_1\left[S_2 - S_2^* \ln\left(\frac{S_2}{S_2^*}\right)\right] + c_2\left[I_2 - I_2^* \ln\left(\frac{I_2}{I_2^*}\right)\right], \quad (21)$$

where $c_1$and $c_2$are positive constants and$\Gamma_2 = \{(S_2, I_2) \in \Gamma_2 / S_2 > 0, I_2 > 0\}$.

As in the previous calculation, the function V_2 can be called a Lyapunov function with the condition that [20]

1. The function V_2^* is continuous and the first partial derivative is continuous at Γ_2.
2. The first derivative of the function V_2^* with respect to time is obtained

$$\frac{dV_2^*(S_2, I_2)}{dt} = \frac{dV_2}{dS_2}\cdot\frac{dS_2}{dt} + \frac{dV_2}{dI_2}\cdot\frac{dI_2}{dt}$$

$$= c_1\left[1-\frac{S_2^*}{S_2}\right][(1-\theta_2\sigma_2)\alpha_1 S_1 - \beta_2 S_2 I_2 - d_2 S_2 - \alpha_2 S_2] + c_2\left[1-\frac{I_2^*}{I_2}\right][\beta_2 S_2 I_2 - d_2 I_2 - \mu_2 I_2 - \gamma_2 I_2]. \quad (22)$$

Based on equations (18) and (19), we get

$$\frac{(1-\theta_2\sigma_2)\alpha_1 S_1}{S_2^*} - \beta_2 I_2^* - \alpha_2 = d_2, \quad (23)$$

and

$$\beta_2 S_2^* - \mu_2 - \gamma_2 = d_2. \quad (24)$$

Then from equations (23) and (24), it can be substituted into the partial derivative (22) so that

$$\frac{dV_2^*}{dt} = c_1\left[1-\frac{S_2^*}{S_2}\right][(1-\theta_2\sigma_2)\alpha_1 S_1 - \beta_2 S_2 I_2 - \alpha_2 S_2 - d_2 S_2] + c_2\left[1-\frac{I_2^*}{I_2}\right][\beta_2 S_2 I_2 - \mu_2 I_2 - \gamma_2 I_2 - d_2 I_2]$$
$$= -(1-\theta_2\sigma_2)\alpha_1 S_1\, c_1\, \frac{[S_2-S_2^*]^2}{S_2 S_2^*} + \beta_2(c_2-c_1)[S_2-S_2^*][I_2-I_2^*].$$

For $c_1 = c_2 = 1$, so we get

$$\frac{dV_2^*(S_2,I_2)}{dt} = -(1-\theta_2\sigma_2)\alpha_1 S_1\, \frac{[S_2-S_2^*]^2}{S_2 S_2^*} < 0.$$

3. $S = \left\{S_2, I_2 \in \Gamma_2 \;\middle|\; \frac{dV^*(S_2,I_2)}{dt} = 0\right\} \Leftrightarrow S = \{S_2 \in \Gamma_2 | S_2 = S_2^*\}$. Because the set S contains no other solutions or only contains equilibrium points E_2^*.

So based on the La Salle Invariant principle, [21] the endemic equilibrium point in group II is globally asymptotically stable in the interior Γ_2

3.2.3. Group III Global Stability Analysis

A. Disease-free Global Stability Analysis

Theorem 5 Disease-free equilibrium point in group II I (E_3^0) from the global asymptotically stable SIR model if $R_0^3 < 1$.

Proof:

Defined $V_3: \Gamma_3 \subset \mathbb{R}^3 \to \mathbb{R}$ and

$$V_3(S_3, I_3, R_3) = I_3. \quad (25)$$

In the same way as the previous group, the function V_3 can be called a Lyapunov function with the condition that [20]

1. The function V_3 is continuous and the first partial derivative is continuous on Γ_3.
2. The first derivative of the function V_3 with respect to time is obtained

$$\frac{dV_3}{dt} = \frac{dI_3}{dt}$$
$$= (\beta_3 S_3^0 - (d_3 + \mu_3 + \gamma_3) I_3)$$
$$= \left(\beta_3 \left(\frac{\alpha_2 S_2}{(d_3 + \alpha_3)} \right) - (d_3 + \mu_3 + \gamma_3) \right) I_3$$
$$= (d_3 + \mu_3 + \gamma_3)(R_0^3 - 1) I_3.$$

When $R_0^3 < 1$, it causes

$$\frac{dV_3}{dt} = (d_3 + \mu_3 + \gamma_3)(R_0^3 - 1) I_3 < 0.$$

So, $\frac{dV_3}{dt} < 0$, provided that $R_0^3 < 1$.

3. $S = \left\{ I_3 \in \Gamma_3 \left| \frac{dV_3}{dt} = 0 \right. \right\} \Leftrightarrow S = \{ I_3 \in \Gamma_3 \, | I_0 = I_3 \}$, the set S contains only equilibrium points E_0^3.

$$\frac{dV_3}{dt} = \frac{dI_3}{dt} = (d_3 + \mu_3 + \gamma_3)(R_0^3 - 1)(0) = 0.$$

Because the set S does not contain any other solutions.

Salle Invariant principle [21], the disease-free equilibrium point in age group III E_3^0 is globally asymptotically stable.

B. Endemic Global Stability Analysis

In determining the global stability analysis, the left-hand endemic equilibrium point is made equal to zero, so it can be written as follows:

$$0 = \alpha_2 S_2 - \beta_3 S_3^* I_3^* - (d_3 + \alpha_3) S_3^* \quad (26)$$
$$0 = \beta_3 S_3^* I_3^* - (d_3 + \mu_3 + \gamma_3) I_3^* \quad (27)$$
$$0 = \gamma_3 I_3^* - d_3 R_3^* \quad (28)$$

Theorem 6 The endemic equilibrium point in group III E_3^* is globally asymptotically stable if $R_0^3 \geq 1$.

Proof:

Defined $V_3^* : \Gamma_3 \subset \mathbb{R}^3 \to \mathbb{R}$ and

$$V_3^*(S_3, I_3) = c_1 \left[S_3 - S_3^* \ln \left(\frac{S_3}{S_3^*} \right) \right] + c_2 \left[I_3 - I_3^* \ln \left(\frac{I_3}{I_3^*} \right) \right]. \quad (29)$$

where c_1 and c_2 are positive constants and $\Gamma_3 = \{ (S_3, I_3) \in \Gamma_3 / S_3 > 0, I_3 > 0 \}$.

As in the previous calculation, the function V_3 can be called a Lyapunov function with the condition that [20]

1. The function V_3^* is continuous and the first partial derivative is continuous at Γ_3.
2. The first derivative of the function V_3^* with respect to time is obtained

$$\frac{dV_3^*(S_3,I_3)}{dt} = \frac{dV_3}{dS_3}\cdot\frac{dS_3}{dt} + \frac{dV_3}{dI_3}\cdot\frac{dI_3}{dt}$$
$$= c_1\left[1-\frac{S_3^*}{S_3}\right][\alpha_2 S_2 - \beta_3 S_3 I_3 - d_3 S_3 - \alpha_3 S_3]$$
$$+c_2\left[1-\frac{I_3^*}{I_3}\right][\beta_3 S_3 I_3 - d_3 I_3 - \mu_3 I_3 - \gamma_3 I_3]. \quad (30)$$

Based on equations (26) and (27), we get

$$\frac{\alpha_2 S_2}{S_3^*} - \beta_3 I_3^* - \alpha_3 = d_3, \quad (31)$$

and

$$\beta_3 S_3^* - \mu_3 - \gamma_3 = d_3. \quad (32)$$

Then equations (31) and (32) can be substituted into the partial derivative (30) so we get

$$\frac{dV_3^*}{dt} = c_1\left[1-\frac{S_3^*}{S_3}\right][\alpha_2 S_2 - \beta_3 S_3 I_3 - \alpha_3 S_3 - d_3 S_3]$$
$$+c_2\left[1-\frac{I_3^*}{I_3}\right][\beta_3 S_3 I_3 - \mu_3 I_3 - \gamma_3 I_3 - d_3 I_3]$$
$$= -\alpha_2 S_2\, c_1\, \frac{[S_3-S_3^*]^2}{S_3 S_3^*} + \beta_3(c_2-c_1)[S_3-S_3^*][I_3-I_3^*].$$

For $c_1 = c_2 = 1$, so we get

$$\frac{dV_3^*(S_3,I_3)}{dt} = -\alpha_2 S_2\, \frac{[S_3-S_3^*]^2}{S_3 S_3^*} < 0.$$

3. $S = \left\{S_3, I_3 \in \Gamma_3 \left| \frac{dV^*(S_3,I_3)}{dt} = 0\right.\right\} \Leftrightarrow S = \{S_3 \in \Gamma_3 | S_3 = S_3^*\}$
   Because the set S contains no other solutions or only contains equilibrium points E_3^*.

So based on the La Salle Invariant principle, [21] the endemic equilibrium point in group III is globally asymptotically stable in the interior Γ_3.

3.2.4. Global Stability Analysis Group IV

A. Disease-free Global Stability Analysis

Theorem 5 Disease-free equilibrium point in group I V (E_4^0) from the global asymptotically stable SIR model if $R_0^4 < 1$.

Proof:

Defined $V_4: \Gamma_4 \subset \mathbb{R}^3 \to \mathbb{R}$ and

$$V_4(S_4, I_4, R_4) = I_4. \quad (33)$$

In the same way as the previous group, the function V_4 can be called a Lyapunov function with the condition that [20]

1. The function V_4 is continuous and the first partial derivative is continuous on Γ_4.

2. The first derivative of the function V_4 with respect to time is obtained

$$\frac{dV_4}{dt} = \frac{dI_4}{dt}$$
$$= (\beta_4 S_4^0 - (d_4 + \mu_4 + \gamma_4)I_4)$$
$$= \left(\beta_4\left(\frac{\alpha_3 S_3}{(d_4)}\right) - (d_4 + \mu_4 + \gamma_4)\right)I_4 = (d_4 + \mu_4 + \gamma_4)(R_0^4 - 1)I_4$$

When $R_0^4 < 1$, it causes

$$\frac{dV_4}{dt} = (d_4 + \mu_4 + \gamma_4)(R_0^4 - 1)I_4 < 0.$$

So, $\frac{dV_4}{dt} < 0$, provided that $R_0^4 < 1$.

3. $S = \left\{I_4 \in \Gamma_4 \left| \frac{dV_4}{dt} = 0\right.\right\} \Leftrightarrow S = \{I_4 \in \Gamma_4 \,|I_0 = I_4\}$, the set S contains only equilibrium points E_0^4.

$$\frac{dV_4}{dt} = \frac{dI_4}{dt} = (d_4 + \mu_4 + \gamma_4)(R_0^4 - 1)(0) = 0.$$

Because the set S does not contain any other solutions. Salle Invariant principle [21], the disease-free equilibrium point in the E_4^0 global asymptotically stable age group IV.

B. Endemic Global Stability Analysis

In determining the global stability analysis, the left-hand endemic equilibrium point in the equation (4) model is made equal to zero, so it can be written as follows:

$$0 = \alpha_3 S_3 - \beta_4 S_4^* I_4^* - d_4 S_4^* \quad (34)$$
$$0 = \beta_4 S_4^* I_4^* - (d_4 + \mu_4 + \gamma_4)I_4^* \quad (35)$$
$$0 = \gamma_4 I_4^* - d_4 R_4^* \quad (36)$$

Theorem 6 The endemic equilibrium point in group IV E_4^* is globally asymptotically stable if $R_0^4 \geq 1$.

Proof:

Defined $V_4^*: \Gamma_4 \subset \mathbb{R}^3 \to \mathbb{R}$ and

$$V_4^*(S_4, I_4) = c_1\left[S_4 - S_4^* \ln\left(\frac{S_4}{S_4^*}\right)\right] + c_2\left[I_4 - I_4^* \ln\left(\frac{I_4}{I_4^*}\right)\right], \quad (37)$$

where $c_1$and $c_2$are positive constants and $\Gamma_4 = \{(S_4, I_4) \in \Gamma_4 / S_4 > 0, I_4 > 0\}$.

As in the previous calculation, the function V_4 can be called a Lyapunov function with the condition that [20]

1. The function V_4^* is continuous and the first partial derivative is continuous at Γ_4.
2. The first derivative of the function V_4^* with respect to time is obtained

$$\frac{dV_4^*(S_4, I_4)}{dt} = \frac{dV_4}{dS_4} \cdot \frac{dS_4}{dt} + \frac{dV_4}{dI_4} \cdot \frac{dI_4}{dt}$$
$$= c_1\left[1 - \frac{S_4^*}{S_4}\right][\alpha_3 S_3 - \beta_4 S_4 I_4 - d_4 S_4]$$

$$+c_2\left[1-\frac{I_4^*}{I_4}\right][\beta_4 S_4 I_4 - d_4 I_4 - \mu_4 I_4 - \gamma_4 I_4]. \quad (38)$$

Based on equations (34) and (35), we get

$$\frac{\alpha_3 S_3}{S_4^*} - \beta_4 I_4^* = d_4, \quad (39)$$

and

$$\beta_4 S_4^* - \mu_4 - \gamma_4 = d_4. \quad (40)$$

Then equations (39) and (40) can be substituted into partial derivatives (38) so we get

$$\frac{dV_4^*}{dt} = c_1\left[1-\frac{S_4^*}{S_4}\right][\alpha_3 S_3 - \beta_4 S_4 I_4 - d_4 S_4]$$
$$+c_2\left[1-\frac{I_4^*}{I_4}\right][\beta_4 S_4 I_4 - \mu_4 I_4 - \gamma_4 I_4 - d_4 I_4]$$
$$= -\alpha_3 S_3\, c_1\, \frac{[S_4 - S_4^*]^2}{S_4 S_4^*} + \beta_4(c_2 - c_1)[S_4 - S_4^*][I_4 - I_4^*].$$

For $c_1 = c_2 = 1$, so we get

$$\frac{dV_4^*(S_4,I_4)}{dt} = -\alpha_3 S_3\, \frac{[S_4 - S_4^*]^2}{S_4 S_4^*} < 0.$$

3. $S = \left\{S_4, I_4 \in \Gamma_4 \left| \frac{dV^*(S_4,I_4)}{dt} = 0\right.\right\} \Leftrightarrow S = \{S_4 \in \Gamma_4 | S_4 = S_4^*\}$

Because the set S contains no other solutions or only contains equilibrium points E_4^*. So based on the La Salle Invariant principle, [21]the endemic equilibrium point in group IV is globally asymptotically stable in the interior Γ_4.

3.3. Numerical Simulation

To understand more clearly will be illustrated the numerical solution of the equation model (1), (2), (3), and (4) with parameter values [10], [11]which differ from $t = 0$ week to $t = 500$ week. To get a clear picture of the SIR model of the spread of measles based on the age structure.

A. The SIR Epidemic Model when $R_0^{1,2,3,4} < 1$

Based on Figure 1, visualize a comparison chart of infection cases in each age group. The pink graph is a graph of the infection population in the first group with vaccination parameters of 85% and vaccination effectiveness of 85%. The yellow graph is a graph of the infection population in the second group with vaccination parameters of 95% and vaccination effectiveness of 80%. The blue graph shows the graph of the infection population in the third group, while the light blue graph shows the graph of the infection population in the fourth group.

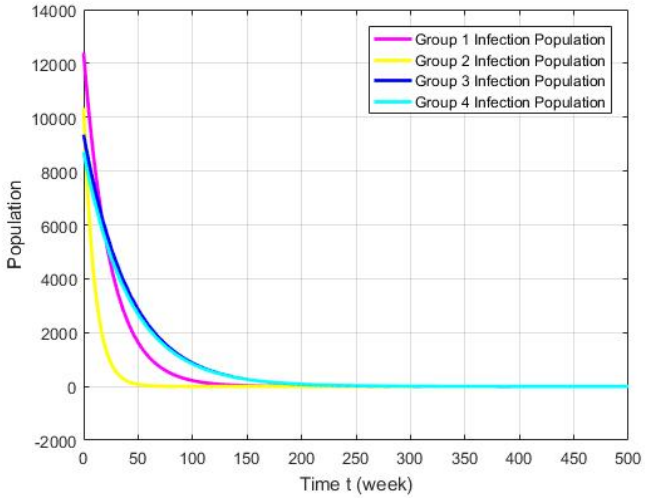

Figure 1 SIR Epidemic Model when $R_0^{1,2,3,4} < 1$

Figure 1 is a graph depicting the dynamics model of the spread of measles in groups I, II, III, and IV when $R_0 < 1$ or $\mathcal{R}_0^1 < 1, \mathcal{R}_0^2 < 1, \mathcal{R}_0^3 < 1, \mathcal{R}_0^4 < 1$. The basic reproduction number is obtained by substituting the parameter values as follows:

$R_0 = \mathcal{R}_0^1 \times \mathcal{R}_0^2 \times \mathcal{R}_0^3 \times \mathcal{R}_0^4 = (0.018002)(0.005272)(0.011594)(0.57) = 0.6272 \times 10^{-6} < 1$.

Based on Figure 1, it can be explained that the infected population in each age group is close to zero. This means that $\mathcal{R}_0 < 1$ there are no infected individuals at any age.

B. SIR Epidemic Model $R_0^{1,2,3,4} > 1$

Based on Figure 2, visualize a comparison chart of infection cases in each age group. The purple graph is a graph of the infection population in group I with vaccination parameters of 85% and vaccination effectiveness of 85%. The yellow graph is a graph of the infection population in group II with vaccination parameters of 95% and vaccination effectiveness of 80% infection in group III, while the light blue graph shows a graph of the population of infections in group IV.

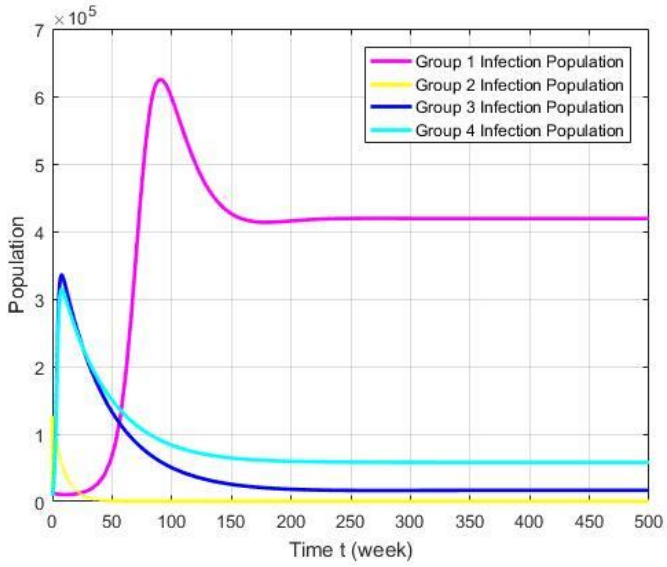

Figure 2 SIR Epidemic Model when $R_0^{1,2,3,4} > 1$.

Figure 2 is a graph illustrating the dynamics model of the spread of measles in groups I, II, III, and IV when $\mathcal{R}_0^{1,2,3,4} > 1$. The basic reproduction number is obtained by substituting the parameter values as follows:

$$R_0 = \mathcal{R}_0^1 \times \mathcal{R}_0^2 \times \mathcal{R}_0^3 \times \mathcal{R}_0^4 = (180.051)(52.72936)(11.59422)(573.178) = 63092696 > 1.$$

Based on Figure 2, it can be explained that the infected population in groups I, II, III, and IV tends to reach the endemic equilibrium point, which means that in groups I, II, III, and IV measles has spread. The infected population in each group experienced asymptotic stability with the population reaching a value, namely:

$$I_1^* = -\frac{\Lambda\beta_1\theta_1\sigma_1 - \Lambda\beta + d_1^2 + \mu_1 d_1 + \gamma_1 d_1 + \alpha_1 d_1 + \alpha_1\mu_1 + \alpha_1\gamma_1}{(d_1+\mu_1+\gamma_1)\beta_1} = 468120.6,$$

$$I_2^* = \frac{(1-\theta_2\sigma_2)\alpha_1 S_1\beta_2 - (d_2^2 + d_2\mu_2 + d_2\gamma_2 + \alpha_2 d_2 + \mu_2\alpha_2 + \gamma_2\alpha_2)}{\beta_2(d_2+\mu_2+\gamma_2)} = 8217.082,$$

$$I_3^* = \frac{\alpha_2 S_2\beta_3 - (d_3^2 + d_3\mu_3 + d_3\gamma_3 + \alpha_3 d_3 + \alpha_3\mu_3 + \alpha_3\gamma_3)}{\beta_3(d_3+\mu_3+\gamma_3)} = 16678.03,$$

$$I_4^* = \frac{\alpha_3 S_3\beta_4 - (d_4^2 + d_4\mu_4 + d_4\gamma_4)}{\beta_4(d_4+\mu_4+\gamma_4)} = 600270.4.$$

Based on the results, it is known that in the group of 0-4 years of age, 468,120 people were infected with measles. Then, in group II there was a drastic decrease of 8,217 people infected with measles. This decrease was because, at the age of 5 – 9 years, children had received measles vaccination. Then in the third age group, there was another increase because there was no vaccination in age groups III and IV, so each person has their immune system.

4. CONCLUSIONS

In the SIR model, by defining $V_k: \Gamma_k \subset \mathbb{R}^3 \to \mathbb{R}$, the Lyapunov function that can be used is that it can be concluded, that the $V_k(S_k, \quad Ik, R_k) = I_k$ global asymptotically stable $\Gamma_k$disease-free

equilibrium point E_k^0 at $k = 1,2,3,4$ if $R_0 \leq 1$, which means that in a long time the population in an area will be free from disease as long as the number of individuals in the population of each group is infected. New arrivals from one infected individual in all groups of susceptible individuals are worth less than one or equal to one $(R_0 \leq 1)$. Then, by defining $V_k: \Gamma_k \subset \mathbb{R}^3 \rightarrow \mathbb{R}$, the Lyapunov function used, it can be concluded that the $V_k^*(S_k, I_k) = c_1 \left[S_k - S_k^* \ln\left(\frac{S_k}{S_k^*}\right)\right] + c_2 \left[I_k - I_k^* \ln\left(\frac{I_k}{I_k^*}\right)\right]$ global asymptotically stable Γ_k endemic equilibrium point is E_k^*at $k = 1,2,3,4$if $R_0 \geq 1$, which means that in a sufficiently long period, the population in an area will cause a disease outbreak if the number of individuals in the newly infected population comes from infected individuals. in all susceptible individuals more than one $(R_0 > 1)$.

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