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ON THE BEHAVIOR ANALYSIS OF SUSCEPTIBLE, INFECTION, RECOVERY (*SIR*) MEASLES SPREAD MODEL WITH AGE STRUCTURE

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Abstract. *This study discusses the behavior analysis model of the Susceptible-Infected-Recovered (SIR) epidemic of the spread of measles based on age structure. The total population is grouped into four age groups, 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 analyzing the behavior of the model can be done by determining the equilibrium point, basic reproduction number, and stability analysis at the equilibrium point. In the measles distribution model with four age groups, where each age group has no interaction with other age groups, sixteen equilibrium points are obtained, which are a combination of the disease-free equilibrium and endemic equilibrium points separately. The stability properties of each equilibrium point can be determined by the value of the basic reproduction number (R_0) which is the product of the basic reproduction number of each age group. The measles disease-free equilibrium point will be locally asymptotically stable when R_0<1, meanwhile the endemic equilibrium point is locally asymptotically stable when R_0>1. This research contributes to providing information to both the government and the public.*

Keywords: *epidemic model, measles, SIR, spread of disease.*

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1. INTRODUCTION

Measles is a disease caused by a virus. This disease comes from the Paramyxviridae family which is contained in the RNA virus of the Morbilivirus genus. Measles is an acute infectious disease that mostly affects children. Measles virus can be spread through the air contaminated by the secretions of an infected person [1-3]. According to the Agency for Disease Control and Prevention [4] states that 90% 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. Otherwise, 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.

The above phenomenon can be explained using a mathematical model [5]. Mathematical models can be described in a differential equation [6], which consists of linear differential equations [7] and nonlinear equations [8]. One of the models that can be used in this problem is the SIR model. The SIR model was first introduced by Kemack and MacKendrick, the SIR (Susceptible – Infected – Recovered) epidemic model is used to explain the spread of disease, where individuals who have recovered from the disease will not be infected again or have an immune system. In this mathematical model contains three individual subclasses in a system of equations consisting of the variables Susceptible (S), Infected (I), Recovered (R).

In previous studies, models of the spread of measles have been constructed with different problem constraints using various approaches [9-11]. In this study, the researchers 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). In constructing the mathematical model of measles distribution, several assumptions are made:

1. All babies born include Susceptible.
2. There is no migration, which means that the population is closed, the increase and decrease in the population is based on births and deaths.
3. Diseases can be cured.
4. Death can occur naturally and due to disease.
5. Individuals who have recovered cannot transmit the disease.
6. Measles vaccination can increase immunity to 99%, so it can be assumed that vaccination efficacy reaches 100% [12].
7. Interaction with infected individuals only occurs in the same age group. Thus, there is no possibility of infected individuals spreading the disease to susceptible individuals in other age groups.

Based on the flow chart, it is possible to form a system of differential equations from the SIR measles spread model with the following age structure:

Group 1: Infant Group (0-4 years)

$$\begin{aligned}\frac{dS_1}{dt} &= (1-\theta_1\sigma_1)\Lambda - \beta_1 S_1 I_1 - d_1 S_1 - \alpha_1 S_1 \\ \frac{dI_1}{dt} &= \beta_1 S_1 I_1 - (d_1+\mu_1+\gamma_1)\, I_1 \\ \frac{dR_1}{dt} &= \theta_1\sigma_1\Lambda + \gamma_1 I_1 - d_1 R_1\end{aligned} \tag{1}$$

Group 2: children group (5-9 years)

$$\begin{aligned}\frac{dS_2}{dt} &= (1-\theta_2\sigma_2)\alpha_1 S_1 - \beta_2 S_2 I_2 - d_2 S_2 - \alpha_2 S_2 \\ \frac{dI_2}{dt} &= \beta_2 S_2 I_2 - (d_2+\mu_2+\gamma_2)\, I_2\end{aligned} \tag{2}$$

$$\frac{dR_2}{dt} = (\theta_2\sigma_2)\alpha_1 S_1 + \gamma_2 I_2 - d_2 R_2$$

Group 3: youth group (10-14 years)

$$\frac{dS_3}{dt} = \alpha_2 S_2 - \beta_3 S_3 I_3 - (d_3 + \alpha_3) S_3$$
$$\frac{dI_3}{dt} = \beta_3 S_3 I_3 - (d_3 + \mu_3 + \gamma_3)\, I_3 \quad (3)$$
$$\frac{dR_3}{dt} = \gamma_3 I_3 - d_3 R_3$$

Group 4: adult group (>15 years)

$$\frac{dS_4}{dt} = \alpha_3 S_3 - \beta_4 S_4 I_4 - d_4 S_4$$
$$\frac{dI_4}{dt} = \beta_4 S_4 I_4 - (d_4 + \mu_4 + \gamma_4)\, I_4 \quad (4)$$
$$\frac{dR_4}{dt} = \gamma_4 I_4 - d_4 R_4$$

From the above model, S_k denotes a population of individuals who have their immune systems susceptible to disease in group k, I_k represents a population of infected individuals who can transmit disease through direct contact in group k, R_k represents a population of individuals who have recovered so that they cannot contract the disease in group k. Λ_k represents the birth of an individual, β_k represents the rate of infection spread of measles in group k, $d_k$represents natural death in group k, μ_k represents disease-caused death rate in group k, α_k represents rate for aging in group k, γ_k represents the recovery rate in group k, σ_1 and σ_2 represent the level of vaccination efficiency in groups 1 and 2, $\theta_1$and θ_2 represent the average coverage of vaccination, with $k = 1,2,3,4$.

2. RESEARCH METHODS

The steps that can be taken in this research:

a) Determine the equilibrium point of the measles distribution model based on the age structure.

b) Determine the basic reproduction number (R_0) using Next Generation Matrix.

c) Analyzing the local stability of the equilibrium point of the measles distribution model.

d) Shows the results of a numerical simulation of the equilibrium point.

3. RESULTS AND DISCUSSION

3.1 Equilibrium Point

In calculating the equilibrium point for the spread of measles with the age structure, to simplify the calculation process, the equilibrium point for each age group will be sought first.

3.1.1 Equilibrium Point Group I

The dynamics model of the spread of measles group I in equation (1) will have an equilibrium point if it satisfies $\frac{dS_1(t)}{dt} = 0, \frac{dR_1(t)}{dt} = 0, \frac{dI_1(t)}{dt} = 0$. So equation 1 can be written as:

$$0 = (1 - \theta_1\sigma_1)\Lambda - \beta_1 S_1^0 I_1^0 - d_1 S_1^0 - \alpha_1 S_1^0 \quad (5)$$

$$0 = \beta_1 S_1^0 I_1^0 - (d_1 + \mu_1 + \gamma_1) I_1^0 \quad (6)$$

$$0 = \theta_1\sigma_1\Lambda + \gamma_1\ I_1^0 - d_1 R_1^0 \quad (7)$$

The disease-free equilibrium point of the group I measles spread model was obtained if the individual was infected ($I = 0$). So that we get a situation where all individuals enter the susceptible population and the population recovers after vaccination. By substituting $I = 0$ in equation (5), we get:

$$S_1^0 = \frac{\Lambda(1 - \theta_1\sigma_1)}{(d_1 + \alpha_1)}$$

Then in the same way substituting $I = 0$ in equation (7) we get:

$$R_1^0 = \frac{\theta_1\sigma_1\Lambda}{d_1}$$

Based on equations (5),(6),(7) the disease-free equilibrium point is obtained for group I (E_1^0)

$$E_1^0 = \left(\frac{\Lambda(1 - \theta_1\sigma_1)}{(d_1 + \alpha_1)}, 0, \frac{\theta_1\sigma_1\Lambda}{d_1}\right) \quad , \quad 0 \le \theta_1\sigma_1 \le 1 \quad (8)$$

The disease endemic equilibrium point of the measles spread model in group I was obtained if the infected individual was not equal to zero I≠0. So that in a population there are individuals who have been infected and can transmit measles in that population. The endemic equilibrium point is obtained by substituting $I \neq 0$ in equation (6), we get

$$S_1^* = \frac{d_1 + \mu_1 + \gamma_1}{\beta_1} \quad (9)$$

By substituting (9) in equation (5)

$$I_1^* = \frac{(1 - \theta_1\sigma_1)\Lambda\,\beta_1 - (d_1^2 + \mu_1 d_1 + \gamma_1 d_1 + \alpha_1 d_1 + \alpha_1\mu_1 + \alpha_1\gamma_1)}{(d_1 + \mu_1 + \gamma_1)\beta_1} \quad (10)$$

By substituting (10) in equation (7)

$$R_1^* = \frac{\theta_1\sigma_1\Lambda\beta_1 d_1 + \theta_1\sigma_1\Lambda\beta_1\mu_1 + \Lambda\beta_1\gamma_1 - \gamma_1(d_1^2 + \mu_1 d_1 + \gamma_1 d_1 + \alpha_1 d_1 + \alpha_1\mu_1 + \alpha_1\gamma_1)}{(d_1^2 + d_1\mu_1 + d_1\gamma_1)\beta_1} \quad (11)$$

Based on equation (5), (6), (7) the endemic equilibrium point for group I (E_1^*) is obtained.

Let $\varphi_1 = d_1^2 + \mu_1 d_1 + \gamma_1 d_1 + \alpha_1 d_1 + \alpha_1\mu_1 + \alpha_1\gamma_1$

$$S_1^* = \frac{d_1 + \mu_1 + \gamma_1}{\beta_1}$$

$$I_1^* = \frac{(1 - \theta_1\sigma_1)\Lambda\,\beta_1 - \varphi_1}{(d_1 + \mu_1 + \gamma_1)\beta_1} \quad (12)$$

$$R_1^* = \frac{\theta_1\sigma_1\Lambda\beta_1(d_1 + \mu_1) + \gamma_1(\Lambda\beta_1 - \varphi_1)}{(d_1^2 + d_1\mu_1 + d_1\gamma_1)\beta_1}$$

3.1.2 Equilibrium Point Group II

The dynamics model of the spread of measles group II in equation (2) will have an equilibrium point if it satisfies $\frac{dS_2(t)}{dt} = 0, \frac{dR_2(t)}{dt} = 0,\ \frac{dI_2(t)}{dt} = 0$. In the same way it can be done to find the equilibrium point free of disease and endemic in group II.

So that the disease-free equilibrium point from the group II measles spread model is obtained if the individual is infected ($I = 0$). So that in equation (2), the disease-free equilibrium point for group II (E_2^0) is

$$E_2^0 = \left(\frac{(1-\theta_2\sigma_2)\alpha_1 S_1}{(d_2+\alpha_2)}, 0, \frac{(\theta_2\sigma_2)\alpha_1 S_1}{d_2}\right) \quad , \quad 0 \le \theta_2\sigma_2 \le 1 \tag{13}$$

The disease endemic equilibrium point of the group II measles distribution model is obtained if the infected individual is not equal to zero $I \neq 0$. So that the endemic equilibrium point (E_2^*) in equation (2) is as follows

Let $\varphi_2 = d_2^2 + d_2\mu_2 + d_2\gamma_2 + \alpha_2 d_2 + \mu_2\alpha_2 + \gamma_2\alpha_2$

$$\begin{aligned} S_2^* &= \frac{d_2+\mu_2+\gamma_2}{\beta_2} \\ I_2^* &= \frac{(1-\theta_2\sigma_2)\alpha_1 S_1\beta_2 - \varphi_2}{\beta_2(d_2+\mu_2+\gamma_2)} \\ R_2^* &= \frac{\theta_2\sigma_2\alpha_1 S_1\beta_2(d_2+\mu_2) + \gamma_2(\alpha_1 S_1\beta_2 - \varphi_2)}{\beta_2(d_2^2+d_2\mu_2+d_2\gamma_2)} \end{aligned} \tag{14}$$

3.1.3 Equilibrium Point Group III

The dynamics model of the spread of measles group III in equation (3) will have an equilibrium point if it satisfies $\frac{dS_3(t)}{dt} = 0, \frac{dR_3(t)}{dt} = 0, \frac{dI_3(t)}{dt} = 0$. In the same way it can be done to find the equilibrium point free of disease and endemic in group III.

So that the disease-free equilibrium point from the group III measles spread model is obtained if the individual is infected ($I = 0$). So that in equation (3), the disease-free equilibrium point for group III (E_3^0) is

$$E_3^0 = \left(\frac{\alpha_2 S_2}{(d_3+\alpha_3)}, 0, 0\right) \tag{15}$$

The disease endemic equilibrium point of the group III measles distribution model is obtained if the infected individual is not equal to zero $I \neq 0$. So that the endemic equilibrium point (E_3^*) in equation (3) is as follows

Let $\varphi_3 = d_3^2 + d_3\mu_3 + d_3\gamma_3 + \alpha_3 d_3 + \mu_3\alpha_3 + \gamma_3\alpha_3$

$$\begin{aligned} S_3^* &= \frac{d_3+\mu_3+\gamma_3}{\beta_3} \\ I_3^* &= \frac{\alpha_2 S_2\beta_3 - \varphi_3}{\beta_3(d_3+\mu_3+\gamma_3)} \\ R_3^* &= \frac{\gamma_3\alpha_2 S_2\beta_3 - \gamma_3\varphi_3}{\beta_3(d_3^2+d_3\mu_3+d_3\gamma_3)} = \frac{\gamma_3(\alpha_2 S_2\beta_3 - \varphi_3)}{\beta_3(d_3^2+d_3\mu_3+d_3\gamma_3)} \end{aligned} \tag{16}$$

3.1.4 Equilibrium Point Group IV

The dynamics model of the spread of measles group IV in equation (4) will have an equilibrium point if it satisfies $\frac{dS_4(t)}{dt} = 0, \frac{dR_4(t)}{dt} = 0, \frac{dI_4(t)}{dt} = 0$. In the same way it can be done to find the equilibrium point free of disease and endemic in group III.

So that the disease-free equilibrium points from the group IV measles spread model is obtained if the individual is infected ($I = 0$). So that in equation (4), the disease-free equilibrium points for group IV (E_4^0) is

$$E_4^0 = \left(\frac{\alpha_3 S_3}{(d_3 + \alpha_3)}, 0,0\right) \tag{17}$$

The disease endemic equilibrium point of the group IV measles distribution model is obtained if the infected individual is not equal to zero $I \neq 0$. So that the endemic equilibrium point (E_4^*) in equation (4) is as follows

Let $\varphi_4 = d_4^2 + d_4\mu_4 + d_4\gamma_4$

$$S_4^* = \frac{d_4 + \mu_4 + \gamma_4}{\beta_4}$$
$$I_4^* = \frac{\alpha_3 S_3 \beta_4 - \varphi_4}{\beta_4(d_4 + \mu_4 + \gamma_4)} \tag{18}$$
$$R_4^* = \frac{\gamma_4 \alpha_3 S_3 \beta_4 - \gamma_4 \varphi_4}{\beta_4(d_4^2 + d_4\mu_4 + d_4\gamma_4)}$$

Based on the calculation of the equilibrium point above, two equilibrium points are obtained, there are the disease-free equilibrium point and the endemic equilibrium point. So that in equation (1)-(4), the equilibrium point conditions are obtained as follows:

1. $E_*^1 = (E_1^0, E_2^0, E_3^0, E_4^0)$
2. $E_*^2 = (E_1^0, E_2^0, E_3^0, E_4^*)$
3. $E_*^3 = (E_1^0, E_2^0, E_3^*, E_4^0)$
4. $E_*^4 = (E_1^0, E_2^*, E_3^0, E_4^0)$
5. $E_*^5 = (E_1^*, E_2^0, E_3^0, E_4^0)$
6. $E_*^6 = (E_1^*, E_2^*, E_3^0, E_4^0)$
7. $E_*^7 = (E_1^0, E_2^*, E_3^*, E_4^0)$
8. $E_*^8 = (E_1^0, E_2^0, E_3^*, E_4^*)$
9. $E_*^9 = (E_1^0, E_2^*, E_3^0, E_4^*)$
10. $E_*^{10} = (E_1^*, E_2^0, E_3^*, E_4^0)$
11. $E_*^{11} = (E_1^*, E_2^*, E_3^*, E_4^*)$
12. $E_*^{12} = (E_1^0, E_2^*, E_3^*, E_4^*)$
13. $E_*^{13} = (E_1^*, E_2^0, E_3^*, E_4^*)$
14. $E_*^{14} = (E_1^*, E_2^*, E_3^0, E_4^*)$
15. $E_*^{15} = (E_1^*, E_2^*, E_3^0, E_4^*)$
16. $E_*^{16} = (E_1^*, E_2^*, E_3^*, E_4^*)$

With $E_1^0, E_2^0, E_3^0, E_4^0$ based on equation (8), (13), (15), (17), while $E_1^*, E_2^*, E_3^*, E_4^*$ according to equation (12), (14), (16), (18).

2. Basic Reproduction Number

The basic reproductive number (R_0) is the average number of susceptible individuals infected due to one infected individual. In determining (R_0) can use the next generation matrix method [13], [14]. In the SIR epidemic model, the infected population is the only population that can transmit measles. To determine the value of the basic reproduction number (R_0) in the first, second, third and fourth groups, it is possible to linearize the infected subsystem at a disease-free equilibrium point, the infected subsystem model is I_1, I_2, I_3, I_4, which can be represented in the Jacobi matrix (J) as follows:

$$\boldsymbol{J} = \begin{bmatrix} \frac{dI_1}{dI_1} & \frac{dI_1}{dI_2} & \frac{dI_1}{dI_3} & \frac{dI_1}{dI_4} \\ \frac{dI_2}{dI_1} & \frac{dI_2}{dI_2} & \frac{dI_2}{dI_3} & \frac{dI_2}{dI_4} \\ \frac{dI_3}{dI_1} & \frac{dI_3}{dI_2} & \frac{dI_3}{dI_3} & \frac{dI_3}{dI_4} \\ \frac{dI_4}{dI_1} & \frac{dI_4}{dI_2} & \frac{dI_4}{dI_3} & \frac{dI_4}{dI_4} \end{bmatrix}$$

Then, the decomposition of the Jacobi matrix above becomes $\boldsymbol{J} = \boldsymbol{\mathcal{F}} - \boldsymbol{V}$:

$$\boldsymbol{\mathcal{F}} = \begin{bmatrix} \beta_1 S_1 & 0 & 0 & 0 \\ 0 & \beta_2 S_2 & 0 & 0 \\ 0 & 0 & \beta_3 S_3 & 0 \\ 0 & 0 & 0 & \beta_4 S_4 \end{bmatrix}$$

$$\boldsymbol{V} = \begin{bmatrix} d_1 + \mu_1 + \gamma_1 & 0 & 0 & 0 \\ 0 & d_2 + \mu_2 + \gamma_2 & 0 & 0 \\ 0 & 0 & d_3 + \mu_3 + \gamma_3 & 0 \\ 0 & 0 & 0 & d_4 + \mu_4 + \gamma_4 \end{bmatrix}$$

Then obtained

$$\boldsymbol{V^{-1}} = \begin{bmatrix} \frac{1}{d_1 + \mu_1 + \gamma_1} & 0 & 0 & 0 \\ 0 & \frac{1}{d_2 + \mu_2 + \gamma_2} & 0 & 0 \\ 0 & 0 & \frac{1}{d_3 + \mu_3 + \gamma_3} & 0 \\ 0 & 0 & 0 & \frac{1}{d_4 + \mu_4 + \gamma_4} \end{bmatrix}$$

To obtain the next generation matrix, we use the multiplication of $\boldsymbol{F}$ by $\boldsymbol{V^{-1}}$

$$\boldsymbol{FV^{-1}} = \begin{bmatrix} \beta_1 S_1 & 0 & 0 & 0 \\ 0 & \beta_2 S_2 & 0 & 0 \\ 0 & 0 & \beta_3 S_3 & 0 \\ 0 & 0 & 0 & \beta_4 S_4 \end{bmatrix} \begin{bmatrix} \frac{1}{d_1 + \mu_1 + \gamma_1} & 0 & 0 & 0 \\ 0 & \frac{1}{d_2 + \mu_2 + \gamma_2} & 0 & 0 \\ 0 & 0 & \frac{1}{d_3 + \mu_3 + \gamma_3} & 0 \\ 0 & 0 & 0 & \frac{1}{d_4 + \mu_4 + \gamma_4} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{\beta_1 S_1}{d_1+\mu_1+\gamma_1} & 0 & 0 & 0 \\ \frac{\beta_2 S_2}{d_2+\mu_2+\gamma_2} & \frac{\beta_2 S_2}{d_2+\mu_2+\gamma_2} & 0 & 0 \\ \frac{\beta_3 S_3}{d_3+\mu_3+\gamma_3} & 0 & \frac{\beta_3 S_3}{d_3+\mu_3+\gamma_3} & 0 \\ \frac{\beta_4 S_4}{d_4+\mu_4+\gamma_4} & 0 & 0 & \frac{\beta_4 S_4}{d_4+\mu_4+\gamma_4} \end{bmatrix}$$

Since there is no dominant absolute value of the resulting eigen values, multiplication is carried out between $|\lambda_1||\lambda_2||\lambda_3||\lambda_4|$, so

$$\mathcal{R}_0 = |\lambda_1||\lambda_2||\lambda_3||\lambda_4|$$

$$\mathcal{R}_0 = \left(\frac{\beta_1 S_1}{d_1+\mu_1+\gamma_1}\right)\left(\frac{\beta_2 S_2}{d_2+\mu_2+\gamma_2}\right)\left(\frac{\beta_3 S_3}{d_3+\mu_3+\gamma_3}\right)\left(\frac{\beta_4 S_4}{d_4+\mu_4+\gamma_4}\right)$$

Then substitute the disease-free equilibrium points for age groups I, II, III, and IV in the above equation, so that we get

$$\mathcal{R}_0 = \left(\frac{\left((1-\theta_1\sigma_1)\beta_1\Lambda\right)}{d_1^2+d_1\mu_1+d_1\gamma_1+\alpha_1 d_1+\alpha_1\mu_1+\alpha_1\gamma_1}\right)\left(\frac{(1-\theta_2\sigma_2)\beta_2\alpha_1 S_1}{d_2^2+d_2\mu_2+d_2\gamma_2+\alpha_2 d_2+\alpha_2\mu_2+\alpha_2\gamma_2}\right) \left(\frac{\beta_3\alpha_2 S_2}{d_3^2+d_3\mu_3+d_3\gamma_3+\alpha_3 d_3+\alpha_3\mu_3+\alpha_3\gamma_3}\right)\left(\frac{\beta_4\alpha_3 S_3}{(d_4^2+\mu_4 d_4+\gamma_4 d_4)}\right) \quad (19)$$

Based on the above calculation, the basic reproduction number from groups I-IV is the product of the basic reproduction number of each group, which can be written as follows:

$$R_0 = \mathcal{R}_0^1 \times \mathcal{R}_0^2 \times \mathcal{R}_0^3 \times \mathcal{R}_0^4$$

By

$$\mathcal{R}_0^1 = \left(\frac{\left((1-\theta_1\sigma_1)\beta_1\Lambda\right)}{d_1^2+d_1\mu_1+d_1\gamma_1+\alpha_1 d_1+\alpha_1\mu_1+\alpha_1\gamma_1}\right)$$

$$\mathcal{R}_0^2 = \left(\frac{(1-\theta_2\sigma_2)\beta_2\alpha_1 S_1}{d_2^2+d_2\mu_2+d_2\gamma_2+\alpha_2 d_2+\alpha_2\mu_2+\alpha_2\gamma_2}\right) \quad (20)$$

$$\mathcal{R}_0^3 = \left(\frac{\beta_3\alpha_2 S_2}{d_3^2+d_3\mu_3+d_3\gamma_3+\alpha_3 d_3+\alpha_3\mu_3+\alpha_3\gamma_3}\right)$$

$$\mathcal{R}_0^4 = \left(\frac{\beta_4\alpha_3 S_3}{(d_4^2+\mu_4 d_4+\gamma_4 d_4)}\right)$$

3.2 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. The analysis of the stability of the equilibrium point can be determined using the Jacobi matrix, then it is

possible to linearize the equilibrium point in a nonlinear differential equation to obtain the eigen values. If the eigen value of the Jacobian matrix is negative, it means that the stability point in the system of equations is stable [15].

3.2.1 Stability Analysis Group I

Analysis of the stability of the equilibrium point of the measles disease model can be determined using the Jacobi matrix, the Jacobi matrix in equation (1) is obtained:

$$J(S,I,R) = \begin{bmatrix} -\beta_1 I_1 - \alpha_1 - d_1 & -\beta_1 S_1 & 0 \\ \beta_1 I_1 & \beta_1 S_1 - (d_1 + \mu_1 + \gamma_1) & 0 \\ 0 & \gamma_1 & -d_1 \end{bmatrix} \tag{21}$$

The local stability analysis of the equilibrium point E_1^0can be determined using the disease-free equilibrium point $E_1^0 = \left(\frac{\Lambda(1-\theta_1\sigma_1)}{(d_1+\alpha_1)}, 0, \frac{\theta_1\sigma_1\Lambda}{d_1}\right)$. Then the disease-free equilibrium point is substituted in the matrix (21), we get

$$J(E_0) = \begin{bmatrix} -(d_1+\alpha_1) & -\beta_1\left(\dfrac{\Lambda(1-\theta_1\sigma_1)}{(d_1+\alpha_1)}\right) & 0 \\ 0 & \beta_1\left(\dfrac{\Lambda(1-\theta_1\sigma_1)}{(d_1+\alpha_1)}\right) - (d_1+\mu_1+\gamma_1) & 0 \\ 0 & \gamma_1 & -d_1 \end{bmatrix}$$

Then the characteristic equation can be determined by means of

$$\det(J_0 - \lambda I) = 0$$

$$\det\begin{pmatrix} -(d_1+\alpha_1) - \lambda & -\dfrac{\beta_1\Lambda(\theta_1\sigma_1 - 1)}{(d_1+\alpha_1)} & 0 \\ 0 & -\dfrac{\beta_1\Lambda(\theta_1\sigma_1 - 1)}{(d_1+\alpha_1)} - (d_1+\mu_1+\gamma_1) - \lambda & 0 \\ 0 & \gamma_1 & -d_1 - \lambda \end{pmatrix} = 0$$

So that the eigen values obtained are as follows:

$$\lambda_1 = -(d_1+\alpha_1)$$

$$\lambda_2 = -\frac{\beta_1\Lambda(\theta_1\sigma_1 - 1)}{(d_1+\alpha_1)} - (d_1+\mu_1+\gamma_1)$$

$$\lambda_3 = -d_1$$

The eigen values of the characteristic equation above are real numbers and are negative if $R_0 < 1$. It can be concluded that the disease-free equilibrium point is locally asymptotically stable if $R_0 < 1$and the disease-free equilibrium point is unstable if $R_0 > 1$. Analysis of the local stability of the equilibrium point E_1^* in age group I. It can be determined by substitution (12) in (21) to obtain

$$J(E_*^1) = \begin{bmatrix} \frac{(1-\theta_1\sigma_1)\Lambda\beta_1 - \varphi_1}{(d_1+\mu_1+\gamma_1)} - \alpha_1 - d_1 & -d_1 - \mu_1 - \gamma_1 & 0 \\ \frac{(1-\theta_1\sigma_1)\Lambda\beta_1 - \varphi_1}{(d_1+\mu_1+\gamma_1)} & \frac{\beta_1(d_1+\mu_1+\gamma_1)}{\beta_1} - (d_1+\mu_1+\gamma_1) & 0 \\ 0 & \gamma_1 & -d_1 \end{bmatrix}$$

Then, in the same way, the characteristic value of will be obtained

$$|A| = (-d_4 - \lambda)\left[\lambda^2 + \left(\left(\frac{\alpha_3 S_3\beta_4 - \varphi_4}{(d_4+\mu_4+\gamma_4)}\right) - d_4\right)\lambda + (\alpha_3 S_3\beta_4 - \varphi_4)\right]$$

So the eigen values obtained are as follows:

$$\lambda_1 = -d_1$$

To find λ_2 and λ_3 by using characteristic equation, where

$$\lambda^2 + a_1\lambda + a_0 = 0$$

So, λ_2 and λ_3 satisfy the above equation, where

$$a_1 = \frac{(1-\theta_1\sigma_1)\Lambda\beta_1 + \varphi_1}{(d_1+\mu_1+\gamma_1)} - \alpha_1 - d_1 = \frac{\varphi_1(\mathcal{R}_0^1 - 1)}{(d_1+\mu_1+\gamma_1)} - (\alpha_1 + d_1) > 0$$

$$a_0 = (1-\theta_1\sigma_1)\Lambda\beta_1 + \varphi_1 = \varphi_1(\mathcal{R}_0^1 - 1) > 0$$

According to the Routh-Hurwitz criteria, the endemic equilibrium point is locally asymptotically stable if $\alpha_1 > 0$ and $\alpha_0 > 0$. Therefore the endemic equilibrium point is locally asymptotically stable when $\mathcal{R}_0^1 > 1$.

3.2.2 Stability Analysis Group II

Analysis of the stability of the equilibrium point of the measles model can be determined using the Jacobi matrix, the Jacobi matrix in equation (2) is obtained:

$$J(S,I,R) = \begin{bmatrix} -\beta_2 I_2 - (d_2+\alpha_2) & \beta_2 S_2 & 0 \\ \beta_2 I_2 & \beta_2 S_2 - (d_2+\mu_2+\gamma_2) & 0 \\ 0 & \gamma_2 & -d_2 \end{bmatrix} \quad (22)$$

The local stability analysis of the equilibrium point E_2^0 can be determined using the disease-free equilibrium point E_2^0. Then, in the same way, we obtain the characteristic equation

$$|A| = (-(d_2+\alpha_2) - \lambda)\left(\frac{(1-\theta_2\sigma_2)\alpha_1 S_1\beta_2}{(d_2+\alpha_2)} - (d_2+\mu_2+\gamma_2) - \lambda\right)(-d_2 - \lambda)$$

So the eigen values obtained are as follows:

$$\lambda_1 = -(d_2+\alpha_2)$$

$$\lambda_2 = -\frac{(1-\theta_2\sigma_2)\alpha_1 S_1\beta_2}{(d_2+\alpha_2)} - (d_2+\mu_2+\gamma_2)$$

$$\lambda_3 = -d_2$$

Therefore, all the eigen values of the characteristic equation above are real numbers and are negative if $R_0 < 1$. It can be concluded that the disease-free equilibrium point is locally asymptotically stable.

The local stability analysis of the endemic equilibrium point E_2^* can be determined in the same way as before so that the characteristic equation is obtained, namely:

$$|A| = (-d_2 - \lambda)\left[\lambda^2 + \left(\left(\frac{(1-\theta_2\sigma_2)\alpha_1 S_1\beta_2 - \varphi_2}{(d_2+\mu_2+\gamma_2)}\right) - (d_2+\alpha_2)\right)\lambda + (1-\theta_2\sigma_2)\alpha_1 S_1\beta_2 - \varphi_2\right]$$

From the above equation, the eigen values are

$$\lambda_1 = -d_2$$

To find λ_2 and λ_3 by using characteristic equation where

$$\lambda^2 + a_1\lambda + a_0 = 0$$

So, λ_2 and λ_3 satisfy the above equation, where

$$a_1 = \left(\frac{(1-\theta_2\sigma_2)\alpha_1 S_1\beta_2 - \varphi_2}{(d_2+\mu_2+\gamma_2)}\right) - (d_2+\alpha_2) = \frac{\varphi_2(\mathcal{R}_0^2-1)}{(d_2+\mu_2+\gamma_2)} - (\alpha_2+d_2) > 0$$

$$a_0 = (1-\theta_2\sigma_2)\alpha_1 S_1\beta_2 - \varphi_2 = \varphi_2(\mathcal{R}_0^2-1) > 0$$

According to the Routh-Hurwitz criteria, the endemic equilibrium point is locally asymptotically stable if $\alpha_1 > 0$ and $\alpha_0 > 0$. Therefore, the endemic equilibrium point is locally asymptotically stable when $\mathcal{R}_0^2 > 1$.

3.2.3 Stability Analysis Group III

Analysis of the stability of the equilibrium point of the measles model can be determined using the Jacobi matrix, the Jacobi matrix in equation (3) is obtained:

$$J(S,I,R) = \begin{bmatrix} -\beta_3 I_3 - (d_3+\alpha_3) & \beta_3 S_3 & 0 \\ \beta_3 I_3 & \beta_3 S_3 - (d_3+\mu_3+\gamma_3) & 0 \\ 0 & \gamma_3 & -d_3 \end{bmatrix} \quad (23)$$

The local stability analysis of the equilibrium point E_3^0 can be determined using the disease-free equilibrium point E_3^0. Then, in the same way, we obtain the characteristic equation

$$|A| = (-d_3 - \lambda)\left(\frac{\beta_4\alpha_3 S_3}{d_4} - (d_4+\gamma_4+\mu_4) - \lambda\right)(-d_4-\lambda)$$

So, the eigen values obtained are as follows:

$$\lambda_1 = -d_4$$

$$\lambda_2 = \frac{\beta_4\alpha_3 S_3}{d_4} - (d_4+\gamma_4+\mu_4) = -(d_4+\mu_4+\gamma_4)\,(1-R_0)$$

$$\lambda_3 = -d_4$$

Therefore, all the eigen values of the characteristic equation above are real numbers and are negative if $R_0 < 1$. It can be concluded that the disease-free equilibrium point is locally asymptotically stable.

The local stability analysis of the endemic equilibrium point E_3^* can be determined in the same way as before so that the characteristic equation is obtained, namely:

$$|A| = (-d_3 - \lambda)) \left[\lambda^2 + \left(\left(\frac{\alpha_2 S_2 \beta_3 - \varphi_3}{(d_3 + \mu_3 + \gamma_3)}\right) - (d_3 + \alpha_3)\right)\lambda + \alpha_2 S_2 \beta_3 - \gamma_3 \varphi_3\right]$$

From the above equation, the eigen values are

$$\lambda_1 = -d_3$$

To find λ_2 and λ_3 by using characteristic equation where

$$\lambda^2 + a_1\lambda + a_0 = 0$$

So, λ_2 and λ_3 satisfy the above equation, where

$$a_1 = \left(\frac{\alpha_2 S_2 \beta_3 - \varphi_3}{(d_3 + \mu_3 + \gamma_3)}\right) - (d_3 + \alpha_3) = \frac{\varphi_3(\mathcal{R}_0^3 - 1)}{(d_3 + \mu_3 + \gamma_3)} - (\alpha_2 + d_2) > 0$$

$$a_0 = \alpha_2 S_2 \beta_3 - \varphi_3 = \varphi_3(\mathcal{R}_0^3 - 1) > 0$$

According to the Routh-Hurwitz criteria, the endemic equilibrium point is locally asymptotically stable if $\alpha_1 > 0$ and $\alpha_0 > 0$. Therefore, the endemic equilibrium point is locally asymptotically stable when $\mathcal{R}_0^3 > 1$.

3.2.4 Stability Analysis Group IV

Analysis of the stability of the equilibrium point of the measles model can be determined using the Jacobi matrix, the Jacobi matrix in equation (4) is obtained:

$$J(S, I, R) = \begin{bmatrix} -\beta_4 I_4 - d_4 & -\beta_4 S_4 & 0 \\ \beta_4 I_4 & \beta_4 S_4 - (d_4 + \gamma_4 + \mu_4) & 0 \\ 0 & \gamma_4 & -d_4 \end{bmatrix} \quad (24)$$

The local stability analysis of the equilibrium point E_4^0 can be determined using the disease-free equilibrium point E_4^0. Then, in the same way, we obtain the characteristic equation

$$|A| = (-(d_3 + \alpha_3) - \lambda)\left(\frac{\alpha_2 S_2 \beta_3}{(d_3 + \alpha_3)} - (d_3 + \mu_3 + \gamma_3) - \lambda\right)(-d_3 - \lambda)$$

So, the eigen values obtained are as follows:

$$\lambda_1 = -(d_3 + \alpha_3)$$

$$\lambda_2 = \left(\frac{\alpha_2 S_2 \beta_3}{(d_3 + \alpha_3)}\right) - (d_3 + \mu_3 + \gamma_3)$$

$$\lambda_3 = -d_3$$

Therefore, all the eigen values of the characteristic equation above are real numbers and are negative if $R_0 < 1$. It can be concluded that the disease-free equilibrium point is locally asymptotically stable.

The local stability analysis of the endemic equilibrium point E_4^* can be determined in the same way as before so that the characteristic equation is obtained, namely:

$$|A| = (-d_4 - \lambda)\left[\lambda^2 + \left(\left(\frac{\alpha_3 S_3 \beta_4 - \varphi_4}{(d_4 + \mu_4 + \gamma_4)}\right) - d_4\right)\lambda + (\alpha_3 S_3 \beta_4 - \varphi_4)\right]$$

From the above equation, the eigen values are

$$\lambda_1 = -d_4$$

To find λ_2 and λ_3 by using characteristic equation where

$$\lambda^2 + a_1\lambda + a_0 = 0$$

So, λ_2 and λ_3 satisfy the above equation, where

$$a_1 = \left(\frac{\alpha_3 S_3 \beta_4 - \varphi_4}{(d_4 + \mu_4 + \gamma_4)}\right) - d_4 = \frac{\varphi_3(\mathcal{R}_0^4 - 1)}{d_4 + \mu_4 + \gamma_4} - d_4 > 0$$

$$a_0 = \alpha_3 S_3 \beta_4 - \varphi_4 = \varphi_4(\mathcal{R}_0^4 - 1) > 0$$

According to the Routh-Hurwitz criteria, the endemic equilibrium point is locally asymptotically stable if $\alpha_1 > 0$ and $\alpha_0 > 0$. Therefore, the endemic equilibrium point is locally asymptotically stable when $\mathcal{R}_0^4 > 1$.

3.3 Numeric Simulation

To understand more clearly will be illustrated the simulation of the equilibrium point of the model equations (1), (2), (3), and (4), obtained 16 equilibrium point conditions. From the 16 equilibrium points above, three equilibrium points will be illustrated with parameter values [11] which differ from $t = 0$ weeks to $t = 2500$ weeks. So as to get a figure of the SIR model of the spread of measles based on the age structure.

a. Equilibrium Point Simulation E_*^1

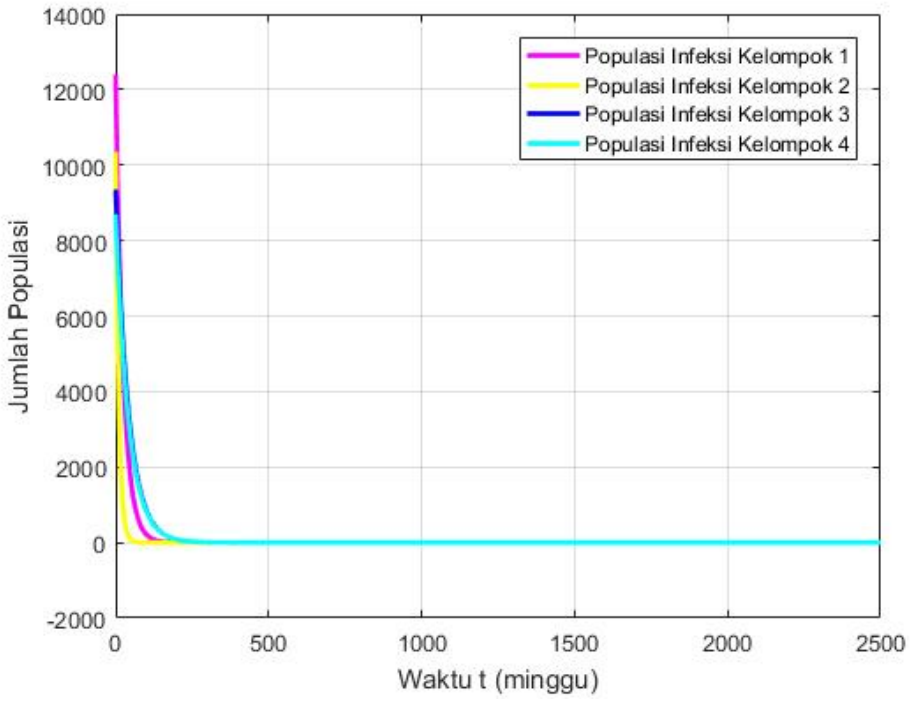

Figure 1. Equilibrium Point Simulation E_*^1

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 the vaccination parameter of 85% and the vaccination effectiveness of 85% with the infection rate of $\beta_1 = 0{,}167989 \times 10^{-8}$. The yellow graph is a graph of the infection population in the second group with 95% vaccination parameters and 80% vaccination effectiveness with an infection rate of $\beta_2 = 0{,}515425 \times 10^{-7}$. The blue graph shows a graph of the infection population in the group with an infection rate of $\beta_3 = 0.262981 \times 10^{-8}$, while the light

blue graph shows a graph of the infection population in the group with an infection rate of $\beta_4 = 0.285701 \times 10^{-8}$.

Figure 1 is a graph depicting the dynamics of measles distribution model in groups I, II, III, IV when $\mathcal{R}_0^1 < 1$. In Figure 1 it can be explained that the infected population in each age group is zero. This means that under conditions of E_*^1 or $\mathcal{R}_0^1 < 1$ there are no infected individuals at any age.

b. Equilibrium Point Simulation E_*^8

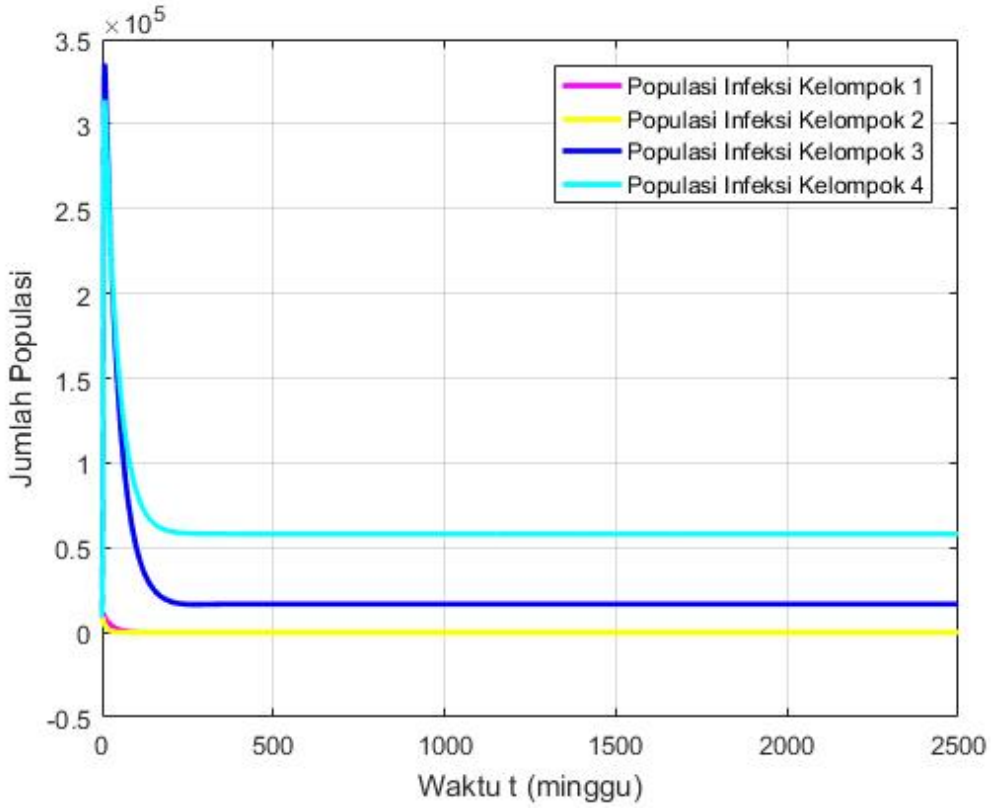

Figure 2 Equilibrium Point Simulation E_*^8

Based on Figure 2, 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 the vaccination parameter of 85% and the vaccination effectiveness of 85% with the infection rate of $\beta_1 = 0{,}167989 \times 10^{-8}$. The yellow graph is a graph of the infection population in the second group with 95% vaccination parameters and 80% vaccination effectiveness with an infection rate of $\beta_2 = 0{,}515425 \times 10^{-7}$. The blue graph shows a graph of the infection population in the group with an infection rate of $\beta_3 = 0.262981 \times 10^{-5}$, while the light blue graph shows a graph of the infection population in the group with an infection rate of $\beta_4 = 0.285701 \times 10^{-5}$.

Figure 2 is a graph depicting the dynamics model of measles distribution in groups I, II, III, IV when $\mathcal{R}_0^{1,2} < 1$ and $\mathcal{R}_0^{3,4} > 1$. In Figure 2 it can be explained that the infected population in groups I and II is zero, which means that in groups I and II there are no infected individuals, while the infected population in groups III and IV is heading to a point which means that in groups III and IV measles has spread. The infected population in groups III and IV experienced asymptotic stability with the population reaching values:

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

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

c. Equilibrium Point Simulation E_*^{16}

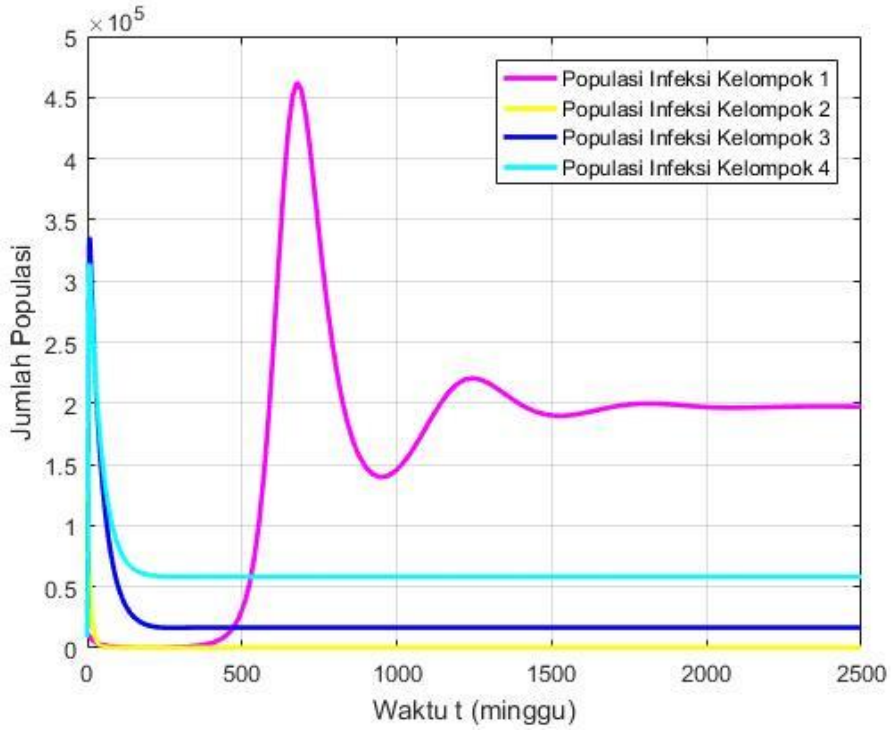

Figure 3 Equlibrium Point Simulation $\mathbf{E}_*^{16}$

Based on Figure 3, visualize a comparison chart of infection cases in each age group. The purple graph is a graph of the infection population in the first group with a vaccination parameter of 85% and a vaccination effectiveness of 85% with an infection rate of $\beta_1 = 0{,}167989 \times 10^{-6}$. The yellow graph is a graph of the infection population in the second group with 95% vaccination parameters and 80% vaccination effectiveness with an infection rate of $\beta_2 = 0{,}515425 \times 10^{-3}$.The blue graph shows a graph of the infection population in the group with an infection rate of $\beta_3 = 0.262981 \times 10^{-5}$, while the light blue graph shows a graph of the infection population in the group with an infection rate of $\beta_4 = 0.285701 \times 10^{-5}$.

Figure 3 is a graph that illustrates the dynamics model of the spread of measles in groups I, II, III and IV when $\mathcal{R}_0^{1,2,3,4} > 1$. In Figure 3 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:

$$I_1^* = -\frac{\Lambda\beta_1\theta_1\sigma_1 - \Lambda\beta + d_1^2 + \mu_1 d_1 + \gamma_1 d_1 + \alpha_1 d_1 + \alpha_1\mu_1 + \alpha_1\gamma_1}{(d_1 + \mu_1 + \gamma_1)\beta_1} = 192193$$

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

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

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

4. CONCLUSIONS

Based on this research, it can be concluded that the measles distribution model with four age groups where each age group inn able to interact with other age groups obtained 16 equilibrium points which are a combination of two equilibrium points for each group separately. Stability properties of each equilibrium

point can be determined using the value of the basic reproduction number (R_0) where the basic reproduction number is the product of each basic reproduction number of each age group which can be expressed by $R_0 = \prod_{i=1}^{4} \mathcal{R}_0^i$.

The results of the analysis are illustrated in a numerical simulation when all R_0 values from each group are less than 1, the infected population from each group will lead into zero, means there are no infected individuals. Then when all R_0 values from each group are more than 1, the infected population from each group will lead into a point of stability, it means that measles has spread within that group. Furthermore, when R_0 in groups I and II was less than 1 and R_0 in groups III and IV was more than one, it was found that age groups I and II were free of measles because there were no infected individuals, while in groups III and IV there was spread of disease measles.

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