Analysis and Solution of The SEIRS Model for The Rubella Transmission with Vaccination Effect using Runge-Kutta Method

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Abstract. Rubella disease is an infectious disease transmitted through the respiratory tract caused by a virus. In some cases, there are diseases that can enter an endemic condition, which is a condition in which the outbreak of a disease in a certain area over a long period of time. This condition can be modeled mathematically by using certain assumptions which will then seek for analytical and numerical solutions. This type of research is a literature study. This study examines the theory and application of the Runge-Kutta method in analyzing the spread of Rubella with the effect of vaccination. The Runge-Kutta method is widely used in solving ordinary differential equations and is more accurate than the Euler method. In this study, two methods were used to analyze it, namely the Runge-Kutta Order 4 and Order 5 methods which were used to analyze and compare the numerical results obtained, and the aim of the study was to obtain and interpret mathematically a mathematical model of the spread of Rubella's disease with the effect of vaccination, and comparing the results obtained from the numerical solution using the Runge-Kutta Order 4 and Runge-Kutta Order 5 methods simulated with Maple software 13. From the results of this study, the results obtained in the 1st iteration of the numerical solution model for Rubella's disease using the Runge-Kutta Order 4 is the value of $S_1 = 8771655$, $E_1 = 142$, $I_1 = 38$, and $R_1 = 30$. While the results in the first iteration of the numerical solution model for Rubella's disease using the Runge-Kutta Order 5 method were that the values of $S_1 = 8771759$, $E_1 = 142$, $I_1 = 37$, and $R_1 = 30$ were obtained. So it can be concluded that the Order 5 Runge-Kutta is better than the Order 4 Runge-Kutta in predicting the state rate of the Rubella disease case population in the Susceptible, Exposed, Infected, Recovered, Suspected (SEIRS) model. Because the image / graph of Order 5 Runge-Kutta is more like / closer to the results of the analytical simulation using maple 13 software, which is as many as 27 infected individuals.
1. INTRODUCTION
Rubella is a contagious viral infection caused by Rubella virus, Togavirus, genus Rubivirus [1]. Immunization with the Measles Rubella (MR) vaccine is the best prevention for this disease. In countries without the implementation of a vaccination control program, Rubella infection is a major cause of miscarriage and birth defects [1]. Each year, through surveillance activities, more than 11,000 cases of suspected measles are reported, and laboratory confirmation results show that 12–39% of them are lab confirmed measles while 16–43% are definite rubella. From 2010 to 2015, there were an estimated 23,164 cases of measles and 30,463 cases of rubella [2].

Several studies on mathematical modeling of disease spread have been conducted [3-18]. This study discusses the SEIRS model in measles with the effect of vaccines and migration which illustrates the effect of permanent vaccines on the spread of measles with the help of the Routh Hurwith method which is used to analyze the stability of the endemic equilibrium point. Furthermore, in another study that has been conducted by [3], namely the Numerical Solution of the Runge-Kutta Order 5 Method in the SIRS Epidemic Model, in which the study conducted an analysis of the stability of the spread of disease by building a mathematical model of the SIRS epidemic in infectious diseases, the numerical solution was obtained through Runge-Kutta fifth order method and simulated with MATLAB R2010 software. So that the model of disease spread is obtained in the form of a system of first order differential equations and their equilibrium points. This study examines the SEIRS mathematical model on the spread of Rubella's disease. Numerical analysis and solutions using RK-4 and RK-5 were also carried out in this study.

2. METHOD
This study was conducted using a literature study research method [4-15] which was examined to obtain a SEIRS model for the spread of Rubella with the effect of vaccination. The first part of this research is the construction of a SEIRS model for the spread of Rubella disease, then analyzing the SEIRS model using the Runge-Kutta method [3] to analyze and determine the numerical results obtained and interpret mathematically from the results obtained. In this case the model uses four populations: suspected, exposed, infected and recovered populations. The model analysis uses the Runge-Kutta method and uses the data as the initial value of the number of cases of Rubella disease and uses the assumption of parameter values as the number of cases of Rubella disease. And then simulate a model using Maple to predict the number of cases of Rubella disease spread over the next few years.

3. RESULT
3.1. SEIRS Mathematical Model for Rubella Disease
Based on the above assumptions, the SEIRS type model diagram for the spread of Rubella can be seen in Figure 1:

![Figure 1: SEIRS Model on the Spread of Rubella](image-url)
According to the Figure 1, the total population of N is divided into 4 sub-populations, namely: the number of human populations that are susceptible to a disease called Susceptible (S), the number of human populations showing or showing symptoms of being infected with a disease called Exposed (E), the number of human populations who have been infected with the disease called Infected (I), and the number of human population who have recovered from the disease known as Recovered (R), with the total population \( N = S + E + I + R \) built in a model mathematics in the form of a system of non-linear differential equations as follows:

\[
\begin{align*}
\frac{dS}{dt} &= (1 - \sigma)N + \delta R - \beta SE - \mu S \\
\frac{dE}{dt} &= \beta SE - \alpha E - \mu E \\
\frac{dI}{dt} &= \alpha E - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I + \sigma \theta N - \delta R - \mu R
\end{align*}
\]

The variables as initial values and parameters used in building a model for the spread of Rubella disease are as listed in table 1 and table 2:

| Variable | Value      | Information                                           |
|---------|------------|-------------------------------------------------------|
| \( S(0) \) | 8.771.761 | Data on the number of human populations susceptible to Rubella disease |
| \( E(0) \) | 142        | Data on the number of human population or symptoms of Rubella disease infection |
| \( I(0) \) | 37         | Data on the number of human populations who have been infected with Rubella disease |
| \( R(0) \) | 30         | Data on the number of human populations who have developed from Rubella disease |

**Source:** Statistics Central, 2018; Health Department, South Sulawesi, 2018

| Parameter | Information                        | Value |
|-----------|------------------------------------|-------|
| \( N \)   | The number of population           | 1     |
| \( \sigma \) | Vaccinated individual level       | 0.309 |
| \( \beta \) | Level of Rubella-exposed individuals | 0,00000002 |
| \( \alpha \) | The rate of Rubella-infected individuals | 0.4   |
| \( \gamma \) | The rate of Rubella-recovered individuals | 0.1667 |
| \( \delta \) | The rate of Rubella-re-suspected individuals | 0.14  |
| \( \mu \)   | The rate of death individual       | 0.0012 |
| \( \theta \) | The rate of birthd population      | 0.0187 |

### 3.2. Solution of SEIR Model for Rubella Disease Using Runge-Kutta Method

#### 3.2.1. Solution of SEIR Model for Rubella Disease Using RK-4 Method

The system of equations (1) is solved using the Runge-Kutta Order method 4 as in the equation \( x_{i+1} = x_i + \frac{1}{6}h(k_1 + 2k_2 + 2k_3 + k_4) \). Then the system of equation (1) is substituted for the Runge-Kutta Order 4 equation in order to obtain the following equation:

\[
S_{i+1} = S_i + \frac{1}{6}h(k_1 + 2k_2 + 2k_3 + k_4)
\]
According to equation 3.4.1.

\[ \begin{align*}
E_{i+1} &= E_i + \frac{1}{6} h(l_1 + 2l_2 + 2l_3 + l_4) \\
I_{i+1} &= I_i + \frac{1}{6} h(m_1 + 2m_2 + 2m_3 + m_4) \\
R_{i+1} &= R_i + \frac{1}{6} h(n_1 + 2n_2 + 2n_3 + n_4)
\end{align*} \] (2)

3.3. Solution of SEIR Model for Rubella Disease Using RK-5 Method

The system of equations (1) is solved using the Runge-Kutta Order method of 5 as in the equation \( x_{i+1} = x_i + \frac{1}{90} h(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6) \). Then the system of equation (1) is substituted for the Runge-Kutta equation of Order 5, so that the following equation is obtained:

\[ \begin{align*}
S_{i+1} &= S_i + \frac{1}{90} h(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6) \\
E_{i+1} &= E_i + \frac{1}{90} h(7l_1 + 32l_3 + 12l_4 + 32l_5 + 7l_6) \\
I_{i+1} &= I_i + \frac{1}{90} h(7m_1 + 32m_3 + 12m_4 + 32m_5 + 7m_6) \\
R_{i+1} &= R_i + \frac{1}{90} h(7n_1 + 32n_3 + 12n_4 + 32n_5 + 7n_6)
\end{align*} \] (3)

3.4. Numerical Solution of the Runge-Kutta Method for SEIRS Model in Rubella Disease

3.4.1. RK-4 Method

According to equation (1)

\[ \begin{align*}
S_{0+1} &= S_0 + \frac{1}{6} h(k_1 + 2k_2 + 2k_3 + k_4) \\
E_{0+1} &= E_0 + \frac{1}{6} h(l_1 + 2l_2 + 2l_3 + l_4) \\
I_{0+1} &= I_0 + \frac{1}{6} h(m_1 + 2m_2 + 2m_3 + m_4) \\
R_{0+1} &= R_0 + \frac{1}{6} h(n_1 + 2n_2 + 2n_3 + n_4)
\end{align*} \]

With the variable values that have been obtained previously are:

| Variable value | 1       | 2       | 3       | 4       |
|----------------|---------|---------|---------|---------|
| \( k \)       | -10546,812 | 10546,719 | -10546,697 | -10546,626 |
| \( l \)       | -32,05859  | -32,0225 | -32,0220  | -31,98660 |
| \( m \)       | 50,6765    | 50,4810398 | 50,4812760 | 50,374851  |
| \( n \)       | 1,93767    | 33,012656 | 1,956440  | 2,0190680 |

Then by substituting the values of \( k_1 \) to \( k_4 \), \( l_1 \) to \( l_4 \), \( m_1 \) to \( m_4 \), and \( n_1 \) to \( n_4 \) into equation (2), the numerical solution of Rubella’s disease model is obtained using the Runge-Kutta Order 4 method as follows:

\[ \begin{align*}
S_{0+1} &= S_0 + \frac{1}{6} h(k_1 + 2k_2 + 2k_3 + k_4) \\
S_1 &= 8771655,532879862 \\
E_{0+1} &= E_0 + \frac{1}{6} h(l_1 + 2l_2 + 2l_3 + l_4) \\
E_1 &= 141,6797774135 \\
I_{0+1} &= I_0 + \frac{1}{6} h(m_1 + 2m_2 + 2m_3 + m_4) \\
I_1 &= 37.50495997
\end{align*} \]
\[ R_{0+1} = R_0 + \frac{1}{6}h(n_1 + 2n_2 + 2n_3 + n_4) \]

\[ R_1 = 30.1231887 \]

with the time \( t = 1 \) year is obtained found \( S = 8771655, (E) = 141.7 \) \( (I) = 37.5 \) and \( (R) = 30.1 \). Then the same thing is done for the next iteration with \( S_i, E_i, I_i, R_i \) where \( i = 1, 2, 3, \ldots \), as initial value.

3.4.2. RK-5 Method

According to the Equation (3):

\[ x_{i+1} = x_i + \frac{1}{90}h(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6) \]

\[ S_{i+1} = S_i + \frac{1}{90}h(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6) \]

\[ E_{i+1} = E_i + \frac{1}{90}h(7l_1 + 32l_3 + 12l_4 + 32l_5 + 7l_6) \]

\[ I_{i+1} = I_i + \frac{1}{90}h(7m_1 + 32m_3 + 12m_4 + 32m_5 + 7m_6) \]

\[ R_{i+1} = R_i + \frac{1}{90}h(7n_1 + 32n_3 + 12n_4 + 32n_5 + 7n_6) \]

With the variable values that have been obtained previously are:

| Variable | 1       | 2       | 3       | 4       | 5       | 6       |
|----------|---------|---------|---------|---------|---------|---------|
| \( k \)  | -105,468,070 | -105,467,65 | -105,467 | -105,467 | -105,466,72 | -105,464,0 |
| \( l \)  | -0,320,58 | -0,320,405 | -0,320,405 | -0,320,22 | -0,320,041 | -0,319,866 |
| \( m \)  | 0,505,877 | 0,505,344 | 0,505,344 | 0,504,81 | 0,504,28 | 0,503,74 |
| \( n \)  | 0,019,376 | 0,019,580 | 0,019,580 | 0,019,78 | 0,019,98 | 0,020,190 |

Then by substituting the values \( k_1 \) to \( k_6 \), \( l_1 \) to \( l_6 \), \( m_1 \) to \( m_6 \), and \( n_1 \) to \( n_6 \) into equation (3), the numerical solution of Rubella's disease model is obtained using the Runge-Kutta Order 5 method as follows:

\[ S_{0+1} = S_0 + \frac{1}{90}h(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6) \]

\[ S_1 = 8771759,9453321 \]

\[ E_{0+1} = E_0 + \frac{1}{90}h(7l_1 + 32l_3 + 12l_4 + 32l_5 + 7l_6) \]

\[ E_1 = 141,996,797,742 \]

\[ I_{0+1} = I_0 + \frac{1}{90}h(7m_1 + 32m_3 + 12m_4 + 32m_5 + 7m_6) \]

\[ I_1 = 37,005,048,122 \]

\[ R_{0+1} = R_0 + \frac{1}{90}h(7n_1 + 32n_3 + 12n_4 + 32n_5 + 7n_6) \]

\[ R_1 = 30,000,197,84 \]

With \( t = 1 \) year, we found \( S = 8771759, (E) = 141.9 \) \( (I) = 37.005 \) and \( (R) = 30,000.1 \). Then the same thing is done for the next iteration with \( S_i, E_i, I_i, R_i \) where \( i = 1, 2, 3, \ldots \), as initial value.

3.5. Simulation Result of SEIRS Model for Rubella Transmission

The iteration results of the numerical solution of the Rubella disease model using the Runge-Kutta Order 4 and Runge-Kutta Order 5 methods up to \( t = 100 \) years for the rate of each class will be shown in the plot of Figure 2 to Figure 6:
Figure 2. Rate of the Susceptible (S) individual for Rubella

Based on Figure 2, it can be seen that the size of the population of the susceptible individual group increases constantly up to $t = 100$. The magnitude of the susceptible rate at $t = 100$ according to the results obtained in the maple simulation is $2.5 \times 8.771.655 = 21.929.138$.

Figure 3. Rate of the Exposed individual for Rubella

Based on Figure 3, it can be seen that the size or number of the individual population of the exposed group drops drastically until the 15th year and is in an equilibrium state after the 15th year with the number of individuals in an equilibrium state is 0, which means it can be said that after the 15th year no more individuals have symptoms of Rubella disease.

Figure 4. Rate of the Infected individual for Rubella

Based on Figure 4, it can be seen that the class rate of Infected (I) individuals which initially increases and decreases drastically at $t = 5$, then is in an equilibrium state when $t = 43$ with the number of infected individuals is 0.
Based on Figure 5, it can be seen that the rate of recovered individuals class (R) increases dramatically and at $t = 50$ begins to balance with the number of recovered individuals as much as $0.04 \times 30 = 2$.

4. DISCUSSION

The SEIRS mathematical model was conducted by [7] using the type of scabies in animal populations using the linearization method. [5] discussed an analysis of an epidemic model of SIR with the effect of random vaccination at birth. In addition, [8] analyzed the spread of measles using the SEIR model with the effect of vaccination and migration. This study discusses the spread of Rubella using the Runge-Kutta method with the effect of vaccination. Model analysis uses the Runge-Kutta method to analyze the numerical results obtained from the method. The simulation results of the SEIRS model use the maple 13 software application. Then the simulation results of this model provide interpretation or information and predictions of the number of cases of Rubella spread for the next few years, so that this model can help improve preventive strategies in controlling the number of infected cases or exposed to Rubella's disease.

5. CONCLUSION

Based on the results and discussion of these studies it can be concluded: Mathematical model of the SEIRS type in the spread of Rubella disease, the results in the first iteration of the numerical solution model for rubella disease using the Runge-Kutta fourth order method were obtained $(S_1) = 8771655$, $(E_1) = 142$, $(I_1) = 38$, and $(R_1) = 30$. While the results in the first iteration of the numerical solution model for rubella disease using the Runge-Kutta were obtained $(S_1) = 8771759$, $(E_1) = 142$, $(I_1) = 37$, and $(R_1) = 30$. Meanwhile, the Runge-Kutta fifth order was better than the Runge-Kutta fourth order in predicting the rate of population conditions for Rubella disease in the SEIRS model. Because the image of Runge-Kutta fifth order is closer to the results of the analytical simulation using maple 13 software, namely 27 individual are infected.

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