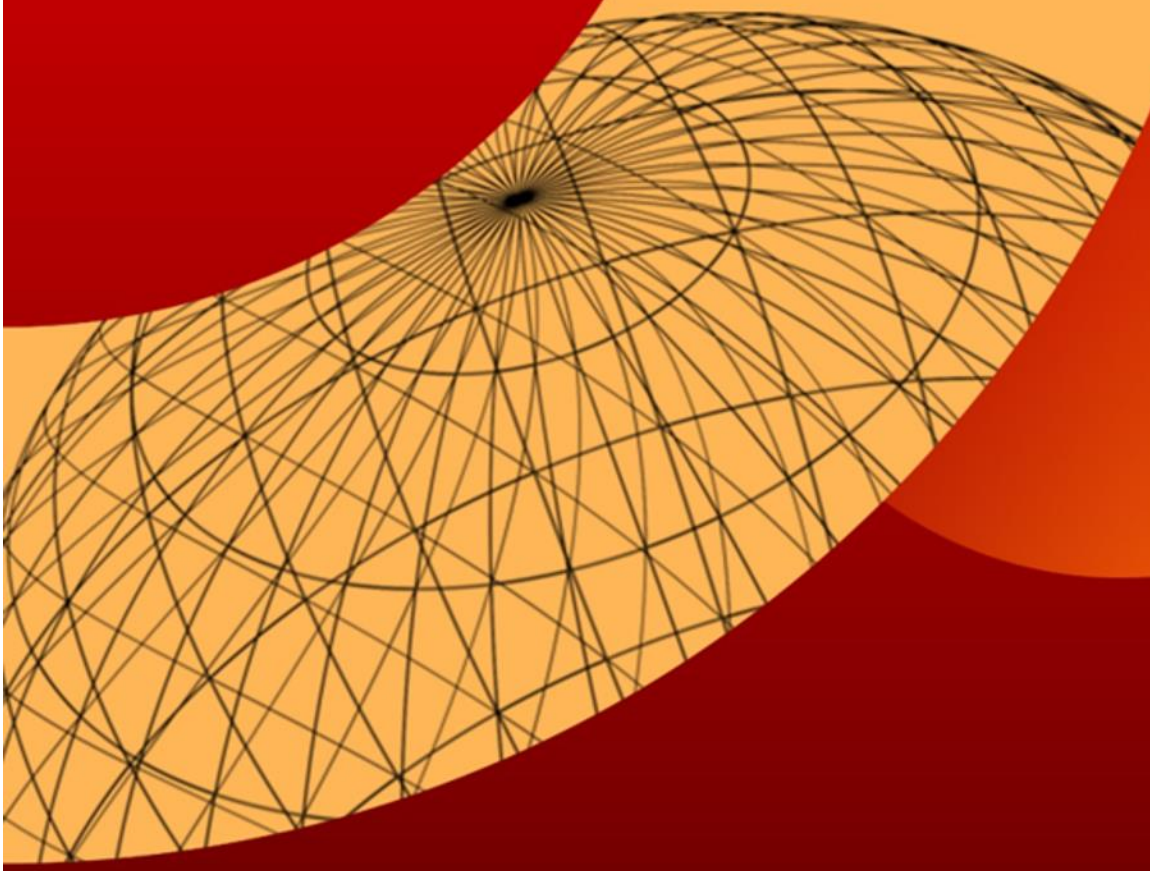
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Modeling the Spread of Hepatitis B Disease from the SEIR Model in East Java Using RKF45

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Abstract: Hepatitis B is an infectious disease that has a major impact on public health, especially in East Java Province with a high prevalence of cases. This study aims to model the spread of Hepatitis B using the *SEIR* model (*Susceptible, Exposed, Infected, Recovered*) and solved numerically with the *Runge-Kutta Fehlberg* method (RKF45). Simulation results for 10 years showed that the susceptible population decreased from 38,654,309 to 36,407,210 individuals, while the *exposed* compartment increased from 134,0419 to 376,213. The *infected* population peaked at around 19,781 individuals in year 2 and decreased to 3,265 individuals, while the cured population continued to increase until it reached 46,565 at the end of the period. The SEIR model with the RKF45 method proved effective in describing the dynamics of the spread of Hepatitis B mathematically and can be utilized as a predictive tool in supporting public health policy.

Keyword: Hepatitis B, *SEIR* model, *Runge-Kutta Fehlberg*, *Disease spread*, *East java.*

1. Introduction

Hepatitis is a disease that is still a serious health problem in Indonesia. Hepatitis or inflammation of the liver is one of the various types of liver disease where other types include liver swelling (*fatty liver*) and liver cancer [2]. According [21] there are various types of hepatitis including Heptitis A,B,C,D and E [5][6][13].

The type of disease studied in this study is hepatitis B disease because it has a wider spread factor, namely through blood or body fluids, as well as through direct contact with hepatitis B sufferers. The World Health Organization (WHO) suggests that by 2022, it is estimated that around 1.3 million people will die from chronic hepatitis B and C virus infections, which means around 3,500 deaths every day. Around 254 million people worldwide are living with hepatitis B, while 50 million people are infected with hepatitis C, with an additional 6,000 people newly infected every day. Many people go undiagnosed (who, 2022).

According to the Ministry of Health of the Republic of Indonesia, published in 2017, there were 2 million people infected in 2013. The most common type of hepatitis infecting the Indonesian population is hepatitis B, with a percentage reaching 21.8%. The increase in the number of hepatitis cases in Indonesia occurred in almost all provinces, including East Java Province [17]. East Java Province is one of the provinces in Indonesia that has experienced an increase in the number of hepatitis B cases. Patients with hepatitis cover a wide range of ages and genders. Based on data from the Ministry of Health, there is no significant difference in the proportion of hepatitis cases between men and women. In May 2022 in East Java there were 114 cases of

acute hepatitis, in addition, East Java is also the province with the highest number of pregnant women infected with hepatitis B in Indonesia, namely 8,269 people.

The spread of hepatitis B virus can occur in two ways, namely horizontally and vertically. Horizontal transmission can take place through the skin or mucous membranes, while vertical transmission occurs when an infected mother passes the virus to her baby during pregnancy or during childbirth [10][11][20]. Hence, transmission of hepatitis can occur in various ways, depending on the type of hepatitis. Hepatitis B can be caused by birth defects from the mother of the patient as well as through the use of contaminated syringes, ear piercing, needle sticks, blood transfusions, and shared razors or toothbrushes. In addition, kissing and having sexual intercourse with people with hepatitis B are also possible ways of transmission [7][20].

Given the high risk of hepatitis B transmission, prevention is very important. The best intervention to prevent mysterious hepatitis infection is to adopt a healthy lifestyle. The Indonesian Ministry of Health has also issued a circular on hepatitis precautions. The vigilance includes recognizing the symptoms of hepatitis and immediately taking the patient to a health facility [3]. Therefore, research related to hepatitis prevention and control efforts is very important to reduce the spread of this disease.

One way to understand how viral hepatitis spreads is to use a mathematical model. The model consists of variables, parameters, and functions that describe how these elements are related. In creating a model, it is important to choose what needs to be included and what can be ignored, depending on the problem being studied. In general, mathematical models are divided into two types: phenomenological models and mechanistic models. For infectious diseases, an epidemic model is usually used, which divides the population into groups based on their health conditions [9][14].

One of the models included in this category is the *SEIR* model, the *SEIR* model divides the population into four groups based on infection-related health status that classifies individuals into: S (*Susceptible*), The population that is susceptible or can contract the disease, where people in this category are not yet infected but can be infected if they come into direct contact with infected individuals. E (*Exposed*), Population that has been exposed to the disease but has not yet shown symptoms or cannot transmit, so this group is in the incubation period, which is the period between exposure and the onset of symptoms; I (*Infected*), Population that has been infected, shows symptoms, and can transmit the disease to others, this group is the source of transmission, R (*Recovered*) Population that has recovered from infection and has immunity to the disease, so they cannot be infected or transmitted again. This model helps understand the dynamics of disease spread from susceptibility to recovery [2].

To obtain the solution of the SEIR model, a system of nonlinear ordinary differential equations (PDB) is used which is solved numerically. Numerical methods enable computational model solving, one of which is the Runge-Kutta Fehlberg (RKF) method, which is effective for solving nonlinear GDP [4][12][14][15][16].

The *Runge-Kutta-Fehlberg* (RKF) method is a numerical technique for solving Ordinary Differential Equations (ODE) with automatic adjustment of the step size developed by Erwin Fehlberg, it combines 4th and 5th order approximations to achieve the desired accuracy efficiently [1][14][18][19] (Mauritis, Rumlawang, & Rijoly, 2023).

2. RESEARCH METHODS

2.1. Research Stages

At this stage, several stages of research are described which will be used to achieve the research objectives. Some of the research stages are as follows:

1. Data Retrieval
2. Determining the solution of the *SEIR* model using the *Runge-Kutta Fehlberg* method
   Steps for solving the *Runge-Kutta Fehlberg* method:

a. Determine the *SEIR* model
b. Determine the initialization
c. Application of *Runge-Kutta Fehlberg* method
d. Determining initial conditions and parameters
e. Calculating the coefficient k_i
f. Calculating 4th order and 5th order solutions
g. Visualization of results

3. Simulation
4. Conclusion drawing

3. RESULTS AND DISCUSSION

3.1 SEIR model for Hepatitis B disease spread

3.1.1 Variable Assumptions and *SEIR* Model Parameters

The *SEIR* model is generally a reduction of the SIR model, only experiencing the addition of an exposed variable (E), which is an individual who has been exposed to the disease but has not shown symptoms or has not been able to transmit. There are several assumptions used in the formation of the model, namely:

1. there are births and deaths in a population
2. every individual born will be vulnerable
4. Every detected individual will become infected
5. the disease is dangerous, if infected it can cause death
6. Susceptible individuals if vaccinated will be immune to the disease 6.
7. Individuals who recover from Hepatitis B are considered unable to be re-infected 7.
8. constant population (covered).

This means $N = S(t) + E(t) + I(t) + R(t)$. The total population in time t is equal to the number of susceptible, exposed, infected, and recovered individuals.

3.1.2 Formation of *SEIR* Model

The changes that occur from each human group can be interpreted in the following form:

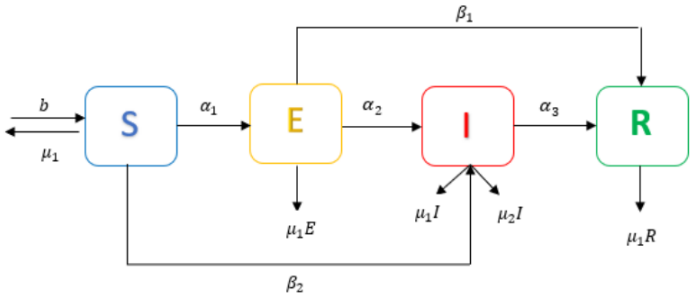


Figure 1. Compartment diagram of the *SEIR* model

Based on Figure 4.1, the mathematical model of the spread of hepatitis B disease is written in the form of differential equations such as the following equation:

$$\frac{dS}{dt} = b - (\alpha_1 + \beta_2 + \mu_1)\, S$$

$$\frac{dE}{dt} = \alpha_1 S - (\alpha_2 + \beta_1 + \mu_1)\, E$$

$$\frac{dI}{dt} = \beta_2 S + \alpha_2 E - (\alpha_3 + \mu_1 + \mu_2)\, I$$

$$\frac{dR}{dt} = \beta_1 E + \alpha_3 I - \mu_1 R$$

With:

N = Total Population
S = Number of vulnerable population.
E = Number of exposed population
I = number of infected population
R = number of recovered population
b = birth rate
β_1 = recovery rate from individual E to individual R
β_2 = transmission rate from individual S to individual I
α_1 = transmission rate from individual S to individual E
α_2 = transmission rate from individual E to individual I
α_3 = recovery rate from individual I to individual R
μ_1 = natural mortality rate
μ_2 = mortality rate due to Hepatitis B disease

3.2 Values of Parameter

Based on data obtained from the results of the 2020 Health Profile report in East Java, it can be seen that the average subpopulation S (Susceptible) is 38,654,309 people, subpopulation E (*Exposed*) is 134,419 people, subpopulation I (*Infected*) is 23,911 people, subpopulation R (*Recovered*) is 15,038, with a total of N 38,827,677 people. Therefore, an initial value can be obtained as in Table 3.1.

Table 1. Initial value

Variabel	Nilai	Keterangan
N	38.827.677	Population size
S_i	38.654.309	Vulnerable population size data
E_i	134.419	Exposed population size data
I_i	23.911	Infected population size data
R_i	15.038	Data on the number of recovered population

The parameter values used in this study can be presented in the form of Table 4.2.

Tabel 1. Parameter Value

Parameter	Description	Value
b	Individual birth rate	0,015
μ_1	The natural mortality rate of individuals	0,014
μ_2	Mortality rate due to Hepatitis B infection	0.01797
β_1	The recovery rate from individual E to individual R	0,1118
β_2	The recovery rate from individual S to individual I	0,00061582
α_1	The recovery rate from individual S to individual E	0,0034
α_2	The recovery rate from individual E to individual I	0,1778
α_3	The recovery rate from individual I to individual R	0,6289

3.3 Solving the *SEIR* model using the *Runge-Kutta Fehlberg* method

In the first iteration, the time interval or step distance used is $h = 0.2$. Then given $S(0) = 38{,}654{,}309$ and $t(0) = 0$ years as the initial value, so that the numerical solution of the equation model using the *Runge-Kutta Fehlberg* method is obtained as in the following equation:

$$y_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5\text{; thus obtained}$$

$$S_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

$$E_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

$$I_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

$$R_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

Whit:

$K_{1S} = h(b - (\alpha_1 + \beta_1 + \mu_1))S_i$

$K_{1E} = h(\alpha_i S_i - (\alpha_2 + \beta_2 + \mu_1))E_i$

$K_{1I} = h(\beta_2(S_i + \alpha_2 E_i)) - (\alpha_3 + \mu_2 + \mu_1)I_i$

$K_{1R} = h(\beta_1(E_i)) + \alpha_3(I_i) - (\mu_1 R_i)$

$K_{2S} = h(b - (\alpha_1 + \beta_1 + \mu_1)(S_i + \frac{1}{4}K_{1S})$

$K_{2E} = h\left(\alpha_1(S_i + \frac{1}{4}K_{1E})\right) - (\alpha_2 + \beta_2 + \mu_1)(E_i + \frac{1}{4}K_{1E})$

$K_{2I} = h\left(\beta_2(S_i + \frac{1}{4}K_{1I})\right) + \alpha_2(E_i + \frac{1}{4}K_{1I}) - (\alpha_3 + \mu_1 + \mu_2)(I_i + \frac{1}{4}K_{1I})$

$K_{2R} = h\left(\beta_1(E_i + \frac{1}{4}K_{1R})\right) + \alpha_3(I_i + \frac{1}{4}K_{1R}) - \mu_1(R_i + \frac{1}{4}K_{1R})$

$K_{3S} = h(b - (\alpha_1 + \beta_1 + \mu_1)(S_i + \frac{2}{32}K_{1S} + \frac{9}{32}K_{2S})$

$K_{3E} = h\left(\alpha_1(S_i + \frac{2}{32}K_{1E} + \frac{9}{32}K_{2E})\right) - (\alpha_2 + \beta_2 + \mu_1)(E_i + \frac{2}{32}K_{1E} + \frac{9}{32}K_{2E})$

$K_{3I} = h\left(\beta_2(S_i + \frac{2}{32}K_{1I} + \frac{9}{32}K_{2I})\right) + \alpha_2(E_i + \frac{2}{32}K_{1I} + \frac{9}{32}K_{2I}) - (\alpha_3 + \mu_1 + \mu_2)(I_i + \frac{2}{32}K_{1I} + \frac{9}{32}K_{2I})$

$K_{3R} = h\left(\beta_1(E_i + \frac{2}{32}K_{1R} + \frac{9}{32}K_{2R})\right) + \alpha_3(I_i + \frac{2}{32}K_{1R} + \frac{9}{32}K_{2R}) - (\mu_i(R_i + \frac{2}{32}K_{1R} + \frac{9}{32}K_{2R})$

$K_{4S} = h\big(b - (\alpha_1 + \beta_1 + \mu_1)\big)(S_i + \frac{1932}{2197}K_{1S} - \frac{7200}{2197}K_{2S} + \frac{7296}{2197}K_{3S})$

$$K_{4E} = h\left(\alpha_1(E_i + \frac{1932}{2197}K_{1E} - \frac{7200}{2197}K_{2E} + \frac{7296}{2197}K_{3E})\right) - (\alpha_2 + \beta_2 + \mu_1)(E_i + \frac{1932}{2197}K_{1E} - \frac{7200}{2197}K_{2E} + \frac{7296}{2197}K_{3E})$$

$$K_{4I} = h\left(\beta_2(S_i + \frac{1932}{2197}K_{1I} - \frac{7200}{2197}K_{2I} + \frac{7296}{2197}K_{3I})\right) + \alpha_2(E_i + \frac{1932}{2197}K_{1I} - \frac{7200}{2197}K_{2I} + \frac{7296}{2197}K_{3I}) - (\alpha_3 + \mu_1 + \mu_2)(I_i + \frac{1932}{2197}K_{1I} - \frac{7200}{2197}K_{2I} + \frac{7296}{2197}K_{3I})$$

$$K_{4R} = h\left(\beta_1(E_i + \frac{1932}{2197}K_{1R} - \frac{7200}{2197}K_{2R} + \frac{7296}{2197}K_{3R})\right) + \alpha_3(I_i + \frac{1932}{2197}K_{1R} - \frac{7200}{2197}K_{2R} + \frac{7296}{2197}K_{3R}) - (\mu_1(R_i + \frac{1932}{2197}K_{1R} - \frac{7200}{2197}K_{2R} + \frac{7296}{2197}K_{3R}))$$

$$K_{5S} = h\big(b - (\alpha_1 + \beta_1 + \mu_1)\big)(S_i + \frac{439}{216}K_{1S} - 8K_{2S} + \frac{3680}{513}K_{3S} - \frac{845}{4104}K_{4S})$$

$$K_{5E} = h\left(\alpha_1(E_i + \frac{439}{216}K_{1E} - 8K_{2E} + \frac{3680}{513}K_{3E} - \frac{845}{4104}K_{4E})\right) - (\alpha_2 + \beta_2 + \mu_1)(E_i + \frac{439}{216}K_{1E} - 8K_{2E} + \frac{3680}{513}K_{3E} - \frac{845}{4104}K_{4E})$$

$$K_{5I} = h\left(\beta_2(S_i + \frac{439}{216}K_{1I} - 8K_{2I} + \frac{3680}{513}K_{3I} - \frac{845}{4104}K_{4I})\right) + \alpha_2(E_i + \frac{439}{216}K_{1I} - 8K_{2I} + \frac{3680}{513}K_{3I} - \frac{845}{4104}K_{4I}) - (\alpha_3 + \mu_1 + \mu_2)(I_i + \frac{439}{216}K_{1I} - 8K_{2I} + \frac{3680}{513}K_{3I} - \frac{845}{4104}K_{4I})$$

$$K_{5R} = h\left(\beta_1(E_i + \frac{439}{216}K_{1R} - 8K_{2R} + \frac{3680}{513}K_{3R} - \frac{845}{4104}K_{4R})\right) + \alpha_3(I_i + \frac{439}{216}K_{1R} - 8K_{2R} + \frac{3680}{513}K_{3R} - \frac{845}{4104}K_{4R}) - (\mu_1(R_i + \frac{439}{216}K_{1R} - 8K_{2R} + \frac{3680}{513}K_{3R} - \frac{845}{4104}K_{4R})$$

$$K_{6S} = h\big(b - (\alpha_1 + \beta_2 + \mu_1)\big)(S_i + \frac{8}{27}K_{1S} + 2K_{2S} - \frac{3544}{2565}K_{3S} - \frac{1858}{4104}K_{4S} - \frac{11}{40}K_{5S})$$

$$K_{6E} = h\left(\alpha_1(E_i + \frac{8}{27}K_{1E} + 2K_{2E} - \frac{3544}{2565}K_{3E} - \frac{1858}{4104}K_{4E} - \frac{11}{40}K_{5E})\right) - (\alpha_2 + \beta_2 + \mu_1)(E_i + \frac{8}{27}K_{1E} + 2K_{2E} - \frac{3544}{2565}K_{3E} - \frac{1858}{4104}K_{4E} - \frac{11}{40}K_{5E})$$

$$K_{6I} = h\left(\beta_2(S_i + \frac{8}{27}K_{1I} + 2K_{2I} - \frac{3544}{2565}K_{3I} - \frac{1858}{4104}K_{4I} - \frac{11}{40}K_{5I})\right) + \alpha_2(E_i + \frac{8}{27}K_{1I} + 2K_{2I} - \frac{3544}{2565}K_{3I} - \frac{1858}{4104}K_{4I} - \frac{11}{40}K_{5I}) - (\alpha_3 + \mu_1 + \mu_2)(I_i + \frac{8}{27}K_{1I} + 2K_{2I} - \frac{3544}{2565}K_{3I} - \frac{1858}{4104}K_{4I} - \frac{11}{40}K_{5I})$$

$$K_{6R} = h\left(\beta_1(E_i + \frac{8}{27}K_{1R} + 2K_{2R} - \frac{3544}{2565}K_{3R} - \frac{1858}{4104}K_{4R} - \frac{11}{40}K_{5R})\right) + \alpha_3(I_i + \frac{8}{27}K_{1R} + 2K_{2R} - \frac{3544}{2565}K_{3R} - \frac{1858}{4104}K_{4R} - \frac{11}{40}K_{5R}) - (\mu_1(R_i + \frac{8}{27}K_{1R} + 2K_{2R} - \frac{3544}{2565}K_{3R} - \frac{1858}{4104}K_{4R} - \frac{11}{40}K_{5R})$$

So from the above calculations, the results in table 4.3 are obtained.

Table 3. Calculation Results of K Value

MODEL	NILAI K					
	K1	K2	K3	K4	K5	K6

S	-139.278	-139.152	-147.058	-142.239	-23.197	-23.210
E	21.112	20.913	20.815	26.067	16.949	20.177
I	6.380	6.226	-7.442	5.458	10.376	4.041
R	5.971	3.391	3.379	3.307	6.950	7.397

Then substituting the value of the evaluation function K_1 to K_6 into the 4th order formulation will obtain the results of the numerical solution to the equation model using the RKF method as follows:

$$S_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

$$S_1 = 38.654.309 + \left(\frac{25}{216}(-139.278)\right) + \left(\frac{1408}{2565}(-147.058)\right) + \left(\frac{2197}{4101}(-142.239)\right) - \left(\frac{1}{5}(-23.197)\right)$$

$$S_1 = 38.485.903$$

$$E_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

$$E_1 = 134.419 + \left(\frac{25}{216}(21.112)\right) + \left(\frac{1408}{2565}(20.815)\right) + \left(\frac{2197}{4101}(26.067)\right) - \left(\frac{1}{5}(16.949)\right)$$

$$E_1 = 158.863$$

$$I_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

$$I_1 = 23.911 + \left(\frac{25}{216}(6.380)\right) + \left(\frac{1408}{2565}(-7442)\right) + \left(\frac{2197}{4101}(5.458)\right) - \left(\frac{1}{5}(10.376)\right)$$

$$I_1 = 21.413$$

$$R_{i+1} = y_i + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$$

$$R_1 = 15.038 + \left(\frac{25}{216}(5.971)\right) + \left(\frac{1408}{2565}(3.379)\right) + \left(\frac{2197}{4101}(3.307)\right) - \left(\frac{1}{5}6.950\right)$$

$$R_1 = 17.965$$

Then the same iteration is done until $t = 10$ or to calculate the population rate for the next 10 years. Next, substitute the values of the evaluation functions k_1 to k_6 into the 5th order formulation to obtain the results of the numerical solution to the logistic equation model using the RKF method as follows:

$$\hat{y}_{i+1} = y_i + \frac{16}{135}k_1 + \frac{6656}{12825}k_3 + \frac{28.561}{56430}k_4 - \frac{9}{50}k_5 + \frac{2}{55}k_6; \quad \text{diperoleh}$$

$$\hat{S}_{i+1} = S_i + \frac{16}{135}k_{1S} + \frac{6656}{12825}k_{3S} + \frac{28561}{56430}k_{4S} - \frac{9}{50}k_{5S} + \frac{2}{55}k_{6S}$$

From the equation, the following results are obtained

$$\hat{S}_1 = 38.654.309 + \left(\frac{16}{135}(-139.278)\right) + \left(\frac{6656}{12825}(147.058)\right) + \left(\frac{28561}{56430}(142.239)\right) - \left(\frac{9}{50}(23.197)\right) + \left(\frac{2}{55}(-23.210)\right)$$

$$S_1 = 38.429.829$$

$$\hat{E}_{i+1} = E_i + \frac{16}{135}k_1 + \frac{6656}{12825}k_{3E} + \frac{28561}{56430}k_{4E} - \frac{9}{50}k_{5E} + \frac{2}{55}k_{6E}$$

$$\hat{E}_1 = 134.419 + \left(\frac{16}{135}(21.112)\right) + \left(\frac{6656}{12825}(20.815)\right) + \left(\frac{28561}{56430}(26.067)\right) - \left(\frac{9}{50}(16.949)\right) + \left(\frac{2}{55}(20.177)\right)$$

$$\hat{E}_1 = 158.598$$

$$\hat{I}_{i+1} = I_i + \frac{16}{135}k_{1I} + \frac{6656}{12825}k_{3I} + \frac{28561}{56430}k_{4I} - \frac{9}{50}k_{5I} + \frac{2}{55}k_6 I$$

$$\hat{I}_1 = 23.911 + \frac{16}{135}(6.380) + \frac{6656}{12825}(-7442) + \frac{28561}{56430}(5.458) - \frac{9}{50}(10.376) + \frac{2}{55}(4.041)$$

$$\hat{I}_1 = 21.846$$

$$\hat{R}_{i+1} = R_i + \frac{16}{135}k_{1R} + \frac{6656}{12825}k_{3R} + \frac{28561}{56430}k_{4R} - \frac{9}{50}k_{5R} + \frac{2}{55}k_{6R}$$

$$\hat{R}_1 = 15.038 + \frac{16}{135}(5.971) + \frac{6656}{12825}(3.379) + \frac{28561}{56430}(3.307) - \frac{9}{50}(6.950) + \frac{2}{55}(7.397)$$

$$\hat{R}_1 = 18.191$$

The calculation can be done up to $t = 10$.
The interval time or step distance used is $h = 0{,}2$. Furthermore, given $S_i = S_0$, $E_i = E_0$, $I_i = I_0$, $R_i = R_0$ as initial values so that the results of the calculation of the numerical solution of the hepatitis B disease spread model using the Fifth Order Fehlberg Runge-Kutta method as in equations (2.9) to (2.14) and t = 1 to t = 10 using *matlab software*.

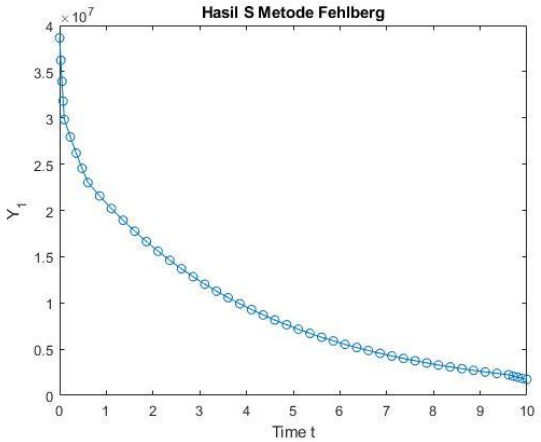


Figure 2. Graph of the number *Susceptible* population (S)

Based on Figure 4.2 the number of individuals in the vulnerable compartment (s) decreased from about 38,654,309 individuals at $t = 0$ to about 36,407,210 individuals at $t = 10$. This decrease occurs due to the movement of individuals to other compartments due to disease transmission. This pattern reflects the dynamics of the $SEIR$ model, where the *susceptible* population continues to decrease over time.

Furthermore, the calculation results for the *exposed* population rate (E) will be shown in the graph as shown in Figure 4.3.

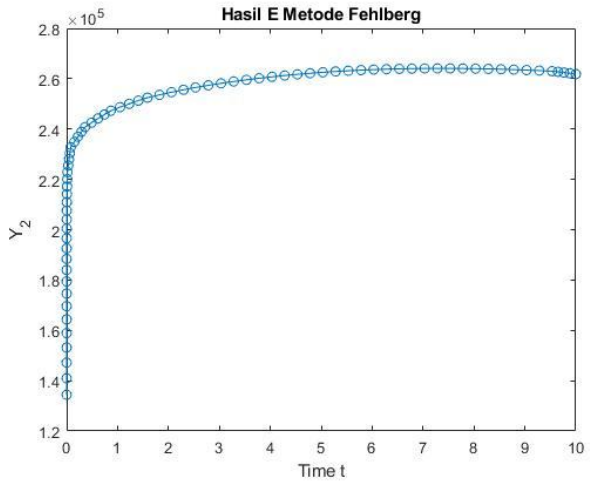


Figure 3. Graph of the number *exposed* population (E)

From Figure 4.3 the number of individuals in the exposed compartment increased from about 134,419 at $t = 0$ to 158,598 at $t = 1$, then the growth slowly slowed down. The peak number of exposed individuals occurred at $t = 6$ with about 279,495 individuals, then slightly increased to 376,213 at $t = 10$. This pattern indicates that the exposed phase lasts a short time before individuals move to the infected or cured phase.

Furthermore, the calculation results for the *infected* population rate (I) will be shown in Figure 4.4.

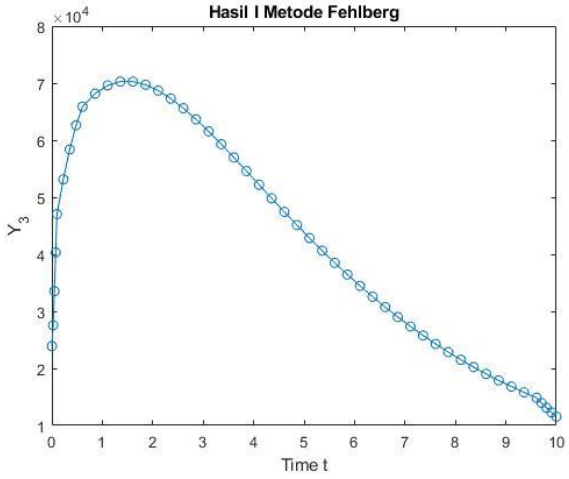


Figure 4. Graph of the number *Infected* population (I)

Based on Figure 4.4 at the beginning of time $t = 0$, the number of infected individuals is around 23,911 individuals. This number increases until it reaches a peak at $t = 2$ with 19,781 individuals. This shows that in the early phase, the transmission rate is very high. After experiencing a peak increase, the number of infected individuals began to decline gradually. At the end of the simulation $t = 10$, the number of individuals decreased to 3,263 people.

Furthermore, the calculation results for the *recovery* population rate (R) will be shown in the graph as shown in Figure 4.5.

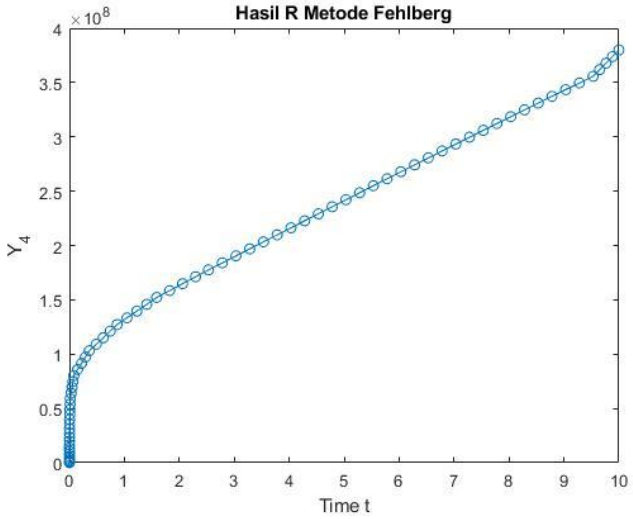


Figure 5. Graph of the number *Recovered* population (R)

Based on Figure 4.5, the number of individuals who recover from the disease continues to increase over time. This shows that the recovery process takes place consistently and effectively in the model used. At the end of the simulation time, i.e. $t = 10$, the number of recovered individuals reached around 46,565, without any decrease in value in the graph, where individuals who have recovered do not return to vulnerable or infected status.

3. CONCLUSION

Based on the results of applying the *Runge-Kutta Fehlberg* (RKF45) method to the *SEIR* model for Hepatitis B disease, it shows the dynamics of the spread of the disease in a certain time span. Here are the main points:

1. Based on the numerical simulation results:

a. The *susceptible* population (S) decreases over time.

b. The *exposed* (E) and infected (I) populations increase at the beginning, then decrease.

c. The *recovered* population (R) increases over time.

This indicates that the disease spreads first before it is finally under control, as the number of cured individuals increases and the number of susceptible individuals decreases.

2. The result graph shows that the RKF45 method is able to provide a stable numerical solution to the system of differential equations of the *SEIR* model for Hepatitis B. Thus, the RKF45 method is proven to be effective.

Thus, RKF45 is proven to be effective for simulating the dynamics of Hepatitis B spread in the study area, as well as providing insight into how the disease develops and declines in the population.

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