

NUMERICAL SOLUTION OF THE SEIR MODEL USING THE FOURTH-ORDER RUNGE-KUTTA METHOD TO PREDICT THE SPREAD OF HEPATITIS B DISEASE IN AMBON CITY

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ABSTRACT

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Hepatitis B is a dangerous type of hepatitis and has a high risk of death. This research aims to predict the spread of Hepatitis B in Ambon using the fourth-order Runge-Kutta method. The mathematical model for the spread of Hepatitis B takes the form of a system of differential equations that includes the variables Susceptible (S) namely the subpopulation that is susceptible to infection with the hepatitis B virus, Exposed (E), namely the subpopulation that is exposed to the hepatitis B virus when it comes into contact with the Infected (I) subpopulation, I, namely the subpopulation infected with hepatitis B and Recovered (R), namely the recovered subpopulation. The values $b, \beta_1, \beta_2, \alpha_1, \alpha_2, \alpha_3, \mu_1$, and μ_2 are the parameter values used to be solved numerically using the fourth order Runge Kutta method which was carried out in 20 iterations with step size $h=1$ using data from the Maluku Provincial Health Service and the Central Bureau of Statistics from 2013 to 2022. Hepatitis B is classified as a type of hepatitis disease that is dangerous and has a high risk of death. This study aimed to construct a model of the spread of Hepatitis B disease in Ambon City and solve the model using the fourth-order Runge-Kutta method. In the research results, it was obtained that subpopulation (S) decreased significantly in the 20th year with a total of 299,239 people, for subpopulation (E) increased in 18th year with a total of 4,309 people, and decreased in 20th year with a total of 4,298 people, for subpopulation (I) subpopulation increased until 20th year with a total of 254 people, and for subpopulation (R) subpopulation increased significantly in 20th year with a total of 10,776 people.



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1. INTRODUCTION

To date, there are approximately seven types of hepatitis that have been discovered, namely Hepatitis A, Hepatitis B, Hepatitis C, Hepatitis D, Hepatitis E, Hepatitis G, and Hepatitis TTV (Transmission Transfusion Virus). Hepatitis B itself is an infectious disease caused by the Hepatitis B Virus (VHB) that can lead to hardening of the liver (liver cirrhosis) and can develop into liver cancer (hepatocellular carcinoma). Hepatitis is an infectious disease affecting morbidity, mortality, public health status, life expectancy, and other socioeconomic impacts [1], [2].

Based on the WHO (World Health Organization) report in 2013, 2 billion people worldwide suffer from hepatitis disease, 240 million people suffer from chronic hepatitis B disease, and 1.46 million of them experience death. The deaths of this disease are comparable to HIV deaths, which is 1.3 million deaths, tuberculosis 1.2 million deaths, and malaria 0.5 million deaths. However, hepatitis has not received serious attention like these three diseases [3]. One way to analyze the spread of viral hepatitis is through mathematical models. A mathematical model is a representation that uses mathematical symbols to study certain real-world systems or phenomena. Mathematical models can be of various kinds: equations, inequalities, and systems of linear and non-linear equations [4].

Previous research on the spread of Hepatitis B has been conducted, such as determining the numerical solution of the mathematical model of Hepatitis B disease in South Sulawesi Province using the fourth-order Runge-Kutta method with the SEIV (Susceptible Exposed Infected Vaccinated) model [5]. Furthermore, research on mathematical models for Hepatitis B disease using the SLAICRV (Susceptible, Latent, Acute Infections, Carrier, Recovered, and Vaccinated) model [6]. There is also research on the numerical solution of the SIR model on the spread of Hepatitis B disease with the Homotopy Perturbation Method [7]. These studies related to the spread of Hepatitis B. In addition, these studies used different methods, case studies, and data used are also different. In these studies, a fairly good numerical solution to the mathematical model of the spread of Hepatitis B disease was obtained.

The SIR model was first developed to determine the rate of spread and extinction of a disease outbreak in a closed and epidemic population. SEIR mathematical modeling is a development of the SIR Model. SIR and SEIR mathematical modeling can be used to detect and predict the spread of disease. Previous research related to the SIR and SEIR models has been carried out, such as analyzing the dynamics of the spread of COVID-19 with vaccination factors using the Fehlberg Runge-Kutta Method [8]. and research to model the spread of Tuberculosis disease [9]. In the research to analyze the stability of the Hepatitis A disease spread model [10], the SIR and SEIR models can model various diseases and obtain good results.

Based on the above considerations and considering previous research in Ambon City [11], this research was conducted to find numerical solutions to the spread of the Hepatitis B disease in Ambon City using the SEIR mathematical model. In particular, research on the numerical solution of the SEIR model for spreading Hepatitis B disease using the fourth-order Runge-Kutta method in Ambon City has never been done. Therefore, this research is fundamental to predicting the spread of Hepatitis B disease in the following years.

2. RESEARCH METHODS

This research uses a numerical data process to solve problems by first compiling concepts as needed regarding the SEIR model using the fourth-order Runge-Kutta method in the form of a system of differential equations. This study's secondary data source is from the Maluku Provincial Health Office and the Central Bureau of Statistics of Ambon City in 2017 - 2021. Researchers simulated the number of people with Hepatitis B disease in Ambon City. The research steps are as follows [12]:

1. Collecting and processing data
2. Constructing the SEIR model.
3. Solving the SEIR model using Fourth Order Runge-Kutta.
4. Numerical simulation using Matlab software

We are concluding the numerical solution of the SEIR model using fourth-order Runge-Kutta.

3. RESULTS AND DISCUSSION

3.1 Mathematical Model of Hepatitis B Disease Spread

The SEIR model of Hepatitis B disease spread described in this study consists of 4 subpopulation variables with the following assumptions:

- Closed population
- Susceptible sub populations (S) are susceptible individuals. Susceptible subpopulation (S) increases due to human births.
- Exposed sub populations (E) are exposed individuals. An individual is declared Exposed (E) if there is contact between a susceptible individual and an infected individual.
- Infected sub population (I) is an infected individual. An individual is declared Infected (I) if there is contact between an exposed individual and an infected individual.
- The Recovered subpopulation (R) is the recovered individuals. Infected individuals (I) can become a Recovered (R) because they have received medical treatment.
- Susceptible subpopulations (S) can become Infected individuals (I) due to sexual contact, shared syringe use, and mother-to-child (pregnant women).
- Exposed subpopulation (E) can become Recovered (R) due to strong immunity and treatment when individuals show symptoms.
- The Recovered subpopulation (R) subpopulation will not revert to Susceptible (S) because they have a high body capacity.

Based on these assumptions, the spread of Hepatitis B disease is schematically presented in a compartment chart, as shown in **Figure 1**.

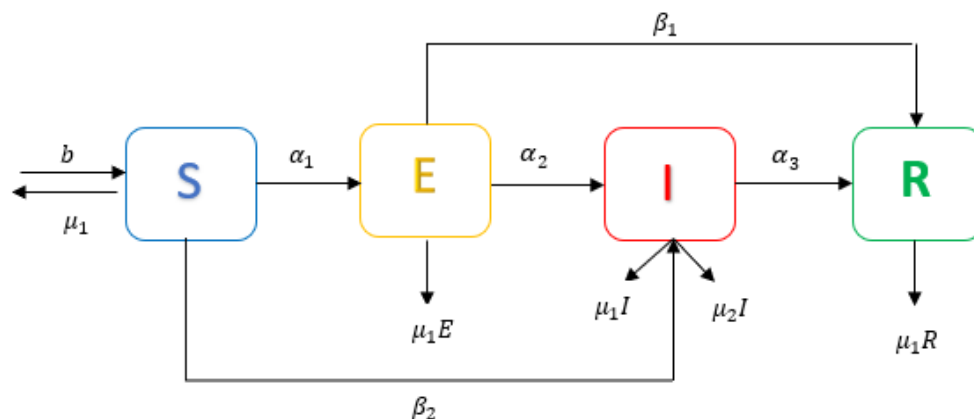


Figure 1. Compartment chart of SEIR model

Based on the compartment chart above, a Mathematical Model of the spread of Hepatitis B disease is formed, written in the form of differential equations as **Equation (1) - Equation (4)**.

$$\frac{dS}{dt} = b - (\alpha_1 + \beta_2 + \mu_1) S \quad (1)$$

$$\frac{dE}{dt} = \alpha_1 S - (\alpha_2 + \beta_1 + \mu_1) E \quad (2)$$

$$\frac{dI}{dt} = \beta_2 S + \alpha_2 E - (\alpha_3 + \mu_1 + \mu_2) I \quad (3)$$

$$\frac{dR}{dt} = \beta_1 E + \alpha_3 I - \mu_1 R \quad (4)$$

with:

- S = Number of vulnerable subpopulations
- E = Number of exposed subpopulations
- I = Number of infected subpopulations
- R = Number of recovered subpopulations
- b = Birth rate
- β_1 = The 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 = The recovery rate from individual I to individual R
- μ_1 = Natural mortality rate
- μ_2 = Hepatitis B disease mortality rate

3.2 Solving the SEIR Model using the Fourth Order Runge-Kutta Method

The Fourth Order Runge-Kutta Method provides high accuracy for solving ODEs. It is a fourth-order method, meaning the error per step is on the order of $O(h^5)$ where h is the step size. This high accuracy allows for reliable and precise solutions. The Fourth Order Runge-Kutta Method is known for its numerical stability. It is suitable for solving stiff differential equations where other methods might fail or require extremely small step sizes. Based on the System of Equations in Equations (1) to (4), it is solved using the fourth-order Runge-Kutta method like in this equation, $y_{k+1} = y_k + \frac{h}{6}(k_1 + 2k_2 + 2k_3 + k_4)$. The Hepatitis B disease spread model to be solved is already a system of equations, so there is no need to change it. The system of equations consisting of **Equation (1)**-**Equation (4)** is substituted into the fourth-order Runge-Kutta equation to obtain **Equation (5)**-**Equation (8)**.

$$S_{0+1} = S_0 + \frac{1}{6}(f_{1S} + 2f_{2S} + 2f_{3S} + f_{4S}) \quad (5)$$

$$E_{0+1} = E_0 + \frac{1}{6}(f_{1E} + 2f_{2E} + 2f_{3E} + f_{4E}) \quad (6)$$

$$I_{0+1} = I_0 + \frac{1}{6}(f_{1I} + 2f_{2I} + 2f_{3I} + f_{4I}) \quad (7)$$

$$R_{0+1} = R_0 + \frac{1}{6}(f_{1R} + 2f_{2R} + 2f_{3R} + f_{4R}) \quad (8)$$

with:

$$f_{1S} = b - (\alpha_1 + \beta_2 + \mu_1) S_i$$

$$f_{1E} = \alpha_1 S_i - (\alpha_2 + \beta_1 + \mu_1) E_i$$

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

$$f_{1R} = \beta_1 E_i + \alpha_3 I_i - \mu_1 R_i$$

$$f_{2S} = b - (\alpha_1 + \beta_2 + \mu_1) \left(S_i + \frac{h}{2} f_{1S} \right)$$

$$f_{2E} = \alpha_1 \left(S_i + \frac{h}{2} f_{1E} \right) - (\alpha_2 + \beta_1 + \mu_1) \left(E_i + \frac{h}{2} f_{1E} \right)$$

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

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

$$f_{3S} = b - (\alpha_1 + \beta_2 + \mu_1) \left(S_i + \frac{h}{2} f_{2S} \right)$$

$$f_{3E} = \alpha_1 \left(S_i + \frac{h}{2} f_{2E} \right) - (\alpha_2 + \beta_1 + \mu_1) \left(E_i + \frac{h}{2} f_{2E} \right)$$

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

$$\begin{aligned}
 f_{3R} &= \beta_1 \left(E_i + \frac{h}{2} f_{2R} \right) + \alpha_3 \left(I_i + \frac{h}{2} f_{2R} \right) - \mu_1 \left(R_i + \frac{h}{2} f_{2R} \right) \\
 f_{4S} &= b - (\alpha_1 + \beta_2 + \mu_1) (S_i + f_{3S}h) \\
 f_{4E} &= \alpha_1 (S_i + f_{3S}h) - (\alpha_2 + \beta_1 + \mu_1)(E_i + f_{3E}h) \\
 f_{4I} &= \beta_2 (S_i + f_{3S}h) + \alpha_2 (E_i + f_{3E}h) - (\alpha_3 + \mu_1 + \mu_2)(I_i + f_{3I}h) \\
 f_{4R} &= \beta_1 (E_i + f_{3E}h) + \alpha_3 (I_i + f_{3I}h) - \mu_1 (R_i + f_{3R}h)
 \end{aligned}$$

3.3 Numerical Model Simulation using the Fourth Order Runge-Kutta Method.

The SEIR model was simulated using the fourth-order Runge-Kutta method. This simulation was done by substituting the initial value in the form of secondary data and parameter values that have been determined. The following data used in the simulation is presented in the form of the following **Table 1**.

Table 1. Hepatitis B disease distribution data

s	Variables				
	N	S	E	I	R
2017	444.797	444.225	536	18	18
2018	443.055	442.335	642	39	39
2019	478.616	477.972	592	26	26
2020	347.288	346.434	768	43	43
2021	347.644	346.599	927	59	59
Total	2.061.400	2.057.565	3.465	185	185
Average	412.280	411.513	693	37	37

(Source: Central Bureau of Statistics of Ambon City and Maluku Provincial Health Office) [13], [14], [15], [16], [17]

Based on data obtained at the Central Bureau of Statistics of Ambon City and the Maluku Provincial Health Office in 2017-2021, it is known that the average subpopulation S (Susceptible) is 411,513 people, subpopulation E (Exposed) is 693 people, subpopulation I (Infected) is 37 people and subpopulation R (Recovered) is 37 people. Therefore, the initial value is obtained as in **Table 2**.

Table 2. Initial value

Variables	Value	Description
S_i	411.513	Data on the average number of human subpopulations susceptible to Hepatitis B disease at the Central Bureau of Statistics of Ambon City
E_i	693	Average data on the number of human subpopulations exposed to Hepatitis B disease at the Maluku Provincial Health Office
I_i	37	Average data on the number of human subpopulations that have been infected with Hepatitis B disease at the Maluku Provincial Health Office
R_i	37	Data on the average number of human subpopulations that recovered after being infected with Hepatitis B disease at the Maluku Provincial Health Office

The birth rate can be calculated based on the baby birth rate of Ambon City 2021. According to data from the Central Bureau of Statistics of Ambon City in 2021, the number of infants born was 5,293. Thus, the birth rate is [18]

$$\begin{aligned}
 b &= \frac{\text{Number of infant births}}{\text{Resident Population}} \\
 &= \frac{5.293}{412.280} \\
 &= 0,01284
 \end{aligned}$$

The natural death rate of individuals can be calculated based on the life expectancy of the people of Ambon City. According to data from the Central Bureau of Statistics of Ambon City in 2021, the life expectancy of Ambon City is 70.63 years [19]. Thus, the natural death rate of individuals in Ambon City is [20]:

$$\begin{aligned}\mu_1 &= \frac{1}{\text{life expectancy rate}} \\ &= \frac{1}{70.63 \text{ years}} \\ &= 0.01416 \text{ year}\end{aligned}$$

Meanwhile, the death rate due to Hepatitis B infection is calculated based on data on patients who died from Hepatitis B infection. Based on the data obtained, it is known that the number of patients who died from Hepatitis B infection is 0 per year. Thus, the individual death rate in Ambon City due to Hepatitis B infection is:

$$\begin{aligned}\mu_2 &= \frac{\text{Number of patients who died of infection}}{\text{average number of infected patients}} \\ &= \frac{0}{37} \\ &= 0.00000\end{aligned}$$

From the data in **Table 1** and **Table 2**, it can be obtained the parameter values of β_1 , β_2 , α_1 , α_2 , and α_3 as follows:

$$\begin{aligned}\beta_1(t) &= \frac{R}{E} = \frac{37}{693} = 0.05339 \\ \beta_2(t) &= \frac{I}{E} = \frac{37}{693} = 0.00009 \\ \alpha_1(t) &= \frac{N}{E} = \frac{412.280}{693} = 0.00168 \\ \alpha_2(t) &= \frac{N}{I} = \frac{412.280}{37} = 0.05339 \\ \alpha_3(t) &= \frac{R}{I} = \frac{693}{37} = 1\end{aligned}$$

The parameter values are then presented in **Table 3** below.

Table 3. Parameter values

Parameters	Definition	Value
b	Individual birth rate	0.01284
β_1	The recovery rate of individual E to the individual R	0.05339
β_2	The transmission rate of individual S to the individual I	0.00009
α_1	The transmission rate of individual S to the individual E	0.00168
α_2	The transmission rate of individual E to the individual I	0.05339
α_3	The recovery rate of individual I to the individual R	1
μ_1	The natural mortality rate of individuals	0.01416
μ_2	Hepatitis B disease mortality rate	0

The total human population (N) in Ambon City in 2017-2021 is 2,061,400 people (Central Bureau of Statistics). The simulation was carried out by substituting the initial values and parameter values in **Table 2** and **Table 3** into **Equation (5) - Equation (8)**, which are numerical solutions to the Hepatitis B disease model using the fourth-order Runge-Kutta method and will then be simulated using the Matlab application.

The step size used was $h = 1$. Furthermore, given $S_i = S_0, E_i = E_0, I_i = I_0, R_i = R_0$ as the initial value that the numerical solution results of the Hepatitis B disease model using the fourth-order Runge-Kutta method as in **Equation (5) to Equation (8)** are obtained. Then, by substituting the value of f_{1S} to f_{4S}, f_{1E} to f_{4E}, f_{1I} until f_{4I} , and f_{1R} until f_{4R} into **Equation (5) - Equation (8)**, the numerical solution of the Hepatitis B disease spread model using the Fourth Order Runge-Kutta method is obtained as follows:

$$\begin{aligned}
S_{0+1} &= S_0 + \frac{1}{6}(f_{1S} + 2f_{2S} + 2f_{3S} + f_{4S}) \\
S_1 &= 411.513 + \frac{1}{6}(-6,555.38925 + 2(-6,503.17557) + 2(-6,503.59146) \\
&\quad - (6,451.78704)) \\
S_1 &= 405,009.54827 \\
E_{0+1} &= E_0 + \frac{1}{6}(f_{1E} + 2f_{2E} + 2f_{3E} + f_{4E}) \\
E_1 &= 693 + \frac{1}{6}(607.53042 + 2(571.30338) + 2(573.46360) + 539.13915) \\
E_1 &= 1,265.70059 \\
I_{0+1} &= I_0 + \frac{1}{6}(f_{1I} + 2f_{2I} + 2f_{3I} + f_{4I}) \\
I_1 &= 37 + \frac{1}{6}(36.51152 + 2(18.97358) + 2(27.39775) + 10.19105) \\
I_1 &= 60.24087 \\
R_{0+1} &= R_0 + \frac{1}{6}(f_{1R} + 2f_{2R} + 2f_{3R} + f_{4R}) \\
R_1 &= 37 + \frac{1}{6}(73.47535 + 2(111.65424) + 2(131.49257) + 210.12637) \\
R_1 &= 165.31589
\end{aligned}$$

time $t = 1$ year was obtained (S) = 405.009, (E) = 1.266, (I) = 60 and (R) = 165. Then, the same thing was done for the next iteration with S_i, E_i, I_i, R_i where $i = 1, 2, 3, \dots$, so forth, as the initial value.

The iteration of the numerical solution of the Hepatitis B disease spread model used the Fourth Order Runge-Kutta method up to $t = 20$ years using Matlab Software. The iteration results for the number of vulnerable individual classes (S) are shown in the graph in **Figure 2**.

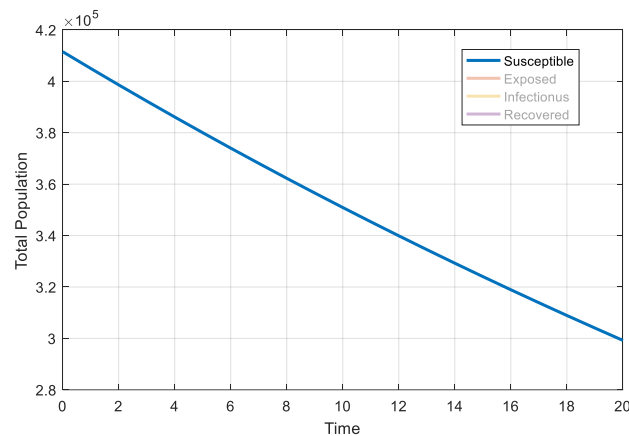


Figure 2. Graph of the number of susceptible individual classes (S)

Based on **Figure 2**, it can be seen that the prediction of the number of susceptible individual classes (S) decreased significantly in 20th year, with a total of 299,239 people. Furthermore, the iteration results for the number of exposed individual classes (E) are shown in **Figure 3**.

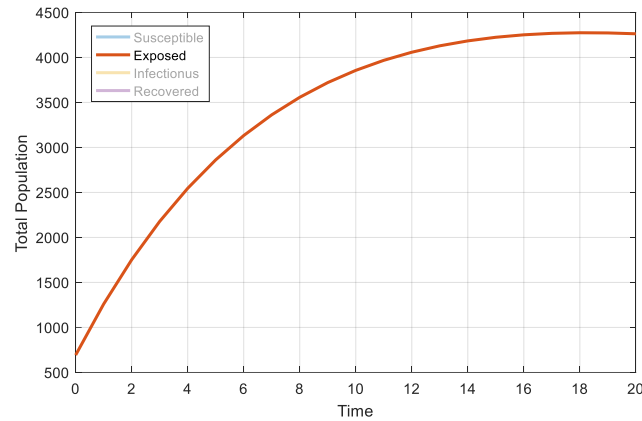


Figure 3. Graph of the number of exposed individuals (E)

Based on **Figure 3**, it can be seen that the prediction of the number of exposed individual classes (E) has increased in 18th year with a total of 4,309 people and has decreased in 20th year with a total of 4,298 people. Furthermore, the iteration results for the number of infected individual classes (I) are shown in **Figure 4**.

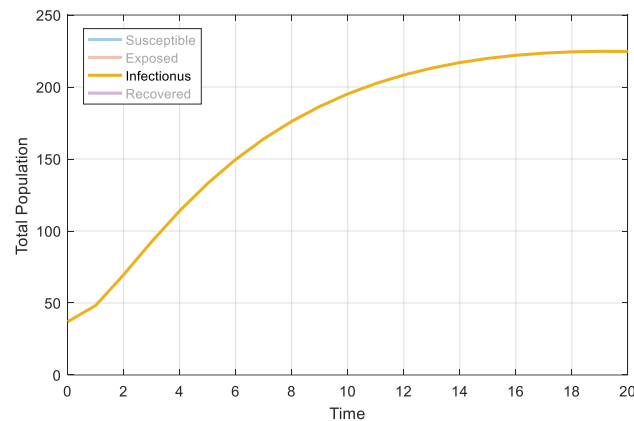


Figure 4. Graph of the number of classes of infected individuals (I)

Based on **Figure 4**, it can be seen that the prediction of the number of infected individual classes (I) has increased in the 20th year with 254 people. Furthermore, the iteration results for the number of recovered individuals (R) are shown in **Figure 5**.

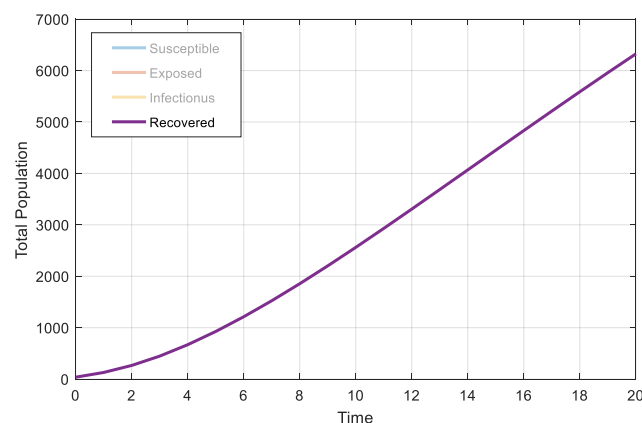


Figure 5. Classes number graph of recovered individuals (R)

Based on **Figure 5**, it can be seen that the prediction of the number of recovered individual classes (R) has increased significantly in 20th year with a total of 10,776 people. Furthermore, the results of iteration $t = 1$ to $t = 20$ are displayed in **Table 4**.

Table 4. Calculation results using Matlab software

Time (t) Year	Sub Population			
	S	E	I	R
0	411.513	693	37	37
1	405.009	1.266	60	165
2	398.609	1.763	87	384
3	392.309	2.193	114	692
4	386.109	2.564	137	1.078
5	380.007	2.883	158	1.530
6	374.002	3.156	176	2.037
7	368.091	3.389	191	2.588
8	362.274	3.585	204	3.174
9	356.549	3.750	215	3.786
10	350.914	3.888	224	4.417
11	345.368	4.000	232	5.062
12	339.910	4.091	238	5.714
13	334.538	4.163	243	6.369
14	329.251	4.218	247	7.024
15	324.048	4.259	250	7.675
16	318.927	4.286	252	8.318
17	313.886	4.303	253	8.952
18	308.926	4.309	254	9.574
19	304.044	4.307	254	10.182
20	299.239	4.298	254	10.776

Based on **Table 4.** we can see that the predicted rate of susceptible individuals classes (S) decreased every year, and in 20th year, with a total 299,239 people, the predicted rate of exposed individuals classes (E), infected individuals classes (I), and recovered individuals classes (R) are increased every year except exposed individuals classes has decreased in 20th year.

4. CONCLUSION

The subpopulation of susceptible individuals (S) saw a significant decrease until the 20th year of 299,239 people, the subpopulation of exposed individuals (E) saw an increase in the 18th year of 4,309 people and a decrease in the 20th year of 4,298 people, the subpopulation of infected individuals (I) saw an increase until the 20th year of 254 people, and the subpopulation of recovered individuals (R) saw a significant increase until the 20th year of 10,776 people. These predictions were made using Matlab software.

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