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Solving Cholera Infection Model Using Runge-Kutta Fourth Order Method

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Abstract: In this study, Runge-Kutta fourth order method (RK4) is used to simulate the spread of cholera in a population. This cholera infection models were solved by using RK4 and the results obtained were compared between two different step sizes: 0.1 and 0.01. The results showed that the choice of step size has a significant impact on the accuracy and computation time of the model. A smaller step size increases the accuracy of the solution but prolongs the computation time, while a larger step size decreases the accuracy but reduces the computation time. We found that a balance needs to be struck between the need for accuracy and the need for computational efficiency when choosing the step size for RK4 method. Our model also showed that as the time progress, the susceptible individuals decrease, vaccinated individuals increase, infectious individuals decrease, concentration of toxigenic vibrio cholerae decrease, and recovery individuals increase. Our study highlights the importance of considering the specific research goals and computational resources when solving a cholera infection model using RK4. Additionally, the model's assumptions and simplifications, data availability, and ethical implications should be taken into account when interpreting the results.

Keywords: Runge-Kutta Fourth Order, Cholera Infection Model

1. Introduction

Aside from war, starvation, and natural calamities, one of the most difficult concerns for the survival of the human population is the spread of infectious illness throughout the planet. Cholera is one of the infectious diseases spread by unclean water and caused by a bacterium named Vibrio cholerae. The cholera epidemic is a life-threatening waterborne disease that causes diarrhoea, dehydration, and vomiting. Cholera is spread through consuming contaminated drinks and food, coming into contact with a cholera patient's faeces, and coming into contact with vomit and a bacterium-killed body without employing protective agents. Mild signs of infection include severe watery diarrhoea, vomiting, leg cramps, low blood pressure, kidney failure, and if left untreated, fast dehydration, acidosis, circulatory

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collapse, and death within 12-24 hours [1]. Every year, an estimated 3 to 5 million people contract cholera, with 100 000 to 120 000 people dying as a result [2].

1.1 Cholera Infection Model

Many research in cholera studied the symptoms, transmission, and treatment of cholera, as well as various models and strategies for controlling its spread. The researchers also discussed the impact of vaccination and control strategies on cholera transmission. For example, [3] proposed a cholera transmission model assuming that an individual can only be infected if they consumed contaminated water. This model emphasized that cholera outbreaks can occur when people consume tainted water, and highlighted the importance of clean water sources in preventing the spread of the disease. [4] discussed the stability of different equilibria in a cholera infection model with vaccination strategy. This study provided insight into how vaccination can be used to control and prevent cholera outbreaks.

[5] and [6] studied the control action to prevent cholera transmission amongst humans and the coinfection of Buruli and cholera. The research recommended that in order to effectively control cholera, both increased awareness and improved sanitation should be taken into account and minimize the Buruli ulcer, cholera infection and its dual infections, respectively. [7] investigated the impact of mass vaccination on cholera transmission and discussed the effectiveness of mass vaccination and its ability to stop transmission and eliminate cholera disease.

1.2 Ordinary differential equation

Ordinary differential equation (ODE) is a differential equation with ordinary derivatives. An ODE expresses a relation between an independent variable, a dependent variable and one or more coefficient of the dependent variable with respects to the independent variable. There are two ways to solve ordinary differential equations which is by analytical method and by numerical method. Analytical solutions provide a precise formula for determining the function's value at any desired point, while numerical solutions offer an estimate of the function's value at a specific point [8]. However, the advantage of numerical method is the solution can be obtained for any difficult problems, even though the analytical solution does not exist. Hence, this study considers numerical method for solving cholera model.

Due to increasing in the number of cholera patients all over the world, Runge-Kutta fourth order (RK4) method is used in running the analysis. RK4 techniques are a class of iterative methods for solving ordinary differential equations in the context of initial value problems (IVP). RK4 method is used since higher order derivatives of variables are not required. Other than that, while RK4 method is a one-step method that only uses the value at the previous time point for computation and can be used under initial conditions, it is more precise than other methods.

The first objective of this study is to examine a mathematical formulation for the cholera infection problem that is applicable for numerical analysis. Next objectives are to solve the cholera infection model by RK4 method and to validate the results with existing results in [4].

2. Materials and Methods

The RK4 method is used to solve the system of first order ODE which is the cholera infection model.

2.1 Cholera Infection Model

Given the cholera infection model [4]

$$\dot{S} = A - \phi S(t) - \frac{\beta S(t) B(t)}{K + B(t)} - \mu S(t) + \eta V(t)$$

$$\dot{V} = \phi S(t) - \frac{\sigma\beta S(t) B(t)}{K + B(t)} - (\mu + \eta) V(t)$$

$$\dot{I} = \frac{\beta S(t) B(t)}{K + B(t)} + \frac{\sigma\beta V(t) B(t)}{K + B(t)} - (\mu + \gamma + d) I(t) \qquad \text{Eq 1}$$

$$\dot{B} = \xi I(t) - \delta B(t)$$

$$\dot{R} = \gamma I(t) - \mu R(t)$$

where $S(t)$, $V(t)$, $I(t)$, and $R(t)$ represent the number of individuals who are susceptible, vaccinated, infected, and recovered at time t respectively, and $B(t)$ is the level of toxic Vibrio cholerae bacteria in the water.

2.2 Runge-Kutta fourth order Method

The Runge-Kutta method, created by German mathematicians Carl Runge and Martin Kutta, is a popular technique for solving ordinary differential equations because of its accuracy and simplicity to use. This method was developed as an alternative to the Taylor series approach, which can be inefficient and difficult to compute due to the need for derivatives. The Runge-Kutta method addresses this issue by carefully selecting a small step size to achieve a high level of precision. While it is possible to derive Runge-Kutta methods of any order, those of higher order can be challenging to derive.

In this method, four approximations of the slope will be used. To estimate the slope at some time t, the following slope approximations will be considered during calculations.

$$\begin{aligned} K_1 &= f\left(y^*(t_i), t_i\right) \\ K_2 &= f\left(y^*(t_i) + K_1 \frac{h}{2}, t_i + \frac{h}{2}\right) \\ K_3 &= f\left(y^*(t_i) + K_2 \frac{h}{2}, t_i + \frac{h}{2}\right) \\ K_4 &= f\left(y^*(t_i) + K_3, t_i + h\right) \end{aligned} \qquad \text{Eq. 2}$$

where K_1 is the slope at the beginning of the time, K_2 is an estimate of the slope at midpoint if the slope K_1 is halfway through the time step, K_3 is another estimate at midpoint if K_2 step halfway through the time step and K_4 is an estimate of slope at the endpoint if K_3 is used to step all the way across the time step.

A weighted sum of these slopes is used to get the final estimation of $y^*(t_i + h)$ as follows:

$$y^*(t_i + h) = y^*(t_i) + \frac{K_1 + 2K_2 + 2K_2 + K_4}{6} h$$

$$= y^*(t_i) + \left(\frac{1}{6}K_1 + \frac{1}{3}K_2 + \frac{1}{3}K_3 + \frac{1}{6}K_4\right) h$$

$$= y^*(t_i) + mh \qquad \text{Eq. 3}$$

where m is a weighted average slope of approximation and h is the step size.

3. Results and Discussion

The results of solving cholera infection model with initial conditions were discussed. This problem is solved numerically using RK4 method. The result of RK4 method is tested using two different step sizes, $h = 0.1$ and $h = 0.01$ to determine the correct step size in order to achieve the accuracy of RK4 method. $h = 0.1$ and $h = 0.01$ are selected to easily differentiate the results obtained.

3.1 Test Problem

Cholera infection model, *Eq 1* will be considered with the parameter values as shown in Table 1 referred from [4]. Hence, the initial condition for *Eq 1* takes the form of $S(0) = 200, V(0) = 300, I(0) = 200, B(0) = 30000$ and $R(0) = 3000$ from [4].

Thus, substituting the parameter values into *Eq 1* resulting in *Eq 4*.

Table 1: Parameter values for cholera infection model

Parameter	Symbol	Values
Rate of newborns birth	A	0.1/day
Rate of vaccination	ϕ	0.01/day
Rate of environment-to-human transmission	β	0.2143/day
Vibrio Cholerae in environment concentration	K	10^6 cells/ml
Rate of waning of vaccine	η	0.005/day
Rate of natural human death	μ	5.48×10^{-5}/day
Vaccine efficacy reduction	σ	10%
Rate of recovery	γ	0.004/day
Rate of cholera-related death	d	0.015/day
Human contribution to Vibrio Cholerae rate	ξ	20 cells/ml-per day
Rate of death of the Vibrios	δ	0.33/day

$$\begin{aligned}
\dot{S} &= 0.1 - 0.01S(t) - \frac{0.2143\,S(t)\,B(t)}{10^6 + B(t)} - 5.48\times 10^{-5}S(t) + 0.005V(t)\\
\dot{V} &= 0.01S(t) - \frac{0.02143\,V(t)\,B(t)}{10^6 + B(t)} - \left(5.0548\times 10^{-3}\right)V(t)\\
\dot{I} &= \frac{0.2143\,S(t)\,B(t)}{10^6 + B(t)} + \frac{0.02143\,V(t)\,B(t)}{10^6 + B(t)} - \left(1.9055\times 10^{-2}\right)I(t)\\
\dot{B} &= 20I(t) - 0.33B(t)\\
\dot{R} &= 0.004I(t) - 5.48\times 10^{-5}R(t)
\end{aligned} \qquad \text{Eq. 4}$$

3.2 Results

The RK4 in *Eq 2* and *Eq 3* is used to find the numerical results for the cholera infection model. The results are calculated using MATLAB software. The performance of the RK4 method is shown in tables 2 through 6, each of which displays the number of susceptible individuals, vaccinated individuals, infected individuals, the concentration of toxic Vibrio cholerae, and the number of recovered individuals over time, for two step sizes, $h = 0.1$ and $h = 0.01$.

Table 2: Susceptible individuals over time t (day) for $h = 0.1$ and $h = 0.01$

t	$h = 0.1$	$h = 0.01$
0	200	200
1	198.6010	198.4705
2	197.5331	197.1520
3	196.5977	195.9854
4	195.7227	194.9299
5	194.8820	193.9567
6	194.0659	193.0463
7	193.2707	192.1847
8	192.4949	191.3624
9	191.7374	190.5725
10	190.9979	189.8102
11	190.2757	189.0722
12	189.5704	188.3558
13	188.8818	187.6593
14	188.1430	186.9814
15	187.5527	186.3209

Table 3: Vaccinated individuals over time t (day) for $h = 0.1$ and $h = 0.01$

t	$h = 0.1$	$h = 0.01$
0	300	300
1	300.3262	300.3052
2	300.6855	300.6229
3	301.0507	300.9467
4	301.4121	301.2720
5	301.8014	301.5985
6	302.1125	301.9161
7	302.4501	302.2314
8	302.7793	302.5409
9	303.1003	302.8439
10	303.4132	303.1402
11	303.7182	303.4296
12	304.0156	303.7149
13	304.3055	303.9875
14	304.5882	304.2561
15	304.8637	304.5179

Table 4: Infectious individuals over time t (day) for $h = 0.1$ and $h = 0.01$

t	$h = 0.1$	$h = 0.01$
0	200	200
1	197.3589	197.5094
2	194.4074	194.8445
3	191.3748	192.0736
4	188.3434	189.2436
5	185.3424	186.3869
6	182.3817	183.5257
7	179.4647	180.6750
8	176.5920	177.8450

9	173.7634	175.0428
10	170.9785	172.2727
11	168.2368	169.5379
12	165.5276	166.8401
13	162.8804	164.1804
14	160.2646	161.5335
15	157.6895	158.9775

Table 5: Concentration of toxigenic Vibrio cholerae over time t (day) for $h = 0.1$ and $h = 0.01$

t	$h = 0.1$	$h = 0.01$
0	30000	30000
1	18498.8965	24504.2675
2	14252.1031	20642.4812
3	12607.9780	17912.0442
4	11898.8063	15965.0442
5	11526.6672	14561.4357
6	11277.1733	13534.2158
7	11073.4386	12768.3878
8	10887.8729	12184.2545
9	10710.5601	11726.6651
10	10537.9204	11357.4516
11	10368.6464	11050.1951
12	10202.2453	10786.6060
13	10038.5168	10554.0185
14	9877.3657	10343.6584
15	9718.7347	10149.4439

Table 6: Recovery individuals over time t (day) for $h = 0.1$ and $h = 0.01$

t	$h = 0.1$	$h = 0.01$
0	3000	3000
1	3000.6311	3000.6307
2	3001.2510	3001.2511
3	3001.8588	3001.8605
4	3002.4544	3002.4587
5	3003.0379	3003.0455
6	3003.6095	3003.6265
7	3004.1693	3004.1847
8	3004.7174	3004.7371
9	3005.2541	3005.2783
10	3005.7795	3005.8083
11	3006.2939	3006.3272
12	3006.7973	3006.8353
13	3007.2900	3007.3326
14	3007.7720	3007.8193
15	3008.2437	3008.2956

The results are graphically depicted in Figure 1 through Figure 5. Figure 1 shows the graph of susceptible individuals over time t while Figure 2 displayed the graph of vaccinated individuals over time t. Figure 3, 4 and 5 exhibit the graph of infectious individuals, concentration of toxigenic V. cholerae and recovery individuals, respectively, over time. Both results for step sizes are plotted in the graph.

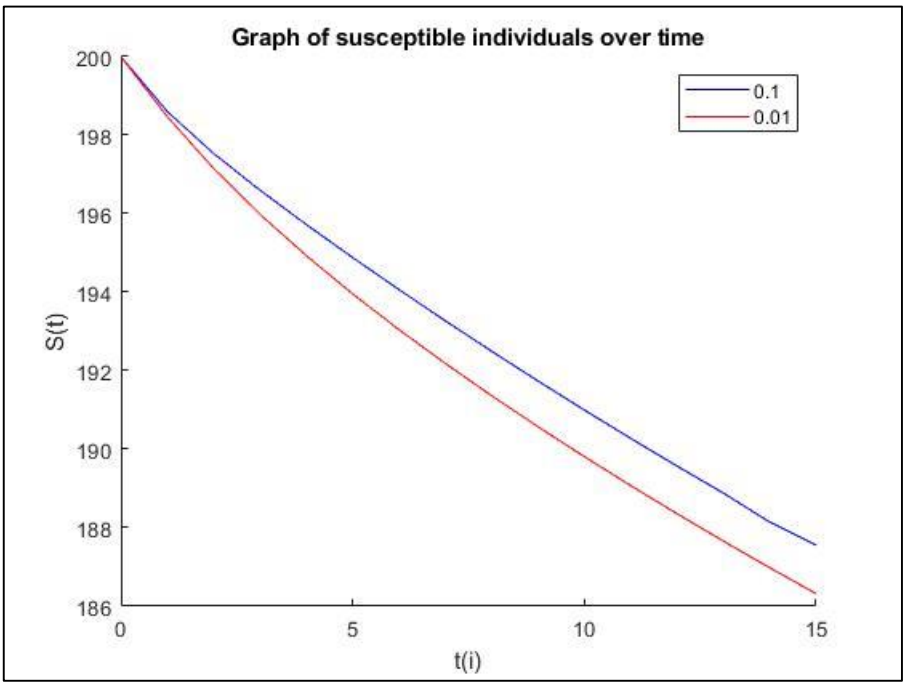

Figure 1: Susceptible individuals over time t (day) for $h = 0.1$ and $h = 0.01$

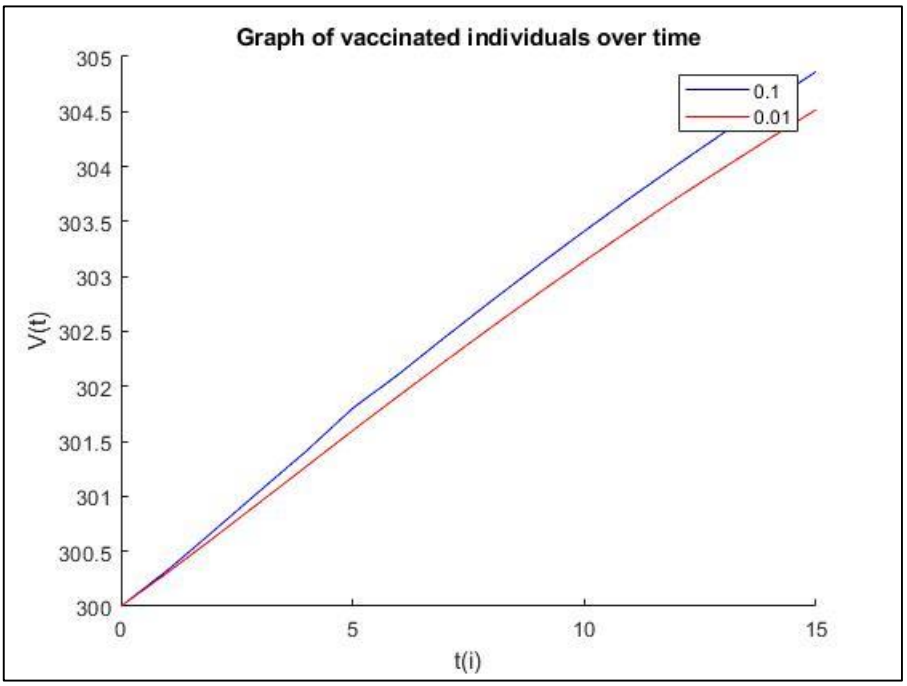

Figure 2: Vaccinated individuals over time t (day) for $h = 0.1$ and $h = 0.01$

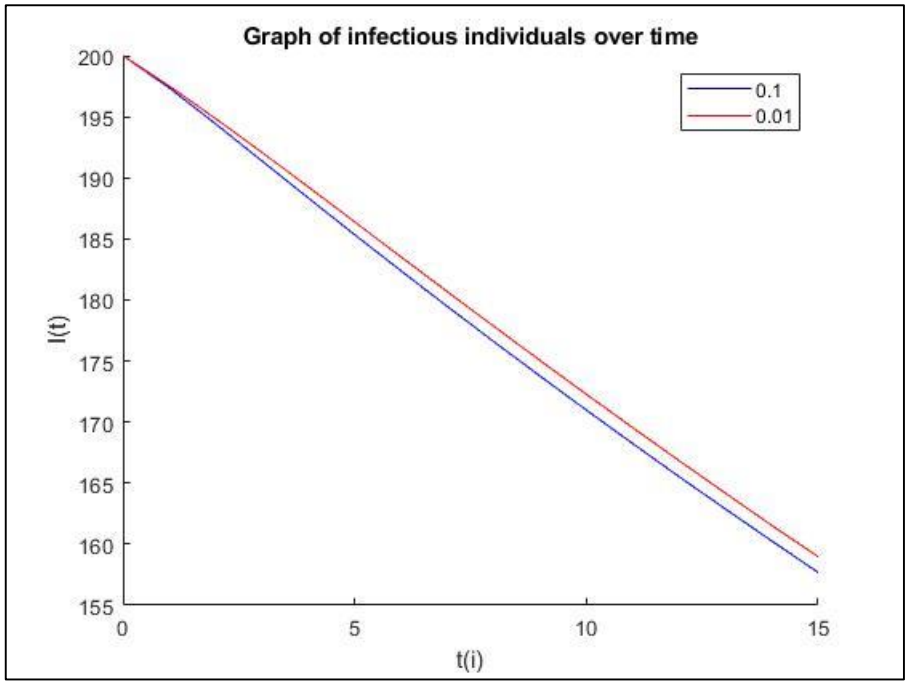

Figure 3: Infectious individuals over time t (day) for $h = 0.1$ and $h = 0.01$

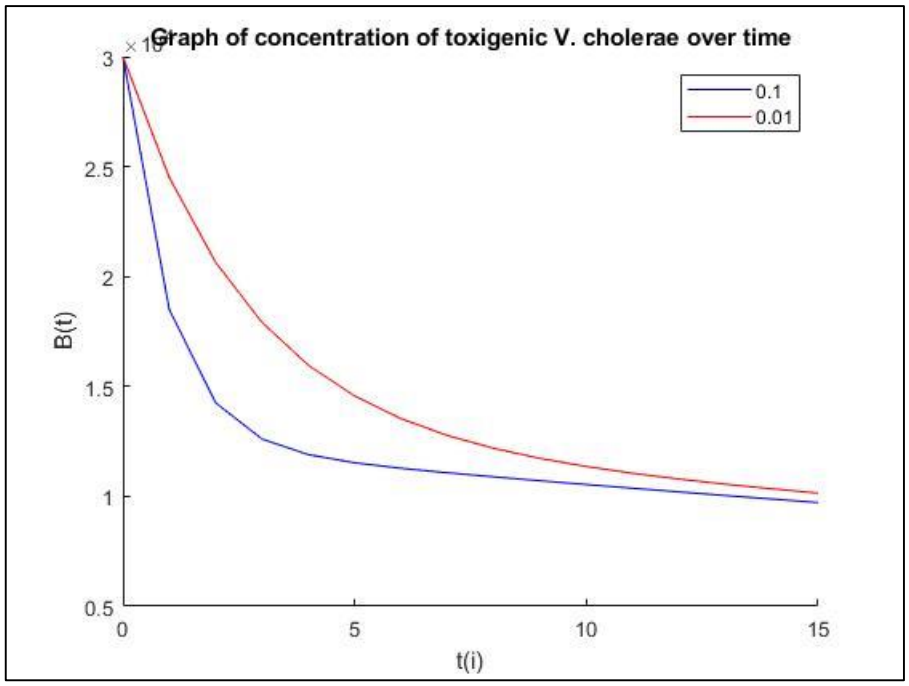

Figure 4: Concentration of toxigenic Vibrio cholerae over time t (day) for $h = 0.1$ and $h = 0.01$

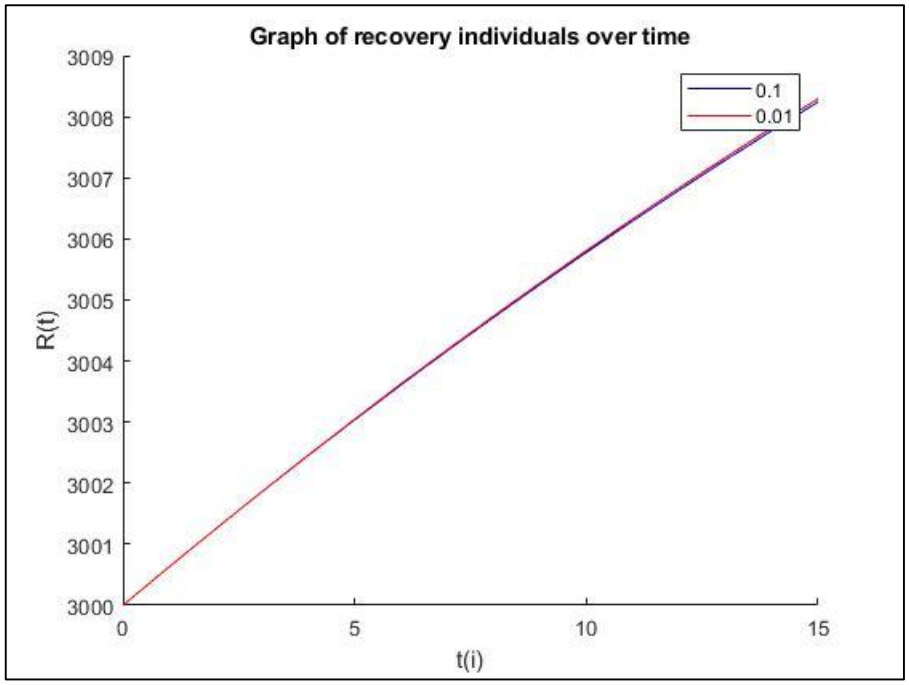

Figure 5: Recovery individuals over time t (day) for $h = 0.1$ and $h = 0.01$

4. Conclusion

The results has been compared with the solutions in [4]. The more accurate solutions are obtained using a smaller step size of 0.01. This is due to the ODE is being solved with a higher degree of precision. However, the computational time is longer, as more steps were required in order to reach the final solution. With larger step size of 0.1, the result is less accurate but the computational time is shorter compared to step size 0.01. The choice of step size is a trade-off between the accuracy of the solution and the computational time. In both cases, by looking at the graph, almost similar results were obtained. Susceptible individuals decrease as the vaccinated individuals increase. As the disease spread, some of the susceptible individuals will become infected and move to the infectious compartment resulting in a decrease in the number of susceptible individuals. Vaccination campaigns will increase the number of vaccinated individuals and significantly decrease the number of infectious individuals as some of them have recover or die. As the infected individuals recover or die, the concentration of toxigenic Vibrio cholerae decreases and the number of recovery individuals increases.

This research focus on solving the cholera infection model using RK4 method. As the result obtained, the susceptible individuals decrease, vaccinated individuals increase, infectious individuals decrease, the concentration of toxigenic Vibrio cholerae decrease and recovery individual increase. The choice of step size in RK4 method can have a significant impact on the accuracy and computation time when solving a cholera infection model. A smaller step size will result in a more accurate solution, but a longer computation time. A larger step size will result in a less accurate solution, but a shorter computation time. It is important to consider the specific requirements of the research and the available computational resources when choosing the step size for solving a cholera infection model using RK4. Additionally, the model's assumptions and simplifications also play a role in the dynamics of the different compartments, and the final values of these compartments will change accordingly. Overall, the cholera infection model is a valuable tool for understanding the spread of the disease and can be used to inform public health policies and interventions aimed at controlling and preventing the spread of cholera.

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