Stability Analysis and Numerical Simulation of Fractional Cholera Model

Sanaa L. Khalaf*

Department of Mathematics, College of science, University of Basrah, Basra, Iraq

*Corresponding author E-mail: sanaasanaa1978@yahoo.com

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ABSTRACT

The Vibrio cholera bacterium, which belongs to the Vibrionaceae family, is the source of the cholera virus. A bacterium known as Vibrio cholerae is the cause of the human disease cholera. This study developed a fractional epidemic model to describe the transmission of cholera. The model consists of four elements: susceptible people, infected people, recovered people, and a setting where the germs may flourish. The endemic and disease-free equilibrium points were calculated. The next-generation matrix was used in order to calculate the reproduction number. It has been proven that a disease-free equilibrium is capable of being locally asymptotically stable. To make sense of them and to compare them to the qualitative answers, numerical simulations of the fractional equations of the epidemic model were performed. According to the findings, the system's susceptible population decreases when more populations are restored. This study suggests that for outbreak and preventive initiatives, health professionals should make good use of the media.

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1. Introduction

Cholera is caused by a type of bacteria called Vibrio cholera. Cholera can be caught when a person eats or drinks something that has been contaminated with the virus that causes cholera, or when they drink water or drinks that have been contaminated with the virus [1]. People die quickly from diseases, especially if the outbreak isn't found in time and people don't get help right away. Children and women have been hurt the most by the cholera outbreak. The cholera outbreak is blamed for between 28,000 and 142,000 deaths each year, and it is thought that between 1.4 million and 4.3 million people get the disease each year around the world. The WHO report states this despite the fact that the actual number of cholera cases cannot be determined due to a lack of a defined monitoring system for various regions and a lack of methods to get comprehensive information through the surveillance system Moreover, According to WHO, Tanzania recorded 33,421 cases between August 2015 and January 2018, leading to 542 deaths. Around 86 percent of all cholera cases during this time period were on the mainland of Tanzania. It was also discovered that 11.4 percent of these cases involved children under five years of age and elderly people [2].

Furthermore, the next-generation matrix method was used to study cholera bacteriophage in the study by authors in [3]. Based on the analysis of the results, both the bacteriophage and the treatment decreased the number of cholera bacteria in the environment. M. Pascual et al. [1] investigated the dynamic behavior of a fractional order of cholera model in Ghana using a Codeco compartmental (SIR) basic model with an environmental component containing V. Cholera in the water supply. Ruth-Hurwitz stability conditions were used to investigate the disease's local stability.

In their investigation of cholera epidemics in Zimbabwe, C. J. Acosta et al. [4] focused on the disease's transmission mechanisms as well as how the environment influences it. Between 41 and 95 percent of the population got cholera as a result of this finding, and many of them recovered. [5] used epidemiological and environmental observations of cholera outbreaks as waterborne diseases to make a mathematical model. The main focus was on how cholera spreads and how bacteria and phage populations change over time. The results showed that the amount of phage in the reservoir was to blame for the rise in cholera outbreaks. With the help of other organizations, a lot has been achieved in the fight against the cholera epidemic [6]. The focus seemed to be on

cholera antibiotic treatment. First, contain the cause of cholera disease. Through initiative and support for a national cholera response plan, affected areas were able to calm the outbreak. This was a model for future public health efforts. According to some assessments, the main factor associated with the severe spread of infection in the region was a lack of safe water and sanitation, as well as adequate water treatment from water sources. Policymakers, epidemiologists, and public health modelers must collaborate to harmonize ideas. Similar cholera outbreak studies are underway in Tanzania, especially in Dar es Salaam, but rarely use modeling. Mathematical modeling of the physical systems of a humanly natural phenomenon is essential for engineering and health practitioners, with direct applications in health science and other fields. The use of fractional calculus theory in the mathematical modeling of biological systems has gotten a lot of attention in recent decades since it carries more memory information and provides a learning mechanism for the spread of disease in the population compared to the ordinary differential equation, which is incapable of this purpose [7-12]. Fractional differential equations and their applications have been studied and used extensively in chemistry, physics, biology, hydrology, medicine, engineering, and biochemistry [13-18].

The structure of this paper is as follows: In section 2, the necessary definitions of fractional derivatives are presented, also a review of some important properties and theorems for stability analysis. In Section 3, the fractional Cholera model is presented and shows that the model's solutions are bounded. In section 4, the infection equilibria points and checks into their stability are computed. The basic reproduction number is also calculated. Section 5 discusses the numerical results, and Section 6 summarizes the conclusions.

2. Fundamentals of fractional calculus

This part will present the definition of the Caputo fractional derivative as well as some important properties and theorems in the field of stability analysis.

Definition 2.1 [19] The right (left) Caputo fractional derivative of order $m-1<\alpha<m,\ m\in\mathbb{N}$ are defined as follows:

$$ {}_{t}^{C}D_{b}^{\alpha}x(t)=\frac{(-1)^{m}}{\Gamma(m-\alpha)}\int_{t}^{b}(\xi-t)^{m-\alpha-1}x^{(m)}(\xi)d\xi, \tag{1}$$

$$ {}_{a}^{C}D_{t}^{\alpha}x(t)=\frac{1}{\Gamma(m-\alpha)}\int_{a}^{t}(t-\xi)^{m-\alpha-1}x^{(m)}(\xi)d\xi. \tag{2}$$

Lemma 2.1 [20] Suppose that the Caputo fractional differential equation is as follows:

$$\begin{cases} {}_{a}^{C}D_{t}^{\alpha}y(t)=g(t,y(t)) \\ y(t_0)=y_0 \end{cases} \tag{3}$$

with $0<\alpha\leq 1$. The Caputo fractional differential equation (3) has equilibrium point y^* if $g(t,y^*)=0$.

Theorem 2.1 [21] The Caputo fractional differential equation (3) is locally asymptotically stable If all the eigenvalues λ of the Jacobian matrix of Eq. (3) satisfy the following condition.

$$|\arg(\lambda)|>\frac{\alpha\pi}{2} \tag{4}$$

Definition 2.2 [22] The Laplace transform $\mathrm{F}(s)$ of the Caputo derivative of the function $\mathrm{F}(t)$ is defined as follows:

$$L\{{}_{a}^{C}D_{t}^{\alpha}F(t),s\}=s^{\alpha}F(s)-\sum_{i=0}^{m-1}s^{\alpha-i-1}F^{(i)}(0)\ ,\quad \alpha\in(m-1,m),\ m\in\mathbb{N} \tag{5}$$

Definition 2.3 [22] The function $E_{\mathrm{r,n}}(t)$ for $t\in\mathbb{R}$ is defined by

$$E_{\mathrm{r,n}}(t)=\sum_{i=0}^{\infty}\frac{t^{i}}{\Gamma(\mathrm{r}\,i+n)}\quad ,\qquad r,\mathrm{n}>0 \tag{6}$$

Where $E_{\mathrm{r,n}}(t)$ is called the generalized Mittag-Leffler function and satisfies

$$1-\ E_{r,n}(t)=\frac{1}{\Gamma(n)}+t\,E_{r,r+n}(t)\ ,\qquad n,r>0 \tag{7}$$

$$2-\ L\{t^{n-1}E_{r,n}(\pm\beta t^{r})\}=\frac{s^{r-n}}{s^{r}\mp\beta} \tag{8}$$

Where L is the Laplace transform of $E_{r,n}(t)$.

3. Fractional Cholera model description and formulation

The model divides the total human population in the system at any time t into four subpopulations based on their disease status. The total population is represented by $N(t)$, which is further subdivided into susceptible humans S, infected humans I, the recovered vector R, and the environment V. The total population is calculated as $N(t) = S(t) + I(t) + R(t)$. Where S: population at risk of Cholera infection, I: population with Cholera symptoms, R: recovered patients with temporary immunity.

In a system of fractional differential equations, the fractional Cholera model is written as follows:

$$\begin{aligned} {}_0^C D_t^\alpha S &= \Omega^\alpha - \rho^\alpha SI - \mu^\alpha S + \eta^\alpha V + \gamma^\alpha R \\ {}_0^C D_t^\alpha I &= \rho^\alpha SI - \mu^\alpha I - \omega^\alpha I - \sigma^\alpha I - \beta^\alpha I \\ {}_0^C D_t^\alpha R &= \beta^\alpha I - \mu^\alpha R - \gamma^\alpha R \\ {}_0^C D_t^\alpha V &= \sigma^\alpha I - \eta^\alpha V \end{aligned} \tag{9}$$

In system (9) of the fractional Cholera model, all parameters are non-negative constants. Table 1 describes the parameters of the fractional Cholera model.

Parameter	Description
Ω	The rate at which susceptible humans are recruited.
ρ	The rate of contact with infectious humans.
μ	The rate of natural death.
η	The rate of infection humans with the bacteria.
γ	The rate of loosed immunity of recovered humans and return to the susceptible compartment.
ω	The cholera infection death rate.
σ	The rate of infectious human contamination.
β	The rate of individuals recover from the disease.

Table 1: parameters used in fractional Cholera model and their meaning

Theorem 3.1 The regionthe fractional Cholera model for $\Psi = \{(S,I,R) \in \mathbf{R}^{+3} : S \geq 0, I \geq 0, R \geq 0\}$ (9) is uniformly bounded.

Proof: From (9) the total population satisfies

$$\begin{aligned} {}_0^C D_t^\alpha N(t) &= \Omega^\alpha - \mu^\alpha S - \mu^\alpha I - \omega^\alpha I - \sigma^\alpha I - \mu^\alpha R \\ &= \Omega^\alpha - \mu^\alpha N(t) - \omega^\alpha I - \sigma^\alpha I \end{aligned} \tag{10}$$

Where $N(t) = S(t) + I(t) + R(t)$

$${}_0^C D_t^\alpha N(t) \leq \Omega^\alpha - \mu^\alpha N(t) \tag{11}$$

Now by using the Laplace transform for Eq. (5) we can get the following equation

$$s^\alpha L\{N(t)\} - s^{\alpha-1} N(0) \leq \frac{\Omega^\alpha}{s} - \mu^\alpha L\{N(t)\} \tag{12}$$

$$(s^\alpha + \mu^\alpha) L\{N(t)\} \leq \frac{\Omega^\alpha}{s} + s^{\alpha-1} N(0) \tag{13}$$

$$L\{N(t)\} \leq \frac{s^{-1}}{s^\alpha + \mu^\alpha} \Omega^\alpha + \frac{s^{\alpha-1}}{s^\alpha + \mu^\alpha} N(0) \tag{14}$$

Then from Eq. (7) and Eq. (8) we get

$$\begin{aligned} N(t) &\leq \Omega^\alpha t^\alpha E_{\alpha,\alpha+1}(-\mu^\alpha t^\alpha) + E_{\alpha,1}(-\mu^\alpha t^\alpha) N(0) \\ &\leq \frac{\Omega^\alpha}{\mu^\alpha} \left[\mu^\alpha t^\alpha E_{\alpha,\alpha+1}(-\mu^\alpha t^\alpha) + E_{\alpha,1}(-\mu^\alpha t^\alpha) \right] \\ &\leq \frac{\Omega^\alpha}{\mu^\alpha} \left[\mu^\alpha t^\alpha E_{\alpha,\alpha+1}(-\mu^\alpha t^\alpha) - \mu^\alpha t^\alpha E_{\alpha,\alpha+1}(-\mu^\alpha t^\alpha) + \frac{1}{\Gamma(1)} \right] \\ &\leq \frac{\Omega^\alpha}{\mu^\alpha} \end{aligned} \tag{15}$$

Solutions in the system (9) are restricted as follows

$$\Psi = \{(S,I,R) \in R^{+3} : 0 \leq N(t) \leq \frac{\Omega^\alpha}{\mu^\alpha}\} \tag{16}$$

4. Infection equilibria points and Basic reproduction number

4.1. Disease free equilibrium and endemic equilibrium

There are two equilibria in the fractional Cholera model (9). The disease-free equilibria E_0, is given as follows:

$$E_0 = (S(0), I(0), R(0), V(0)) = \left(\frac{\Omega^\alpha}{\mu^\alpha}, 0, 0, 0 \right) \tag{17}$$

The other type of equilibrium is endemic equilibrium points would be in the form;

$$\begin{aligned} E^* &= (S^*, I^*, R^*, V^*) \\ &= \left(\frac{\mu^\alpha + \omega^\alpha + \sigma^\alpha + \beta^\alpha}{\rho^\alpha}, \frac{(\gamma^\alpha + \mu^\alpha)R^*}{\beta^\alpha}, \frac{(\rho^\alpha I^* + \mu^\alpha)S^* - \Omega^\alpha}{\gamma^\alpha}, \frac{\sigma^\alpha(\gamma^\alpha + \mu^\alpha)R^*}{\eta^\alpha \beta^\alpha}\right) \end{aligned} \tag{18}$$

4.2. Calculating the basic reproduction number R_0

These are the threshold parameters that govern disease spread in the population. Whether the disease would persist or die out in the system over time is unknown. The basic reproduction number indicates or explains the progression of the disease over time. The next-generation matrix at the disease-free equilibrium is used to figure out the basic reproductive number R_0 [23].

From system (9) the infective compartments are

$$\begin{aligned} {}_0^C D_t^\alpha S &= \Omega^\alpha - \rho^\alpha SI - \mu^\alpha S + \eta^\alpha V + \gamma^\alpha R \\ {}_0^C D_t^\alpha I &= \rho^\alpha SI - \mu^\alpha I - \omega^\alpha I - \sigma^\alpha I - \beta^\alpha I \end{aligned} \tag{19}$$

Using the next-generation matrix approach, the matrices F and V that correspond to the newly discovered infection terms and the remaining transfer terms, respectively, are as follows:

$$F = \begin{bmatrix} 0 & \frac{-\rho^\alpha \Omega^\alpha}{\mu^\alpha} \\ 0 & \frac{\rho^\alpha \Omega^\alpha}{\mu^\alpha} \end{bmatrix} \tag{20}$$

and

$$V=\begin{bmatrix}\mu^{\alpha} & 0\\ 0 & \mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha}\end{bmatrix} \tag{21}$$

The inverse of matrix from is given by V

$$V^{-1}=\begin{bmatrix}\frac{1}{\mu^{\alpha}} & 0\\ 0 & \frac{1}{\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha}}\end{bmatrix} \tag{22}$$

Now, we compute the eigenvalues of the matrix $G=FV^{-1}$ to get the basic reproduction number R_0.

$$\lambda=\begin{bmatrix}0\\ \frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha})}\end{bmatrix} \tag{23}$$

Therefore, the basic reproduction number R_0 is given by the relation

$$R_0=\max\{0,\frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha})}\} \tag{24}$$

Theorem 4.1 The disease-free equilibrium point E_0 is locally asymptotically stable if $R_0<1$ and unstable if $R_0>1$.

Proof: To determine local stability, we apply the Jacobian matrix at the disease-free equilibrium of the Caputo fractional system (9) as follows:

$$J_{E_0}=\begin{bmatrix}-\mu^{\alpha} & \frac{-\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}} & \gamma^{\alpha} & 0\\ 0 & \frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}}-(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha}) & 0 & 0\\ 0 & \beta^{\alpha} & -(\mu^{\alpha}+\gamma^{\alpha}) & 0\\ 0 & \sigma^{\alpha} & 0 & -\eta^{\alpha}\end{bmatrix} \tag{25}$$

Now, we compute the determinant of the Jacobian matrix at free equilibrium as follows;

$$\begin{vmatrix} -\mu^{\alpha}-\lambda_1 & \frac{-\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}} & \gamma^{\alpha} & 0 \\ 0 & \frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}}-(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha})-\lambda_2 & 0 & 0 \\ 0 & \beta^{\alpha} & -(\mu^{\alpha}+\gamma^{\alpha})-\lambda_3 & 0 \\ 0 & \sigma^{\alpha} & 0 & -\eta^{\alpha}-\lambda_4 \end{vmatrix}=0 \quad (26)$$

The eigenvalues of the Jacobian matrix in Eq. (26) are

$$\lambda_1=-\mu^{\alpha} \quad (27)$$

$$\lambda_2=\frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}}-(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha}) \quad (28)$$

$$\lambda_3=-(\mu^{\alpha}+\gamma^{\alpha}) \quad (29)$$

$$\lambda_4=-\eta^{\alpha} \quad (30)$$

Note that λ_1,λ_3 and λ_4 have a real negative part. Now, we will proof the λ_2 has a real negative part. Suppose $\lambda_2<0$, we get

$$\frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}}-(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha})<0$$

$$\frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}}<\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha}$$

$$\frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha})}<1 \quad (31)$$

Since $R_0=\frac{\rho^{\alpha}\Omega^{\alpha}}{\mu^{\alpha}(\mu^{\alpha}+\omega^{\alpha}+\sigma^{\alpha}+\beta^{\alpha})}$, then from Eq. (31) we have $R_0<1$.

Then the disease-free equilibrium point E_0 is locally asymptotically stable.

5. Numerical results

By using systems of fractional differential equations that were solved over a predetermined period of time using the fractional Adams method, numerical simulation was done to demonstrate the effects of the model parameters. Table 2 contains the parameter values used in the simulations. Also, we will use the proposed initial values of the state variables in Table 3. The simulation was carried out three months after the cholera epidemic started. To determine the changes in the various populations of these compartments over time, we ran numerical simulations of the system of fractional differential equations of susceptible humans, recovered humans, and infectious humans. There seems to be a continuous decrease in the number of susceptible humans as the number of the recovered population increases with time.

Parameter	Value	Reference
Ω	0.000096274	[24]
ρ	0.011	[24]
μ	0.00002537	[24]
η	0.075	Assumed
γ	0.002	Assumed
ω	0.0004	[24]
σ	10	[24]
β	5	[24]

Table 2: Parameter values in the fractional Cholera model

Variable	Initial values	Reference
$S(t)$	10	[24]
$I(t)$	1	[24]
$R(t)$	1	[24]
$V(t)$	100	[24]

Table 3: The initial values in the fractional Cholera model

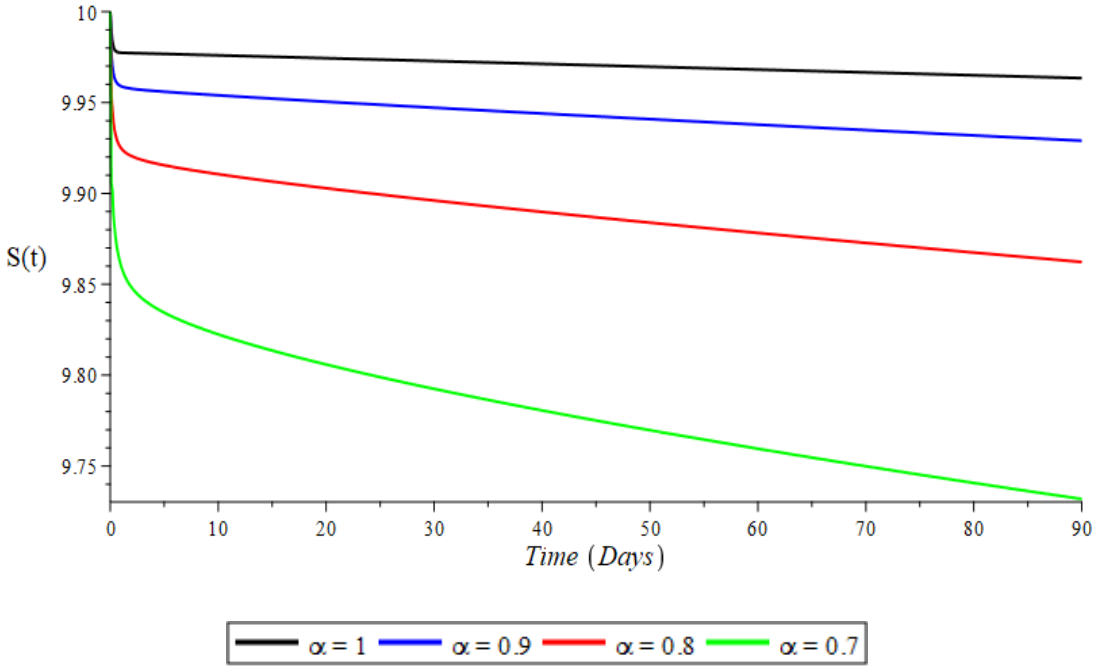

Figure 1: Susceptible population with $0 < \alpha \leq 1$.

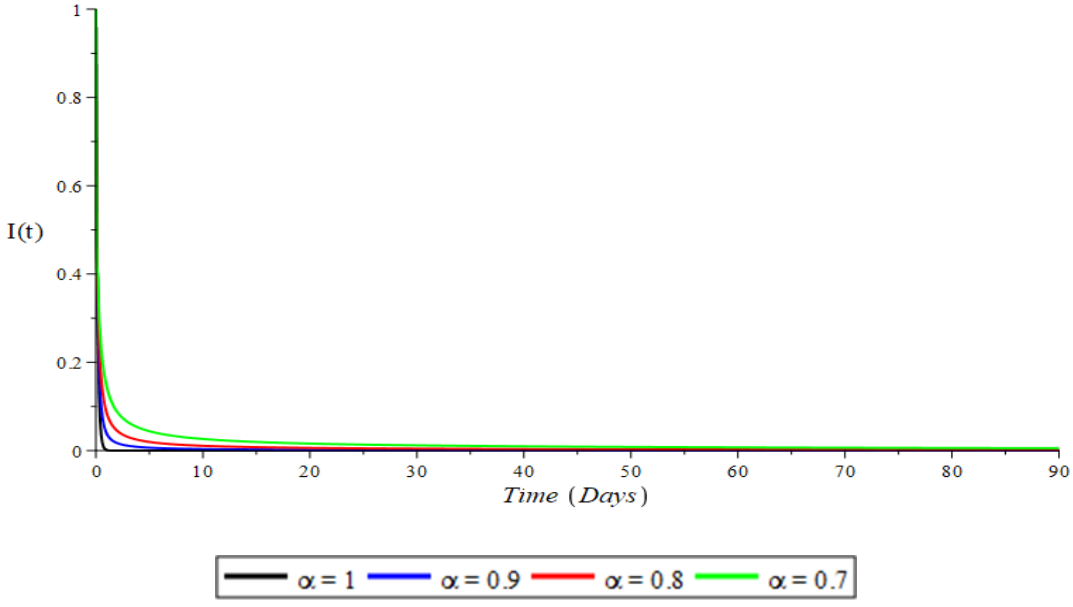

Figure 2: Infected population with $0 < \alpha \leq 1$.

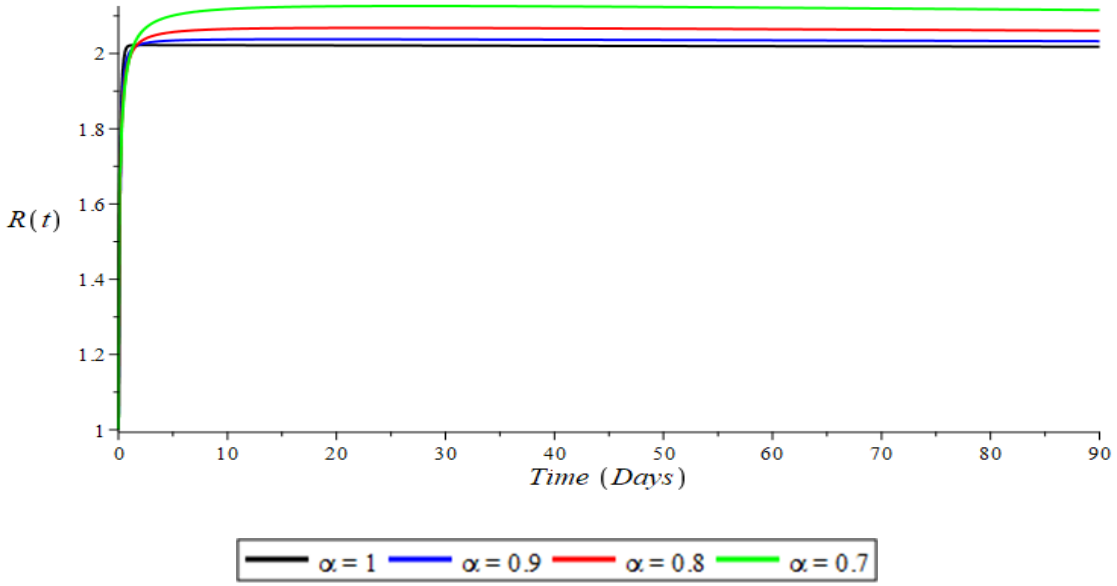

Figure 3: Recovered population with $0 < \alpha \leq 1$.

6. Conclusions

The fractional Cholera model has been shown to have limited solutions. The basic reproductive number was identified, and it was demonstrated that our model possesses a locally asymptotically stable infection-free equilibrium when the basic reproductive number is smaller than one. The computer calculations demonstrated that there has been a rise in the overall number of recovered persons as the susceptible population has decreased. The vulnerable human and the recovered human have an inversely proportionate connection. The influence of the order of the fractional derivative (the memory property of fractional derivatives) on the fractional Cholera model has been recommended to be examined using Adams' approach for numerical simulations.

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تحليل الاستقرار والمحاكاة العددية لنموذج الكوليرا الكسري

سناء لفته خلف

جامعة البصرة، كلية العلوم، قسم الرياضيات

المستخلص

فيروس الكوليرا يسببه بكتيريا ضمة الكوليرا ، وهي أحد أفراد عائلة Vibrionaceae. الكوليرا مرض يصيب البشر وينتج عن كائن حي يسمى ضمة الكوليرا. في هذا البحث، تم عمل نموذج وبائي كسري لشرح كيفية انتشار الكوليرا. يتكون النموذج من أربعة أجزاء هي: البشر المعرضون للخطر، والبشر المصابون، والبشر الذين تعافوا، والبيئة التي يمكن أن تنمو فيها البكتيريا. تم حساب نقاط التوازن الخالية من الأمراض والمتوطنة. تم تطبيق مصفوفة الجيل التالي في عملية حساب رقم الاستنساخ R_0 . لقد ثبت أن التوازن الخالي من الأمراض يمكن أن يكون مستقرًا محليًا بشكل مقارب عندما $R_0 < 1$. تم إجراء المحاكاة العددية لنظام المعادلات الكسرية في النموذج الوبائي للمساعدة في فهمها ومقارنتها بالحلول النوعية. وأظهرت النتائج أنه مع ارتفاع عدد السكان المتعافين، ينخفض عدد الأشخاص المعرضين للخطر في النظام. وفقًا لهذه الدراسة، يجب على الممارسين الصحيين استخدام تغطية إعلامية فعالة لحملات تفشي المرض والوقاية.