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An Irregular Finite Variation Technique Pro Partial Solution−Array Replica of Covid19 Infection

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Abstract

The present paper comprises the study of array replica of Covid19 infection. We study the effect of the changing the average number of viral particles N with different sets of initial conditions on the dynamics of the presented replica. The irregular finite difference scheme is implemented to examine the dynamic behaviors in the array replica Covid19 infection model. Numerical results show that the approach is simple and accurate for solving fractional-order Covid19 infection replica.

Keywords - Covid19, Array, Replica etc.

Introduction-

Covid19 causes Corona pandemic a condition in humans in which the immune system begins to fail, leading to danger to life vital infection. Covid19 infects primarily vital cells in the human immune system, bulk phages, and cells. When cell numbers decline below a critical level, cell-mediated immunity is lost and the body becomes progressively more vulnerable to vital infections. The Covid19 pandemic is widely recognized to be the most severe health crisis at present.Covid19 continues to spread at danger rates through many parts of the world, and there have been few victories in the efforts to contain it.For those who are able to obtain treatment with antiretroviral drugs, Covid19 infection has been transformed from a fatal illness into a chronic condition. Though, on the medical frontier there have been many advances, but still there is no effective cure or vaccine available for Covid19.Mathematical models have been proven valuable in understanding the dynamics of Covid19 infection. Many researchers discussed on these models.

In Person Covid19 was developed a simple model for the primary infection . This model has been important in the field of mathematical modeling of Covid19 infection, and many other models have been proposed, which take this model as their inspiration. The researchers extended the model and discussed some behavior of the model. They defined the model by considering four categories: uninfected CD4+P-cells, latently infected CD4+ P-cells, productively infected CD4+ P-cells and Corona virus inhabitants. Further the model was developed by incorporating anti-retroviral effects to study the evolution of drug resistance. They considered three classes of CD4+P-cells: uninfected cells, infected cells in eclipse phase and productively infected cells. The model depends on the observation that for a virus, when it enters a resting CD4+ P-cell, viral RNA may not be completely reverse transcribed into DNA.

Haiping modified the system of ordinary differential equations (ODEs) model proposed by Culshaw and into a system of fractional-order. Following , we assume here that a fraction of infected CD4+ P- cells return to the uninfected class-

P*= R− kQP − dP + bP#

P∗′ = kQP − (b + δ)P∗, (1)

Q′ = nδP∗ − cQ,

with initial conditions:

P(0) = P0* P∗(0) = P∗Q(0) = Q0.

In this model, P*, P# and Q denote the concentration of uninfected CD4+ cells, infected CD4+ P-cells and free Corona virus particles in the blood, respectively .The parameters stand for the inflow rate of CD4+ P-cells and d its natural death rate. The parameter k represents the rate of infection of P-cells, δ represents death rate of infected P-cells and includes the possibility of death by bursting of infected P-cells, hence $\delta \geq d$. The factor b is the rate at which infected cells return to uninfected class. In addition, c presents the death rate of virus and N is the average number of viral particles produced by an infected cell. Features of the procedures for constructing NSFD schemes for systems of ODEs.We introduce fractional-order into the model that describes Covid19 infection of CD4+ P-cells and also stability theorem and Routh-Hurwitz stability conditions are given for the local asymptotic stability of the fractional systems.We will discuss the stability analysis of fractional system.We present the idea of scheme for solving the fractional-order Covid19 infection of CD4+ P-cells model. Finally in the last section, numerical results demonstrate that the approach is easy to be implemented and accurate when applied to the fractional-order Covid19 infection model.

Here some basic definitions and properties of the fractional calculus theory and nonstandard discretization are mentioned-

To study the Covid19 fractional differential equations have gained considerable importance due to their applications in various sciences, such as physics, mechanics, chemistry and engineering. Covid19 Replica by GL Approximation

Covid19 Replica by the GL method of approximation for the one-dimensional fractional derivative is as follows -

$D\alpha$a(p) = f(p, a(p)), a(0) = a0, p ∈ [0, pf], (2)

pf[q] $D\alpha$a(t) = lim h−α ∑(−1)j (α) q(t − jh),

q→0

j

j=0

where 0 < α < 1, $D\alpha$ denotes the fractional derivative, q is the step size and [af]

q represents the integer part of af. n

∑ $c\alpha$an−j

= f(pn, xn),

n = 1, 2, 3, …

j=0 where pn = n h and $c\alpha$ are the GL coefficients defined as:

$c\alpha = (1 - 1 + \alpha)\, c\alpha$, $c\,\alpha = h - \alpha$, j = 1, 2, 3, …

j j j−1 0

The starting foundation of schemes came from the exact finite difference schemes. These schemes are well developed by Mickens in the past decades. Regarding the positivity, boundedness and monotonicity of solutions, the schemes have a better performance over the standard finite difference schemes, due to its flexibility to construct a scheme that can preserve certain properties and structures, which are obeyed by the original equations.

The advantages of schemes have been shown in many numerical applications. Schemes to solve population and biological models. Constructed schemes for heat transfer problems. We now give an outline of the critical points which will allow the construction of discretization. Consider the equation given by

p′ = f(p), p(0) = p0, p ∈ [0, pf],

where f(a) is, in general, a nonlinear function of x.

Δp = q, we replace the independent variable p by

p ≈ pn = nq, n = 0, 1, 2, … , N

where q = tf. The dependent variable a(p) is replaced by

Na(p) ≈ xn,where bn is the approximation of a(pn).

The first requirement is that the dependent functions should be replicated nonlocally on the discrete–time computational grid- ⎧ ab ≈ 2an+1bn − an+1bn+1,

⎩ a ≈ an+1bn,

⎪ 3an+1 + bn−1 2

la ≈ (2) an.

a′ ≅ an+1 − an.q

However, the scheme requires that x' has the more general representation

a′ ≅ an+1 − an,

$\emptyset(h)$ where the denominator function, i.e. $\emptyset$ has the properties:

(i) $\emptyset(h) = h + O(h2)$,

(ii) $\emptyset(h)$ is *an increasing function of* h,

(iii) $\emptyset(h)$ *may depend on the parameters appearing* in *the differential equations*.The paper gives a general procedure for determining $\emptyset(h)$ for systems. An example of the discretization process is its application to the decay equation

a′ = −λa, where λ is a constant. The discretization scheme is an+1 − bn

( ) 1 − e−ƨh ∅ = −λan, ∅ q, λ =

Another example is given byλ where the scheme is

an+1 – an a′ = λ1a − λ2a2 ,( ) eƨ1h − 1

∅ = λ1an − λ2an+1an, ∅ h, λ1 = λ1 .

It should be noted that the schemes for both are exact in the sense that

an = a(pn) for all applicable values of h > 0. In general, polynomial terms,

P′ = xa + (nl), nl ≡ $nonlinear\ terms$

the discretization for the linear expressions is derived as-

an+1 − an = ax∅+ (nl),

where the denominator function is

∅(q, a)eaq − 1= a .

It follows that if x' is a function of x which does not have a linear term, then the denominator function would be just h, i.e. ∅(q) = q. By applyingthis technique and using the GL discretizationmethod, it yields the following relations:

∑n+1 $c\alpha$an+1−j + f(pn+1 , an+1)

xn+1 =

where $c\alpha$ = ∅(h)−α.

j=1 j $c\alpha$

n = 0, 1, 2, …

Fractional Order Covid19 Infection Epidemic Model-In this section, we introduce fractional-order into the model (1) of Covid19 infection of the CD4+ P-cells.

The Jacobian matrix at the equilibrium point E1(T˜, T˜∗, V˜) is

− $skNR$0 − skN + dcR0 b − (b + δ)

$J(T$˜, T˜∗, V˜) = cR0(R0 − 1) −b − δcR0 $N\delta$ $c(b + \delta)$ $N\delta$

h 0 $N\delta$ −c

with the characteristic equation

(λ) = λ3 + a1λ2 + a2λ + a3 = 0,

where a1 =(R0 − 1) + dcR0 + R0δc + c2R0 + cR0bcR0

$a2 = (R0 - 1) + skN(R0 - 1) + dcR0b + dcR0\delta + dc2R0\ cR0$,3= $s(1).R0$

Observe that if $R0 > 1$ then $a1 > 0$, $a2 > 0$ and $a3 > 0$.

$n+1$

$\sum c\alpha 1 P n+1-j = s - kPn+1Qn - dPn+1 + bP*,$

$j \quad nj=0 n+1$

$\sum c\alpha 2 P* = kPn+1Qn - (b + \delta)P* ,$

$jj=0 n+1-jn+1n+1$

$\sum c\alpha 3 Qn+1-j = N\delta P* - cQn+1.$

$jj=0\ n+1$,Comparing with system , we note the following statements-

$-PQ \approx -Pn+1Q , \quad - PQ \approx -Pn+1, \quad P* \approx Q*.$

$PQ \approx Pn+1Q , \quad - P* \approx -Q* .$

$P* \approx Q* , \quad - Q \approx -Pn+1.$

Invoking some algebraic manipulations on,the following relations are obtained:$- \sum n+1\ c\alpha 1\ Pn+1-j + s + bQ*$

$Pn+1 = j=1j$

$c\alpha 1 + d + kVnn ,- \sum n+1\ c\alpha 2\ T* + kTn+1Vn$

$P* = j=0 \quad jn+1-j ,+1$

$c\ \alpha 2 + b + \delta - \sum n+1\ c\alpha 3\ Qn+1-j + N\delta T*$

$Pn+1 = j=1j\ c\alpha 3 + cn+1$,where

$c\alpha 1 = \emptyset 1(Q) - \alpha 1 , \quad c\alpha 2 = \emptyset 2(q) - \alpha 2 , \quad c\alpha 3 = \emptyset 3(q) - \alpha 3 ,$

$0( )dh - 10\ \ 0( ) \quad (\eth + b)q - 1( )\ ech - 1\emptyset 1\ q =$

$d \quad , \quad \emptyset 2\ h = (\delta + b) , \quad \emptyset 3 \quad q = c$

The approximate solutions are displayed in Figures 1*4, for different $0 < \alpha i \leq 1$ and i = 1, 2, 3.We exploited the following data set: $s = 10$, $b = 0.2$, $k = 0.000024$, $d = 0.01$, $= 0.16$, $c = 3.4$ and $N = 1000$. For this set of data $R0 = 3.137 > 1$, $(P) = -4.868$and $a1 = 3.818$,$a2 = 0.208$, $a3 = 0.026$,with $a1a2 - a3 = 0.771$. Thus, the disease free equilibrium point $E1$ is locally asymptotically stable for $\alpha < 2$. It can be verified that the system goes to infected steady state (318.75, 42.57, 2003.9). The results are depicted

We exploited the following data set: s = 10, b = 0.2, k = 0.000024, d = 0.01, = 0.16, c = 3.4 and N = 1600. For this set of data $R0$ = 5.019 > 1, (P) = −8.417 And $a1$ = 3.860, $a2$ = 0.359, $a3$ = 0.049,with $a1a2 - a3$ = 1.338. Thus, the disease free equilibrium point $E1$ is locally asymptotically stable for α < 2. 3state (199.218, 3768.382, 50.048). The results are depicted in Figures 3 and 4 for the initial conditions in the second case study are (0) = 1000, $T*(0)$ = 10, $V(0)$ = 10 with simulation time 3000s and step size h = 1.5.

Conclusion-

In this paper we studied the fractional-order Covid19 array replica. From the obtained results in the presented figures, it turns out that in the primary stage of the infection with the Covid19 virus, a dramatically decrease in the level of the CD4+P-cells occurs because of the death of such infected cells. On the other hand, the number of the free Covid19 virus particles and the number of susceptible CD4+ P-cells increase. This assumes that the growth of healthy P-cells slows down during the course of Covid19 infection. The basic reproduction number is given in as:$R0N\delta ks\ cd(b + \delta)$. The concentration of the free Covid19 virus particles at N = 1600 with step size q = 1.5. The concentration of the free Covid19 virus particles at N = 1600 with step size q = 1.5.It represents the average number of secondary infection caused by a single infected p-cell in an entirely susceptible p-cell population, through out its infectious period.if the basic reproduction number $N_0 \leq 1$, the virus is cleared and no Covid19 infection persists. If No > 1, the Covid19 infection persists in the P-cell population. In the two presented cases, N_0 = 3.137 when N = 1000 and R_0 = 5.019 when N = 1the system goes to infected steady state. From the definition of N_0, it can be seen that N_0 decreases as there verting rate, y of infected cells increases. Hence N_0 can be low for a high parametric value of y. Increasing the value of N will decrease the numbers of uninfected $CD4^+$ P-cells and increases the number of free viruss ubstantially, but does not change the stability of the steady state. The concentration of susceptible $CD4^+$ P-cells P(p), the recent appearance of fractional differential equations as replica in some fields of applied Mathematical Science and Chemical Science.

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