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Fractional SVIR model for COVID-19 under Caputo derivative

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Abstract

COVID-19 has been an outbreak since December 2019 all around the world. There exist many studies in literature that examines the future of the pandemic and the effect of control strategies via mathematical modeling. Main aim of mathematical modeling in epidemiology and health sciences is applying the theory to real world health problems. In this paper, world population is divided into four compartments for the construction of SVIR model. That is, it is assumed that population consists of susceptible (*S*), vaccinated (*V*), infected (*I*), and recovered (*R*) individuals. Fractional mathematical models are very popular nowadays since it counts previous state of problems. While the construction of this model, fractional derivative is added with the purpose of seeing memory effect.

Keywords: Mathematical modeling, Fractional Caputo derivative, COVID-19, Vaccinations

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1. Introduction

The outbreak of the typical coronavirus strain COVID-19 (SARS-COV2) started out in the late December in the Wuhan, a region of China (WHO, 2020). Researchers and scientists all over the world had been attracted to the epidemic due to its severity (He et al., 2020). It has become a global pandemic, alleged to have increased illness, contamination and loss of life; in addition to devastating the economy as a result the series of lockdown and travel restrictions (Bedford et al., 2020; Chaturvedi et al., 2020). It has been discovered that a growing range of countries have begun banning worldwide travel and large gatherings, and has only recently started relieving the restrictions. The virus has a genetic hyperlink to acute breathing syndrome (SARS-COV) (Hon et al., 2020), but is much less extreme than the Middle East Respiration Syndrome (MERS-COV) (Gorbalenya et al., 2020; Peeri et al., 2020). While an infected character inhales the breathing droplets, the virus is transmitted to healthy people via the eyes, mouth and nostril (CDC, 2019); because of coughing and sneezing, or contact with infected surfaces. The average incubation length is about two to fourteen days (Singhal, 2020).

A large variety of medical doctors and professionals have also contributed to the fight in opposition to the epidemic by carrying out studies in their regions of expertise (Han et al., 2020). Scientists have been studying the novel virus from a ramification of angles, along with virology, infectious illnesses, microbiology, place of business environmental health, veterinary technological know-how, sociology, media research, and political economic system. The rapid development of COVID-19 vaccines in 2020 was a welcome source of hope in another dark year. Many people saw the approval of several vaccines as a milestone in the global epidemic response, raising hopes that national vaccination strategies would soon address public health risks, and finally, restrictions on daily life can be lifted.

Mathematicians have advanced new mathematical models that can be used for simulation to flatten the contamination and dying curve (Tahir et al., 2019; Yavuz et al., 2021). Many researches have been completed withinside the literature at the mathematical version of the COVID-19 pandemic in a quick time (Kaymakamzade, 2017; Ahmad et al., 2020). They will be used to offer and have a look at viable conditions of the dynamics to hand, such as clinical

establishments, politicians, armies, regulation enforcement, industrialists, chemists, physicists, engineers, and many others; sectors round the sector are making efforts to stop the unfold of COVID-19. It is important to take a look at the mathematical model of infectious illnesses for a higher information and assessment, as the classical strategies of mathematical models do not decide the excessive degree of accuracy to represent those diseases (Abdo et al., 2020). Fractional differential equations have been delivered to address such troubles, which have many applications in fields like manufacturing troubles, optimization hassle, synthetic intelligence, scientific diagnoses, robotics, cosmology and masses of extra. Also, the fractional-order differential method has been applied in mathematical modeling of natural phenomena. Researchers, therefore have integrated the classical calculus to the fractional-order via fractional-order modeling in using special mathematical techniques, considering that mathematical models are powerful device to analyze infectious disease. Fractional mathematical model allows us to understand the future of epidemic with the help of memory effect. Recently some authors have considered mathematical models of COVID-19 beneath fractional order derivatives and produced first-rate consequences (Garrappa, 2014; Baleanu et al., 2020).

In this paper, a fractional-order SVIR COVID-19 model is proposed in the sense of Caputo derivative for representing and studying the pandemic. Then, analysis of the model is given. Afterwards, numerical simulations of the model are represented. Finally, the results of the model are explained.

2. Material and Methods

A mathematical model is constructed by dividing the world population into four compartments. Total population, denoted by *N(t)*, at time *t*, consists of susceptible individuals, *S(t)*, vaccinated individuals, *V(t)*, infected individuals, *I(t)*, and recovered individuals, *R(t)*. The model is obtained by means of system of ordinary differential equations. For determining the infectiousness of the disease, basic reproduction number, denoted by R_0, is calculated with the help of Next Generation Matrix method. Disease-free Equilibrium point, denoted by E_0, is found and its existence is proved with the help of Lyapunov function idea.

2.1. Mathematical model

The model is constructed as follows.

$$\begin{aligned}
&{}_0^c\mathrm{D}_t^\alpha\, S(t) = \Lambda^\alpha - \beta^\alpha SI - r^\alpha S - \mu^\alpha S,\\
&{}_0^c\mathrm{D}_t^\alpha\, V(t) = r^\alpha S - k^\alpha VI - \mu^\alpha V,\\
&{}_0^c\mathrm{D}_t^\alpha\, I(t) = \beta^\alpha SI + k^\alpha VI - (d^\alpha + \gamma^\alpha + \mu^\alpha)I,\\
&{}_0^c\mathrm{D}_t^\alpha\, R(t) = \gamma^\alpha I - \mu^\alpha R,
\end{aligned} \tag{1}$$

where ${}_0^c\mathrm{D}_t^\alpha$, for $\alpha \in (0,1)$, is the standard Caputo derivative. Explanation of the variables and parameters are given in Table 1 and Table 2.

Table 1. Description of variables of the model

Variable	Description
S	Susceptible individuals
V	Vaccinated individuals
I	Infected individuals
R	Recovered individuals

Table 2. Description of parameters of the model

Parameter	Description
Λ	Recruitment rate
β	Infection rate of susceptible individuals
r	Vaccination rate of susceptible individuals
k	Infection rate of vaccinated individuals
d	COVID-19 caused death rates
γ	Recovery rate
μ	Natural death rate

2.1.1. Existence and uniqueness of the system

$$\begin{aligned}
{}_0^c\mathrm{D}_t^\alpha \mathrm{N(t)} &= (\Lambda^\alpha - \beta^\alpha SI - r^\alpha S - \mu^\alpha S) + (r^\alpha S - k^\alpha VI - \mu^\alpha V) + (\beta^\alpha SI + k^\alpha VI - (d^\alpha + \gamma^\alpha + \mu^\alpha)I) + (\gamma^\alpha I - \mu^\alpha R)\\
&= \Lambda^\alpha - \mu^\alpha(S + V + I + R) - d^\alpha I\\
&= \Lambda^\alpha - \mu^\alpha N(t) - d^\alpha I\\
&\le \Lambda^\alpha - \mu^\alpha N(t)\,.
\end{aligned}$$

Applying the Laplace transform method to solve Grönwall's inequality, with initial condition $N(t_0) \ge 0$, we get,

$$\lfloor \mathcal{L}\{{}_0^c\mathrm{D}_t^\alpha N(t) + \mu^\alpha N(t)\} \le \mathcal{L}\{\Lambda^\alpha\},$$

using the properties of Laplace transforms (linearity) we obtain,

$$\lfloor \mathcal{L}\{{}_0^c\mathrm{D}_t^\alpha N(t)\} + \mu^\alpha \mathcal{L}\{N(t)\} \le \mathcal{L}\{\Lambda^\alpha\}\,.$$

Employing the definition of Laplace transform,

$$S^{\alpha}\mathcal{L}\{N(t)\} - \sum_{m=0}^{n-1} S^{\alpha-m-1}N^{(m)}(t_0) + \mu^{\alpha}\mathcal{L}\{N(t)\} \leq \frac{\Lambda^{\alpha}}{S}$$

$$\mathcal{L}\{N(t)\}(S^{\alpha}+\mu^{\alpha}) \leq \sum_{m=0}^{n-1} S^{\alpha-m-1}N^{(m)}(t_0) + \frac{\Lambda^{\alpha}}{S} \tag{2}$$

$$\mathcal{L}\{N(t)\} \leq \sum_{m=0}^{n-1} \frac{S^{\alpha-m-1}}{(S^{\alpha}+\mu^{\alpha})}N^{(m)}(t_0) + \frac{\Lambda^{\alpha}}{S(S^{\alpha}+\mu^{\alpha})}.$$

Applying partial fractions, we arrive at,

$$\begin{aligned}\mathcal{L}\{N(t)\} &\leq \sum_{m=0}^{n-1} \frac{S^{\alpha-m-1}}{(S^{\alpha}+\mu^{\alpha})}N^{(m)}(t_0) + \frac{\Lambda^{\alpha}}{S(S^{\alpha}+\mu^{\alpha})}. \\ &= \Lambda^{\alpha}\left(\frac{1}{S(S^{\alpha}+\mu^{\alpha})}\right) + \sum_{m=0}^{n-1} \frac{S^{\alpha-m-1}}{(S^{\alpha}+\mu^{\alpha})}N^{(m)}(t_0)\,.\end{aligned} \tag{3}$$

Using Taylor series expansion, $\Sigma_{n=0}^{\infty}\left(\frac{-\mu^{\alpha}}{s^{\alpha}}\right)^n$ is the Taylor series expansion for $F(t) = \frac{1}{(1+\frac{\mu^{\alpha}}{s^{\alpha}})}$ from definition. So, from Eq. 3 we have that,

$$\begin{aligned}\mathcal{L}\{N(t)\} &\leq \Lambda^{\alpha}\left[\frac{1}{S} - \frac{1}{S}\sum_{n=0}^{\infty}\left(\frac{-\mu^{\alpha}}{s^{\alpha}}\right)^n\right] + \sum_{m=0}^{n-1}\frac{1}{S^{m+1}}\left(\sum_{n=0}^{\infty}\left(\frac{-\mu^{\alpha}}{s^{\alpha}}\right)^n\right)N^{(m)}(t_0) \\ &= \Lambda^{\alpha}\left[\frac{1}{S} - \sum_{n=0}^{\infty}\frac{-\mu^{\alpha n}}{s^{\alpha n+1}}\right] + \sum_{m=0}^{n-1}\left(\sum_{n=0}^{\infty}\frac{-\mu^{\alpha n}}{s^{\alpha n+m+1}}\right)N^{(m)}(t_0)\,.\end{aligned}$$

Taking Laplace inverse function, we see that,

$$N(t) \leq \Lambda^{\alpha}\mathcal{L}^{-1}\left\{\frac{1}{s}\right\} - \Lambda^{\alpha}\sum_{n=0}^{\infty}(-\mu^{\alpha})^n\mathcal{L}^{-1}\left\{\frac{1}{s^{\alpha n+1}}\right\} + \sum_{m=0}^{n-1}\sum_{n=0}^{\infty}(-\mu^{\alpha})^n N^{(m)}(t_0)\mathcal{L}^{-1}\left\{\frac{1}{s^{\alpha n+m+1}}\right\}.$$

Recall that,

$$\mathcal{L}\{x^n\} = \frac{n!}{S^{n+1}} = \frac{\Gamma(n+1)}{s^{n+1}},$$

$$\mathcal{L}^{-1}\left(\frac{1}{s^{n+1}}\right) = \frac{x^n}{\Gamma(n+1)}.$$

So, we get,

$$\begin{aligned}N(t) &\leq \Lambda^{\alpha} - \Lambda^{\alpha}\sum_{n=0}^{\infty}(-\mu^{\alpha})^n t^{\alpha n} + \sum_{m=0}^{n-1}\sum_{n=0}^{\infty}(-\mu^{\alpha})^n N^{(m)}(t_0)\frac{t^{\alpha n+m}}{\Gamma(\alpha n+m+1)} \\ &\leq \Lambda^{\alpha} - \Lambda^{\alpha}\sum_{n=0}^{\infty}\left(\frac{-\mu^{\alpha}t^{\alpha}}{\Gamma(\alpha n+1)}\right)^n + \sum_{m=0}^{n-1}\sum_{n=0}^{\infty}\left(\frac{-\mu^{\alpha}t^{\alpha}}{\Gamma(\alpha n+m+1)}\right)^n t^m N^{(m)}(t_0)\,.\end{aligned}$$

Employing the Mittag-Leffler function, $E_{a,b} = \Sigma_{n=0}^{\infty}\frac{z^m}{\Gamma(am+b)}$, $a>0,\ b>0$, and $E_a(z) = E_{a,1}(z) = \Sigma_{n=0}^{\infty}\frac{z^m}{\Gamma(am+1)}$, we arrive at,

$$N(t) \leq \Lambda^{\alpha}[1 - E_1(-\mu^{\alpha}t^{\alpha})] + \sum_{n=0}^{\infty}E_{m+1}(-\mu^{\alpha}t^{\alpha})N^{(m)}(t_0)t^m\,,$$

where the series of the Mittag-Leffler function are $E_1(-\mu^{\alpha}t^{\alpha})$ and $E_{m+1}(-\mu^{\alpha}t^{\alpha})$ and they converge. Therefore, the system is bounded and the solution exists.

Next, we rewrite the system as follows;

Given the Eq. 1,

$$ {}_0^c\mathrm{D}_t^{\alpha} y(t) = G(t,y), \quad y(0) = y_0. \tag{4} $$

$$ G(t,y) = A(y) + B(y) + C, $$

$$ y = y(t). $$

$$
\begin{aligned}
|G(t,y) - G(t,y^*)| &= |A(y) + B(y) + C - (A(y^*) + B(y^*) + C)| \\
&= \left|A\big((y(t) - y^*(t)\big) + B(y(t) - y^*(t))\right| \\
&\leq \left\|A\big((y(t) - y^*(t)\big)\right\| + \|B(y(t) - B(y^*(t))\| \\
&= \|A\|.\|(y(t) - y^*(t)\| + \|G(y(t) - G(y^*(t))\| \\
&\leq \|A\|.\|y(t) - y^*(t)\| + \|(y(t) - y^*(t)\| \\
&= (\|A\| + 1)\|y(t) - y^*(t)\| \\
&= M\|y(t) - y^*(t)\|,
\end{aligned}
$$

where $M\|y(t) - y^{\alpha}(t)\| < \infty$.

So, *G* is continuous and bounded. Therefore, from Picard-Lindelof theorem, we have that the system is uniformly Lipschitz continuous and has a unique solution

$$ \Omega = \left\{ \big(S(t), V(t), I(t), R(t)\big) \in \mathbb{R}_+^4 : S(t), V(t), I(t), R(t) \leq \Lambda^{\alpha}[1 - E_1(-\mu^{\alpha} t^{\alpha})] + \sum_{m=0}^{\infty} E_{m+1}(-\mu^{\alpha} t^{\alpha}) N^{(m)}(t_0) \right\}. $$

2.2. Equilibrium points and basic reproduction number (R_0)

In this model, two equilibrium points are obtained; disease-free equilibrium point, denoted by E_0, and endemic equilibrium point, denoted by E^*.

The disease-free equilibrium point is the set

$$ E_0 = \{(S_0, V_0, I_0, R_0) : S, V, I, R \in \mathbb{R}_+^4, I = 0, R = 0\}. $$

That is,

$$ E_0 = (S_0, V_0, I_0, R_0) = \left(\frac{\Lambda^{\alpha}}{r^{\alpha} + \mu^{\alpha}}, \frac{r^{\alpha}\Lambda^{\alpha}}{\mu^{\alpha}(r^{\alpha} + \mu^{\alpha})}, 0, 0\right). $$

The basic reproduction number is found as:

$$ R_0 = \frac{\beta^{\alpha} S_0 + k^{\alpha} V_0}{d^{\alpha} + \gamma^{\alpha} + \mu^{\alpha}} = \frac{\Lambda^{\alpha}(\beta^{\alpha}\mu^{\alpha} + k^{\alpha} r^{\alpha})}{\mu^{\alpha}(r^{\alpha} + \mu^{\alpha})(d^{\alpha} + \gamma^{\alpha} + \mu^{\alpha})}. $$

Theorem 2.2.1. The Eq. 1is globally asymptotically stable at the given positive equilibriums.

Proof. Consider the constructed Lyapunov function:

$$ W(x_1, x_2, x_3, \dots, x_n) = \sum_{i=1}^{n} (x_i(t)x')^{\frac{1}{2}}, $$

$$ W(S(t), V(t), I(t), R(t)) = (S(t)S')^{\frac{1}{2}} + (V(t)V')^{\frac{1}{2}} + (I(t)I')^{\frac{1}{2}} + (R(t)R')^{\frac{1}{2}}. $$

Applying the linearity of Caputo operator, and the relation $(ab)^{\frac{1}{2}} \leq \frac{(a+b)}{2}, a > 0, b > 0$, we get:

$$
\begin{aligned}
{}_0^c\mathrm{D}_t^{\alpha} W\big(S(t), V(t), I(t), R(t)\big) &= {}_0^c\mathrm{D}_t^{\alpha} \left((S(t)S')^{\frac{1}{2}} + (V(t)V')^{\frac{1}{2}} + (I(t)I')^{\frac{1}{2}} + (R(t)R')^{\frac{1}{2}} \right) \\
&\leq \frac{1}{2} ({}_0^c\mathrm{D}_t^{\alpha}(S(t)+S') + {}_0^c\mathrm{D}_t^{\alpha}(V(t)+V') + {}_0^c\mathrm{D}_t^{\alpha}(I(t)+I') + {}_0^c\mathrm{D}_t^{\alpha}(R(t)+R')
\end{aligned}
$$

$$= \frac{1}{2}\left({}_0^c\mathrm{D}_t^{\alpha}(N(t)+N')\right)$$

$$= \frac{1}{2}[\Lambda^{\alpha} - \mu^{\alpha}(N(t)+N') - d^{\alpha}(I(t)+I')\,.$$

Case 1: Substituting the disease-free equilibrium $E_0(N^0) = \left(\frac{\Lambda^{\alpha}}{r^{\alpha}+\mu^{\alpha}}, \frac{r^{\alpha}\Lambda^{\alpha}}{\mu^{\alpha}(r^{\alpha}+\mu^{\alpha})}\right)$, we get:

$${}_0^c\mathrm{D}_t^{\alpha}W\big(S(t),V(t),I(t),R(t)\big) \leq \frac{1}{2}\left[\Lambda^{\alpha} - \mu^{\alpha}(N(t) + \left(\frac{\Lambda^{\alpha}}{r^{\alpha}+\mu^{\alpha}} + \frac{r^{\alpha}\Lambda^{\alpha}}{\mu^{\alpha}(r^{\alpha}+\mu^{\alpha})}\right)) - d^{\alpha}I(t)\right]$$

$$= \frac{1}{2}\left[\Lambda^{\alpha} - \mu^{\alpha}\left(N(t) + \frac{\Lambda^{\alpha}}{\mu^{\alpha}}\right) - d^{\alpha}I(t)\right],$$

$$= -\frac{1}{2}\left[\mu^{\alpha}\big(N(t)\big) + d^{\alpha}I(t)\right],$$

$$= -M(x(t))\,.$$

Where $M\big(x(t)\big) = \frac{1}{2}[\mu^{\alpha}\big(N(t)\big) + d^{\alpha}I(t)]$.

Case 2: The endemic equilibrium point is $E_1 = (S^*, V^*, I^*, R^*) = \left(\frac{\Lambda^{\alpha}}{\beta^{\alpha}I^*+r^{\alpha}+\mu^{\alpha}}, \frac{\Lambda^{\alpha}r^{\alpha}}{(\beta^{\alpha}I^*+r^{\alpha}+\mu^{\alpha})(k^{\alpha}I^*+\mu^{\alpha})}, I^*, \frac{\gamma^{\alpha}I^*}{\mu^{\alpha}}\right)$.

I^* is the solution of

$AI^{*2} + BI^* + C = 0,$

where

$A = \beta^{\alpha}k^{\alpha}d^{\alpha},$

$B = (\beta^{\alpha}\mu + k^{\alpha}r^{\alpha} + \mu k^{\alpha})(d^{\alpha} + \gamma^{\alpha} + \mu^{\alpha}) + \beta^{\alpha}k^{\alpha}(\gamma^{\alpha} + \mu^{\alpha} - \Lambda^{\alpha})\,,$

$C = \mu^{\alpha}(d^{\alpha} + \gamma^{\alpha} + \mu^{\alpha})(r^{\alpha} + \mu^{\alpha}) - \Lambda^{\alpha}(k^{\alpha}r^{\alpha} + \beta\mu^{\alpha}).$

The endemic equilibrium is biologically meaningful if $I(t) > 0$. Employing the Routh-Hurwitz criterion, it is easy to see that it is the case when $C < 0$ and $B > 0$. We can easily see that $B > 0$ and $C < 0$ when $R_0 > 1$.

So, substituting the endemic equilibrium $E_1(N)$ we get,

$${}_0^c\mathrm{D}_t^{\alpha}W\big(S(t),V(t),I(t),R(t)\big)$$

$$\leq \frac{1}{2}\left[\Lambda^{\alpha} - \mu^{\alpha}(N(t) + (\frac{\Lambda^{\alpha}}{\beta^{\alpha}I^*+r^{\alpha}+\mu^{\alpha}} + \frac{\Lambda^{\alpha}r^{\alpha}}{(\beta^{\alpha}I^*+r^{\alpha}+\mu^{\alpha})(k^{\alpha}I^*+\mu^{\alpha})} + I^* + \frac{\gamma^{\alpha}I^*}{\mu^{\alpha}})) - d^{\alpha}I^*\right]$$

$$= \frac{1}{2}\left[-\mu^{\alpha}\left(N(t) + \frac{\Lambda^{\alpha}r^{\alpha} + \Lambda^{\alpha}(k^{\alpha}I^*+\mu^{\alpha})}{(\beta^{\alpha}I^*+r^{\alpha}+\mu^{\alpha})(k^{\alpha}I^*+\mu^{\alpha})} + I^* + \frac{\gamma^{\alpha}I^*}{\mu^{\alpha}} - \frac{\Lambda^{\alpha}}{\mu^{\alpha}}\right) - d^{\alpha}I^*\right]$$

$$= -\frac{1}{2}\left[\mu^{\alpha}\left(N(t) + \frac{\Lambda^{\alpha}r^{\alpha} + \Lambda^{\alpha}(k^{\alpha}I^*+\mu^{\alpha})}{(\beta^{\alpha}I^*+r^{\alpha}+\mu^{\alpha})(k^{\alpha}I^*+\mu^{\alpha})} + I^* + \frac{\gamma^{\alpha}I^*}{\mu^{\alpha}} - \frac{\Lambda^{\alpha}}{\mu^{\alpha}}\right) + d^{\alpha}I^*\right]$$

$$= -M(x(t),$$

where $M\big(x(t)\big) = \frac{1}{2}\left[\mu^{\alpha}\left(N(t) + \frac{\Lambda^{\alpha}r^{\alpha}+\Lambda^{\alpha}(k^{\alpha}I^*+\mu^{\alpha})}{(\beta^{\alpha}I^*+r^{\alpha}+\mu^{\alpha})(k^{\alpha}I^*+\mu^{\alpha})} + I^* + \frac{\gamma^{\alpha}I^*}{\mu^{\alpha}} - \frac{\Lambda^{\alpha}}{\mu^{\alpha}}\right) + d^{\alpha}I^*\right]$.

Hence by the theorem of global stability of non-autonomous fractional order systems (Delavari et al., 2012), the Eq. 1 is globally stable at the positive equilibriums. ■

3. Numerical Simulations

For the numerical simulations of the constructed model, MATLAB code fde12.m which implements the Predictor-Corrector Method proposed by (Diethelm & Freed, 1998). Real data taken from World Health Organization are used for the figures. Figure 1, Figure 2, and Figure 3 are obtained by changing the α values.

4. Results and Discussion

The basic reproduction number of the model showed that the disease-free equilibrium point E_0 exists and it is globally asymptotically stable for R_0<1. Also, another equilibrium point, endemic equilibrium point E^* exists and for R_0>1, it is globally asymptotically stable. With the real data used, R_0 value is obtained as higher than 1.

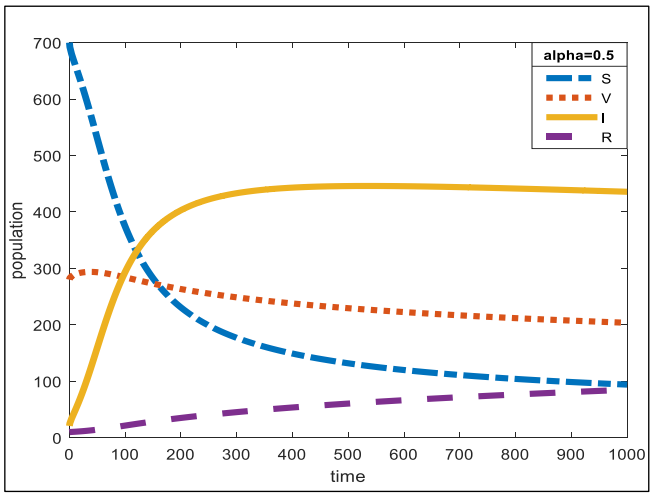

Figure 1. Pattern of compartments for α=0.5

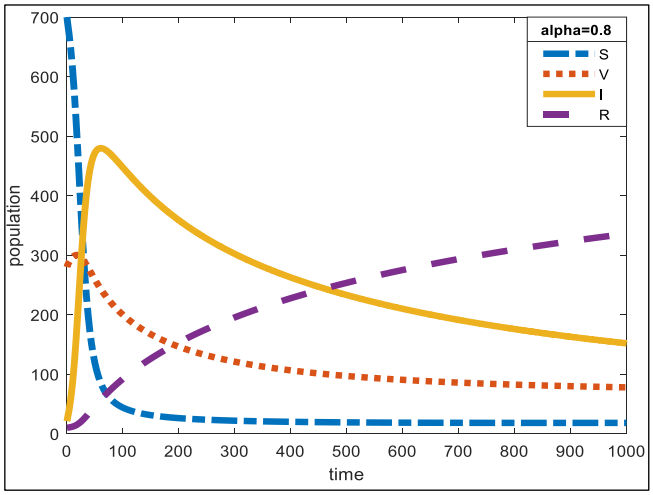

Figure 2. Pattern of compartments for α=0.8

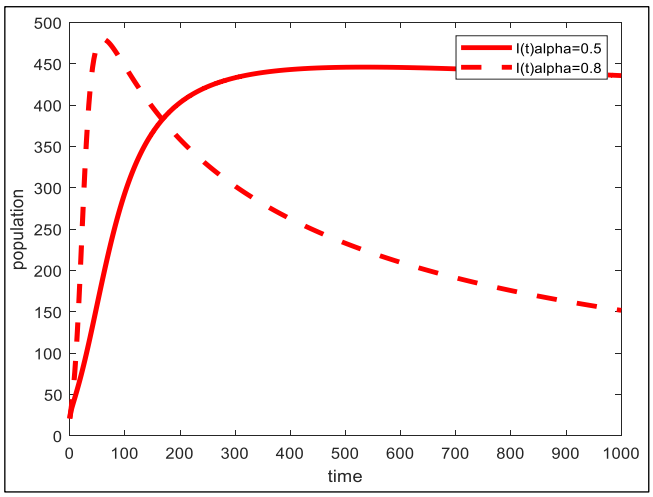

Figure 3. Comparison of compartment *I* by means of α

As the value of alpha reduces, the compartments converge faster. According to the results, for α=0.5, the infected compartment *I* is higher than the case of α=0.8 which is given in Figure 3. Similarly, in the vaccination compartment *V*, as the value of alpha decreases, the population will be higher. On the other hand, the converse of this situation happens in the recovery compartment *R*, that is, as alpha decreases, there are less people in the recovery compartment. This result can be seen from the comparison of Figure 1 and Figure 2.

5. Conclusion

According to the findings, as the value of alpha decreases, the various compartments converge faster. In other words, the process occurs quicker and the memory effect is revealed so that we can see what occurs at different compartments irrespective of time. Reduce in alpha showed an increase in the infected and vaccinated compartment; a decrease in the recovery compartment, which is expected to happen in the endemic case.

Beside, R_0 is greater than 1 which means that the disease still exists and continues to spread. The existence of E_0 and E^* proves that it is possible to have an environment without COVID-19 or an endemic environment with COVID-19.

Conflict of interest

The authors declare that there is no conflict of interest.

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