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An analysis of a nonlinear susceptible-exposed-infected-quarantine-recovered pandemic model of a novel coronavirus with delay effect

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**ABSTRACT**

In the present study, a nonlinear delayed coronavirus pandemic model is investigated in the human population. For study, we find the equilibria of susceptible-exposed-infected-quarantine-recovered model with delay term. The stability of the model is investigated using well-posedness, Routh Hurwitz criterion, Volterra Lyapunov function, and Lasalle invariance principle. The effect of the reproduction number on dynamics of disease is analyzed. If the reproduction number is less than one then the disease has been controlled. On the other hand, if the reproduction number is greater than one then the disease has become endemic in the population. The effect of the quarantine component on the reproduction number is also investigated. In the delayed analysis of the model, we investigated that transmission dynamics of the disease is dependent on delay terms which is also reflected in basic reproduction number. At the end, to depict the strength of the theoretical analysis of the model, computer simulations are presented.

**Introduction**

Coronavirus is a group of viruses that causes illness like the common cold, respiratory syndrome, and severe acute respiratory syndrome. A novel coronavirus (COVID-19) firstly saw in humans. This is the new one that has not been seen in humans previously [1]. The antibiotic has been discovered as a novel covered RNA coronavirus-2 that has been currently named as SARS coronavirus-2 (SARS-COV-2) which has emerged evolution similarly to SARS-COV-3. Infected people have been recorded both in the infirmary and in-home. The world health organization (WHO) has recently declared coronavirus disease 2019 (COVID-19) as a pandemic. Due to the rapid spread of COVID-19, we established that an updated analysis of the world might help to identify the dynamics of coronavirus. Many peoples have died around the world due to this novel coronavirus [2]. Arif et al. [3,4] investigated the stochastic analysis of typhoid fever and hepatitis B diseases. Baleanu et al. [5] presented the dynamics of influenza which is basically the symptoms of coronavirus, in the human population with constant vaccination strategy. Li et al. [6] studied the classification of brain waves in the human population. Lin et al. [7] presented the coronavirus model in the population of China under the assumption of an individual’s reactions and government action. Shereen et al [8] investigated the characteristics of coronavirus in the human population. Shim et al. [9] studied the dynamics of coronavirus in the population of South Korea. Tahir et al. [10] presented the dynamics of middle east respiratory syndrome in the human population. Zhao et al. [11] studied control techniques regarding the pandemic of coronavirus. World Health Organization (WHO) declared the outbreak of coronavirus is a global issue. Due to this pandemic, this project is a platform for all researchers to introduce new delayed mathematical modeling for a better understanding of the extinction and persistence of coronavirus. Thus, the biologically consistent mathematical modeling for the transmission and...
dynamics of COVID-19 is an extensive need around the world. Ivorra et al. [12] investigated the mathematical modeling of coronavirus disease by taking undetected infections. Yang et al. [13] presented a mathematical model for novel coronavirus the case study Wuhan, China. Sameni [14] presented the mathematical modeling of different epidemic diseases and discussed a special case about Covid-19. Rajagopal et al. [15] investigated the fractional order model for the outbreak of coronavirus and predict different results in the field of a fractional derivative. Baleanu et al. [16] presented the coronavirus model by using the Caputo-Fabrizio derivative in the field of a fractional derivative. Goufo et al. [17] investigated the joint dynamical analysis of the equilibria of the mathematical model of HIV and COVID-19. Kouidere et al. [18] studied the dynamics of the coronavirus pandemic model with an optimal control strategy and its transmission. Mandal et al. [19] presented the prediction and control techniques for the coronavirus model with the concept of mathematical modeling. Naveed et al. [20] designed the compartmental modeling of the coronavirus pandemic with delay strategies in the subpopulation of humans as susceptible-exposed-systematical infected-a systematical infected and recovered. Shatanawi et al. investigated the nonstandard computational method on the dynamics of stochastic coronavirus model in which main focus is positivity, boundedness, consistency and stability of aforementioned purpose [24,25]. Atangana et al. gives an authentic idea for the modeling of coronavirus pandemic in which sea food market, asymptomatic and symptomatic humans are the main sources for the prevalence of virus. How the effective use of facemask may eradicate the dreadful virus [26]. On the other way, great idea was delivered by scientist in which the use of fractal fractional derivative technique and how the lack down strategy may help to cure the virus and better than any type of vaccination [27]. Atangana et al. studied the dynamics of Ebola virus homologic fever in the west countries of Africa. Also, give the suitable precautions for the treatment of such dreadful infection [28]. Raza et al. studied the effect of delay tactics on the transmission dynamics of HIV/AIDS [29]. Due to the unavailability of vaccines for the coronavirus worldwide, delay factors such as social distance, quarantine, travel restrictions, extended holidays, hospitalization, and isolation have contributed to controlling the coronavirus epidemic. That is the reason, we motivated to do mathematical modeling of coronavirus pandemic model with delay strategy. So, we have investigated the delay differential equations in this study due to the delay term. The flow of paper has based on the following sections: In Section “Formulation of the model”, described the invention of the nonlinear delayed model and its equilibrium points. In Section “Local stability”, the local stability of the proposed model is discussed. In Section “Global stability”, the global stability of the proposed model is presented. Before closing, in Section “Computer simulations”, computer simulations for the solution of susceptible-exposed-infected-quarantine-recovered pandemic models with a different strategy. In the end, the conclusion of the study is presented.

**Formulation of the model**

In this section, we considered the total population of humans, presented as $N$. Define a function of population dynamics $f : N \rightarrow [0, \infty)$, for all $t \in [-\tau, 0], \tau \in [0, \infty)$. The susceptible component of humans is represented as $S$, the exposed component of humans is represented as $E$, the infected component of humans is represented as $I$, the quarantine component of humans is represented as $Q$ and the recovered component of humans is represented as $R$, as desired (Fig. 1).

Assume, the nonnegative constants of the model as $\Lambda$ (denote the natural birth rate of humans), $\beta_1$ (denotes the infection rate of infected humans who are interaction with susceptible humans), $\beta_2$ (denotes the infection rate of exposed humans who are interaction with susceptible humans), $q_1$ (denotes the rate of exposed humans who are directly moving to quarantine component), $K$ (denotes the rate of natural immunity), $\alpha$ (denotes the rate of exposed humans who are infected), $r$ (denotes the rate of infected humans who are recovered after vaccina-

\[ \begin{align*} \frac{dS}{dt} &= \Lambda - \beta_1 IS(t) - \beta_2 ES(t) - \mu S, \\
\frac{dE}{dt} &= \beta_1 IS(t) - \alpha E - \mu E, \\
\frac{dI}{dt} &= \beta_2 ES(t) - r I, \\
\frac{dQ}{dt} &= \alpha E - \mu Q, \\
\frac{dR}{dt} &= r I - \mu R. \end{align*} \]
tion or quarantine), $d_1$ (denotes the rate of death of infected humans due to corona virus), $q$ (denotes the rate of quarantine humans who are recovered) $d_2$ (denotes the rate of quarantine humans who dies after quarantine because they have a weak immune system or having diseases) and $\mu$ (denotes the natural death rate of humans components).

After that, the dynamics with nonlinear delayed equations are as follows:

$$\frac{dS(t)}{dt} = \Lambda - (\beta_1(t-t) + \beta_2 E(t-t)) S(t) e^{-\mu t} - \mu S(t), \forall t$$

$$E(t) = (\beta_1 E(t-t) + \beta_2 E(t-t)) S(t) e^{-\mu t} - q I(t-t) - KE(t) - \alpha E(t) - \mu E(t), \forall t \in[-\tau, 0], t \in[0, \infty).$$

$$I(t) = \alpha E(t) - r I(t) - \mu I(t) - d_1 I(t), \forall t \in[-\tau, 0].$$

$$Q(t) = q I(t) - q Q(t) - d_2 Q(t), \forall t \in[-\tau, 0].$$

$$R(t) = \mu E(t) + r I(t) + Q(t) - \mu R(t), \forall t \in[-\tau, 0].$$

with initial conditions $S_0 = S(0), E_0 = E(0), I_0 = I(0), Q_0 = Q(0), R_0 = R(0)$. Also, the feasible region of the equations (1) to (5) is $\Omega = \{(S, E, I, Q, R) : S > E + I + Q + R \leq \frac{q}{\beta}, S \geq 0, E \geq 0, I \geq 0, Q \geq 0, R \geq 0\}$. Note that, the solutions of a given system are positive and bounded, and lies in the feasible region.

**Model equilibria**

At the analysis that the system (1–5) has three types of equilibria as follows: Trivial equilibrium (TE) is $C_1 = (S^*, E^*, I^*, Q^*, R^*) = (\frac{\beta_2}{q}, 0, 0, 0, 0)$, virus absenteeism equilibrium (VAE) is $C_2 = (S^*, E^*, I^*, Q^*, R^*)$, where, $S^1 = \frac{q}{\beta r + d_1}$ and $R^1 = \frac{\beta_2}{\beta r + d_2}$. 

**Reproduction number**

In this section, we employ the next generation matrix (NGM) method to the system (1–5), for obtaining reproduction number with calculating the transmission and transition matrices as follows:

$$E = \begin{bmatrix}
    \beta_2 Se^{-\mu t} & \beta_1 Se^{-\mu t} & 0 & 0 & 0
\end{bmatrix}$$

$$Q = \begin{bmatrix}
    0 & 0 & 0 & 0 & 0
\end{bmatrix}$$

$$R = \begin{bmatrix}
    0 & 0 & 0 & 0 & 0
\end{bmatrix}$$

$$V = \begin{bmatrix}
    (k + \alpha + \mu + q_1) & 0 & 0 & 0 & 0
    -\alpha & (r + \mu + d_1) & 0 & 0 & 0
    -q_1 & 0 & (q + \mu + d_2) & 0 & 0
    -k & -r & -q & -\mu & 0
\end{bmatrix}$$

Notice that, the spectral radius of $FV^{-1}$, is called reproduction number and $R_0 = \frac{\beta_2 q}{(k + \alpha + \mu + d_1) (r + \mu + d_2) \mu}.$

**Local stability**

In this section, we satisfied the well-posed theorem at the both equilibria as follows:

**Theorem.** The virus absenteeism equilibrium (VAE), $C_1 = (S^*, E^*, I^*, Q^*, R^*) = (\frac{\beta_2}{q}, 0, 0, 0, 0)$ is locally asymptotical stable (LAS) if $R_0 < 1$, forgiven $t \in[-\tau, 0]$ and $t \in[0, \infty).$

**Proof.** Considering the Jacobean matrix (JM) for the system (1–5) at $C_1$ is estimated as follows:

$$J(C_1) = \begin{bmatrix}
    -\mu & \frac{\beta_2 Se^{-\mu t}}{\mu} & -\frac{\beta_1 Le^{-\mu t}}{\mu} & 0 & 0
    0 & -\frac{\beta_1 Se^{-\mu t}}{\mu} & 0 & 0
    \beta_1 Le^{-\mu t} - (k + \alpha + \mu + q_1) & \frac{\beta_1 Se^{-\mu t}}{\mu} & 0 & 0
    0 & 0 & \alpha & -\frac{(r + \mu + d_1) - (q + \mu + d_2)}{q - \mu}
    0 & 0 & -q & -\mu
\end{bmatrix}$$

Notice that, two eigenvalues are repeated as $\lambda_1 = -\mu < 0, \lambda_2 = -\mu < 0$ and third eigenvalue is $\lambda_3 = -(q + \mu + d_2) < 0$ and $|J(C_1) - \lambda I| = \begin{bmatrix}
    \frac{\beta_2}{\mu} & 0 & -\frac{\beta_1}{\mu} & 0
    0 & \frac{\beta_1}{\mu} & 0 & 0
    \frac{\beta_1}{\mu} & 0 & \alpha
    0 & 0 & -q & -\mu
\end{bmatrix} = 0.$

$$J^2 + \lambda (\beta_2 - \alpha a_2 + \alpha_1) + (a_2 a_2 - \alpha_2 a_2 - \alpha a_2 a_1) = 0$$

where, $\sigma = \alpha_1, (k + \alpha + \mu + q_1) = a_2, (r + \mu + d_1) = a_3.$

By using the second order Routh-Hurwitz Criterion as, $a_3 + a_2 - \alpha a_2 > 0$, if $k + \alpha + \mu + q_1 + (r + \mu + d_1) - \frac{\beta_2}{\mu} > 0$, $R_0 = \frac{\beta_2 q}{(k + \alpha + \mu + d_1) (r + \mu + d_2) \mu} < 1$ and $(q_2 a_2 - \alpha a_2 a_2 - \alpha a_2 a_1) > 0$ if $R_0 < 1$.

Hence, by Routh Hurwitz criteria, the given equilibria, $C_1$ is locally asymptotical stable because all eigenvalues are negative.

**Theorem.** The virus incidence equilibrium (VIE), $C_2 = (S^*, E^*, I^*, Q^*, R^*)$ is locally asymptotical stable (LAS) if $R_0 > 1$, forgiven $t \in[-\tau, 0]$ and $t \in[0, \infty).$

**Proof.** Considering the Jacobean matrix (JM) for the system (1–5) at $C_2$ is estimated as follows:

$$R^1 = \begin{bmatrix}
    0 & 0 & 0 & 0 & 0
\end{bmatrix}$$

Notice that, the eigen values are $\lambda_1 = -\mu < 0, \lambda_2 = -(q + \mu + d_2) < 0$ and $|J(C_2) - \lambda I| = \begin{bmatrix}
    \frac{\beta_2}{\mu} & 0 & 0 & 0
    0 & \frac{\beta_1}{\mu} & 0 & 0
    0 & 0 & \alpha
    0 & 0 & -q & -\mu
\end{bmatrix} = 0.$

$$J^2 + \lambda \left( (k + \alpha + \mu + q_1) + (r + \mu + d_1) - \frac{\beta_2}{\mu} \right) > 0$$

Notice that, two eigenvalues are repeated as $\lambda_1 = -\mu < 0, \lambda_2 = -\mu < 0$ and third eigenvalue is $\lambda_3 = -(q + \mu + d_2) < 0$ and $|J(C_2) - \lambda I| = \begin{bmatrix}
    \frac{\beta_2}{\mu} & 0 & 0 & 0
    0 & \frac{\beta_1}{\mu} & 0 & 0
    \frac{\beta_1}{\mu} & 0 & \alpha
    0 & 0 & -q & -\mu
\end{bmatrix} = 0.$

$$J^2 + \lambda \left( (k + \alpha + \mu + q_1) + (r + \mu + d_1) - \frac{\beta_2}{\mu} \right) > 0$$

Notice that, two eigenvalues are repeated as $\lambda_1 = -\mu < 0, \lambda_2 = -\mu < 0$ and third eigenvalue is $\lambda_3 = -(q + \mu + d_2) < 0$ and $|J(C_2) - \lambda I| = \begin{bmatrix}
    \frac{\beta_2}{\mu} & 0 & 0 & 0
    0 & \frac{\beta_1}{\mu} & 0 & 0
    \frac{\beta_1}{\mu} & 0 & \alpha
    0 & 0 & -q & -\mu
\end{bmatrix} = 0.$

$$J^2 + \lambda \left( (k + \alpha + \mu + q_1) + (r + \mu + d_1) - \frac{\beta_2}{\mu} \right) > 0$$
Theorem: The virus absenteeism equilibrium (VAE), $C_1 = (S^a, E^a, I^a, Q^a)$, $R^a = \left(0, 0, 0, 0\right)$ is globally asymptotically stable (GAS) if $R_0 < 1$, forgiven $t \in (-\infty, 0]$ and $t \in (0, \infty)$.

Proof: Considering the Volterra Lyapunov function $V : \Omega \rightarrow R$, as well-defined:

$$V = \left( S - S^0 \right) \log \frac{S}{S^0} + E + I + Q + R, \forall (S,E,I,Q,R) \in \Omega.$$ 

By using third order Routh-Hurwitz Criterion,

$$\begin{vmatrix}
    -b_1 - \mu - \lambda & -b_2 & -b_3 & -b_4 \\
    b_1 & b_2 - \lambda & b_3 & b_4 \\
    0 & \alpha & -b_3 - \lambda & 0 \\
    0 & 0 & 0 & -\mu - \lambda
\end{vmatrix} = 0$$

and

$$\lambda^2 + (b_1 - b_2 + b_1 + b_3 + \mu)\lambda + (b_1 b_2 - b_2 b_3 + b_3 b_4 - b_3 \mu + b_3 \mu + b_3 \mu = 0$$

where,

$$b_1 = \beta_1 e^{-\mu \tau}, b_2 = \beta_2 e^{-\mu \tau}, b_3 = k + \mu + q_1, b_4 = \beta_1 e^{-\mu \tau} + \beta_2 e^{-\mu \tau}, b_5 = r + \mu + d_4$$

By using third order Routh-Hurwitz Criterion,

$$\begin{vmatrix}
    -b_1 - b_2 + b_3 + b_4 + b_5 + \mu & (b_1 b_2 b_3 - b_2 b_3 b_4 + b_3 b_4 \mu - b_4 \mu) \\
    b_1 b_2 b_3 - b_2 b_3 b_4 + b_3 b_4 \mu - b_4 \mu & r + \mu + d_4 \\
    0 & \alpha & -b_4 - \mu \\
    0 & 0 & 0 & -\mu
\end{vmatrix} = 0,$$

if $R_0 > 1$, then $b_1 b_2 b_3 - b_2 b_3 b_4 + b_3 b_4 \mu - b_4 \mu$, if $R_0 > 1$.

Thus, we have concluded that all eigenvalues are negative and by Routh Hurwitz (RH) criteria, the given equilibria, $C_2$ is locally asymptotically stable.

Global stability

In this section, we satisfied the well-known theorems on both equilibria as follows:

Theorem: The virus incidence equilibrium (VIE), $C_2 = (S^I, E^I, I^I, Q^I)$, $R^I = \left(\frac{m}{a}, 0, 0, 0\right)$ is globally asymptotically stable (GAS) if $R_0 > 1$, forgiven $t \in (-\infty, 0]$, and $t \in (0, \infty)$.

Proof: Considering the Volterra Lyapunov function $V : \Omega \rightarrow R$, as well-defined:

$$V = \left( S - S^I \right) \log \frac{S}{S^I} + E + I + P + Q + R, \forall (S,E,I,P,Q,R) \in \Omega.$$
Fig. 3. Graph of the system (1) to (5) at the presence of corona virus. (a) susceptible humans at VIE (b) Exposed humans at VIE (c) Infected Humans at VIE (d) quarantine humans at VIE (e) Recovered humans at VIE.
In this section, we discuss the simulations of the Eq. (1) to Eq. (5), by using the physical values of parameters presented in Table 1.

Example 1: (Simulation at virus incidence equilibrium) In this study, we present the graph of virus incidence equilibrium (VIE) at the given real data as the value of the threshold reproduction number is $R_0 = 1.0222 > 1$. Therefore, the system converges to the $C_2 = 0.4891, 0.4353, 0.0621, 0.00069721, 0.0128$. Fig. 2 exhibits the solution of the system (1) to (5) with the absence of delay by using the values of the parameters presented in Table 1 and touches to true equilibria of the model, as desired.

Example 2: (Simulation at virus incidence equilibrium) In this example, we depict the graph of virus incidence equilibrium (VIE) at the given real data as the value of the threshold reproduction number is $R_0 = 1.0222 > 1$. Therefore, the system converges to the $C_2 = 0.4891, 0.4353, 0.0621, 0.00069721, 0.0128$. Fig. 3 exhibits the solution of the system (1) to (5) with the absence of delay by using the values of the parameters presented in Table 1 and converges to true equilibria of the system, as desired.

Example 3: (Simulation for the effect of delay term on reproduction number) Let, $\tau = 1.022$. We can observe that, the effective use of delay tactics may decrease the value of threshold number and even though the given system switch from virus incidence equilibrium to virus absenteeism equilibrium. Thus, the absence of coronavirus is stable. But, Fig. 4 shows that, infection could be controlled due to the effective uses of different kind of delay tactics, as desired.

Example 4: (Simulation for the effect of delay term on the infected component of model) Let now assume for different values of $\tau$ (delay term). We can see that, the infected step by step moves towards zero means infection is controlled. Therefore, Fig. 5 shows that the delay strategy or delay tactics such as vaccination, quarantine, travel restriction, holidays and distancing measure, etc. are a vital role to control the current strain of coronavirus.

Conclusion

In the present study, we have analyzed the dynamics of the coronavirus model in the human population with the technique of mathematical modeling of the delayed term. We have categorized the whole population into five components of subpopulations. We have studied the system of nonlinear delayed differential equations for the dynamics of coronavirus in humans. We have proved its stability locally and globally by using well-known theorems. We have examined the validity of delay term on the reproduction number and the infected component of humans. The dynamics of the investigated system depends on the use of delay terms. Furthermore, delay strategies such as social distancing, placement of isolation, extension in holidays, restriction on travels are helpful to overcome the dreadful situation of coronavirus. In the future, our study can be extended in stochastic spatiotemporal and fraction order models, in the sense of delayed models [22,23]. This type of modeling could also be studied with different fractal fractional derivatives as presented in [30,31]. Also, numerical algorithms may be designed in the modeling of epidemic diseases using fuzzy differential equations and stochastic differential equations of fractional order [32-35]. We have concluded that the analysis of delayed mathematical modeling (DMM) plays a significant role in the dynamics of pandemic models.

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Declaration of Competing Interest

All the authors have no conflict of interest.
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