A mathematical model to study the spread of COVID-19 and its control in India

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Abstract: In this article, a nonlinear mathematical model is proposed and analyzed to study the spread of coronavirus disease (COVID-19) and its control. Due to sudden emergence of a peculiar kind of infection, no vaccines were available, and therefore, the nonpharmaceutical interventions such as lockdown, isolation, and hospitalization were imposed to stop spreading of the infectious disease. The proposed model consists of six dependent variables, namely, susceptible population, infective population, isolated susceptible population who are aware of the undesirable consequences of the COVID-19, quarantined population of known infectives (symptomatic), recovered class, and the coronavirus population. The model exhibits two equilibria namely, the COVID-19-free equilibrium and the COVID-19-endemic equilibrium. It is observed that if basic reproduction number $R_0 < 1$, then the COVID-19-free equilibrium is locally asymptotically stable. However, the endemic equilibrium is locally as well as nonlinearly asymptotically stable under certain conditions if $R_0 > 1$. Model analysis shows that if safety measures are adopted by way of isolation of susceptibles and quarantine of infectives, the spread of COVID-19 disease can be kept under control.

Keywords: endemic equilibrium, isolated susceptible, basic reproduction number, quarantined infectives

MSC 2020: 92-08, 92-10, 34D20, 34D23, 92D30, 92Bxx

1 Introduction

The coronavirus disease (COVID-19) pandemic is of great concern to researchers, governments, and the general public because of its worldwide escalation and high number of deaths associated with it. The COVID-19 disease is an infectious disease caused by coronavirus, which causes illness in animals and humans. On December 31, 2019, a new and unusual case of pneumonia was reported at the World Health Organization (WHO) country office in China. A large number of such cases have taken place in the Chinese city of Wuhan. It was noted that all cases were linked to the Wuhan Seafood Market, which trades in live and fish species, including poultry, bats, marmots, and snakes [21]. It was later discovered that this infection occurred due to a new coronavirus called 2019 novel coronavirus (2019-n COV) [15]. Later, on February 11, 2020, the International committee on viral rehabilitation renamed acute respiratory syndrome coronavirus 2 as SARS-COV-2. Coronavirus SARS-COV-2, which causes COVID-19, is thought to have originated from bats and spread to snakes and pangolins, which is why it has spread to humans, possibly
through the contamination of wildlife as sold in Chinese meat markets [3]. In India, the first case of COVID-19 was reported in Kerala on January 30, 2020. In the same year, on March 9, 44 confirmed cases were reported in India, and as of April 5, according to the Ministry of Health and Family Welfare, a total of 3,577 cases of COVID-19 were reported [24].

According to WHO, the symptoms of this deadly disease are dry cough, difficulty in breathing, and fever. Some patients may also experience diarrhea, pain, or runny nose, and symptoms may begin gradually. In some cases, the infected persons show no symptoms, and many recover from the disease without any special treatment. Older people and those with some medical problems, such as diabetes and high blood pressure, are at greater risk of developing the disease [24]. It is easily transmitted directly from a person to another one in proximity by inhaling small droplets released by a person affected with COVID-19 during coughing, sneezing, etc. These droplets may also deposit on the objects, surfaces, and areas or remain airborne for a period of time and if susceptible individuals come in contact with these objects or areas and touch their eyes, nose, or mouth after touching these surfaces can also catch COVID-19 infection. Thus, the infection not only spreads directly by susceptible-infective interaction but also indirectly through effective contacts with affected surfaces.

Several nonpharmaceutical measures such as regular hand washing, wearing of face cover/mask, social distancing, and avoidance of crowds were suggested to stop the escalation of pandemic. In 2021, the second phase of COVID-19 was more dangerous than the previous one in 2020 where only those who have traveled abroad tested positive for respiratory diseases. At this stage, the community spread did not occur. Thus, the spread of COVID-19 disease was relatively small. In the second phase, local infections started to occur and susceptibles became infected through contacts with people who already had it. The people also experienced infection in situations such as parties, weddings, or family reunions. Although the number of infected individuals increased at this stage, they were still able to detect the disease and were provided medical care. In the third stage, transmission of disease to the public occurred and outbreaks spread rapidly.

Some mathematical models have been proposed and analyzed for COVID-19 outbreaks in different countries [1,2,8–10,18,20,23,25]. Persistence of coronaviruses on inanimate surfaces and their inactivation with biocidal agents are discussed by Kampf et al. [12]. They concluded that human coronaviruses can persist in nonliving areas for up to 9 days. In addition, Khan and Atangana [14] designed a dynamic model for the novel coronavirus and observed that the marine fish market has enough sources of infection that can infect humans. The conditions for the eradication of this disease are determined in the model proposed by Monterio [19], which shows that the number of infected people increases as time goes on. In addition, Khajanchi and Sarkar [13] proposed a compartmental model to explain the transport capacity of COVID-19 and measured the model with daily and aggregate cases in four Indian provinces. The authors have conducted a detailed analysis of the theories in terms of basic reproduction numbers. Modified SIR model is used in ref. [18] to indicate the actual number of cases of infection and certain loads on isolation wards and several care centers. Sarkar et al. [21] proposed a mathematical model predicting the dynamics of COVID-19 in 17 regions of India. Their findings highlighted the fact that the level of communication between uninfected and infected people can be reduced by the strong segregation that is imposed on the affected people. The authors further pointed out that the precise course of an epidemic depends largely on the costs of monitoring, isolation, and forced isolation [11,16]. The closure strategy is one of the major steps taken to curb the spread of disease [5,17]. Since the virus can easily spread to overcrowded areas, social distancing measures are taken to increase physical space between people to slow down the spread of the virus. Batista [4] has learned to process growth retardation model used for measurement with the final size of the coronavirus epidemic.

In the aforementioned studies, the mathematical models are proposed with many facts related to the spread of COVID-19 but the growth of viral density is not taken into account. As has been pointed above, the COVID-19 disease can also spread indirectly upon contacts with small droplets deposited on objects, surfaces, areas, or through suspended air borne virus as a result of coughing, sneezing, or exhalation of an affected person, and the susceptibles may get exposed to COVID-19 infection after coming in contact with the aforementioned factors.
Keeping this aspect in view, the objective of this article is to explore the role of viral density in order to study the spread of COVID-19 pandemic where the viral density is assumed to be proportional to the infected individuals (symptomatic or asymptomatic). A mathematical model is formulated by considering the total population to be variable using simple mass action incidence.

2 Mathematical model

To formulate a pandemic model, let \( N(t) \) be the total human population in a region under consideration affected by coronavirus disease (COVID-19) at any time \( t \). The population is divided into five subpopulations, namely, susceptible population \( X(t) \), infective population \( Y(t) \), isolated susceptibles population \( X_i(t) \) who are aware of undesirable consequences of the COVID-19, population of quarantined infectives (symptomatic) \( Y_i(t) \), and recovered class with density \( R(t) \). Let \( V(t) \) be the cumulative density of COVID-19 virus present in the environment, emitted from infectives at any time \( t \).

The following assumptions are made to model the dynamics of the transmission of the coronavirus disease (COVID-19),
(i) The recruitment rate of susceptibles \( A \) is constant.
(ii) Susceptibles become infected directly by coming in contact with infectives with a contact rate \( \beta \) (i.e., \( \beta XY \)).
(iii) Susceptibles become infected indirectly by coming in contact with contaminated surfaces having coronaviruses with a contact rate \( \lambda \) (i.e., \( \lambda XV \)).
(iv) Isolated aware susceptibles obtain infected by a rate upon contact with infectives (i.e., \( \gamma \varepsilon X_iY \), \( 0 \leq \varepsilon \leq 1 \)).
(v) Isolated aware susceptibles also obtain infected by a rate \( \gamma(1 - \varepsilon) \) upon contact with coronavirus present on the contaminated surfaces (i.e., \( \gamma(1 - \varepsilon)X_iV \)).

In view of the aforementioned assumptions and considerations, the transmission dynamics of the spread of COVID-19 is expressed in the following system of nonlinear differential equations:

\[
\frac{dX}{dt} = A - \beta XY - \lambda VX - dX + \lambda_1 X_i, \tag{1}
\]

\[
\frac{dY}{dt} = \beta XY + \lambda VX + \gamma((1 - \varepsilon)VX_i + \varepsilon YX_i) - (d + \delta_1 + \beta_1)Y, \tag{2}
\]

\[
\frac{dX_i}{dt} = \lambda_i X_i - d \lambda X_i - \gamma((1 - \varepsilon)VX_i + \varepsilon YX_i), \tag{3}
\]

\[
\frac{dY_i}{dt} = \beta_i Y_i - (d + a + \delta_2)Y_i, \tag{4}
\]

\[
\frac{dR}{dt} = \delta_1 Y + \delta_2 Y_i - dR, \tag{5}
\]

\[
\frac{dV}{dt} = \theta Y - \theta_0 V, \tag{6}
\]

where \( X(0) > 0, Y(0) \geq 0, X_i(0) \geq 0, Y_i(0) \geq 0, R(0) \geq 0, \) and \( V(0) \geq 0 \).

As mentioned earlier, susceptibles get infected by rates \( \beta XY \) and \( \lambda VX \), which increase the growth rate of infective individuals. The constants \( \beta \) and \( \lambda \) are the transmission rates of disease directly by infectives \( Y \) and indirectly by coming in contact with contaminated surfaces having viral density \( V \), respectively. It is assumed that knowing the undesirable consequences of the pandemic, aware susceptibles keep themselves in isolation. The constant \( \lambda_i \) is the rate of transfer of susceptible people to isolated aware susceptible class. It is reasonable to assume that some of the isolated susceptible people may become susceptible again joining susceptible population class. Thus, \( \lambda_{1i} \) is the rate at which people from the isolated aware susceptible class move to susceptible class. The constant \( d \) is the natural death rate coefficient of human population. Further, the isolated susceptible people may also get infected upon casual contact with infectives and contaminated...
surfaces filled with coronaviral density, thus increasing the growth rate of infectives. The constant \( y < \min(\beta, \lambda) \), is the rate of transfer of isolated susceptibles to infected class (i.e., \( yX_iY \)). A fraction of this transmission (i.e., \( yeX_iY, 0 \leq \varepsilon \leq 1 \)) is due to interaction of susceptibles with infectives and the other (i.e., \( y(1 - \varepsilon)X_iV \)) is due to coming in contact with virus density present on the contaminated surfaces. It is observed that if proper safety precautions (such as use of face cover/mask, comply with social distancing, not touching the surfaces, and use of soap and/or sanitizer for hand wash) are taken by both susceptibles and infectives, then the possibility of the susceptibles to get infected will reduce and some of the infectives may get well and join recovered class. Further, if infected individuals are found COVID-19 positive, they are quarantined in hospitals for proper treatment for a prescribed time period. Thus, infected individuals are hospitalized by a rate \( \beta_1 \) and are recovered by a rate \( \delta_1 \), thus joining quarantined and recovered class, respectively. After undergoing proper treatments during hospitalization and getting well, these people join recovered class by a rate \( \delta_2 \). The constant \( \alpha \) is the disease-induced death rate. It is assumed that when an infected person (known or unknown COVID-19-positive individuals) touches a surface, the surface also gets infected with COVID-19 virus. Therefore, it is reasonable to assume that the growth rate of COVID-19 viral density is directly proportional to the infected human population. The constant \( \theta \) represents the growth rate of COVID-19 virus on the surfaces, \( \theta_0 \) being its natural depletion rate.

Using the assumption \( N = X + Y + X_i + Y_i + R \), Models (1)–(6) reduces to the following system:

\[
\begin{align*}
\frac{dN}{dt} &= A - dN - aY_i, \\
\frac{dY}{dt} &= \beta Y(N - Y - X_i - Y_i - R) + \lambda V(N - Y - X_i - Y_i - R) - (d + \delta_1 + \beta_1)Y + yeXY + y(1 - \varepsilon)X_iV, \\
\frac{dX_i}{dt} &= \lambda_i(N - Y - X_i - Y_i - R) - (d + \lambda_{1i})X_i - yeXY + y(1 - \varepsilon)X_iV, \\
\frac{dY_i}{dt} &= \beta_1Y - (d + \alpha + \delta_2)Y_i, \\
\frac{dR}{dt} &= \delta_1Y + \delta_2Y_i - dR, \\
\frac{dV}{dt} &= \theta Y - \theta_0 V.
\end{align*}
\]

Now, we will proceed with reduced Models (7)–(12).

**Remark 1.** From the model system, it is noted here that \( \beta > y \) and \( \lambda > y \).

**Lemma 1.** The set

\[
\Omega = \{(N, Y, X_i, Y_i, R, V) : \frac{A}{a + d} \leq N \leq \frac{A}{d}, 0 < Y \leq \frac{A}{a + d}, 0 < X_i \leq X_{im}, 0 < Y_i \leq Y_{im}, 0 \leq R \leq R_m, 0 \leq V \leq V_m\},
\]

where \( X_{im} = \frac{\lambda A}{d(d + \lambda_i)} < \frac{A}{d}, Y_{im} = \frac{\beta_i A}{(a + d)(d + a + \delta_2)}, R_m = \frac{A}{d(a + d)} \left[ \delta_1 + \frac{\beta_1 \delta_2}{(d + a + \delta_2)} \right], \) and \( V_m = \frac{\alpha A}{\delta_2 (a + d)} \) attract all solutions initiating in the interior of positive orthant.

(See Appendix A for proof)

### 3 Equilibrium analysis and basic reproduction number

Models (7)–(12) have the following two equilibria:
The COVID-19-free equilibrium $E_0(N_0, X_{00}, 0, 0, 0), \]

where $N_0 = \frac{A}{d}$ and $X_{00} = \frac{A \lambda}{d(h_1 + d + h_0)}$.

The existence of $E_0$ is obvious. The equilibrium $E_0(N_0, X_{00}, 0, 0, 0)$ implies that in the absence of infective individuals and COVID-19 virus density deposited on surfaces, areas, etc., the disease will not persist.

To determine basic reproduction number $R_0$ [7], it is sufficient to take equations (8), (10), and (12) satisfying necessary constraints:

\[
\frac{dY}{dt} = \beta Y (N - Y - X_i - Y_i - R) + \lambda Y (N - Y - X_i - Y_i - R) - (d + \delta_i + \beta_1) Y + \gamma \xi X_i Y + \gamma (1 - \xi) X_i V,
\]

\[
\frac{dY_i}{dt} = \beta_i Y - (d + \alpha + \delta_i) Y_i,
\]

\[
\frac{dV}{dt} = \theta Y - \theta_0 V.
\]

From the aforementioned system, the infectious matrix $F$, corresponding to new infections in the population at disease-free equilibrium, is

\[
F = \begin{bmatrix}
\frac{\beta A (d + \lambda_{11}) + \gamma \xi \lambda_i A}{d(d + \lambda_i + \lambda_{11})} & 0 & \frac{\lambda A (d + \lambda_{11}) + \gamma (1 - \xi) \lambda_i A}{d(d + \lambda_i + \lambda_{11})} \\
0 & 0 & 0 \\
0 & 0 & 0
\end{bmatrix}.
\]

The nonsingular matrix $V$, denoting the transfer terms at disease-free equilibrium, is

\[
V = \begin{bmatrix}
d + \delta_i + \beta_1 & 0 & 0 \\
-\beta_i & d + \alpha + \delta_2 & 0 \\
-\theta & 0 & \theta_0
\end{bmatrix}.
\]

Now, basic reproduction number $R_0$ is the spectral radius of the next-generation matrix $FV^{-1}$ and is given as $R_0 = R_1 + R_2$, where

\[
R_1 = \frac{A}{d} \frac{\beta (d + \lambda_{11}) + \gamma \xi \lambda_i}{(d + \lambda_i + \lambda_{11})(d + \delta_i + \beta_1)} \quad \text{and} \quad R_2 = \frac{A}{d} \frac{(\lambda(d + \lambda_{11}) + (1 - \xi)\lambda_i)\theta}{\theta_0(d + \lambda_i + \lambda_{11})(d + \delta_i + \beta_1)}.
\]


The equilibrium $E^*(N^*, Y^*, X_i^*, Y_i^*, R^*, V^*)$ implies that in the presence of infective individuals and surfaces contaminated with COVID-19 virus, disease will always persist. Some infective individuals, which are kept under proper treatment in the form of isolation and hospitalization, may get recovered.

The solution of endemic equilibrium $E^*(N^*, Y^*, X_i^*, Y_i^*, R^*, V^*)$ is given by the following system of simultaneous equations:

\[
N = \frac{A}{d} - \frac{a \beta_1}{d(d + \alpha + \delta_2)} Y,
\]

\[
\beta Y (N - Y - X_i - Y_i - R) + \lambda Y (N - Y - X_i - Y_i - R) - (d + \delta_i + \beta_1) Y + \gamma \xi X_i Y + \gamma (1 - \xi) X_i V = 0,
\]

\[
X_i = \frac{\lambda_i}{(d + \lambda_i + \lambda_{11})} \left( \frac{(d + \delta_i + \beta_1) Y}{(\lambda + d + \lambda_{11}) + (\xi (1 - \xi) \theta_0) Y} \right),
\]

\[
Y_i = \frac{\beta_i}{(d + \alpha + \delta_2)} Y,
\]

\[
R = \frac{\delta_1 Y + \delta_2 Y_i}{d} = \frac{1}{d} \left( \delta_1 + \frac{\delta \beta_1}{d + \alpha + \delta_2} \right) Y_i.
\]
\[ V = \frac{\theta}{\theta_0} Y. \] (18)

Using equations (13) and (15)–(18) in equation (14), we obtain
\[ aY^2 + bY - c = 0, \] (19)
where
\[
\begin{align*}
a &= \left(\beta + \lambda \frac{\theta}{\theta_0}\right) \left(\frac{d + \beta_1 + \delta_1}{d}\right) \left(\varepsilon + (1 - \varepsilon) \frac{\theta}{\theta_0}\right) Y > 0, \\
b &= \left(\frac{d + \beta_1 + \delta_1}{d}\right) \left[\left(\beta + \lambda \frac{\theta}{\theta_0}\right) (d + \lambda_{ii}) + (d + \lambda_i) \left(\varepsilon + (1 - \varepsilon) \frac{\theta}{\theta_0}\right) Y\right] - \frac{A}{d} \left(\beta + \lambda \frac{\theta}{\theta_0}\right) \left(\varepsilon + (1 - \varepsilon) \frac{\theta}{\theta_0}\right) Y, \\
c &= \frac{A}{d} \left[\left(\beta + \lambda \frac{\theta}{\theta_0}\right) (d + \lambda_{ii}) + \gamma_i \left(\varepsilon + (1 - \varepsilon) \frac{\theta}{\theta_0}\right) Y\right] - (d + \beta_1 + \delta_1) (\lambda_i + d + \lambda_{ii}) \\
&= (d + \beta_1 + \delta_1) (\lambda_i + d + \lambda_{ii}) (R_0 - 1).
\end{align*}
\]

A unique positive root (say \( Y = Y^* \)) of equation (19) exists if \( R_0 > 1 \).

**Remark 2.** It is noted from the model system (7)–(12), corresponding to the endemic equilibrium \( E^* \), that \((\beta Y^* + AV^*) + (d + \beta_1 + \delta_1) - \beta(N^*, Y^*, X^*_i, Y^*_i, R^*, V^*) - eyX^*_i > 0\).

**Remark 3.** Differentiating equation (19), we obtain \( \frac{dY}{\beta X} < 0 \), which implies that as the recovery rate of the infectives due to various processes involved in the treatment of infectives (such as efforts made by the government) increases, then the equilibrium level of infectives in the society decreases. In view of this result, it can easily be shown that \( \frac{dX}{\lambda X} < 0 \), which implies that as the recovery rate of the infectives due to various processes involved in the treatment of infectives (such as hospitalization) increases, then the equilibrium level of quarantined infectives decreases.

**Remark 4.** Differentiating equation (19) with respect to \( \beta \) and \( \lambda \), respectively, we obtain \( \frac{dY}{\beta X} \) and \( \frac{dY}{\lambda X} \), which are all positive. This implies that as the transmission rate of disease directly from the infectives to the susceptibles and indirectly by coming in contact with COVID-19 virus density present on the contaminated surfaces increases, the equilibrium level of infected individuals increases.

### 4 Stability analysis

#### 4.1 Local stability analysis

Computing Jacobian matrix for the model system (7)–(12) corresponding to the equilibrium \( E_0(N_0, 0, X_0, 0, 0, 0) \), it is noted that the four eigenvalues corresponding to \( E_0 \) are \(-d, -(d + \lambda_1 + \lambda_{ii}), -(d + a + \delta_2), -d\) and the remaining two are given by the following equation:
\[ \mu^2 + a_1 \mu + a_2 = 0, \]
where
\[
\begin{align*}
a_1 &= \theta_0 + (d + \delta_1 + \beta_1) - \frac{A (\beta (d + \lambda_{ii}) + ey\lambda_i)}{d (d + \lambda_i + \lambda_{ii})} = \theta_0 + (d + \delta_1 + \beta_1) (1 - R_0), \\
a_2 &= \theta_0 (d + \delta_1 + \beta_1) - \frac{A (\beta (d + \lambda_{ii}) + ey\lambda_i) \theta_0 + (\lambda (d + \lambda_{ii}) + (1 - \varepsilon) \gamma \lambda_i) \theta}{(d + \lambda_i + \lambda_{ii})} = \theta_0 (d + \delta_1 + \beta_1) (1 - R_0).
\end{align*}
\]
Thus, the COVID-19-free equilibrium $E_0(N_0, 0, X_0, 0, 0, 0)$ is locally asymptotically stable if $R_0 < 1$ and disease will die out due to no further infection in the population. But, if $R_0 > 1$, it is unstable and the endemic equilibrium $E^*$ exists and the disease always persists in the population.

**Theorem 2.** The endemic equilibrium $E^*$ is locally asymptotically stable provided the following conditions hold:

\[ c_0 \theta < \frac{c_0 \theta_0}{10}, \]
\[ (\beta Y^* + \lambda V^*) \beta_0 \sigma^2 < \frac{4c_0 d^2(d + \alpha + \delta_1)}{45}, \]
\[ c_j (\lambda_1 + \gamma e X_i^*) < \frac{c_j}{25}, \]
\[ \beta_1 \delta_2^2 < \frac{d \delta_1(d + \alpha + \delta_1)}{3}, \]
\[ c_0 < (\lambda_1 + \gamma e X_i^*) \min(\phi_1, \phi_2, \phi_3), \]

where $\phi_1 = \frac{c_0 (\beta Y^* + \lambda V^*) (d + \alpha + \delta_1)}{54 \lambda_1 \beta_1}$, $\phi_2 = \frac{4 c_0 d \beta Y^* + \lambda V^*)}{154 \delta_1}$, $\phi_3 = \frac{2c_0 \theta_0}{59 \gamma (1 - e)^2 X_i^*}$, and $\phi_4 = \frac{4c_0 d^2(d + \alpha + \delta_1)(\beta Y^* + \lambda V^*)}{454 \lambda_1}$. 

(See Appendix B for proof).

**4.2 Nonlinear stability analysis**

In this section, the stability [22] behavior of the endemic equilibrium $E^*$ is studied for whole region of attraction $\Omega$ near the equilibrium $E^*$.

**Theorem 3.** The endemic equilibrium $E^*$ is nonlinearly asymptotically stable provided the following conditions hold inside the region of attraction $\Omega$:

\[ \frac{A}{d} \left( \lambda + \frac{\lambda_1 (1 - e) y}{d + \lambda_1} \right) \theta < \frac{\theta_0}{10} \left\{ (\beta Y^* + \lambda V^*) + (d + \delta_1 + \beta_1) + (\beta - e y) X_i^* - \beta \frac{A}{d} \right\}, \]
\[ (\beta Y^* + \lambda V^*) \beta_0 \sigma^2 < \frac{d \delta_1(d + \alpha + \delta_1)}{45} \left\{ (\beta Y^* + \lambda V^*) + (d + \delta_1 + \beta_1) + (\beta - e y) X_i^* - \beta \frac{A}{d} \right\}, \]
\[ \frac{(\beta - e y) A}{a + d} + (\lambda - (1 - e) y) V^* \left( \frac{a + d + \lambda_1}{25} \right) \frac{(\beta Y^* + \lambda V^*) + (d + \delta_1 + \beta_1) + (\beta - e y) X_i^*}{(\beta Y^* + \lambda V^*) + (d + \delta_1 + \beta_1) + (\beta - e y) X_i^*}, \]
\[ \beta_1 \delta_2^2 < \frac{d \delta_1(d + \alpha + \delta_1)}{3}, \]

where $\phi_1 = \frac{(\beta Y^* + \lambda V^*) (d + \alpha + \delta_1)(a + d + \lambda_1)}{54 \lambda_1 \beta_1}$, $\phi_2 = \frac{4d \beta Y^* + \lambda V^*) (a + d + \lambda_1)}{154 \delta_1}$, $\phi_3 = \frac{A}{d} \left( \lambda + \frac{\lambda_1 (1 - e) y}{d + \lambda_1} \right) \theta_0 (a + d + \lambda_1)(1 - e)^2 X_i^*$, and $\phi_4 = \frac{4d \beta Y^* + \lambda V^*) (a + d + \lambda_1)(\beta Y^* + \lambda V^*)}{454 \lambda_1}$. 

(See Appendix C for proof).
Remark 5. The aforementioned theorems imply that if \( \beta \) and \( \lambda \) are very small, then the possibility of the satisfying local and nonlinear stability conditions is more plausible. Thus, it can be speculated that the transmission rate of disease directly from the infectives to the susceptibles and the rate of contact of susceptibles with COVID-19 virus density present on the contaminated surfaces have a destabilizing effect on the model system. For small values of \( \beta \) and \( \lambda \), the equilibrium values of \( E^* \) obtain stabilized.

5 Numerical simulation

The numerical simulation of the model system (7)–(12) is given here to show the existence of equilibrium and the feasibility of stability conditions. We integrate the model system by the fourth-order Runge-Kutta method using MATLAB with the following set of parameter values given in Table 1. Some of the parameter values taken from “Coronavirus statistics by India” [6] and other values are estimated.

The equilibrium values of endemic equilibrium \( E^* \) are computed as: \( Y^* = 774672.0396, N^* = 262838217.5267, X_i^* = 20183759.3694, Y_i^* = 110433.9453, R^* = 204878365.4484, \) and \( V^* = 0.0000194. \)

The eigenvalues of the Jacobian matrix corresponding to the endemic equilibrium \( E^* \) of the model system are \(-0.070148, -0.065102811454311, -0.0108768558137863, -9.24424226463753 \times 10^{-5} \pm 0.00112473808393725i, \) and \(-3.80000000000011 \times 10^{-5}. \) Thus, the endemic equilibrium is locally asymptotically stable for the aforementioned set of parameter values, as all the eigenvalues are negative or have a negative real part.

The graphical representation of the results of numerical simulation is displayed in Figures 1–4.

In Figure 1(a), the comparison between the confirmed reported values of infected people in India by WHO [6,23] and that predicted by the mathematical model using the aforementioned set of parameter values is shown. It is seen from the figure that the model system fits well with the real data. For simulation, the fraction of the population initially is assumed as follows:

\( Y(0) = 0, N(0) = 130000000, X_i(0) = 0, Y_i(0) = 1, R(0) = 0, \) and \( V(0) = 0.004. \)

In Figure 1(b), the variation of confirmed infective population density is displayed with time \( t \) for distinct values of \( \lambda \), the transmission coefficient of disease to susceptibles due to virus density present in the environment. It is observed from the figure that as the value of \( \lambda \) increases, the infective population increases, which indicates the faster spread of the disease with an increase in the indirect contact of susceptibles with contaminated surfaces.

<table>
<thead>
<tr>
<th>Parameter</th>
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<tbody>
<tr>
<td>Description</td>
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<tr>
<td>Recruitment rate of susceptibles ( A )</td>
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<tr>
<td>Transmission rate of susceptibles via infectives ( \beta )</td>
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<tr>
<td>Transmission rate of susceptibles via virus density ( \lambda )</td>
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<tr>
<td>Natural death rate coefficient of human population ( d )</td>
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<tr>
<td>Disease-induced death rate ( \alpha )</td>
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<tr>
<td>The rate at which infected individuals are quarantined ( \beta_i )</td>
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<tr>
<td>Growth rate of virus density ( \theta )</td>
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<tr>
<td>Natural depletion rate of virus density ( \theta_0 )</td>
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<tr>
<td>The transfer rate of susceptible people to isolated aware susceptible class ( \lambda_1 )</td>
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<tr>
<td>The rate at which people from the isolated aware susceptible class move to susceptible class ( \lambda_{11} )</td>
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<tr>
<td>The rate of transfer of isolated susceptibles to infected class ( \gamma )</td>
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<tr>
<td>A fraction of transfer rate of isolated susceptibles to infected class ( \epsilon )</td>
</tr>
<tr>
<td>Recovery rate of infected population ( \delta_1 )</td>
</tr>
<tr>
<td>Recovery rate of quarantined infectives ( \delta_2 )</td>
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Table 1: Description of parameters
Figure 1: (a) Confirmed infectives reported cases of COVID-19 in India and (b) variation of confirmed infective population with time for distinct values of $\lambda$.

Figure 2: (a) Variation of infective population with time for distinct values of $\lambda_1$ and (b) variation of virus density with time for distinct values of $\lambda_1$.

Figure 3: (a) Variation of quarantined infectives with time for distinct values of $\beta_1$ and (b) variation of virus density with time for distinct values of $\beta_1$.

Figure 4: (a) Variation of quarantined infectives with time for distinct values of $\delta_2$ and (b) variation of recovered population with time for distinct values of $\delta_2$. 

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Figure 2 represents the variation of infective population and virus density with time for different values of $\lambda$, the rate of transfer of susceptible population to isolated aware susceptible class. It is seen from Figure 2(a) that the infective population decreases with an increase in the value of $\lambda$. This is due to the fact that as more people isolate themselves, the spread of disease decreases, which decreases the number of infective population. This decline in the infective population ultimately decreases the density of virus in the environment (Figure 2(b)). Thus, if more susceptible people isolate themselves from direct interaction with infectives or from indirect interaction with contaminated surfaces, the spread of disease decreases, which in turn decreases the density of virus present in the environment (Figure 2(b)).

The variation of quarantined infectives and virus density, respectively, with time is displayed in Figure 3 for distinct values of $\beta$, the rate at which infected individuals are quarantined. It is seen that with an increase in the value of $\beta$, the quarantined infective population increases (Figure 3(a)), and this increment in quarantined infective population, not spreading the diseases anymore, in turn decreases the density of the virus (Figure 3(b)). Thus, if the infective population is quarantined, then the density of virus decreases.

Figure 4 displays the variation of quarantined infectives and recovered population, respectively, with time for different values of $\delta$, the recovery rate of quarantined infectives. It is noted from Figure 4(a) that the quarantined infectives decreases with an increase in the value of $\delta$, as more people obtain recovered during quarantine period. Thus, the spread of disease decreases, which leads to a decline in the infective population and, as such, the recovered population increases (Figure 4(b)).

6 Conclusion

In the article, a nonlinear mathematical model has been proposed and analyzed to study the spread of coronavirus disease COVID-19 in the human population with constant immigration of susceptibles. In the modeling process, the total human population is divided into five subclasses, namely, susceptibles, infectives, isolated aware susceptibles, quarantined symptomatic infectives, and the recovered population. The effect of some critical parameters on the spread of the disease is studied. The analysis of the model has been performed using the stability theory and numerical simulation, and some inferences have been drawn by establishing the local and nonlinear stability results. The model results indicate similar pattern as seen with the reported data. The model analysis shows that if more people are exposed to virus deposited on contaminated surfaces or areas, the infective population increases. However, if the rate of transfer of susceptible population to isolated aware susceptible class increases, the infective population declines, leading to a decreased virus density in the environment. This also highlights the importance of social distancing, use of face cover/mask, avoidance of social gatherings, etc., to make effective isolation so that disease spread is decreased. The increased density of virus present in the environment, however, leads to faster spread of the deadly coronavirus disease COVID-19 if proper safety measures are not adopted.

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References


Appendix

A Proof of lemma

From equation (7), we note that $\frac{dN}{dt} \leq A - dN$. This implies that $\lim_{t \to \infty} \sup N(t) \leq \frac{A}{a + d}$, from which we obtain $N(t) \leq \frac{A}{a + d}$. Similarly, it can be obtained that $N(t) \geq \frac{A}{a + d}$. Further, it is noted that $Y(t) < N(t)$, and therefore, $0 < Y \leq \frac{A}{a + d} \leq \frac{A}{d}$.

From equation (9), we note that $\frac{dX}{dt} \leq \lambda_i N - (d + \lambda_{11})X_i$, which implies that $\lim_{t \to \infty} \sup X_i(t) \leq \frac{\lambda_i A}{(d + \lambda_{11})} < \frac{A}{d}$. Similarly, it can be proved that $\lim_{t \to \infty} \sup Y_i(t) \leq \frac{\beta A}{(a + d + \alpha + \delta_2)} = Y_m$.

From equation (11), we note that $\frac{dR}{dt} \leq \delta_1 Y_m + \delta_2 Y_m - dR$, which implies that $\lim_{t \to \infty} \sup R(t) \leq \frac{A}{d(a + d)} \left[ \delta_1 + \frac{\beta \delta_2}{(d + a + \delta_2)} \right] = R_m$.

Similarly, it can be proved that $\lim_{t \to \infty} \sup V(t) \leq \frac{\theta A}{\delta_2(a + d)} = V_m$.

Hence, the lemma.

B Proof of Theorem 1

To determine the local stability behavior of $E^*$, the linearized system of the model (7)–(12) about $E^*(N^*, Y^*, X^*_i, Y^*_i, R^*, V^*)$ is expressed as follows:

$$
\begin{bmatrix}
n \\
y \\
x_i \\
y_i \\
r \\
v
\end{bmatrix} =
\begin{bmatrix}
-d & 0 & 0 & -\alpha & 0 & 0 \\
\beta Y^* + \lambda V^* & -c_1 & -c_2 & -\beta Y^* + \lambda V^* & -\beta Y^* + \lambda V^* & c_4 \\
\lambda_i - (\lambda_i + \gamma \epsilon X^*_i) & -c_3 & -\lambda_i & -\lambda_i & -\gamma(1 - \epsilon)X^*_i \\
0 & \beta_1 & 0 & -(d + \alpha + \delta_2) & 0 & 0 \\
0 & \delta_1 & 0 & \delta_2 & -d & 0 \\
0 & \theta & 0 & 0 & 0 & -\theta_0
\end{bmatrix}
\begin{bmatrix}
n \\
y \\
x_i \\
y_i \\
r \\
v
\end{bmatrix}.$$

where “.” denotes $\frac{d}{dt}$ and $n, y, x_i, y_i, r, v$ are the small perturbations about the equilibrium $E^*$, i.e., $N = N^* + n, Y = Y^* + y, X_i = X_i^* + x_i, Y_i = Y_i^* + y_i, R = R^* + r, V = V^* + v$ and

$$
c_1 = (\beta Y^* + \lambda V^*) + (d + \beta_1 + \delta_1) - \beta(N^* - Y^* - X_i^* - Y_i^* - R^* - V^*) - \epsilon \gamma X_i^* > 0, \\
c_2 = (\beta - \epsilon \gamma)Y^* + (\lambda - (1 - \epsilon)\gamma)V^* > 0, \\
c_3 = (\lambda_i + d + \lambda_{11}) + \gamma \epsilon Y^* + \gamma(1 - \epsilon)Y^* > 0, \\
c_4 = \lambda(N^* - Y^* - X_i^* - Y_i^* - R^* - V^*) + (1 - \epsilon)\gamma X_i^* > 0.
$$

Now, consider the following positive definite function:

$$
U_1 = \frac{1}{2}(k_1 n^2 + k_2 y^2 + k_3 x_i^2 + k_4 y_i^2 + k_5 r^2 + k_6 v^2),
$$

where $k_i (i = 1 \ldots 6)$ are the positive constants to be chosen appropriately.

Differentiating $U$ with respect to “t” along the solutions of linearized system of (7)–(12), we obtain
\[
\frac{dU}{dt} = -k_d n^2 - k_5 c y^2 - k_3 c x^2 - k_4 (d + \alpha + \delta_2) y_i^2 - k_d r^2 - k_6 \theta \nu^2
\]
\[
+ k_6 (\beta Y^* + \lambda V^*) n y + k_3 \lambda u x_i - k_4 a y_i - (k_5 c_2 + k_3 (\lambda + y e X_i^*)) y x_i
\]
\[
+ (-k_6 (\beta Y^* + \lambda V^*) + k_6 \beta) y y_i + (-k_6 (\beta Y^* + \lambda V^*) + k_6 \beta) y r + (k_5 c_4 + k_6 \theta) y v
\]
\[
- k_3 a x x_i - k_3 a x r - k_6 (1 - \epsilon) X_i^* x \nu + k_6 \delta y r.
\]

Now, \(\frac{dU}{dt}\) will be negative definite provided the following conditions are satisfied:

\[
k_6 (\beta Y^* + \lambda V^*)^2 < \frac{4k_6 d \xi}{15},
\]

\[
k_3 \lambda_i^2 < \frac{4k_6 d \xi}{15},
\]

\[
k_6 a^2 < \frac{k_6 d (d + \alpha + \delta_2)}{3},
\]

\[
(k_5 c_2 + k_3 (\lambda + y e X_i^*))^2 < \frac{4k_6 k_3 c_2 \xi}{25},
\]

\[
(-k_6 (\beta Y^* + \lambda V^*) + k_6 \beta)^2 < \frac{k_6 k_3 c_2 (d + \alpha + \delta_2)}{5},
\]

\[
(-k_6 (\beta Y^* + \lambda V^*) + k_6 \beta)^2 < \frac{4k_6 k_3 c_2 d}{15},
\]

\[
(k_5 c_4 + k_6 \theta)^2 < \frac{2k_6 k_3 c_2 \theta}{5},
\]

\[
k_5 \lambda_i^2 < \frac{k_6 c_2 (d + \alpha + \delta_2)}{5},
\]

\[
k_5 \lambda_i^2 < \frac{4k_6 \xi d}{15},
\]

\[
k_6 \lambda_i^2 < \frac{k_6 \xi (1 - \epsilon) X_i^* \nu}{5},
\]

\[
k_6 \delta_i^2 < \frac{k_6 d (d + \alpha + \delta_2)}{3}.
\]

Choosing \(k_1 = \frac{d(d + \alpha + \delta_2)(\beta Y^* + \lambda V^*)}{3 a \beta_i^2}\), \(k_2 = 1\), \(k_4 = \frac{(\beta Y^* + \lambda V^*)}{\beta_i}\), \(k_5 = \frac{(\beta Y^* + \lambda V^*)}{\delta_i}\), and \(k_6 = \frac{c_4}{\theta^*}\), \(\frac{dU}{dt}\) will be negative definite under conditions (20)–(24), which implies that is a Lyapunov function and hence the theorem.

### C Proof of Theorem 2

Consider the following positive definite function:

\[
W = \frac{1}{2} m_1 (N - N^*)^2 + \frac{1}{2} m_2 (Y - Y^*)^2 + \frac{1}{2} m_3 (X_i - X_i^*)^2 + \frac{1}{2} m_4 (Y_i - Y_i^*)^2 + \frac{1}{2} m_5 (R - R^*)^2
\]
\[
+ \frac{1}{2} m_6 (V - V^*)^2,
\]

where \(m_i (i = 1 \ldots 6)\) are the positive constants to be chosen appropriately. Differentiating \(W\) with respect to “t” along the solutions of system (7)–(12), we obtain
\[
\frac{dW}{dt} = -m_3d(N - N^*)^2 - m_2(\beta Y^* + \lambda V^*) + (d + \beta_1 + \delta_1) - \beta(N - Y - X_i^* - Y_i - R) - \psi X_i^*(Y - Y^*)^2 \\
- m_3(\lambda_i + d + \lambda_{i1}) + yeY + y(1 - \epsilon)V(X_i - X_i^*)^2 - m_3d + a + \delta_2)(Y_i - Y_i^*)^2 \\
- m_3d(R - R^*)^2 - m_3d(\lambda N - N^*(V - V^* + m_2(\beta Y^* + \lambda V^*)(N - N^*)(Y - Y^*) + m_3d(X_i - X_i^*)(N - N^*) \\
\] 
\[
- m_3d(N - N^*)(Y_i - Y_i^*) + [(m_2(\beta - \psi)yY + (\lambda - (1 - \epsilon)y)V) + m_3(\lambda_i + yeX_i^*)][(Y - Y^*)(X_i - X_i^*) \\
+ (-m_2(\beta Y^* + \lambda V^*) + m_3\beta_i)(Y - Y^*)(Y_i - Y_i^*) + (-m_2(\beta Y^* + \lambda V^*) + m_3\delta_i)(Y - Y^*)(R - R^*) \\
+ (m_3(\lambda(N - Y - X_i - Y_i - R) + (1 - \epsilon)yX_i) + m_3\delta_i)(Y - Y^*)(V - V^*) - m_3\lambda_i(X_i - X_i^*)(Y_i - Y_i^*) \\
- m_3\lambda_i(X_i - X_i^*)(R - R^*) - m_3d(1 - \epsilon)X_i^*(X_i^* - X_i^*)(V - V^*) + m_3\delta_i(Y - Y^*)(R - R^*). \\
\]
\]

Now, \(\frac{dW}{dt}\) will be negative definite provided the following conditions are satisfied:

\[
m_3(\beta Y^* + \lambda V^*)^2 < \frac{4}{15}m_3d\beta, \quad \tag{A16}
\]
\[
m_3\lambda_i^2 < \frac{4}{15}m_3d(\lambda_i + d + \lambda_{i1}) + yeY + y(1 - \epsilon)V, \quad \tag{A17}
\]
\[
m_3\alpha^2 < \frac{m_3d(d + a + \delta_2)}{3}, \quad \tag{A18}
\]
\[
[(m_2(\beta - \psi)yY + (\lambda - (1 - \epsilon)y)V^*) + m_3(\lambda_i + yeX_i^*)]^2 < \frac{4m_2m_3}{25}((\lambda_i + d + \lambda_{i1}) + yeY + y(1 - \epsilon)V)\beta, \quad \tag{A19}
\]
\[
(-m_2(\beta Y^* + \lambda V^*) + m_3\beta_i)^2 < \frac{m_3m_6}{5}(d + a + \delta_2)\beta, \quad \tag{A20}
\]
\[
(-m_2(\beta Y^* + \lambda V^*) + m_3\delta_i)^2 < \frac{4m_2m_6}{15}d\beta, \quad \tag{A21}
\]
\[
(m_3(\lambda(N - Y - X_i - Y_i - R) + (1 - \epsilon)yX_i) + m_3\delta_i)^2 < \frac{2m_2m_6}{5}\theta_0\beta, \quad \tag{A22}
\]
\[
m_3\lambda_i^2 < \frac{m_3d(d + a + \delta_2)(\lambda_i + d + \lambda_{i1}) + yeY + y(1 - \epsilon)V), \quad \tag{A23}
\]
\[
m_3\lambda_i^2 < \frac{4m_6}{15}d(\lambda_i + d + \lambda_{i1}) + yeY + y(1 - \epsilon)V, \quad \tag{A24}
\]
\[
m_3\psi(1 - \epsilon)^2X_i^* < \frac{2m_3\theta_0(\lambda_i + d + \lambda_{i1}) + yeY + y(1 - \epsilon)V), \quad \tag{A25}
\]
\[
m_3\delta_i^2 < \frac{m_3d(d + a + \delta_2)}{3}, \quad \tag{A26}
\]

where \(\beta = ((\beta Y^* + \lambda V^*) + (d + \beta_1 + \delta_1) - \beta(N - Y - X_i^* - Y_i - R) - \psi X_i^*)\). Now, maximizing left-hand side and minimizing right-hand side (A16)–(A26) and choosing \(m_1 < \frac{d(d + a + \delta_2)(\beta Y^* + \lambda V^*)}{2\beta_0^\alpha^2}, \ m_2 = 1, \ m_3 = \frac{d(d + a + \delta_2)(\beta Y^* + \lambda V^*)}{\beta_0^\alpha^2}\)
\(m_5 = \frac{d(d + a + \delta_2)(\beta Y^* + \lambda V^*)}{\beta_0^\alpha^2}, \ m_6 = \frac{\lambda_i + d + \lambda_{i1}}{\beta_0^\alpha^2}\), and \(\frac{dW}{dt}\) will be negative definite under the conditions (25)–(29) inside the region of attraction \(\Omega\), which implies that \(W\) is a Lyapunov function and hence the theorem.