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Modeling the dynamics of novel coronavirus (COVID-19) via stochastic epidemic model

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\textbf{A B S T R A C T}

In this article we propose a stochastic model to discuss the dynamics of novel corona virus disease. We formulate the model to study the long run behavior in varying population environment. For this purposes we divided the total human population into three epidemiological compartments: the susceptible, covid-19 infected, recovered and recovered along with one class of reservoir. The existence and uniqueness of the newly formulated model will be studied to show the well-possedness of the model. Moreover, we investigate the extinction analysis as well as the persistence analysis to find the disease extinction and disease persistence conditions. At the end we perform simulation to justify the investigation of analytical work with the help of graphical representations.

\textbf{Introduction}

Corona viruses consist of a wide family of viruses This can cause human diseases, ranging from the popular Severe Acute Respiratory Syndrome (SARS) colds. In the previous two decade, two epidemics of coronavirus have been reported. The one called SARS caused a large-scale epidemic devastation in China and targeting two dozen countries with reported 8000 cases along with 800 deaths. The other epidemic was Middle East Respiratory Syndrome Coronavirus (MERS), which initially reported in the Kingdom of Saudi Arabia and consequently 2,500 number of individuals infected with 800 deaths [1–4].

In December 2019, a serious outbreak of respiratory disease started in Wuhan city, China [5,4]. The causative agent is the novel corona virus that was detected in early January and isolated from one single patient. The pandemic of the novel corona virus infected approximately 21,101,574 confirmed cases, including 758,025 deaths till 14 August, 2020. The World Health Organization reveal it as a Public Health Emergency of International Concern. This new virus appears to be extremely infectious and has spread rapidly across the globe making it a global pandemic. The potential spreading of these disease become pandemic worldwide and therefore seems to be a very serious public health risk. The COVID-19 infection normal symptoms including fever, cough, breathing, fatigue and difficulties like (MERS-CoV) and (SARS-CoV) infection.

The literature reveals that the novel corona virus disease (COVID-2019) has been identified as a global issue and therefore got the attention of many researchers. Many mathematician as well as biologists performed experiments to forecast the future possible progression via various mathematical models [6]. A variety of mathematical studies for the dynamics of novel corona virus outbreak as well as other infectious diseases have already been carried out, see for detail [7–15]. While there is an onset of epidemic, human–human transmission occur resulting in the rise of cases of corona virus disease worldwide. Due to limited resources, the most important thing for health care providers becomes the forecasting about the disease. It could be also noted to the best of our knowledge from the resent literature that most of the deterministic modeling approach were used for the dynamics of novel corona virus while modeling the transmission dynamics of infectious disease stochastic differential equations model is more appropriate, for example see [16–28]. Similarly according to the characteristic of the novel corona virus disease the stochastic modeling approach is more suitable then deterministic one.

In this study, we propose and analyze a stochastic epidemic compartmental model for covid-19 according to the characteristics of novel corona virus disease. It could be noted form the spreading of the novel corona virus disease that the ratio of transmission is different from place to place and therefore the random fluctuation of the environment is taken to be in the transmission rate and so distributed. We formulated the model with the fact that adding the noise term in the transmission rate. Once formulate the model we discuss the existence analysis and
uniqueness by using the stochastic Lyapnov function theory to investigate the well posedness of the proposed problem. We also find the condition for the extinction and persistence by discussing the extinction and persistence analysis. At the end we use the well known purely numerical technique of stochastic Euler Maruyama technique to perform the numerical simulation and show the feasibility of the analytical work graphically.

Model formulation

We formulate a stochastic model for the dynamics of novel Corona virus disease in this section. Without the direct representation of the model, we put some assumptions.

a. All variables, constants as well as parameters of the model are non-negative.

b. The total human population is represented by $N(t)$ and consequently divided into three epidemiological groups of susceptible, infected and recovered population.

c. It could be noted that the corona pandemic rises from the human to human contact worldwide and the stochastic behaviors of population groups of the proposed model are supposed to be driven by the same source or randomness $B(t)$. This can be seen as the model proposes that variations in population groups are linked to the same source of information represented by the Brownian motion filtration $\mathcal{F} = (\mathcal{F}_t)_{t \in \mathbb{R}_+}$, where $\mathcal{F}_t := \sigma(B(t))$ is the $\sigma$-algebra generated by $B(t)$ leads to the fact that any change in one population group has directly an impact on the other groups. Therefore the random fluctuation of the environment are to be taken in the transmission rate, such that $\beta_1 \rightarrow \beta_1 + \eta \beta_4(t)$ and $\beta_2 \rightarrow \beta_2 + \eta \beta_3(t)$. Here $B(t)$ symbolize the standard Brownian motion, while $\beta_1$ and $\beta_2$ are white noise intensities. Clearly the Brownian motion obey the property of $B(0) = 0$ and $\eta_1^2, \eta_2^2 > 0$.

Thus keeping in view (2019-nCoV) characteristics along with the above assumptions, we explore the problem in term of the nonlinear model:

\[
\begin{align*}
\frac{ds}{dt} & = \frac{\beta_1 s(t) i(t) + \beta_2 s(t) w(t) + d s(t)}{d} - \eta_1 s(t) i(t) d B(t) - \eta_2 s(t) w(t) d B(t), \\
\frac{di}{dt} & = (\beta_1 s(t) i(t) + \beta_2 s(t) w(t) - (d + d_1 + \sigma) i(t)) d t + \eta_2 s(t) i(t) d B(t) + \eta_1 s(t) w(t) d B(t), \\
\frac{dw}{dt} & = (\sigma(i(t)) - d w(t)) d t, \\
\frac{dr}{dt} & = (\sigma(i(t)) - d r(t)) d t,
\end{align*}
\]

where the new born rate is $\Pi$, while $\beta_1$ and $\beta_2$ are assumed to be the two transmission routes i.e., from infected individuals and reservoir. We also denote the natural death by $d$ and the disease death by $d_1$. Moreover, it is assumed that $\sigma$ is the recovery of the infected population. Finally the rate of virus contributing to the seafood market is taken to be $\alpha$, while $\eta$ is the removal proportion of the virus.

Clearly the proposed model (1) reduces to its associated deterministic form, if the intensities of white noise $\eta_1 = \eta_2 = 0$. In addition the associated deterministic model having two type of equilibria: disease free and endemic equilibrium respectively denoted by $e_0 = (s_0, 0, 0, 0)$ and $e^* = (s^*, i^*, r^*, w^*)$, where

\[
\begin{align*}
s_0 & = \frac{\Pi}{d}, \quad s_0 = \frac{(d + d_1 + \sigma) \eta_1}{\beta_1 \eta_1 + \beta_2 \alpha}, \\
\dot{i}^* & = \frac{\eta_1 (R_0 - 1) (d + d_1)}{\beta_1 \eta_1 + \beta_2 \alpha}, \\
\dot{r}^* & = \frac{\alpha \eta_1 (R_0 - 1) (d + d_1)}{\beta_1 \eta_1 + \beta_2 \alpha}.
\end{align*}
\]

where $R_0$ is the threshold parameter or also known the basic reproductive number of the associated deterministic model of system (1). To find this quantity, let $X = (i, w)^T$, then

\[
\frac{dX}{dt} = F - V,
\]

where

\[
F = \begin{pmatrix} \beta_1 i(t) s(t) + \beta_2 w(t) s(t) \\ 0 \end{pmatrix}, \quad V = \begin{pmatrix} (d + d_1 + \sigma) i(t) & 0 \\ \eta w(t) & -\alpha \end{pmatrix}.
\]

Calculating the Jacobian of the above matrices $F$ and $V$ around the disease free state $e_0 = (s_0, 0, 0, 0)$, we may arrives at

\[
F = \begin{pmatrix} \beta_1 s_0 & 0 \\ 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} (d + d_1 + \sigma) s_0 & 0 \\ \eta w \end{pmatrix}.
\]

The threshold quantity is the spectral radius of the matrix, $H = FV^{-1}$, and so consequently having the following expression is given by

\[
R_0 = \frac{\Pi \beta_1}{(d + d_1 + \sigma) s_0} + \frac{\alpha \Pi \beta_2}{(d + d_1 + \sigma) \eta w}.
\]

Existence and uniqueness analysis

The current section is dedicated to find the existence analysis and uniqueness analysis of the stochastic model (1).

The Itô formula presented in the next lemma will be very useful in getting our results. It is a special case of the Multidimensional Itô formula that can be found in many books on stochastic calculus e.g. [29].

Lemma 1. Let $a = (a_1, \ldots, a_n)$ and $b = (b_1, \ldots, b_n)$ denote two $n$-dimensional square-integrable adapted processes. We consider the process $X = (X_1, \ldots, X_n)$, where for $k \in \{1, \ldots, n\}$, $X_k$ is driven by the stochastic differential equation

\[
dX_k(t) = a_k(t) dt + b_k(t) d B(t), \quad X_k(0) \in \mathbb{R}.
\]

Given a function $F$ twice continuously differentiable from $\mathbb{R}^n$ to $\mathbb{R}$, then we have

\[
dF(X(t)) = \sum_{i=1}^n \frac{\partial F}{\partial X_i}(X(t)) dX_i(t) + \sum_{i,j=1}^n \frac{1}{2} \frac{\partial^2 F}{\partial X_i \partial X_j}(X(t)) \langle dX_i(t), dX_j(t) \rangle,
\]

where

\[
\langle dX_i(t), dX_j(t) \rangle = b_i(t) b_j(t) dt.
\]

since $(dB(t), dB(t)) = dt$ and $(dB(t), dt) = (dB(t), dt) = (dt, dt) = 0$. We have the following results to discuss the properties of existence and uniqueness.
Theorem 2. For every initial sizes \((s(0), i(0), r(0), w(0))\) in \(R^4_+\), the model (1) solution i.e., \((s(t), i(t), r(t), w(t))\) is unique and remains in \(R^4_+\) almost surely (as).

Proof. We first show existence and uniqueness of local positive solution then we prove that the local solution is global. Our proof is based on results from [30–32]. In the following, we adopt the same method used in [33] and more recently in [34], So in view of the properties of locally Lipschitz continuity for the proposed model (1) holds, therefore, we assume that if \(r(t)\) is the explosion time then the solution \((s, i, r, w)\) for \(t \in [0, r(t)]\) along with non-negative initial population sizes \((s(0), i(0), r(0), w(0))\) in \(R^4_+\) is unique local. Further to perform that the solution is global, we need to investigate the axioms of \(\tau \equiv \infty\) a.s. For this we assume that \(k_0\) a positive constant i.e., \(k_0 > 0\) be sufficiently large such that
\[\frac{1}{k_0} < (s(0), i(0), r(0), w(0)) < k_0.\]
The stopping time for each \(k_0 > k_0\) is define to be
\[\tau_k = \inf \left\{ t \in [0, \tau_k) \mid : \min \left( \frac{s(t)}{k}, \frac{i(t)}{k}, \frac{r(t)}{k}, \frac{w(t)}{k} \right) \right\}. \quad (7)\]

Let us assume that \(\phi\) is the null set, then setting \(\omega = \inf \phi\). It could be noted that the increasing of \(\tau_k\) depends on the value of \(k\) and consequently increasing if the value of \(k\) is increasing i.e., \(\tau_k\) rises with \(k\) approaches \(\omega\). The substitution of \(\inf delta = \tau_k\) as \(t \to \infty\) along with the investigation of \(\tau_\omega = \infty\) a.s leads to \((s(t), i(t), r(t), w(t)) \in R^4_+\) is non-negative t a.s. It clearly shows that only we need to prove that \(\tau_k = \infty\). Thus we assume that there are two constants such that \(T > 0\) and \(\epsilon \in (0, 1)\), such that
\[P\{\tau_\omega \leq T\} > \epsilon. \quad (8)\]
So \(k \geq k_0\) is an integer that
\[P\{\tau_k \leq T\} \geq \epsilon, \text{ for every } k \geq k_0. \quad (9)\]

Let us assume that \(N = N_1 + N_2\), where \(N_1 = s + i + r\) and \(N_2 = w\). Then for any \(t \leq \tau_k\), we may arrive to the following assertions
\[dN_1(t) = (\Pi - (s(t) + i(t)) + r(t)d - \Pi d(r(t))dt. \quad (10)\]

Using some algebraic manipulation the above Eq. (10) ultimately takes the following form
\[dN_1(t) = (\Pi - N_1(\Pi))d\Pi dt. \quad (11)\]

Solving Eq. (11), we obtain the following assertion is given by
\[N_1(t) = \begin{cases} \frac{\Pi}{d} \text{ if } N_1(0) \leq \frac{\Pi}{d} \\ N_1(0) \text{ if } N_1(0) > \frac{\Pi}{d}. \end{cases} \quad (12)\]

Similarly the temporal differentiation of \(N_2(t)\) takes the following form
\[dN_2(t) = (ai(t) - \eta w(t))dt. \quad (13)\]

The use Eq. (12) in Eq. (13) with little re-arrangement gives the solution is represented by
\[N_2(t) = \begin{cases} \frac{\alpha \Pi}{d} \text{ if } N_2(0) \leq \frac{\alpha \Pi}{d} \\ N_2(0) \text{ if } N_2(0) > \frac{\alpha \Pi}{d}. \end{cases} \quad (14)\]

Thus the combination of Eq. (12) and Eq. (14) lead to the following assertion is symbolized by
\[N(t) = \begin{cases} \Pi \text{ if } N_1(0) \leq \Pi \\ N_1(0) \text{ if } N_1(0) > \Pi \frac{d}{d} \\ N_2(0) \text{ if } N_2(0) > \frac{\alpha \Pi}{d}. \end{cases} \quad := M. \quad (15)\]

Moreover, let \(H \in C^2\), i.e., \(H : R^4_+ \rightarrow R\). define by
\[H(s, i, r, w) = s + i + r + w - 4 - \log (s + i + r + w). \quad (16)\]

It could be noted from the above Eq. (16) that \(H\) is non-negative. Thus for \(k_0 \leq k\) and \(0 \in T\), we apply the \(ito\) formula which lead to the following assertion
\[dH = \frac{\Pi}{d} \left( i - s \right) \left( \eta_1 + \frac{\eta_2w}{d} \right) dB(t), \quad (17)\]

where
\[dH(s, i, r, w) = \left( 1 - \frac{1}{s} \right) \left( \Pi - \beta_1 si - \beta_2 sw - ds - d(r(t))dt \right) + \frac{1}{2\Pi} \left( ds \right)^2 \left( 1 - \frac{1}{s} \right) \left( \beta_1 si + \beta_2 sw - (d + d\Pi + \sigma) i \right) + \frac{1}{2\Pi} \left( ds \right)^2 + \left( 1 - \frac{1}{r} \right) (\eta_1 + \frac{\eta_2w}{d}) \left( ai - \eta w \right). \quad (18)\]

Simplifying and the use of algebraic manipulation gives the following
\[dH(s, i, r, w) = \Pi + 2d + d\Pi + \sigma + \eta - ds - \Pi s + \frac{1}{2\Pi} \left( \eta_1 i + \eta_2 w \right) \left( i + \frac{1}{r} \right) - \sigma i + \frac{\sigma w}{d} - \eta w - ai + \frac{i}{w}. \quad (19)\]

which implies that
\[dH(s, i, r, w) = \Pi + 2d + d\Pi + \sigma + \eta + \frac{1}{2\Pi} \left( \eta_1 i + \eta_2 w \right) + ai. \quad (20)\]

Let \(\rho = \max \{\eta_1, \eta_2\}\) then the above equation i.e., Eq. (20) can be re-written as
\[dH(s, i, r, w) = \Pi + 2d + d\Pi + \sigma + \eta + \rho \left( i^2 + \frac{i^2}{r} + w^2 \right) + ai. \quad (21)\]

It is very much clear that \(s^2 + b^2 + c^2 \leq (a + b + c)^2\), so Eq. (21) may be expressed in the following form
\[dH(s, i, r, w) = \Pi + 2d + d\Pi + \sigma + \eta + \rho \left( s^2 + i^2 + w^2 \right) + ai. \quad (22)\]

Furthermore it could be noted from the fact that \(N = N_1 + N_2\), therefore making use of the Eq. (15) in Eq. (23) leads to the assertion is give by
\[dH(s, i, r, w) = \Pi + 2d + d\Pi + \sigma + \eta + \rho M^2 + \alpha M := K. \quad (23)\]

Hence
\[ E[H(s(\tau_1 ∧ T), i(\tau_1 ∧ T), r(\tau_1 ∧ T), w(\tau_1 ∧ T))] = \mathcal{H}(s(0), i(0), r(0), w(0)) + E \left[ \int_0^{\tau_1 ∧ T} Kdt \right], \]
\[ \mathcal{H}(s(0), i(0), r(0), w(0)) + TK. \] (24)

Set \( \Omega_k = T ≥ \tau_k \) for \( k \leq k \). As a result, Eq. (8) reads \( P(\Omega_k) ≥ s \). So for all \( \omega \in \Omega_k \), there is at least one \( s(\omega, \tau_k), i(\omega, \tau_k), r(\omega, \tau_k), w(\omega, \tau_k) \) exists, which will be equal to \( \frac{1}{k} \). So \( H \) is not less than \( \frac{1}{k} + \log k - 1 \) or \( \log k - k - 1 \). Then
\[ H ≥ E \left[ \frac{1}{k} + \log k \right] ∧ (− \log k - k - 1). \] (25)

Using Eq. (8) and Eq. (24), we write
\[ H(s(0), i(0), r(0), w(0)) + TK ≥ E[1_{\Omega_k}ωH(s(\tau_1), i(\tau_1), r(\tau_1), w(\tau_1))] \]
\[ ≥ E \left( \log k + \frac{1}{k} - 1 \right) \] \[ ∧ \left| − \log k - k - 1 \right|. \] (26)

where the notion \( 1_{\Omega_k} \) is used for the indicator function of \( \Omega_k \). Let \( k \rightarrow ∞ \) then it contradict that \( \infty > H(s(0), i(0), r(0), w(0)) + MT \) \( = \infty \), which ultimately implies that \( t_m = \infty \) a.s. \( \square \)

Remark 1. It could be noted from the existence analysis that for any initial population sizes \( (s(0), i(0), r(0), w(0)) \) \( \in \mathbb{R}^+_4 \) the unique global solution \( (s(t), i(t), r(t), w(t)) \) \( \in \mathbb{R}^+_4 \) exists almost surly (a.s) for the proposed problem (1), therefore
\[ d(s(t) + i + r) ∈ (Π - (s + i + r))dt \] (27)
and
\[ dw = (ai - w)dt \] (28)

Solving Eq. (27) and (28) with some manipulation we get the following assertions
\[ \lim_{t \rightarrow \infty} (s(t) + i(t) + r(t) + w(t)) = 0. \] (29)

Hence the feasible region for the proposed problem (1) is given by the following bounded set
\[ Ω = \{ (s, i, r, w) ∈ \mathbb{R}^+_4 : s > 0, i, r, w ≥ 0 : (s + i + r) ∈ Π/d, w ∈ Ω \} \] (30)

is invariant positively subjected to the proposed system (1).

Theorem 3. The solutions \( s(t), i(t), r(t), w(t) \) of the proposed system (1) are positive for \( s(0), i(0), r(0), w(0) \) \( ∈ \mathbb{R}^+_4 \) a.s for \( t > 0 \).

Proof. We suppose that the solutions of stochastic corona model (1) exists in the interval \( (0, +\infty) \). To solve the first and second equations of model (1), as in [35] we consider the process \( (\xi(t), t ∈ \mathbb{R}) \) defined by the SDE
\[ d\xi(t) = a(t)\xi(t)dt + b(t)\xi(t)dB(t), \quad ξ(0) = 1, \] (31)

where \( (a(t), t ∈ \mathbb{R}) \) and \( (b(t), t ∈ \mathbb{R}) \) are two stochastic processes satisfying the required conditions to assure a solution of (31) as follows
\[ ξ(t) = \exp \left( \int_0^t a(u) - \frac{b^2(u)}{2} du + \int_0^t b(u) dB(u) \right), \quad t ∈ \mathbb{R}_+. \] (32)

Then the variation of constants method will be utilized to assume that the solution of the first equation of our model can be written as \( s(t) = y(t)ξ(t), \) with \( y(t) := s(t), \) \( a(t) := -(β_is(t) + β_dw(t) + d), \) and \( b(t) := -η_i(s(t) - Π) + η_w(t). \) Then \( y(t) \) can be obtained using the below integration by parts for stochastic processes
\[ dy(t) = d(\xi^{-1}(t)s(t)) = ξ^{-1}(t)s(t)dt + s(t)dt\xi^{-1}(t) + [d\xi^{-1}(t), ds(t)]. \]

Here \( d\xi^{-1}(t) \) is calculated using Ito formula applied to
\[ f(ξ(t)) = \frac{1}{\sqrt{η}}. \]

The solution of first equation of model (1) is then given by
\[ s(t) = s(0) + Π \int_0^t ξ^{-1}(u)du, \quad t ∈ \mathbb{R}_+. \]

The second equation of stochastic corona model (1) can be also obtained using the same methodology as above but with \( (t) = Π(ξ(t)), \) with \( s(0) := s(0), a(t) := β_is(t) - (d + d_1 + σ), \) and \( b(t) := η_is(t). \) The solution of second equation of model (1) is then given by
\[ i(t) = i(0) + \int_0^t (β_i - b(u))w(u)i(u)ξ^{-1}(u)du \]
\[ + \int_0^t η_is(u)w(u)ξ^{-1}(u)dB(u)ξ(t), \]

where \( t ∈ \mathbb{R}_+. \) Similarly it is not tedious to show that \( r(t) ≥ 0 \) and \( w(t) ≥ 0. \) Hence the solutions of the model (1) are positive. \( \square \)

Extinction and Persistence Analysis

The current section is devoted to discuss the extinction as well as persistence analysis. We find the condition that how the disease will be extinct from the community, we have the

...
following theorems.

**Theorem 4.** Since \((s_{i.r.w})\) is the solution of system (1) and \((s(0),r(0),\Omega(0))\) is the initial sizes of the populations, then

\[
\lim_{t \to \infty} \left( \log \left( \frac{t}{s(t)} \right) \right) = 0, \quad \text{a.s., i.e., the infection of novel corona virus disease will dies surely, if the}
\]

or consequently we can write that \(i(t) \to 0\), \(r(t) \to 0\) and \(w(t) \to 0\) exponentially a.s., i.e., the infection of novel corona virus disease will dies surely, if the following conditions are satisfied

\[
R_0^1 < 1 \quad \text{and} \quad 2\tilde{\eta}(\beta_1 + \beta_2 w + d + d_1 + \sigma) \geq \Pi (\tilde{\eta}_1^2 + \tilde{\eta}_2^2) + \alpha \tilde{\eta}_1^2 \Pi.
\]

Moreover,

\[
im_i \lim_{t \to \infty} \left( \frac{r(t)}{i(t)} \right) = \lim_{t \to \infty} \left( \frac{\log \left( \frac{t}{s(t)} \right) \log \left( \frac{t}{i(t)} \right) \log \left( \frac{t}{r(t)} \right) \log \left( \frac{t}{w(t)} \right)}{t} \right) = 0.
\]

**Proof.** We follow the same methodology as reported in Lei et al., we get the following system of equations

\[
\int_0^t \left( \Pi - \int_0^t (\beta_1 i(x) + \beta_2 w(x) + d) s(x) \right) dx - \int_0^t (\eta_1 s(x) i(x) + \eta_2 s(x) w(x)) dB(x),
\]

\[
\int_0^t \left( \Pi - \int_0^t (\beta_1 i(x) + \beta_2 w(x)) s(x) \right) dx - \frac{d + d_1 + \sigma}{\Pi} \int_0^t i(x) dB(x),
\]

\[
\int_0^t \left( \Pi - \int_0^t (\beta_1 i(x) + \beta_2 w(x) + d) s(x) \right) dx - \frac{d + d_1 + \sigma}{\Pi} \int_0^t i(x) dB(x),
\]

\[
\int_0^t \left( \Pi - \int_0^t (\beta_1 i(x) + \beta_2 w(x)) s(x) \right) dx - \frac{d + d_1 + \sigma}{\Pi} \int_0^t i(x) dB(x),
\]

where \(\psi_2(t) = -1/t \left( \frac{s(t-i(t))}{d + d_1 + \sigma} + \frac{r(t-i(t))}{d + \sigma} \right) \). Clearly if \(t\) approaches to \(\infty\), then \(\psi_1(t)\) and \(\psi_2(t)\) tend to zero.

Moreover the application of Itô formula to the 2nd equation of system (1) leads to the following equation

\[
di(t) = (\beta_1 i + \beta_2 w - (d + d_1 + \sigma) - \eta_1^2 x^2/2)
\]

\[
- \eta_2^2 w^2/2 dt + (\eta_1 s + \eta_2 w) dB(t).
\]

Integrating both side of the above Eq. (43) with limit from 0 to \(t\) and then dividing the resultant expression by \(t\) we get the following assertion

\[
\frac{1}{t} \int_0^t \left( \log \left( \frac{t}{i(t)} \right) - \log \left( \frac{t}{0(t)} \right) \right) dB(x) \leq \frac{\beta_1}{t} \int_0^t s(x) i(x) dB(x) - \frac{d + d_1 + \sigma}{t} \int_0^t s(x) w(x) dB(x),
\]

\[
\frac{1}{t} \int_0^t \left( \log \left( \frac{t}{r(t)} \right) - \log \left( \frac{t}{0(t)} \right) \right) dB(x) \leq \frac{\beta_1}{t} \int_0^t s(x) i(x) dB(x) + \frac{d + d_1 + \sigma}{t} \int_0^t s(x) w(x) dB(x),
\]

\[
\frac{1}{t} \int_0^t \left( \log \left( \frac{t}{w(t)} \right) - \log \left( \frac{t}{0(t)} \right) \right) dB(x) \leq \frac{\beta_1}{t} \int_0^t s(x) i(x) dB(x).
\]

It is clear from Eq. (33) that \(\langle a^2(x) \rangle \leq \langle a(x) \rangle^2\), therefore the above Eq. (44) may take the following form

\[
\frac{1}{t} \int_0^t \left( \log \left( \frac{t}{i(t)} \right) - \log \left( \frac{t}{0(t)} \right) \right) dB(x) \leq \frac{\beta_1}{t} \int_0^t s(x) i(x) dB(x) - \frac{d + d_1 + \sigma}{t} \int_0^t s(x) w(x) dB(x),
\]

Adding first and second equation of the above system and making use of \(\psi_2(t) = -1/t \left( \frac{s(t-i(t))}{d + d_1 + \sigma} + \frac{r(t-i(t))}{d + \sigma} \right) \), we obtain

\[
\langle s(t) \rangle = \Pi/\psi_2(t),
\]

\[
\langle w(t) \rangle = \Pi/\psi_2(t).
\]

Similarly the addition of first, second and third equation of the above system gives the following expression

\[
\langle w(t) \rangle = \Pi/\eta_1 \psi_2(t).
\]
\[
\frac{1}{t} \left( \log(i(t)) - \log(0) \right) \leq \beta_i \left( s \right) + w_i(t) \beta_i - \left( d_i + d + \sigma \right) - \eta_f \left( s \right)^2 / 2 - \eta_f \left( w \right)^2 / 2 + M_i(t) / \left( t + M_i(t) / t \right).
\] (46)

Plugging Eq. (41) and (42) in the above Eq. (46) lead to the assertion is given by
\[
\frac{1}{t} \left( \log(i(t)) - \log(0) \right) \leq \beta_i \left( \Pi/d - (d + d_i + \sigma)(i(t)) \right) + \eta_f \left( s \right)^2 / 2 - \eta_f \left( w \right)^2 / 2 + M_i(t) / \left( t + M_i(t) / t \right),
\] (47)

\[
\frac{1}{t} \left( \log(i(t)) - \log(0) \right) \leq \left( d + d_i + \sigma + \eta_f \left( \Pi \right)^2 + \eta_f \left( \Pi \right)^2 \right) \left( 1 - R^2 \right) - \left( d + d_i + \sigma \right) \left( \beta_i \eta_f + \beta_i \Pi \right) - \left( \Pi^2 \eta_f + \Pi^2 \right) / d - \eta_f \Pi \eta_f \left( \eta \right) / d - \eta_f \Pi \eta_f \left( \eta \right) / d.
\] (48)

Following the strong law of large number for the local continues martingales that \( \limsup M_i(t)/t = 0 \), \( \limsup M_2(t)/t = 0 \) and \( \lim \Phi(t) = 0 \) as \( t \) approaches \( \infty \) a.s. Moreover, Eq. (47) implies that
\[
\Phi(t) = \beta_i \left( r \right) + \beta_i \left( r \right) - \eta_f \left( \eta \right) / \left( \Pi \right) + \left( \Pi \right) + \left( \Pi \right) / \left( \Pi \right).
\] (49)

If \( R^2 < 1 \) and \( \left( d \beta_i \eta_f + \beta_i \Pi \right) - \left( \Pi \right) + \left( \Pi \right) / \left( \Pi \right) \), then we may write the above inequality in the following form
\[
\lim_{t \to \infty} \frac{1}{t} \left( \log(i(t)) - \log(0) \right) \leq \left( d + d_i + \sigma + \eta_f \left( \Pi \right)^2 + \eta_f \left( \Pi \right)^2 \right) \left( 1 - R^2 \right) - \left( d + d_i + \sigma \right) \left( \beta_i \eta_f + \beta_i \Pi \right) - \left( \Pi \right) \left( \Pi \right) / \left( \Pi \right) / \left( \Pi \right). \] (50)

Alternatively Eq. (50) shows that \( \lim \Phi(t) = 0 \) as \( t \to \infty \), which implies that \( \lim \Phi(t) = 0 \) as \( t \to \infty \). Also we know that
\[
\left\langle w(t) \right\rangle = \frac{1}{t} \left\langle \eta \left( \eta \right) / \left( \Pi \right) \right\rangle - \frac{\left\langle w(t) \right\rangle - \left\langle \eta \left( \eta \right) / \left( \Pi \right) \right\rangle}{t}
\] (51)

It could be noted from \( \lim \Phi(t) = 0 \) and the above Eq. (51) that \( \lim r(t) = 0 \) and \( \lim \left\langle w(t) \right\rangle = 0 \) as \( t \to \infty \). Using all these data i.e., \( \lim \Phi(t) = 0 \), \( \lim r(t) = 0 \) and \( \lim \left\langle w(t) \right\rangle = 0 \), Eq. (41) implies that \( \lim i(t) = \Pi/d \) a.s as \( t \) approaches \( \infty \). Thus it could be concluded that the extinction of the disease depend on the choice of parameters \( R^2 < 1 \) as well as \( \left( d \beta_i \eta_f + \beta_i \Pi \right) - \left( \Pi \right) + \left( \Pi \right) / \left( \Pi \right) \), and if these conditions holds the novel corona virus disease will extinct from the community.

**Persistence analysis**

We discuss the analysis of persistence in this subsection. We find that how the novel corona virus disease will persist in the community and therefore for analysis of persistence the following theorems are described.

**Theorem 5.** For any initial sizes \((i(0), \eta(0), r(0), w(0)) \in \Omega\), the solution \((s, i, r, w)\) of system (1) satisfying the property is given by
\[
i_i \lim_{t \to \infty} \inf \left\langle i(t) \right\rangle \leq \limsup_{t \to \infty} \left\langle i(t) \right\rangle \leq i_1 \text{ a.s.},
\] (52)

and
\[
w_1 \lim_{t \to \infty} \inf \left\langle w(t) \right\rangle \leq \limsup_{t \to \infty} \left\langle w(t) \right\rangle \leq w_1 \text{ a.s.}
\] (53)

In Eq. (52) and (53), the value of \( i_1, i_2, w_1, w_2 \) are defined by
\[
i_1 = \frac{\left( d + d_i + \sigma + \eta_f \left( \Pi \right)^2 + \eta_f \left( \Pi \right)^2 \right) \left( R^2 - 1 \right)}{\left[ d + d_i + \sigma \right] \left( \beta_i \eta_f + \beta_i \Pi \right) - \left( \Pi \right) \left( \Pi \right) / \left( \Pi \right)}
\] (54)

\[
w_1 = \frac{\left( d + d_i + \sigma + \eta_f \left( \Pi \right)^2 + \eta_f \left( \Pi \right)^2 \right) \left( R^2 - 1 \right)}{\left[ d + d_i + \sigma \right] \left( \beta_i \eta_f + \beta_i \Pi \right) - \left( \Pi \right) \left( \Pi \right) / \left( \Pi \right)}
\] (55)

**Proof.** By following the work of Lei et al., [33], it could be noted from Eq. (47) that
\[
\frac{1}{t} \left( \log(i(t)) - \log(0) \right) \leq \left( d + d_i + \sigma + \eta_f \left( \Pi \right)^2 + \eta_f \left( \Pi \right)^2 \right) \left( R^2 - 1 \right)
\] (56)

Consequently the above inequality can be written as
\[
\left\langle \left( \Phi \right) \right\rangle \leq \frac{\left( d + d_i + \sigma + \eta_f \left( \Pi \right)^2 + \eta_f \left( \Pi \right)^2 \right) \left( R^2 - 1 \right)}{\left[ d + d_i + \sigma \right] \left( \beta_i \eta_f + \beta_i \Pi \right) - \left( \Pi \right) \left( \Pi \right) / \left( \Pi \right)}
\] (57)

Taking the supremum as well as lim of both side, we get the following assertion is given by
\[
\left\langle \left( \Phi \right) \right\rangle \leq \left( d + d_i + \sigma + \eta_f \left( \Pi \right)^2 + \eta_f \left( \Pi \right)^2 \right) \left( R^2 - 1 \right)
\] (58)

On the other hand the substitution of Eq. (15), (41) and (42) in Eq.
The section is devoted to perform the simulation analysis of the novel corona virus model (1). The purposes of numerical simulation is to verify the analytical findings.

We first give a short overview on simulating stochastic differential equations-SDEs\footnote{for more details on simulating SDEs the reader can refer to the books [36,37].} since our model system in (1) is driven by SDEs. Consider a one dimensional stochastic process $X := (X_t)_{t\in[0,T]}$ driven by the following SDE

$$dX(t) = a(t, X(t))dt + b(t, X(t))dB(t), \quad X(0) = x.$$ \hfill (68)

The aim is to reproduce the evolution of $X(t)$ over a continuous time period. It is possible to generate a sample of $X(t)$ at a given time $t$ utilizing the SDE solution in case (68) is solved. Nonetheless, in general this can be done by simulating the SDE. As for deterministic differential equations, a discretization $\tilde{X}$ of the SDE at a finite number of points is needed. For seek of simplification, we use the notations $\tilde{X}_k$ instead of $X(k\Delta t)$ and $B_k$ instead of $B(k\Delta t)$, then a discretization of (68) can be given by $\tilde{X}_{k+1} = \tilde{X}_k + a(k\Delta t, \tilde{X}_k)\Delta t + b(k\Delta t, \tilde{X}_k)\Delta B_k$, \hfill (69)

for $k = 0, \ldots, N-1$. Notice that $\Delta B_k = B_{k+1} - B_k$. We will omit, from now on, the use of the symbol $\tilde{}$ for discretized version of a given SDE.

The application of stochastic Euler Maruyama technique to the model (1) gives the system

\begin{align*}
{s}_{i+1} - s_i &= \left[\Pi - \beta_i s_i - \beta_2 w_i - \delta s_i - \delta s_i\right] \Delta t - \left[\eta_i s_i + \eta_2 w_i\right] \Delta B_i, \\
{i}_{i+1} - i_i &= \left[\beta_i s_i + \beta_2 w_i - \delta (d + i) + \sigma_i\right] \Delta t + \left[\eta_i s_i + \eta_2 w_i\right] \Delta B_i, \\
{r}_{i+1} - r_i &= \left[\sigma_i - d_i\right] \Delta t + \left[a_i - \eta_2\right] \Delta t.
\end{align*}

Consequently the above system (70) can be re-written as

\begin{align*}
{s}_{i+1} &= s_i + \left[\Pi - \beta_i s_i - \beta_2 w_i - \delta s_i - \delta s_i\right] \Delta t - \left[\eta_i s_i + \eta_2 w_i\right] \Delta B_i, \\
{i}_{i+1} &= i_i + \left[\beta_i s_i + \beta_2 w_i - \delta (d + i) + \sigma_i\right] \Delta t + \left[\eta_i s_i + \eta_2 w_i\right] \Delta B_i, \\
{r}_{i+1} &= r_i + \left[\sigma_i - d_i\right] \Delta t + \left[a_i - \eta_2\right] \Delta t.
\end{align*}

Moreover we code the above algorithm via Matlab software along with the biological feasible value of parameters and initial sizes of populations to show the stochastic process influence with the help of graphs. We use two different set of parameters values i.e., one for the extinction analysis and one for the persistance analysis to verify the analytical findings. Let $S = \left[\Pi, \beta_1, \beta_2, \eta_1, \eta_2, d, d, \sigma, \alpha, \eta\right] = (p)$ be the set of parameter whose values are assumed to perform the verification of extinction analysis. The choice of parameters value in the case of extinction analysis are as: $\Pi = 0.5, \beta_1 = 0.045, \beta_2 = 0.15, \eta_1 = 0.5, \eta_2 = 0.1, d = 0.2, d_1 = 0.028, \sigma = 0.2, \alpha = 0.2, \eta = 0.25$, while the value for
the analysis of persistence are assumed as: 

\[ I(0) = 0.5, \beta_1 = 0.6, \beta_2 = 0.15, \eta_1 = 0.4, \eta_2 = 0.3, d = 0.015, d_i = 0.18, \sigma = 0.001, \alpha = 0.1, \eta = 0.12. \]

After executing with all these data we obtain the results as given in Fig. 1. The different trajectories of Fig. 1a demonstrate the susceptible dynamics, covid-19 infected, recovered and reservoir, which shows the extinction of the novel corona virus disease as shown in Theorem 4.1. This clearly splash that the susceptible population exist always while the remaining will vanishes after some time. Similarly the analysis of persistent are shown in Fig. 1b, which verify the analytical result as discussed in Theorem 4.2. In this case the solution trajectories of the various compartment of susceptible, infected, recovered and reservoir show that the disease persist as shown in Fig. 1b. Moreover, we also observe the influence of noise on the disease transmission that the increasing of noise intensity is directly proportional to the disease transmission while inversely proportional to the persistence of the disease.

Conclusion

We proposed a stochastic model for the novel corona virus disease, because spreading of the covid-19 is not deterministic and having stochastic effect. We formulated the model for covid-19 by varying the transmission co-efficient. Moreover we discussed the existence analysis along with uniqueness for the global solution and showed that the model is well-posed. We then also showed the extinction of the problem as well as persistence and obtained conditions in term of parameters and intensity of white noise. To support the theoretical findings, we used a numerical method of stochastic Euler Maruyama technique and presented numerical simulation. It could be noted from the simulation of the proposed model that there is a great influence of the white noise intensity on the transmission of the novel corona virus disease. The extinction of the covid-19 infected population is directly proportional to the noise intensity, i.e., to increase the value of the noise intensity will exponentially decrease the infection. Beside from this one the persisting of the novel corona virus are proportional inversely to the intensity of white noise i.e., disease persisting decreases if we increase the intensity of white noise.

In a near future a more general model with different sources of randomness where each population group has a different Brownian motion could be investigated.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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