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A proposed modified SEIQR epidemic model to analyze the COVID-19 spreading in Saudi Arabia

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Received 7 April 2021; revised 3 June 2021; accepted 25 June 2021
Available online 02 July 2021

KEYWORDS
SEIQR model; COVID-19; Reproduction; Jacobian matrix; Lyapunov stability; Number

Abstract The key aim of this paper is to construct a modified version of the SEIQR essential disease dynamics model for the COVID-19 emergence. The modified SEIQR pandemic model takes a groundbreaking approach to evaluate and monitor the COVID-19 epidemic. The complex studies presented in this paper are based on real-world data from Saudi Arabia. A reproduction number and a systematic stability analysis are included in the new version of SEIQR model dynamics. Using the Jacobian linearization process, we can obtain the domain of the solution and the state of equilibrium based on the modified SEIQR model. The equilibrium and its importance have been identified, and the disease-free stability of the equilibrium has been investigated. The reproduction number was calculated using internal metrics, and the global stability of the current model’s equilibrium was demonstrated using Lyapunov’s stability theorem. To see how well the SEIQR proposed model went, it was compared to real COVID-19 spread data in Saudi Arabia. According to the results, the new SEIQR proposed model is a good match for researching the spread of epidemics like COVID-19. In the end, we presented an optimal protocol to prevent the dissemination of COVID-19. Staying at home and transporting sick people as far as possible to a safe region is the most effective strategy to prevent COVID-19 spread. It is critical to offer infected people safe and effective treatment, as well as antibiotics and nutrients to non-affected people. To detect confirmed infections, we must provide more effective and reliable diagnostic methods. Furthermore, increasing
1. Introduction

From a medical engineering perspective, scientists and experts all over the world are attempting to develop an antidote or cure for the COVID-19 epidemic and to control possible pandemics. Any infectious disease can be well-known and understood using mathematical models. This idea began in 1927. After that, many different mathematical models have been constructed for various diseases and infections. For some essential studies, we refer to [1–8].

To explain transmission dynamics and estimate domestic and global disease spread based on data recorded from December 31, 2019, to January 28, 2020, Wu et al. [9] have implemented the Susceptible Exposed Infectious Recovered Model (SEIR). They also found that COVID-19 had a fundamental reproductive number of approximately 2.68. Read et al. [10] registered a value of 3.1 for the fundamental reproductive number based on the SEIR model data adaptation, assuming that the daily time spent by Poisson increases. Tang et al. [11] proposed a compartmental model of chronic disease development, human epidemiological status, and intervention measures that was deterministic. The authors found that the number of reproductive controls can be up to 6.47 and those engagement techniques, such as simplified traceability accompanied by insulation and quarantine, may minimize reproductive control numbers and risk of transmission effectively. To determine the scale of the disease outbreak in Wuhan, Iman [12] carried out calculational modeling of the possible epidemic tracks with an emphasis on human-to-human transmissions. Its findings suggest that controls must be efficiently controlled by well over 60% of the transmission. To analyze and forecast the infectivity of the new coronavirus, Guo et al. [13] developed a deep learning algorithm. They found that two animal hosts of this virus were bats and minks. Most of the models illustrate the significant role of a direct transmission mechanism between humans and humans in the outbreak, as demonstrated by the fact that many individuals infected in the Wuhan area have no interaction and the number of infections has been growing rapidly and spreading across the Chinese provinces and over 20 people [14]. There is a relatively long incubation period in many infected individuals, so they do not show symptoms and have not been aware of their infection for 10–14 days. Over time, the disease can easily be spread by direct exposure to other people. On the other hand, the published models have not, to date, considered the environmental position of COVID-19 transmission. Several different models have been constructed to study the COVID-19 outbreak [6,8,15–27].

Statistical epidemiology is based on the dynamics of health and disease and related population factors. The presence of a pathogenic microbial agent identifies an infectious disease as a clinically obvious disease. For modeling purposes, there are four types of transmission: straightforward, if the causative disease agent is an individual; vector, if the causative disease agent is transmitted from a vector to a person; normal, if a pathogen infects a human through the environment; and vertical, if the disease agent is transmitted from mother to child at birth. Airborne and personal infections are often believed to be spread immediately as people come into contact with one another [28].

Farman et al. [29] studied the stability and control of the glucose-insulin glucagon system in humans. The dynamical behavior of fractional-order cancer model with vaccine strategy has been discussed by Farman et al. [30]. Gondim and Machado [31] introduced the optimal strategies of the quarantine for the COVID-19 pandemic in a discrete age population. Davies et al. [32] studied the age-dependent effects in the rate of transmission and control of COVID-19 spreading. Youssef et al. [33] modified the SEIR model and used it to the real data of COVID-19 spreading in Saudi Arabia.

Feng and Thieme [34,35] considered SEIQR (Susceptible-Exposed-Infected-Quarantined-Recovered) models of arbitrarily spaced durations of illness, including quarantine, and a general occurrence concluded that all affected persons passed through the quarantine stage and examined the model dynamics. Junpen1 et al. [36] proposed a pandemic influenza SEIQR model and analyze the model properties and introduced a differential evolution (DE) algorithm for determining the numerical values of the parameters in the model. Gerberry and Milner [37] used the SEIQR model for childhood diseases.

Thus, the goal of this paper is to construct a new COVID-19 vital dynamical model that is more applicable to cases in any country through mathematical analysis of the model in question by using a system of similar models with different considerations and new in/out flows between population divisions. Besides, this paper presents a new formula that explores the sensitivity of a reproduction number. The mechanisms of virus transmission by humans are to be discovered. Another aim is to investigate and learn the optimal procedures, controls, and techniques to minimize the outbreak substantially.

2. Materials and methods

2.1. Formulation of a coronavirus disease (SEIQR model)

In any country where COVID-19 is spreading, the population can be divided into five critical diverse subpopulations or classes, which are depicted in Fig. 1 and can be defined as follows [4,6,16,23,32,36,38]:

The main group \(S(t)\) is dedicated to healthy people but who may get the disease population. For certain diseases, the infected person may not become infectious immediately, but the latent phase is not contagious. The pathogen requires time to reproduce and establish itself in its new host. In general, the exposed (latent) cycle follows the sensitive process [4,6,18,20,38].

As a result, the category \(E(t)\) is devoted to the exposed population or compromised but non-infectious persons.

The population that has been reported infected is the focus of the group \(I(t)\) . (individuals who have contracted the disease...
and are now sick with it and infected individuals are also infected. The group \( Q(t) \) is dedicated to the quarantined population (separated from the general population even in their houses).

The group \( R(t) \) is defined as the recovered population (individuals who have recovered and cannot contract the COVID-19 again), as in Fig. 1.

The transmission rate from a susceptible population to infected but undetected by the testing population is defined by the parameter \( K_a \). We consider the net inflow of the susceptible population at a non-negative rate \( \Lambda > 0 \) per unit value of time (comprising new births and new residents).

For any group, the outflow based on the natural death rate is defined by the nonnegative rate \( d_i \).

The total population size is \( N(t) \), which is defined as \[ N(t) = S(t) + E(t) + I(t) + Q(t) + R(t) \] (1)

For the group \( S(t) \), we have two outflows; a population flows out to the exposed group \( E(t) \) by the rate \( \alpha S(t) \) (each one in \( S(t) \) can transfer the infection to \( E(t) \)), so the total number of outflows is equal to \( \alpha S(t) \). The outflow of the natural death is \( dS(t) \).

The group of exposed \( E(t) \) has only one inflow \( \beta_1 E(t) \) and \( \beta_2 I(t) \), while it has four outflows. The first outflow is the population that flows out to the group \( Q(t) \) by the rate of transmission \( \beta_1 \). The second outflow is the population that flows out to the recovery group directly without needing treatment by transmission rate of recovery \( \sigma_1 \). The third outflow is a population that flows out to the infected group \( I(t) \) with the transmission rate of infection \( \beta_2 \), and the fourth outflow is the population that experiences natural death by the transmission rate \( d_1 \).

For the group of the confirmed infected population \( I(t) \), we have only one inflow, which comes from the group \( E(t) \), with the transmission rate \( \beta_2 \), while it has three outflows of population. The first outflow is the population that must go to the quarantine area \( Q(t) \) by the transmission rate \( \beta_1 \), and the second outflow comes from the population in which treatment has succeeded; individuals in this population can go out to the recovery group \( R(t) \) by recovery transmission rate \( \sigma_2 \). The last outflow from the infected group is the total death, which comes from natural death by transmission rate \( d_1 \) and death due to the COVID-19 virus by transmission rate of mortality \( d_2 \).

For the recovery population \( R(t) \), three inflows exist, and only one outflow. The first inflow comes from the quarantine area \( Q(t) \) by transmission rate of recovery \( \sigma_1 \), the second inflow is the population that comes out from the infected by the transmission recovery rate \( \sigma_2 \), and the third inflow is the population that flows out from the exposed area directly by transmission recovery rate \( \sigma_3 \). The only outflow from the recovering group is death by the natural transmission rate of mortality \( d_1 \).

For the quarantine group \( Q(t) \), two inflows \( \beta_1 E(t) \) and \( \beta_2 I(t) \) two outflows are present. The first outflow is the population flow out to the recovery group \( R(t) \) with transmission rate \( \sigma_1 \), while the second outflow is the total death, which comes from natural death by transmission rate of death \( d_1 \) and by the transmission rate of death due to the COVID-19 virus \( d_2 \).

All inflows and outflows are shown in the flowchart in Fig. 1, and the five groups can be converted into equations to formulate the following system of first-order ordinary nonlinear differential equations [4,6,16,22,23,39,40]:

\[
\begin{align*}
\frac{dS(t)}{dt} &= \Lambda - \alpha S(t) I(t) - d_1 S(t) \\
\frac{dE(t)}{dt} &= \alpha S(t) I(t) - \varepsilon_1 E(t) \\
\frac{dI(t)}{dt} &= \beta_1 E(t) + \beta_2 I(t) - \varepsilon_1 I(t) \\
\frac{dQ(t)}{dt} &= \beta_1 E(t) + \beta_2 I(t) - \varepsilon_3 Q(t) \\
\frac{dR(t)}{dt} &= \sigma_3 E(t) + \sigma_2 I(t) + \sigma_1 Q(t) - d_1 R(t)
\end{align*}
\]

where \( \varepsilon_1 = (r + \beta_1 + \sigma_1 + d_1), \varepsilon_2 = (\beta_2 + \sigma_2 + d_1 + d_2), \) and \( \varepsilon_3 = (\sigma_1 + d_1 + d_2) \).

We can see that the current model in Eqs. (2)–(6) is more general than the model by Gerberry and Milner [37], where...

![Fig. 1](image_url)
the model coincides with the current model when $\beta_1 = \sigma_2 = \sigma_3 = 0$. Moreover, when $\beta_i = 0$ the current model coincides with the model proposed by Jumpen et al. [36].

2.2. Theorem 1 (all solutions are definite positive)

Let the initial conditions $\{S(0), E(0), I(0), Q(0), R(0)\} \geq 0$. Then, the solutions of the SEIQR model in Eqs. (2)–(6) are non-negative in the interval $[0, \infty)$ [6].

Proof: Assume that $t_1 = \sup \{t > 0 : S > 0, E > 0, I > 0, Q > 0, R > 0, \in [0, t]\}$. Thus, $t_1 > 0$.

From the Eq. (2), we obtain that:

$$\frac{dS(t)}{dt} = \Lambda - (\lambda + d_1) S(t)$$

$$\lambda = xI$$

It can be re-written in the following form [3]:

$$\frac{d}{dt} \left[ S(t) \exp \left( d_1 t + \int_0^t \lambda(\tau) d\tau \right) \right] = \dot{S}(t) \exp \left( d_1 t + \int_0^t \lambda(\tau) d\tau \right)$$

Hence, we have:

$$S(t_1) \exp \left( d_1 t_1 + \int_0^{t_1} \lambda(\tau) d\tau \right) = S(0)$$

$$= \int_0^{t_1} \Lambda \exp \left( d_1 x + \int_0^x \lambda(\tau) d\tau \right) dx$$

For $S(0) > 0$, it gives:

$$S(t_1) \geq \int_0^{t_1} \Lambda \exp \left( d_1 x + \int_0^x \lambda(\tau) d\tau \right) dx$$

Thus, we obtain:

$$S(t_1) \geq \exp \left( -d_1 t_1 - \int_0^{t_1} \lambda(\tau) d\tau \right) \times \int_0^{t_1} \Lambda \exp \left( d_1 x + \int_0^x \lambda(\tau) d\tau \right) dx > 0$$

Then, we get:

$$S(t_1) > 0$$

It can also be shown that $I(t) > 0, E(t) > 0, Q(t) > 0$, and $R(t) > 0$[3].

2.3. Theorem 2 (the domain of solutions)

All the solutions of the proposed model structure that initiate in $\mathbb{R}_+^5$ are bounded inside the region $\psi$ defined by

$$\psi = \left\{ (S, E, I, Q, R) \in \mathbb{R}_+^5 : 0 \leq N(t) \leq \frac{\Lambda}{d_1} \right\}$$

Proof: After making the first derivative for both sides of the Eq. (1), we obtain

$$N'(t) = S'(t) + E'(t) + I'(t) + Q'(t) + R'(t)$$

Substituting from the model (2)–(6), we obtain

$$N'(t) = \Lambda - d_1 N(t) - d_2 (Q(t) + I(t))$$

From theorem 1, we have $d_2 (Q(t) + I(t)) \geq 0$; hence, the following inequality is valid:

$$N'(t) + d_1 N(t) \leq \Lambda$$

Then, we obtain:

$$N(t) \leq \left( N(0) - \frac{\Lambda}{d_1} \right) e^{-d_1 t} + \frac{\Lambda}{d_1}$$

Then, when $t \to \infty$ we obtain the solution:

$$0 \leq N(t) \leq \frac{\Lambda}{d_1}$$

which completes the proof [3,6,39].

2.4. The SEIQR model’s equilibrium

By Setting all the derivatives to zero and solve the system, we can find the equilibrium of this process as follows [3,6,39]:

$$S'(t) = E'(t) = I'(t) = Q'(t) = R'(t) = 0 \rightarrow \{ S, E, I, Q, R \} \equiv \text{Constants}$$

which gives

$$0 = \Lambda - \alpha SI - d_1 S$$

$$0 = \alpha SI - \alpha E$$

$$0 = \alpha E - \alpha I$$

$$0 = \beta_1 E + \beta_2 I - \alpha Q$$

$$0 = \alpha Q + \alpha I + \alpha E - d_1 R$$

From the Eq. (21), we have

$$I = \frac{\sigma_2}{\beta_2} E$$

Substituting Eq. (24) into the Eq. (20) for $E \neq 0$, we obtain

$$S = \frac{\alpha_1 \alpha_2}{\alpha r}$$

Substituting Eqs. (24) and (25) into the Eq. (19), we obtain

$$E = \frac{\alpha_1 \beta_1}{\beta_2} (\mathfrak{R}_0 - 1)$$

where

$$\mathfrak{R}_0 = \frac{\alpha r \Lambda}{d_1 \alpha_1 \alpha_2}$$

Substituting Eq. (26) into the Eq. (24), we obtain

$$I = \frac{\alpha_1}{\mathfrak{R}_0} (\mathfrak{R}_0 - 1)$$

Substituting Eqs. (26) and (28) into the Eq. (22), we obtain

$$Q = \frac{(\beta_1 \alpha_2 + \beta_2 \alpha_1) d_1}{\alpha r} (\mathfrak{R}_0 - 1)$$

Substituting Eqs. (26), (28), and (29) into the Eq. (23), we obtain
We can see that at disease-free equilibrium (DFE) 
\( \mathcal{R}_0 = 1 \) i.e. \( \frac{\alpha}{\sigma} \leq \frac{\lambda}{d_1} \), which leads to \( E = I = Q = R = 0 \), as in
Eqs. (19) and (25), which agrees with the domain of solution
in (17).

The number \( \mathcal{R}_0 \) is called the reproduction number (RBN),
which takes the form [3,6,39]:
\[
\mathcal{R}_0 = \frac{\lambda \sigma}{d_1 \beta_1 \bar{e}_2} = \frac{\lambda \sigma}{d_1 (r + \beta_1 + \sigma_1 + d_1)(\beta_2 + \sigma_2 + d_1 + d_2)} \tag{31}
\]

Then, if \( \mathcal{R}_0 > 1 \), The system has a one-of-a-kind endemic
equilibrium [8]:
\[
E_0 = (S^*, E^*, I^*, Q^*, R^*) \tag{32}
\]
where
\[
S^* = \frac{\alpha}{\sigma,C} E^* = \frac{\alpha}{\sigma,C} (\lambda \mathcal{R}_0 - 1), I^* = \frac{\lambda}{d_1} (\lambda \mathcal{R}_0 - 1),
\]
and
\[
Q^* = \frac{\beta_1 \sigma_1 \sigma_2}{\sigma_1 + \sigma_2 + d_2} (\lambda \mathcal{R}_0 - 1),
\]

Thus, the system has a unique disease-free equilibrium \( E_0 = \left( \frac{\lambda}{d_1}, 0, 0, 0, 0 \right) \) when \( \mathcal{R}_0 = 1 \), and has a unique endem-
ismic equilibrium \( E_0 = (S^*, E^*, I^*, Q^*, R^*) \) when \( \mathcal{R}_0 > 1 \)[6,8].

When \( \mathcal{R}_0 = 0 \) there is no transmission, which is considered as the number of secondary cases or the current inci-
dence of infection (transmission rate at which the susceptible
individuals converted to an exposed individual) [6,8].

2.5. Reproduction number by using the Jacobian matrix

To obtain the reproduction number \( \mathcal{R}_0 \) by applying the Jacobian
matrix method, the disease-free equilibrium (DFE) of the
SEIQR proposed model is acquired by setting\( E = I = Q = R = 0 \) in Eqs. (19)–(23) has been considered.

Then, we get DFE in the form \( E_0 = \left( \frac{\lambda}{d_1}, 0, 0, 0, 0 \right) \) [6].

The Jacobian matrix of the SEIQR proposed model as follows:
\[
J = \begin{bmatrix}
-\lambda I - d_1 & 0 & -\lambda S & 0 & 0 \\
\lambda I & -\varepsilon_1 & \lambda S & 0 & 0 \\
0 & r & -\varepsilon_2 & 0 & 0 \\
0 & \sigma_3 & \sigma_2 & -d_1 & \sigma_1 \\
0 & \beta_1 & \beta_2 & 0 & -\varepsilon_3 
\end{bmatrix} \tag{33}
\]

First, we will linearize the first two equations by using the
Jacobian method. The first two equations have a disease-free
equilibrium (DFE) situation when \( E = 0 \) the and \( S = \frac{\lambda}{d_1} \).

Hence, we consider \( S'(t) = F(S, I) \) and
\[
E'(t) + \varepsilon_1 E(t) = G(S, I) \text{such that} [6]:
\]
\[
F(S, I) = \Lambda - \lambda S(t) I(t) - d_1 S(t) \tag{34}
\]
\[
G(S, I) = \lambda S(t) I(t) \tag{35}
\]

Then, we have
\[
\begin{bmatrix}
S'(t) \\
E'(t) + \varepsilon_1 E(t)
\end{bmatrix} = \begin{bmatrix}
\frac{\alpha}{\sigma_1} & \frac{\alpha}{\sigma_2} & \frac{\alpha}{\sigma_3} \\
\frac{\sigma_1}{\lambda C} & \frac{\sigma_2}{\lambda C} & \frac{\sigma_3}{\lambda C}
\end{bmatrix}
\begin{bmatrix}
S(t) - S(0) \\
I(t) - I(0)
\end{bmatrix}
\]
\[
= \begin{bmatrix}
-\varepsilon_1 I(t) - \alpha S(t) \\
\alpha I(t)
\end{bmatrix}
\begin{bmatrix}
0 \\
\lambda S(t)
\end{bmatrix}
\begin{bmatrix}
S(t) - S(0) \\
I(t) - I(0)
\end{bmatrix} \tag{36}
\]

By using the equilibrium point, we get:
\[
\begin{bmatrix}
S'(t) \\
E'(t) + \varepsilon_1 E(t)
\end{bmatrix} = \begin{bmatrix}
-\varepsilon_1 & \frac{\alpha}{\lambda} \\
\frac{\alpha}{\lambda} & 0
\end{bmatrix}
\begin{bmatrix}
S(t) - S(0) \\
I(t)
\end{bmatrix} \tag{37}
\]

Hence, the system of nonlinear Eqs. (2) and (3) has been converted
to the following linear system [6]:
\[
\begin{bmatrix}
S'(t) \\
E'(t) + \varepsilon_1 E(t)
\end{bmatrix} = \begin{bmatrix}
-\varepsilon_1 & \frac{\alpha}{\lambda} \\
\frac{\alpha}{\lambda} & 0
\end{bmatrix}
\begin{bmatrix}
S(t) - S(0) \\
I(t)
\end{bmatrix} \tag{38}
\]

For the full equilibrium system, the consistency of the
disease-free equilibrium (DFE) is determined by the Jacobian
matrix:
\[
J_{E_0} = \begin{bmatrix}
-\varepsilon_1 & \frac{\alpha}{\lambda} & 0 & 0 \\
0 & -\varepsilon_1 & \frac{\alpha}{\lambda} & 0 & 0 \\
0 & r & -\varepsilon_2 & 0 & 0 \\
0 & \sigma_3 & \sigma_2 & -d_1 & \sigma_1 \\
0 & \beta_1 & \beta_2 & 0 & -\varepsilon_3 
\end{bmatrix} \tag{40}
\]

Calculation of the characteristic equation given by
\[
|J_{E_0} - \lambda I_{5}| = 0, \text{ where } \lambda \text{ is the parameter of the eigenvalue}
\text{and } I_5 \text{ is the identity matrix of order 5}, \text{ then the eigenvalues}
of the matrix } J_{E_0} \text{ take the following values:}
\]
\[
\begin{bmatrix}
\lambda_1 \\
\lambda_2 \\
\lambda_3 \\
\lambda_4 \\
\lambda_5
\end{bmatrix} = \begin{bmatrix}
-\varepsilon_1 \\
-\varepsilon_1 \\
-\varepsilon_1 \\
-\varepsilon_2 - \lambda \\
-\varepsilon_2 - \lambda
\end{bmatrix} \tag{41}
\]

and the rest of the roots are the solution to the following
equation:
\[
\begin{bmatrix}
-\varepsilon_1 & \frac{\alpha}{\lambda} \\
\frac{\alpha}{\lambda} & 0
\end{bmatrix}
\begin{bmatrix}
\lambda_1 - \lambda \\
\lambda_2 - \lambda
\end{bmatrix} = 0 \tag{42}
\]

which gives
\[
(\varepsilon_1 + \lambda)(\varepsilon_2 + \lambda) - \frac{\alpha \lambda}{d_1} = 0 \tag{43}
\]

After inserting \( \mathcal{R}_0 \), the roots of the Eq. (43) have the forms:
\[
\lambda_4 = -\frac{1}{2} \left( \varepsilon_1 + \varepsilon_2 - \sqrt{(\varepsilon_1 - \varepsilon_2)^2 + 4 \varepsilon_1 \varepsilon_2 \mathcal{R}_0} \right) \tag{44}
\]
\[
\lambda_5 = -\frac{1}{2} \left( \varepsilon_1 + \varepsilon_2 + \sqrt{(\varepsilon_1 - \varepsilon_2)^2 + 4 \varepsilon_1 \varepsilon_2 \mathcal{R}_0} \right)
\]

The formulas (44) generate the following cases [6]:
1. If $R_0 < 1$, then we have $\lambda_4 < 0$ and $\lambda_5 < 0$ in which the disease-free equilibrium $E_{0\text{df}}$ is locally asymptotically stable.

2. If $R_0 > 1$, then we have $\lambda_4 > 0$ and $\lambda_5 < 0$ in which the endemic equilibrium $E_{0\text{end}}$ is locally asymptotically unstable.

3. If $R_0 = 1$, then we have $\lambda_4 = 0$ and $\lambda_5 < 0$ in which the disease-free equilibrium $E_{0\text{df}}$ is locally asymptotically unstable.

### 2.6. Condition of equilibrium (Hartman-Grobman theorem)

The Hartman-Grobman theorem states that the solutions of a square system of nonlinear ordinary differential Eqs. (2)–(5) in a neighborhood of a steady-state look “qualitatively” similar to the solutions of the linearized system near the point $E_0 = \left( \frac{S_0}{\lambda}, 0, 0, 0, 0 \right)$. This finding only applies when the equilibrium is hyperbolic [6].

Thus, from the Eq. (41) we obtain the following condition of equilibrium:

$$\alpha r \Lambda - d_1 e_1 e_2 \neq 0$$

### 2.7. The uniqueness of the equilibrium state

When the matrix $J_{E_0}$ has been obtained from the linearization and the Jacobian is evaluated at equilibrium $D(\frac{E_0}{\lambda}) = \left( \frac{S_0}{\lambda}, 0, 0, 0, 0 \right)$, then, the condition $|J_{E_0}| \neq 0$ means that the equilibrium situation is isolated (there is a disk around $E_0$ that has no other equilibria) [6,18,23,39].

Hence, from the Eq. (40), we have:

$$|J_{E_0}| = 
\begin{vmatrix}
-d_1 & 0 & -\frac{\alpha r \Lambda}{e_1} & 0 & 0 \\
0 & -e_1 & -\frac{\alpha r \Lambda}{e_1} & 0 & 0 \\
0 & r & -e_2 & 0 & 0 \\
0 & \sigma_3 & \sigma_2 & -d_1 & \sigma_1 \\
0 & \beta_1 & \beta_2 & 0 & -e_1 \\
\end{vmatrix}
$$

which gives:

$$|J_{E_0}| = e_3 d_1 (x r \Lambda - d_1 e_1 e_2) = e_3 e_2 (x \frac{r \Lambda}{e_1 e_2} - 1) \neq 0$$

Hence, the condition in the Eq. (45) is the only one of the equilibria of the SEIQR proposed model. Thus, the unique condition of equilibrium of the SEIQR proposed model as follows:

$$\frac{x r \Lambda}{e_1 e_2} - 1 = R_0 - 1 \neq 0$$

The reproduction number (RBN) $R_0 = \frac{x r \Lambda}{e_1 e_2}$ is also unique [6].

### 2.8. The analysis of the local sensitivity of RBN($R_0$)

The analysis of the local sensitivity examines the increment in the output values due to a change in any parameter (input value) [6].

The sensitivity of a quantity $G$ with respect to a parameter $p$ is given by:

$$\psi_p = \frac{\partial G}{\partial p} \frac{G}{p} = \frac{\% \Delta G}{\% \Delta p}$$

The sensitivity of $G$ concern $p$ is negative if $G$ decreases concerning $p$ and is positive if $G$ increases concerning $p$.

Applying the formula in the Eq. (49) into reproduction number $R_0$, which takes the form [6]:

$$R_0 = \frac{x r \Lambda}{d_1 e_1 e_2} = \frac{x r \Lambda}{d_1 (r + \beta_1 + \sigma_1 + d_1)(\beta_2 + \sigma_2 + d_1 + d_2)}$$

Hence, from the Eq. (40), we have:

$$\psi_{R_0} = \frac{\partial R_0}{\partial R} \frac{R_0}{\alpha} = 1 > 0$$

Then,

$$\psi_{R_0} = \frac{\partial R_0}{\partial r} \frac{R_0}{\alpha} = 1 - \frac{r}{e_1} > 0$$

$$\psi_{R_0} = \frac{\partial R_0}{\partial e_1} \frac{R_0}{\alpha} = - \frac{d_1 (r + \sigma_2 + d_1)}{\sigma_1 e_1 e_2} + 1 < 0$$

$$\psi_{R_0} = \frac{\partial R_0}{\partial \beta_1} \frac{R_0}{\alpha} = - \frac{\beta_1}{e_1} < 0$$

$$\psi_{R_0} = \frac{\partial R_0}{\partial \beta_2} \frac{R_0}{\alpha} = - \frac{\beta_2}{e_2} < 0$$

$$\psi_{R_0} = \frac{\partial R_0}{\partial \sigma_1} \frac{R_0}{\alpha} = - \frac{\sigma_1}{e_1} < 0$$

$$\psi_{R_0} = \frac{\partial R_0}{\partial \sigma_2} \frac{R_0}{\alpha} = - \frac{\sigma_2}{e_2} < 0$$

$$\psi_{R_0} = \frac{\partial R_0}{\partial \sigma_3} \frac{R_0}{\alpha} = - \frac{\sigma_3}{e_1} < 0$$

It means that a 1% increase in each one($d_1, \beta_1, \sigma_1, d_2, \sigma_2, \beta_2$) will produce $\left( \left( \frac{d_1 (r + \sigma_2 + d_1)}{\sigma_1 e_1 e_2} + 1 \right) \frac{d_1 (r + \sigma_2 + d_1)}{\sigma_1 e_1 e_2} \right)$, a decrease in $R_0$, respectively, and a 1% increase in $r$ will give $\left( 1 - \frac{\beta_1}{e_1} \right)$ a rise in RBN($R_0$). From the Eq. (51), $\psi_{R_0} = 1$ gives that a 1% increase $z$ will produce an increase of 1% in $R_0$ [6].

### 2.9. Global stability of equilibria (Lyapunov stability theorem)

One of the most often used functions is the Lyapunov equation. Lyapunov functions are scalar functions that can be used to demonstrate the global stability of equilibrium. Lyapunov states that if $V(x)$ is a globally positively definite function and radially unbounded and its first derivative is globally negative, $V'(x) < 0$ for all $x \neq x'$, then the equilibrium position $x'$ is globally stable for the autonomous system $x' = f(x)$, where $V(x)$ is a Lyapunov function [6].

### 2.10. Theorem 5 (Global stability)

The SEIQR proposed model $DFE(E_0) = \left( \frac{S_0}{\lambda}, 0, 0, 0, 0 \right)$ is a globally stable system in disease-free equilibrium under the condition $R_0 < 1$. 

Proof. We propose the SEIQR model on the space of only the first three variables \((S, E, I)\). If the disease-free equilibrium for the first three differential equations only is stable globally, then \((R, Q)\) is the disease-free equilibrium for the full SEIQR proposed model is stable globally.

We assume a Lyapunov function on \(\mathbb{R}^3_+\) in the following form:
\[
V = \kappa \left( S - S' - S \ln \left( \frac{S}{S'} \right) \right) + \frac{E}{\epsilon_1} + \frac{I}{r} \tag{59}
\]

where \(\kappa\) is a constant which will be determined later on, and \(S' = \frac{\Delta}{\epsilon_1} \).

The Eq. (59) means that \(V = 0\) at the disease-free equilibrium \((\Delta, 0, 0)\).

Now, we must prove that \(V > 0\) for all \((S, E, I) \geq (\Delta, 0, 0)\).

Re-write the Eq. (59) as follows:
\[
V = \kappa S' \left( \frac{S}{S'} - \ln \left( \frac{S}{S'} \right) - 1 \right) + \frac{E}{\epsilon_1} + \frac{I}{r} \tag{60}
\]

The first term of the Eq. (60) is positive for any value of \(S\), moreover, the other two terms are non-negative also. Hence, \(V > 0\).

We apply the first derivative to the Eq. (59), we get:
\[
V' = \kappa \left( 1 - \frac{S'}{S} \right) S' + \frac{E'}{\epsilon_1} + \frac{I'}{r} \tag{61}
\]

Substituting from the first three equations of the SEIQR proposed model and by using the Eq. (25), we get:
\[
V' = 2 \Delta \kappa - \frac{\kappa_2 \epsilon_3}{r} SI - d_1 \kappa S - \frac{\Lambda_2 \kappa_3}{d_1 r} S + \frac{d_1 \kappa S}{\epsilon_1 r} I + \frac{\lambda_3}{\epsilon_1 r} SI - \frac{\epsilon_3}{r} I \tag{62}
\]

We choose \(\kappa = \frac{1}{\Delta}\), then we have:
\[
V' = -\frac{\Lambda}{\epsilon_1} (\frac{\Lambda}{d_1 S} + \frac{d_1 S}{\Lambda} - 2) + \frac{\epsilon_3}{r} (9 \theta_0 - 1) I \tag{63}
\]

Since \(9 \theta_0 < 1\) then, the last term in the Eq. (63) is non-positive.

Consider \(\frac{d_1 S}{\epsilon_1} = x\), then, the term \((\frac{\Lambda}{d_1 S} + \frac{d_1 S}{\Lambda} - 2)\) takes the form \((x + \frac{1}{x} - 2) = \frac{(x-1)^2}{x} > 0\).

The point of equilibrium \(S = S' = \frac{\Delta}{\epsilon_1}\) gives \(x = 1\). So, the first term completely vanishes, and the last term only is already non-negative. Hence, \(V' < 0\). Otherwise, \(x \neq 1\), which means that the two terms are non-positive. Thus, \(V' < 0\).

Therefore, \(V' < 0\) for every \((S(t), E(t), I(t)) \geq (\frac{\Delta}{\epsilon_1}, 0, 0)\)

[6].

Thus, by the Lyapunov theorem, the disease-free equilibrium is globally asymptotically stable for the system of the SEIQR model in all.

2.11. The SEIQR proposed model’s solutions

Consider the initial conditions of the SEIQR system in (38), (39), and (4)-(6) take the forms:
\[
\begin{align*}
\{S(t), E(t), I(t), Q(t), R(t)\}_{t=0} = \{S(0), E(0), I(0), Q(0), R(0)\} \\
\{S(0), E(0), I(0), Q(0), R(0)\} \leq \{S(t), E(t), I(t), Q(t), R(t)\}_{t=0}
\end{align*}
\]

We solved this system by using MAPLE software. Hence, we obtain:
\[
I(t) = \frac{1}{2\Lambda} \left[ (\frac{\epsilon_1}{\epsilon_2} - \delta) \gamma_1 e^{\frac{\epsilon_1}{\epsilon_2} t} + (\frac{\epsilon_1}{\epsilon_2} - \delta) \gamma_2 e^{\frac{\epsilon_1}{\epsilon_2} t} \right] e^{-\epsilon_3 t} \tag{65}
\]

where \(\delta = \sqrt{4\Lambda \epsilon_3 d_1 + d_1^2 \epsilon_2^3 - 2d_1 \epsilon_1 \epsilon_2 + d_1^2 \epsilon_2^2}, \quad \gamma_1 = (d_1 (\epsilon_1 - \epsilon_2) - \delta) E(0) + 2\Lambda_2 I(0), \quad \gamma_2 = (d_1 (\epsilon_1 - \epsilon_2) + \delta) E(0) + 2\Lambda_2 I(0)\). Consequently, we can obtain the other functions \(S, E, I, Q\).

2.12. Model verification and predictions

To verify the SEIQR model, we will apply it to the real data regarding the COVID-19 outbreak in Saudi Arabia. The COVID-19 has started in Saudi Arabia since March 3, 2020. Cases continued to be discovered in small numbers until the beginning of April, and then the number of detected cases increased. Therefore, we decided in this study to consider April 1, 2020, as the real beginning of the spread of the COVID-19 in Saudi Arabia.

The tables of statistics issued by the Saudi Ministry of Health [41] and the daily official statement issued by the ministry as well as Wikipedia [42] will be used, which also depends on the ministry’s website and other websites that would announce these statistics.

Another source of these data is the “Saudi Centre for Disease Prevention and Control [43].” We used the official website of the General Statistics Authority of Saudi Arabia for more data about the kingdom’s population, population growth rate, and mortality rate.

To study the spread of COVID-19 in Saudi Arabia before June 13, 2020, we will represent the curves of the number of daily infections and time series of the total infections, as in Figs. 2 and 3:

Fig. 2 shows that the number of cases on April 1, 2020, was 157 infections, and it reached 4233 infections on June 13, 2020. Between the two numbers, the curves passed through many up and down variations.

Fig. 3 represents the total number of cases at the same interval which started with 157 infections and obtained an accumulated amount of 122,259 infections on June 13, 2020. Therefore, we will use these data by the present SEIQR proposed model to determine if there is a convergence between the model results and the actual data [41-43].

3. Results

3.1. Using the SEIQR model to Saudi Arabia data of the spread of Covid-19

According to the official information of Saudi Arabia, we have the following initial data, which are considered the initial conditions of the system based on the SEIQR model, as in Table 1 [41-43]:
where $S(0) = 34,218,169$ is the total population in Saudi Arabia up to June 13, 2020. The total number of exposed populations infected but not detected by testing has been assumed $E(0) = 5000$, while the number of infections $I(0) = 157$. The recovery number of the population at the same time was $R(0) = 99$, and the population number in quarantine is $Q(0) = 1720$.

The total number of new births and residents of Saudi Arabia $K$ is $25230$ per person/day and the natural death rate is approximately $1030$ people/day, which results in $d = 3/10$. Some of the above parameters have been calculated, estimated, or assumed, as in Table 2. The estimated data has been calculated by using the most powerful methods, which is called curve fitting. MAPLE software has been used for the fitting curves and to estimate the parameters we need.

After using the above values of the parameter and by using MAPLE software, we obtain the results that indicate the number of daily infections as outcomes of the SEIQR model. The following figure shows the numerical results of the SEIQR model against the real data with different values of the rate of transmission from susceptible populations to infection in Saudi Arabia, $\alpha = (2.0, 2.2, 2.4) \times 10^{-5}$. Some of the above parameters have been calculated, estimated, or assumed, as in Table 2. The estimated data has been calculated by using the most powerful methods, which is called curve fitting. MAPLE software has been used for the fitting curves and to estimate the parameters we need.

![Fig. 2](image.png) The real number of daily infections in Saudi Arabia between 4/1/2020 and 6/13/2020.

It is noted that an increase in the parameter $\alpha$ leads to a rise in the number of infections and $RBN(90)$. Moreover, the reproduction number $RBN(90)$ is $90 = (6.81, 7.49, 8.17) > 1$. In other words, the rate of transmission at which the susceptible individuals converted to an exposed individual is greater than one. It means that the spreading of COVID-19 in Saudi Arabia was unstable in this interval. Fig. 4 shows the number of daily infections based on the SEIQR model against the real data in Saudi Arabia between 4/1/2020 and 6/13/2020 with three different values of the rate of transmission from susceptible populations to infection in Saudi Arabia, $\alpha = (2.0, 2.2, 2.4) \times 10^{-5}$ which gives three different values of $RBN(90) = (6.81, 7.49, 8.17) > 1$. It is noted that the three curves that come as results from the SEIQR model work as three trends to the curves belong to the real data, which makes the results due to applying the SEIQR model close to the actual data.

To illustrate the convergence of the results by the SEIQR proposed model and the real data, we displayed Fig. 5, which shows the cumulatively infected numbers within the same interval referred to earlier. It is noted that the curve of the real data is set between the three cases of the SEIQR model with the mentioned values of $\alpha$ and $RBN(90)$ parameters.

Now, we will calculate the COVID-19 spreading in Saudi Arabia depending on the real current data and parameters with the same rates without any change in the procedures. We will calculate the total number of infections by applying the SEIQR model for the next three months, starting from April 1, 2020, and ending on October 18, 2020. As shown in Fig. 6, the curves and results show whether the number of infections will be reduced and whether the spread of COVID-19 continues to be unstable. The curves have been established by using the same three values of the two parameters $\alpha$ and $RBN(90)$. 


Fig. 6 shows that the spread of COVID-19 will continue with an unstable situation without being slowed and that the number of daily infections will rise to extremely high numbers.

3.2. Study of the sensitivity of the RBN ($R_0$) based on the current data of Saudi Arabia

To study the sensitivity of the critical parameters against the reproduction number ($R_0$), we use the Eqs. (51)–(58) and represent Fig. 7, which shows the increment of the value of RBN($R_0$) concerning the parameters $a$, $r$, $b_1$, $r_3$, $r_2$, and $b_2$, respectively. For the parameters $d_1$ and $d_2$, we do not need to study its effects where we cannot change its values. Therefore, we will use the values of that parameter in this study.

Fig. 7a shows that the parameter $a$ has a significant effect on the value of the reproduction number $R_0$, where an increase in the parameter $a$ leads to an increase in the value of the reproduction number $R_0$. The Saudi Arabia data indicate that for a stable epidemic spreading of COVID-19 $R_0 < 1$, the value of the parameter $a$ must be smaller than or equal to the value $2 \times 10^{-3}$. Fig. 7b-7f show that the values of the other parameters have significant effects on the reproduction number $R_0$. The value of each parameter that gives a stable reproduction number ($R_0 < 1$) individually, when the other parameters remain constant, is provided as follows:

$$r \leq 0.001, \quad d_1 > 0.002, \quad \beta_1 > 0.2, \quad \sigma_1 \geq 0.18, \quad d_2 \geq 0.4, \quad \sigma_2 \geq 0.04, \quad \beta_2 \geq 0.045$$

(66)

---

**Table 1** The initial conditions of the SEIQR proposed model.

| Parameter | Value     | Background |
|-----------|-----------|------------|
| $S(0)$    | 34,218,169| Assumed    |
| $E(0)$    | $5.0 \times 10^4$ | Assumed |
| $I(0)$    | 157       | Calculated |
| $R(0)$    | 99        | Estimated  |
| $Q(0)$    | 1720      | Estimated  |

**Table 2** The values of parameters in SEIQR [3,8,10,16,20,22,39,40]

| Parameter | Value     | Background |
|-----------|-----------|------------|
| $\beta_1$ | 0.02      | Assumed    |
| $\beta_2$ | 0.005     | Assumed    |
| $\sigma_1$ | 0.001     | Calculated |
| $\sigma_2$ | 0.002     | Estimated  |
| $\sigma_3$ | 0.002     | Estimated  |
| $r$       | 0.01      | Estimated  |
| $d_1$     | $3.0 \times 10^{-3}$ | Calculated |
| $d_2$     | $3.5 \times 10^{-7}$ | Calculated |

Fig. 3 The total number of infections in Saudi Arabia between 4/1/2020 and 6/10/2020.
The other parameters change within its suitable range, making all its significant private effects, even the value of the reproduction number $R_0$ higher or smaller than one.

4. Discussions

4.1. The current situation and how to stop the spread of Covid-19 in Saudi Arabia

Now, we are in the most critical part of the assessment of the current situation and evaluate what needs to take place later in Saudi Arabia to control the COVID-19 spread. Therefore, in this section, we will apply the SEIQR model to analyze the current situation with new initial conditions and different values of the system parameters according to the current state. We will consider June 14, 2020, as a new start, and we will renew all the initial conditions in Table 1. The number of infections on this day was $I(0) = 4223$[41–43]. We will keep the values of the parameters $d_1$ and $d_2$ as it is without any change, while the other parameters will take the values in Table 3.

Fig. 8 shows how the current state of spreading COVID-19 in Saudi Arabia up to March 6, 2020.

It is noted in Fig. 8 that the spreading of COVID-19 in Saudi Arabia passed through its peak point on 18 July 2020, which agrees with the actual data; after that, the spread has slowed down and kept this attitude until the current days, and the reproduction number takes the value $R_0 = 0.1 < 1$ which means the situation is stable.

According to this curve, we can also see that the number of daily infections on November 15, 2020, for example, was 450 infections/day, and we can predict that the spreading situation will go to a more stable position and better state.

4.2. The ideal protocol to halt COVID-19 spreading in Saudi Arabia

To obtain the ideal state which can help to break the spread of COVID-19 in Saudi Arabia, we must begin to implement the following procedures:

1. Decrease the transmission rate from the susceptible population to infected but not detected by testing the population to be in the following interval $a_1 \in \left(\frac{1}{C_2}, \frac{1}{C_0}\right)$.

2. Increase the transmission coefficient from the infected population but not detected by testing to a quarantine population $b_1$ to be $b_1 P_0$, which means expanding the detection work and the need to isolate infected people in compulsory quarantine areas as an example.

3. Increase the transmission coefficient from the confirmed detected population by testing to a quarantine population $b_2$ to be $b_2 P_0$, which means we must help the confirmed infected population, which they need to be in the quarantine zone.
Fig. 5 The total number of infections using the SEIQR proposed model against the real data in Saudi Arabia between 4/1/2020 and 6/13/2020.

Fig. 6 The number of daily infections using the SEIQR model in Saudi Arabia between 4/1/2020 and 10/18/2020.
4. Increase the transmission rate from the quarantine population to the recovery zone \( r_1 \) to be \( r_1 = 0.001 \), which means we must apply a successful treatment on the quarantine area and help them recover.

5. Increase the transmission rate from the confirmed detected population to the recovery population \( r_2 \) to be \( r_2 = 0.01 \) by applying a successful treatment for the confirmed infected population and help them recover without needing to go to the quarantine zone.

6. Increasing the value of the transmission rate \( r_3 \) from infected and undetected populations to the recovery zone directly to be \( r_3 = 0.02 \) by using a successful treatment and supplying with vitamins, health awareness, social spacing, and applying the principle of prevention is better than cure.

7. Increase the rate of infected but not detected individuals by checking the population to infected population for treatment \( r_1 \) to be \( r_1 = 0.001 \), which means we have to offer the more effective and accurate methods of diagnosis to determine the confirmed infections. Moreover, raising awareness about ways to identify the disease and the symptoms and ways of confirming the infection.

\[
\begin{align*}
\text{Table 3} & \quad \text{The new values of parameters in SEIQR that give an ideal situation.} \\
\hline
\text{Parameter} & \text{Value} & \text{Background} \\
\hline
\beta_1 & 0.2 & \text{Assumed} \\
\beta_2 & 0.01 & \text{Assumed} \\
\sigma_1 & 0.01 & \text{Calculated} \\
\sigma_2 & 0.01 & \text{Estimated} \\
\sigma_3 & 0.02 & \text{Estimated} \\
\gamma & 0.003 & \text{Calculated} \\
\delta_1 & 3.0 \times 10^{-5} & \text{Calculated} \\
\delta_2 & 3.5 \times 10^{-7} & \text{Calculated} \\
\alpha & 1.1 \times 10^{-9} & \text{Assumed} \\
\end{align*}
\]
5. Conclusion

For this analysis, a new statistical outbreak (SEIQR) model was developed for the introduction of the current COVID-19 coronavirus. Throughout the estimation and treatment of the COVID-19 outbreak, this pandemic paradigm offers a different method. In Saudi Arabia, the original COVID-19 details were used to validate the effects of the current model. The findings suggest that the SEIQR approach is an excellent tool for the study in Saudi Arabia and other countries of the transmission of diseases, such as COVID-19.

Five measures are included in the optimal procedure, and guidance has been comprehensive in helping delay the spread of COVID-19 in Saudi Arabia. Prevention is safer than recovery, one of the key targets in this procedure.

The main method to slow down the transmission of COVID-19 in Saudi Arabia or any country is to remain home and to put sick individuals in a distant location or a protected place as far as possible.

To evaluate the reported infections, we need more reliable and effective diagnostic methods. Besides, awareness-raising on ways in which the infection can be confirmed, the disease symptoms, and ways.

Author contributions

H.Y., M.E., and N.A. Project administration, Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation. A.E. and A.S. Methodology, Resources, Software, Supervision, Validation, Visualization. H. Y, M. E, N. A., A.E., and A.S. Writing - original draft, Writing - review & editing.

Availability of data and materials

The datasets analyzed during the current study are available in the following repositories:
1. Saudi Ministry of Health (www.moh.gov.sa/en/Pages/default.aspx)
2. COVID-19 in Saudi_Arabia (https://en.wikipedia.org/wiki/COVID-19_pandemic_in_Saudi_Arabia)
3. Saudi Center for Diseases Prevention and Control (https://covid19.cdc.gov.sa/ar/).

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.

Acknowledgment

The authors are grateful and thank the Research and Development Grants Program for National Research Institutions and Centers (GRANTS), Target Research Program, Infectious Diseases Research Grant Program, King Abdulaziz City for Science and Technology (KACST), Kingdom of Saudi Arabia, grant number (5-20-01-007-0002), to fund this project and this work.
Funding

This work was funded by Research and Development Grants Program for National Research Institutions and Centers (GRANTS), Target Research Program, Infectious Diseases Research Grant Program, King Abdulaziz City for Science and Technology, Kingdom of Saudi Arabia, grant number (5-20-01-007-0002).

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