A New Dynamical Modelling of the Epidemic Diseases to Assessing the Rates of Spread of COVID-19 in Saudi Arabia: SEIRQ Model

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Abstract

A new model of critical epidemic dynamics for the emergence of the new coronavirus COVID-19 is being established in this paper. A new approach to the assessment and control of the COVID 19 epidemic is given with the SEIRQ pandemic model. This paper uses real knowledge on the distribution of COVID-19 in Saudi Arabia for mathematical modeling and dynamic analyses. The reproductive number and detailed stability analysis are provided in the SEIRQ model dynamics. In a Jacobian method of linearization, we will address the domain of the solution and the equilibrium situation based on the SEIRQ model. The equilibrium and its

importance have been proven, and a study of the stability of the equilibrium free from diseases has been implemented. The reproduction number was evaluated in accordance with its internal parameters. The Lyapunov theorem of stability has proven the global stability of the current model's equilibrium. The SEIRQ model was contrasted by comparing the results based on the SEIRQ model with the real COVID-19 spread data in Saudi Arabia. Numerical evaluation and predictions were given. The results indicate that the SEIRQ model is a strong model for the study of the spread of epidemics, such as COVID-19. At the end of this work, we implemented an optimum protocol that can quickly stop the spread of COVID-19 among the Saudi populations.

Keywords: COVID-19, Jacobian matrix, Lyapunov stability, Novel coronavirus, Reproduction number, SEIR model, SEIRQ model

1. Introduction

As COVID-19 outbreaks continue, the number of infections steadily increases. This is due to the presence of many factors that increase the complexities of COVID-19 infection and create barriers to disease management. Since scientists and researchers all over the world are trying to establish a vaccine or a cure for the outbreak to control such pandemics in the future, from a medical engineering framework, an infectious disease can be well known and understood through the use of 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] suggested a deterministic compartmental model that included clinical disease progression, individual epidemiological status, and intervention steps. The authors found that the number of reproductive controls can be up to 6.47 and that 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. 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, taken into account the environmental position of COVID-19 transmission. Several other modeling studies for the COVID-19 outbreak have also been carried out [6, 8, 14-22].

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, four forms of transmission are

characterized: straightforward, if the causative disease agent is individual; vector, if the causative agent is transmitted from a vector to a person; natural, if the touch of a pathogen infects the human via the environment; and vertical, if the disease agent is transmitted from mother to child at birth. Airborne and personal diseases are generally known to be transmitted directly where transmission occurs through contact between individuals and others. [23].

Mathematical modeling of infectious diseases is important and critical with the advent of HIV epidemics. Since then, several models for investigating infectious diseases have been developed, studied, and applied. Mathematical modeling currently applies enormously to public health and mathematics. [3, 14, 17, 22, 24].

In the emergence of HIV epidemics, the mathematical modeling of infectious diseases is significant. Since then, numerous models have been developed, studied, and applied for the investigation of infectious diseases. Today, mathematical modeling is extremely important for public health and mathematics. [4, 6, 15, 22].

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 / outflows between population divisions. In addition, 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 novel coronavirus disease (SEIRQ model)

During the spread of COVID-19 in any country, the population can be divided into five vital dynamic subpopulations or five groups, which are represented in Fig. 1 and can be described as follows [4, 6, 15, 22, 25]:

The main group $S(t)$ is dedicated to the vulnerable (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. It takes time for the pathogen to replicate and develop itself in the new host. In general, the exposed (latent) cycle follows the sensitive process [4, 6, 17, 19, 25].

Thus, the group $E(t)$ is dedicated to the exposed population or individuals who are infected but not yet infectious.

The group $I(t)$ is devoted to the population who are confirmed infected (individuals who have contracted the disease and are now sick with it and infected individuals are also infectious).

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.

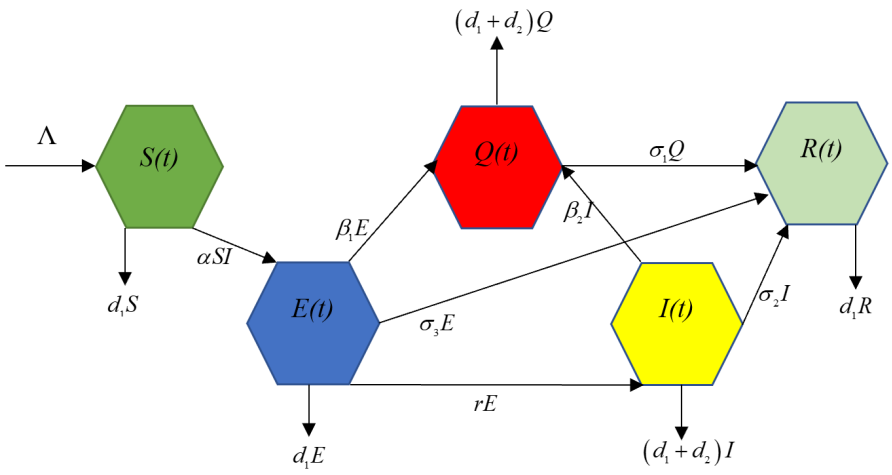

Figure 1. The flowchart of the SEIRQ model

The parameter α is defined as the transmission rate from a susceptible population to infected but not detected by the testing population. 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_1.

The total population size is $N(t)$, which is defined as [4, 6, 15, 21, 22, 24, 26]:

$$N(t) = S(t) + E(t) + I(t) + R(t) + Q(t) \tag{1}$$

Starting with group $S(t)$, we have two outflows; a population flows out to the exposed group $E(t)$ by the rate $\alpha I(t)$ (each one in $S(t)$ can transfer the infection to $\alpha I(t)$), so the total number of outflows is equal to multiple $\alpha S(t) I(t)$), and the outflow of the natural death is $d_1 S$.

The group of exposed $E(t)$ has only one inflow $\alpha I(t) S(t)$, while it has four outflows. The first outflow is the population that flows out to group $Q(t)$ by the rate of transmission β_1. The second outflow is the population that flows out to the recovery group directly without needing treatment by transmission rate of recovery σ_3. The third outflow is a population that flows out to the infected group $I(t)$ with the transmission rate of infected r, and the fourth outflow is the population that experiences natural death by the transmission rate d_1 [4, 6, 15, 21, 22, 24, 26].

For the group of confirmed infected population $I(t)$, we have only one inflow, which comes from the group $E(t)$, with the transmission rate r, 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 β_2, 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 σ_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 σ_1, the second inflow is the population that comes out from the infected group by transmission recovery rate σ_2, and the third inflow is the population that flows out from the exposed area directly by transmission recovery rate σ_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 σ_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, 15, 21, 22, 24, 26]:

$$\frac{dS(t)}{dt} = \Lambda - \alpha S(t) I(t) - d_1 S(t) \tag{2}$$

$$\frac{dE(t)}{dt} = \alpha S(t) I(t) - \varepsilon_1 E(t) \tag{3}$$

$$\frac{dI(t)}{dt} = rE(t) - \varepsilon_2 I(t) \tag{4}$$

$$\frac{dR(t)}{dt} = \sigma_3 E(t) + \sigma_2 I(t) - d_1 R(t) + \sigma_1 Q(t) \tag{5}$$

$$\frac{dQ(t)}{dt} = \beta_1 E(t) + \beta_2 I(t) - \varepsilon_3 Q(t) \tag{6}$$

where $\varepsilon_1 = (r + \beta_1 + \sigma_3 + d_1), \varepsilon_2 = (\beta_2 + \sigma_2 + d_1 + d_2)$, and $\varepsilon_3 = (\sigma_1 + d_1 + d_2)$.

2.2 Theorem 1 (all solutions are definite positive)

Each solution of the SEIRQ model with its initial condition is a subset in the interval $[0, \infty)$ and $\{S(t), E(t), I(t), R(t), Q(t)\} \geq 0$ for all values $0 \leq t < \infty$ [6].

Proof:

All the right-hand sides of the SEIRQ model are completely continuous and locally Lipschitzian on~ . The solutions $\{S(t), E(t), I(t), R(t), Q(t)\}$ with their initial conditions exist and are unique in the interval $[0, \infty)$.

From equation (2) where $(\alpha I(t) + d_1) = M > 0$ and $\Lambda > 0$, we obtain the following inequality:

$$\frac{dS(t)}{dt} \geq -M\, S(t) \tag{7}$$

which gives after the solution

$$S(t) \geq S(0) e^{-Mt} \geq 0 \tag{8}$$

Hence, $S(t)$ it is a nonnegative function for all values $t \in [0, \infty)$.

From equation (3), we have

$$\frac{dE(t)}{dt} \geq -\varepsilon_1 E(t) \tag{9}$$

which gives after the solution

$$E(t) \geq E(0) e^{-\varepsilon_1 t} \geq 0 \tag{10}$$

Hence, $E(t)$ it is a nonnegative function for all values $t \in [0, \infty)$.

In similar manners, from the other equations in the model system, we have

$$\frac{dI(t)}{dt} \geq -\varepsilon_2 I(t) \rightarrow I(t) \geq I(0)e^{-\varepsilon_2 t} \geq 0 \tag{11}$$

$$\frac{dR(t)}{dt} \geq -d_1 R(t) \rightarrow R(t) \geq R(0)e^{-d_1 t} \geq 0 \tag{12}$$

$$\frac{dQ(t)}{dt} \geq -\varepsilon_3 Q(t) \rightarrow Q(t) \geq Q(0)e^{-\varepsilon_3 t} \geq 0 \tag{13}$$

Hence, $I(t), R(t), \text{and}\, Q(t)$ are nonnegative functions for all values of $t \in [0,\infty)$ that complete the proof.

2.3 Theorem 2 (the domain of solutions)

All the solutions of the model structure that initiate in $\sim_{+}^{5}$ are bounded inside the region ψ defined by $\psi = \left\{ (S,E,I,R,Q) \in \sim^{5} : 0 \leq N(t) \leq \frac{\Lambda}{d_1} \right\}_{t\to\infty}^{6}$.

Proof:

By differentiating both sides of equation (1), we obtain

$$N'(t) = S'(t) + E'(t) + I'(t) + R'(t) + Q'(t) \tag{14}$$

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

$$N'(t) = \Lambda - d_1 N(t) - d_2 \left(Q(t) + I(t) \right) \tag{15}$$

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

$$N'(t) + d_1 N(t) \leq \Lambda \tag{16}$$

Then, we obtain

$$N(t) \leq \left(N(0) - \frac{\Lambda}{d_1} \right) e^{-d_1 t} + \frac{\Lambda}{d_1} \tag{17}$$

Then, when $t \rightarrow \infty$ we obtain the solution

$$N(t) \subset \left[0, \frac{\Lambda}{d_1}\right] \tag{18}$$

which completes the proof [3, 6, 24].

2.4 The equilibrium of the SEIRQ model

To determine the equilibrium of this model, we set all the derivatives equal to zero and solve the system as follows [3, 6, 24]:

$$S'(t) = E'(t) = I'(t) = R'(t) = Q'(t) = 0 \rightarrow \{S, E, I, R, Q\} \equiv \text{constants} \tag{19}$$

which gives

$$0 = \Lambda - \alpha SI - d_1 S \tag{20}$$

$$0 = \alpha SI - \varepsilon_1 E \tag{21}$$

$$0 = rE - \varepsilon_2 I \tag{22}$$

$$0 = \sigma_1 Q + \sigma_2 I + \sigma_3 E - d_1 R \tag{23}$$

$$0 = \beta_1 E + \beta_2 I - \varepsilon_3 Q \tag{24}$$

From equation (22), we have

$$I = \frac{r}{\varepsilon_2} E \tag{25}$$

Substituting equation (25) into equation (21) for $E \neq 0$, we obtain

$$S = \frac{\varepsilon_1 \varepsilon_2}{\alpha r} \tag{26}$$

Substituting equations (25) and (26) into equation (20), we obtain

$$E = \frac{\varepsilon_2 d_1}{r\alpha}(\Re_0 - 1) \tag{27}$$

where

$$\Re_0 = \frac{\alpha r \Lambda}{d_1 \varepsilon_1 \varepsilon_2} \tag{28}$$

Substituting equation (27) into equation (25), we obtain

$$I = \frac{d_1}{\alpha}\left(\Re_0 - 1\right) \tag{29}$$

Substituting equations (27) and(29) into equation (24), we obtain

$$Q = \frac{\left(\beta_1\varepsilon_2 + \beta_2 r\right)d_1}{\alpha r}\left(\Re_0 - 1\right) \tag{30}$$

Substituting equations (27), (29), and (30) into equation (23), we obtain

$$R = \left(\frac{\sigma_1\left(\beta_1\varepsilon_2 + \beta_2 r\right) + \sigma_2 r + \varepsilon_2\sigma_3}{\alpha r}\right)\left(\Re_0 - 1\right) \tag{31}$$

We can see that at disease-free equilibrium (DFE) $\Re_0 = 1$ i.e. $\frac{\varepsilon_1\varepsilon_2}{r\alpha} = \frac{\Lambda}{d_1}$, which leads to $E = I = Q = R = 0$, and $S = \frac{\Lambda}{d_1} = \frac{\varepsilon_1\varepsilon_2}{r\alpha}$ as in equations (20) and (26), which agrees with the domain of solution in (18).

The number $\Re_0$ is called the reproduction number (RBN), which takes the form [3, 6, 24]:

$$\Re_0 = \frac{\alpha r\Lambda}{d_1\varepsilon_1\varepsilon_2} = \frac{\alpha r\Lambda}{d_1\left(r + \beta_1 + \sigma_3 + d_1\right)\left(\beta_2 + \sigma_2 + d_1 + d_2\right)} \tag{32}$$

Then, if $\Re_0 > 1$ the system has a unique endemic equilibrium [7]:

$$E_0^* = \left(S^*, E^*, I^*, R^*, Q^*\right) \tag{33}$$

where

$$S^* = \frac{\varepsilon_1\varepsilon_2}{r\alpha}, E^* = \frac{\varepsilon_2 d_1}{r\alpha}\left(\Re_0 - 1\right), I^* = \frac{d_1}{\alpha}\left(\Re_0 - 1\right) R^* = \left(\frac{\sigma_1\left(\beta_1\varepsilon_2 + \beta_2 r\right) + \sigma_2 r + \varepsilon_2\sigma_3}{\alpha r}\right)\left(\Re_0 - 1\right),$$

and $Q^* = \frac{\left(\beta_1\varepsilon_2 + \beta_2 r\right)d_1}{\alpha r}\left(\Re_0 - 1\right)$.

Thus, the system has a unique disease-free equilibrium E_0 when $\Re_0 = 1$ and has a unique endemic equilibrium E_0^* when $\Re_0 > 1$ [6].

When $\Re_0 = 0$ there is no transmission, where $\alpha = 0.0$, it can be interpreted as the number of secondary cases or the new infection rate (transmission rate at which the susceptible individual converted to an exposed individual) [6].

2.5 Achieving equilibrium by applying a Jacobian matrix

To obtain the reproduction number $\Re_0$ by using the Jacobian matrix method, we consider that the disease-free equilibrium (DFE) of the SEIRQ model is acquired by setting $E = I = R = Q = 0$ in equations (20)-(24). Hence, we obtain DFE in form $E_0 = \left(\frac{\Lambda}{d_1}, 0, 0, 0, 0\right)$[6].

The Jacobian matrix of the SEIRQ model takes the following form:

$$J_{E_0} = \begin{bmatrix} -\alpha I - d_1 & 0 & -\alpha S & 0 & 0 \\ \alpha I & -\varepsilon_1 & \alpha S & 0 & 0 \\ 0 & r & -\varepsilon_2 & 0 & 0 \\ 0 & \sigma_3 & \sigma_2 & -d_1 & \sigma_1 \\ 0 & \beta_1 & \beta_2 & 0 & -\varepsilon_3 \end{bmatrix} \tag{34}$$

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 $I = 0 \rightarrow E = 0$ and $S = \frac{\Lambda}{d_1}$.

Hence, we consider that [6]:

$$F(S,I) = \Lambda - \alpha S(t) I(t) - d_1 S(t) \tag{35}$$

$$G(S,I) = \alpha S(t) I(t) - \varepsilon_1 E(t) \tag{36}$$

Then, we have

$$\begin{bmatrix} F(S,I) \\ G(S,I) \end{bmatrix} = \begin{bmatrix} \frac{\partial F}{\partial S} & \frac{\partial F}{\partial I} \\ \frac{\partial G}{\partial S} & \frac{\partial G}{\partial I} \end{bmatrix} \begin{bmatrix} S(t) - S(0) \\ I(t) - I(0) \end{bmatrix} = \begin{bmatrix} -\alpha I(0) - d_1 & -\alpha S(0) \\ \alpha I(0) & \alpha S(0) \end{bmatrix} \begin{bmatrix} S(t) - S(0) \\ I(t) - I(0) \end{bmatrix} \tag{37}$$

By substituting from the equilibrium position, we obtain

$$\begin{bmatrix} S'(t) \\ E'(t) \end{bmatrix} = \begin{bmatrix} -d_1 & -\dfrac{\alpha\Lambda}{d_1} \\ 0 & \dfrac{\alpha\Lambda}{d_1} \end{bmatrix} \begin{bmatrix} S(t) - \dfrac{\Lambda}{d_1} \\ I(t) \end{bmatrix} + \begin{bmatrix} 0 \\ -\varepsilon_1 E(t) \end{bmatrix} \tag{38}$$

Hence, the system of nonlinear equations (2) and (3) has been converted to the following linear system [6]:

$$\frac{dS(t)}{dt} = \Lambda - d_1 S(t) - \frac{\alpha\Lambda}{d_1} I(t) \tag{39}$$

and

$$\frac{dE(t)}{dt} = \frac{\alpha\Lambda}{d_1} I(t) - \varepsilon_1 E(t) \tag{40}$$

For the complete system at equilibrium, the stability of the disease-free equilibrium (DFE) is given by the Jacobian matrix [7]:

$$J_{E_0} = \begin{bmatrix} -d_1 & 0 & -\dfrac{\alpha\Lambda}{d_1} & 0 & 0 \\ 0 & -\varepsilon_1 & \dfrac{\alpha\Lambda}{d_1} & 0 & 0 \\ 0 & r & -\varepsilon_2 & 0 & 0 \\ 0 & \sigma_3 & \sigma_2 & -d_1 & \sigma_1 \\ 0 & \beta_1 & \beta_2 & 0 & -\varepsilon_3 \end{bmatrix} \tag{41}$$

By calculating the characteristic equation given by $\left| J_{E_0} - \lambda I_5 \right| = 0$, where λ is the eigenvalue parameter and I_5 is the identity matrix of order 5, then the eigenvalues of the matrix J_{E_0} take the following values:

$$\begin{bmatrix} \lambda_1 \\ \lambda_2 \\ \lambda_3 \end{bmatrix} = \begin{bmatrix} -\varepsilon_3 \\ -d_1 \\ -d_1 \end{bmatrix} \tag{42}$$

and the remaining roots are the solution to the following equation:

$$\begin{vmatrix} -\varepsilon_1 - \lambda & \dfrac{\alpha\Lambda}{d_1} \\ r & -\varepsilon_2 - \lambda \end{vmatrix} = 0 \tag{43}$$

which gives

$$(\varepsilon_1 + \lambda)(\varepsilon_2 + \lambda) - \frac{r\alpha\Lambda}{d_1} = 0 \tag{44}$$

The roots of the above equation after inserting $\Re_0$ will take the forms:

$$\lambda_4 = -\frac{1}{2}\left[(\varepsilon_1 + \varepsilon_2) - \sqrt{(\varepsilon_1 - \varepsilon_2)^2 + 4\varepsilon_1\varepsilon_2\Re_0}\right],\ \lambda_5 = -\frac{1}{2}\left[(\varepsilon_1 + \varepsilon_2) + \sqrt{(\varepsilon_1 - \varepsilon_2)^2 + 4\varepsilon_1\varepsilon_2\Re_0}\right] \tag{45}$$

The formulas (45) generate the following cases [6]:

1- If $\Re_0 < 1$, then we have $\lambda_4 < 0$ and $\lambda_5 < 0$ in which the disease-free equilibrium E_0 is locally asymptotically stable.

2- If $\Re_0 > 1$, then we have $\lambda_4 > 0$ and $\lambda_5 < 0$ in which the endemic equilibrium E_0^* is locally asymptotically unstable.

3- If $\Re_0 = 1$, then we have $\lambda_4 = 0$ and $\lambda_5 < 0$ in which the disease-free equilibrium E_0 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 equations (2)-(5) in a neighborhood of a steady-state look "qualitatively" similar to the solutions of the linearized system near the point $E_0 = \left(\frac{\Lambda}{d_1}, 0, 0, 0, 0\right)$. This result holds only when the equilibrium is hyperbolic, that is, when none of the eigenvalues of the matrix J_{E_0} have zero real part [6].

Thus, from (42), we obtain the following condition of equilibrium:

$$\alpha r\Lambda - d_1\varepsilon_1\varepsilon_2 \neq 0 \tag{46}$$

2.7 The uniqueness of equilibrium condition

If the matrix J_{E_0} is obtained from the linearization and is the Jacobian evaluated at equilibrium $DFE(E_0) = \left(\frac{\Lambda}{d_1}, 0, 0, 0, 0\right)$, the condition $\left|J_{E_0}\right| \neq 0$ means that the equilibrium is isolated, which means there is a disk around it that does not contain other equilibria [6, 17, 22, 24].

Hence, from (41), we have

$$\left|J_{E_0}\right| = \begin{vmatrix} -d_1 & 0 & -\frac{\alpha\Lambda}{d_1} & 0 & 0 \\ 0 & -\varepsilon_1 & \frac{\alpha\Lambda}{d_1} & 0 & 0 \\ 0 & r & -\varepsilon_2 & 0 & 0 \\ 0 & \sigma_3 & \sigma_2 & -d_1 & \sigma_1 \\ 0 & \beta_1 & \beta_2 & 0 & -\varepsilon_3 \end{vmatrix} \tag{47}$$

which gives

$$\left|J_{E_0}\right| = \varepsilon_3 d_1 \left(\alpha r\Lambda - d_1\varepsilon_1\varepsilon_2\right) = \frac{\varepsilon_3 d_1}{\varepsilon_1\varepsilon_2}\left(\frac{\alpha r\Lambda}{d_1\varepsilon_1\varepsilon_2} - 1\right) \neq 0 \tag{48}$$

Thus, the condition (46) is the only condition of the equilibrium of the SEIRQ model.

Therefore, the unique equilibrium condition of the SEIRQ model is

$$\frac{\alpha r\Lambda}{d_1\varepsilon_1\varepsilon_2} - 1 = \Re_0 - 1 \neq 0 \tag{49}$$

The reproduction number (RBN) $\Re_0 = \frac{\alpha r\Lambda}{d_1\varepsilon_1\varepsilon_2}$ is also unique [6].

2.8 Local sensitivity analysis of RBN$\left(\Re_0\right)$

Local sensitivity analysis is a sensitivity analysis that examines the change in the output values that results from a change in one input value (parameter) [6].

The sensitivity or elasticity of quantity G concerning parameter p is given by:

$$\wp_G^p = \frac{\partial G}{\partial p} \Big/ \frac{G}{p} = \pm \frac{\%\Delta G}{\%\Delta p} \tag{50}$$

The sensitivity of G concern p is positive if G is increasing concerning p and negative if G is decreasing concerning p.

Applying formula (50) into reproduction number $\Re_0$, which takes the form [6]:

$$\Re_0 = \frac{\alpha r \Lambda}{d_1 \varepsilon_1 \varepsilon_2} = \frac{\alpha r \Lambda}{d_1 \left(r + \beta_1 + \sigma_3 + d_1\right)\left(\beta_2 + \sigma_2 + d_1 + d_2\right)} \tag{51}$$

Then,

$$\wp_{\Re_0}^{\alpha} = \frac{\partial \Re_0}{\partial \alpha} \Big/ \left(\frac{\Re_0}{\alpha}\right) = 1 > 0 \tag{52}$$

$$\wp_{\Re_0}^{r} = \frac{\partial \Re_0}{\partial r} \Big/ \left(\frac{\Re_0}{r}\right) = 1 - r > 0 \tag{53}$$

$$\wp_{\Re_0}^{d_1} = \frac{\partial \Re_0}{\partial d_1} \Big/ \left(\frac{\Re_0}{d_1}\right) = -\left(\frac{d_1\left(\varepsilon_1 + \varepsilon_2\right)}{\varepsilon_1 \varepsilon_2} + 1\right) < 0 \tag{54}$$

$$\wp_{\Re_0}^{\beta_1} = \frac{\partial \Re_0}{\partial \beta_1} \Big/ \left(\frac{\Re_0}{\beta_1}\right) = -\frac{\beta_1}{\varepsilon_1} < 0 \tag{55}$$

$$\wp_{\Re_0}^{\sigma_3} = \frac{\partial \Re_0}{\partial \sigma_3} \Big/ \left(\frac{\Re_0}{\sigma_3}\right) = -\frac{\sigma_3}{\varepsilon_1} < 0 \tag{56}$$

$$\wp_{\Re_0}^{d_2} = \frac{\partial \Re_0}{\partial d_2} \Big/ \left(\frac{\Re_0}{d_2}\right) = -\frac{d_2}{\varepsilon_2} < 0 \tag{57}$$

$$\wp_{\Re_0}^{\sigma_2} = \frac{\partial \Re_0}{\partial \sigma_2} \Big/ \left(\frac{\Re_0}{\sigma_2}\right) = -\frac{\sigma_2}{\varepsilon_2} < 0 \tag{58}$$

$$\wp_{\Re_0}^{\beta_2} = \frac{\partial \Re_0}{\partial \beta_2} \Big/ \left(\frac{\Re_0}{\beta_2}\right) = -\frac{\beta_2}{\varepsilon_2} < 0 \tag{59}$$

It means that a 1% increase in each one $(d_1, \beta_1, \sigma_3, d_2, \sigma_2, \beta_2)$ will produce $\left(\left(\frac{d_1(\varepsilon_1+\varepsilon_2)}{\varepsilon_1\varepsilon_2}+1\right), \frac{\beta_1}{\varepsilon_1}, \frac{\sigma_3}{\varepsilon_1}, \frac{d_2}{\varepsilon_2}, \frac{\sigma_2}{\varepsilon_2}, \frac{\beta_2}{\varepsilon_2}\right)$% a decrease in $\Re_0$, respectively, and a 1% increase in r will produce $(1-r)$ an increase in RBN($\Re_0$). From relation (52), $\wp_{\Re_0}^{\alpha}=1$ means that a 1% increase α will produce a rise of 1% in $\Re_0$ [6].

2.9 Global stability of equilibria of the SEIRQ model (Lyapunov stability theorem)

One of the most commonly used functions is the Lyapunov function. Lyapunov functions are scalar functions that may be used to prove the global stability of equilibrium. Lyapunov states that if a function $V(x)$ is globally positively definite and radially unbounded and its time derivative is globally negative, $V(x)<0$ *for all* $x \neq x^*$ then the equilibrium x^* is globally stable for the autonomous system $x' = f(x)$, and $V(x)$ is called a Lyapunov function [6].

2.10 Theorem 5 (global stability)

The SEIRQ model $DFE(E_0)=\left(\frac{\Lambda}{\varepsilon_1}, 0, 0, 0, 0\right)$ is globally stable in disease-free equilibrium under the condition $\Re_0 < 1$.

Proof:

We will consider the SEIRQ model on the space of the first three variables only (S, E, I). It is clear that if the disease-free equilibrium for the first three equations is globally stable, then $(R, Q) \to 0$ and the disease-free equilibrium for the full SEIRQ model is globally stable.

We construct the Lyapunov function on $\sim_{+}^{3}$ in the following form:

$$V = \kappa\left(S - S^* - S^* \ln\left(\frac{S}{S^*}\right)\right) + \frac{E}{\varepsilon_1} + \frac{I}{r} \tag{60}$$

where κ is a parameter that will be determined later, and $S^* = \frac{\Lambda}{d_1}$.

The equation (60) shows that at the disease-free equilibrium $\left(S^* = \frac{\Lambda}{d_1}, 0, 0\right)$, $V = 0$.

Now, we have to show that $V > 0$ for all $(S, E, I) \geq \left(\frac{\Lambda}{d_1}, 0, 0\right)$.

The equation (60) can be rewritten as follows:

$$V = \kappa S^* \left(\frac{S}{S^*} - 1 - \ln\left(\frac{S}{S^*}\right)\right) + \frac{E}{\varepsilon_1} + \frac{I}{r} \tag{61}$$

The first term is positive for any value of S / S^*, and the other two terms are also non-negative, so $V > 0$

Now, we take the derivative of equation (60); we obtain

$$V' = \kappa\left(1 - \frac{S^*}{S}\right)S' + \frac{E'}{\varepsilon_1} + \frac{I'}{r} \tag{62}$$

Substituting from the first three equations of the SEIRQ model and using the equation (26), we obtain

$$V' = 2\Lambda\kappa - \frac{\kappa\alpha\varepsilon_3}{r} SI - d_1\kappa S - \frac{\Lambda^2\kappa}{Sd_1} + \frac{\kappa\alpha\Lambda\varepsilon_3}{d_1 r} I + \frac{\alpha\varepsilon_3}{\varepsilon_1 r} SI - \frac{\varepsilon_3}{r} I \tag{63}$$

We choose $\kappa = \frac{1}{\varepsilon_1}$, then we have

$$V' = -\frac{\Lambda}{\varepsilon_1}\left(\frac{\Lambda}{d_1 S} + \frac{d_1 S}{\Lambda} - 2\right) + \frac{\varepsilon_2}{r}\left(\Re_0 - 1\right) I \tag{64}$$

Since $\Re_0 < 1$ then, the last term is non-positive.

For the first term, consider $\frac{d_1 S}{\Lambda} = x$; then, the term inside the brackets takes the form

$\left(x + \frac{1}{x} - 2\right) = \frac{(x-1)^2}{x} > 0$, and now we have two possibilities. The first term is at the equilibrium point, where we have $S = S^* = \frac{\Lambda}{d_1}$, and it gives $x = 1$. Then, the first term

completely vanishes, and then we have the last term only, which is already non-negative. Thus, $V' < 0$.

The second possibility is $x \neq 1$; then, the two terms are non-positive. Thus, $V' < 0$.

Hence, we have $V' < 0$ for every $\left(S(t), E(t), I(t)\right) \geq \left(\frac{\Lambda}{d_1}, 0, 0\right)$ [6].

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

2.11 Solutions for the system of the SEIRQ model

We assume the initial conditions of the SEIRQ system in (39), (40), and (4)-(6) to take the form

$$\left\{S(t), E(t), I(t), R(t), Q(t)\right\}\Big|_{t=0} = \left\{S(0), E(0), I(0), R(0), Q(0)\right\} \tag{65}$$

We solved this system by using MAPLE software. Hence, we obtain

$$I(t) = \frac{1}{\alpha\Lambda\delta}\left[\left((-\varepsilon_1 + \varepsilon_2) - \delta\right)\gamma_1 e^{\frac{\delta}{2d_1}t} + \left((\varepsilon_1 - \varepsilon_2) - \delta\right)\gamma_2 e^{-\frac{\delta}{2d_1}t}\right] e^{-\frac{1}{2}(\varepsilon_1 + \varepsilon_2)t} \tag{66}$$

where $\delta = \sqrt{4\Lambda\alpha r d_1 + d_1^2\varepsilon_1^2 - 2d_1^2\varepsilon_1\varepsilon_2 + d_1^2\varepsilon_2^2}$, $\gamma_1 = \left(d_1(\varepsilon_1 - \varepsilon_2) - \delta\right)E(0) + 2\Lambda\alpha I(0)$, and $\gamma_2 = \left(d_1(\varepsilon_1 - \varepsilon_2) + \delta\right)E(0) + 2\Lambda\alpha I(0)$

Consequently, we can obtain the other functions S, E, I, and Q.

2.12 Model verification and predictions

To verify the SEIRQ model, we will apply it to the real data regarding the COVID-19 outbreak in Saudi Arabia. COVID-19 has been 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 epidemic in Saudi Arabia.

We used tables of statistics issued from the Saudi Ministry of Health [27] and the daily official statement issued by the ministry as well as Wikipedia [28], 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 [29]." We used the official website of the General Statistics Authority of Saudi Arabia for more information about the kingdom's population, mortality rate, and population growth rate.

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

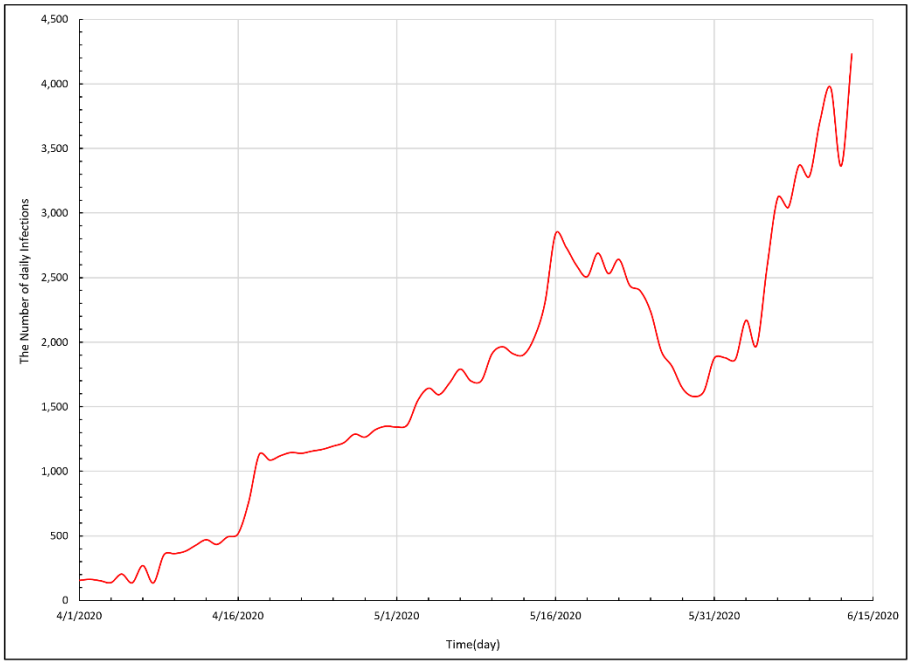

Figure 2. The real number of daily infections in Saudi Arabia between 4/1/2020 and 6/13/2020

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.

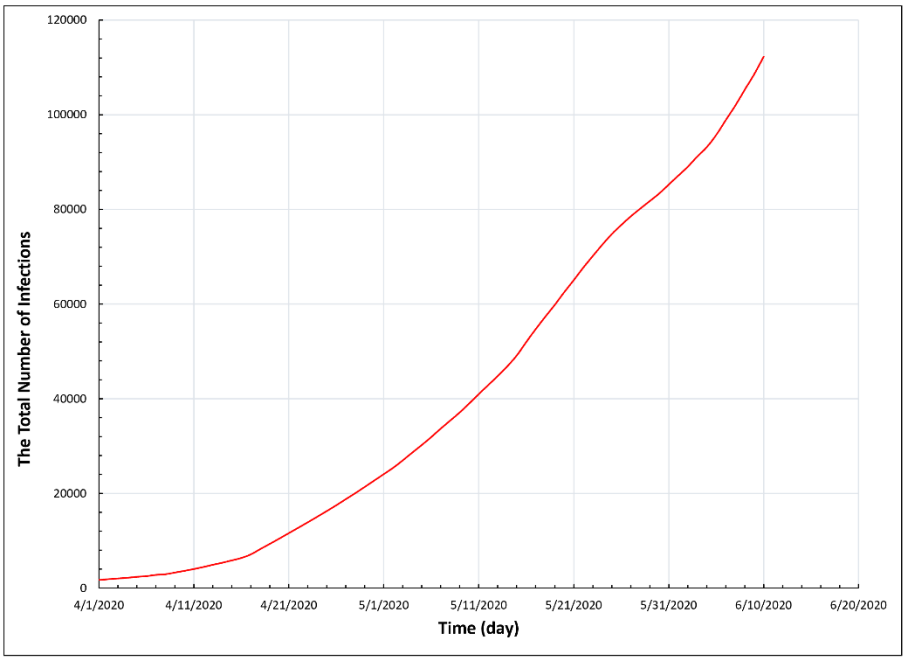

Figure 3. The total number of infections in Saudi Arabia between 4/1/2020 and 6/10/2020

Fig. 3 shows that the total number of cases at the same interval started with 157 infections and reached an accumulated amount of 122,259 infections on June 13, 2020. Therefore, we will use these data through the present SEIRQ model to discern whether there is a convergence between the model results and the real data [27-29].

3. Results

3.1 Applying the SEIRQ model to Saudi Arabia data of the spread of Covid-19

According to the official data of Saudi Arabia, we have the following initial data, which are considered the initial conditions of the system based on the SEIRQ model, as in Table 1 [27-29]:

Table 1: The initial conditions of the SEIRQ model

$S(0)$	$E(0)$ Assumed	$I(0)$	$R(0)$	$Q(0)$
34,218,169	5.0×10^{3}	157	99	1720

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 of Saudi children and new residents $\Lambda \approx 2300$ person/day and the rate of natural deaths is approximately 1030 people/day, which results in $d_1 \approx 3\times10^{-5}$. Some of the other parameters have been calculated, estimated, or assumed, as in Table 2.

Table 2: The values of parameters in SEIRQ [3, 8, 10, 15, 19, 21, 24, 26]

Parameter	Value	Background
β_1	0.02	Assumed
β_2	0.005	Assumed
σ_1	0.001	Calculated
σ_2	0.002	Estimated
σ_3	0.002	Estimated
r	0.01	Estimated
d_1	3.0×10^{-5}	Calculated
d_2	3.5×10^{-7}	Calculated

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 SEIRQ model. The following figure shows the numerical results of the SEIRQ model against the real data with different values of the parameter α and RBN $(\Re_0)$ to show the convergence between them. It

is noted that an increase in the parameter α leads to a rise in the number of infections and RBN $(\Re_0)$. The value of the parameter α (the rate of transmission from the susceptible population to infection in Saudi Arabia) within the abovementioned interval is $\alpha = (2.0, 2.2, 2.4) \times 10^{-9}$. Moreover, the reproduction number RBN $(\Re_0)$ is $\Re_0 = (6.81, 7.49, 8.17) > 1$. In other words, the transmission rate at which the susceptible individual converted to an exposed individual is higher than one, which means the spread of COVID-19 is unstable.

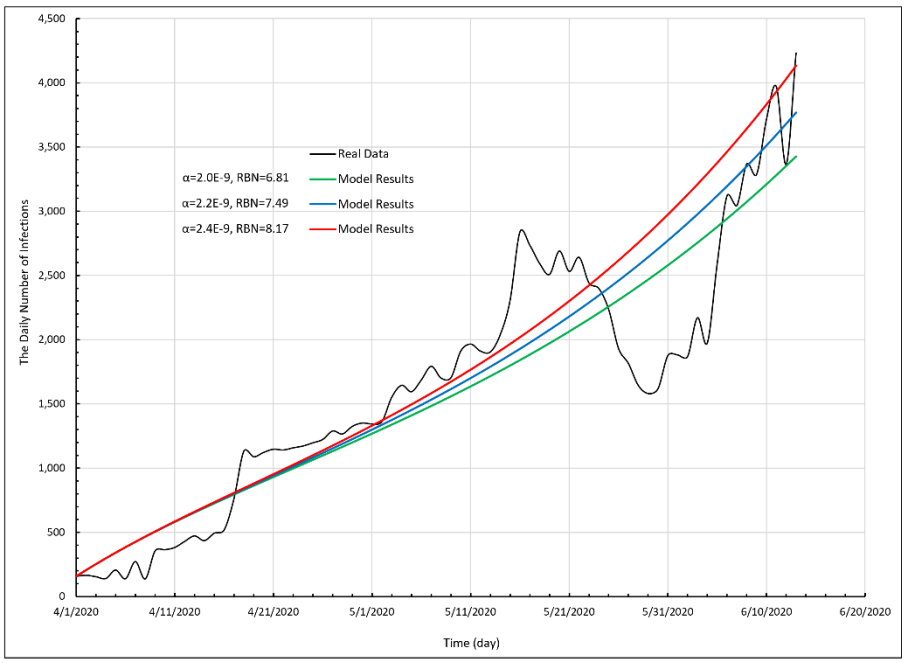

Figure 4. The number of daily infections based on the SEIRQ model against the real data in Saudi Arabia between 4/1/2020 and 6/13/2020

Fig. 4 shows the number of daily infections based on the SEIRQ 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, $\alpha = (2.0, 2.2, 2.4) \times 10^{-9}$ which gives three different values of RBN $\Re_0 = (6.81, 7.49, 8.17) > 1$. It is noted that the three

curves that come as results from the SEIRQ model work as three trends to the curves belong to the real data, which makes the results due to applying the SEIRQ model close to the actual data.

To illustrate the convergence between the results of the proposed SEIRQ model and the real results, 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 SEIRQ model with the mentioned values of α and $\Re_0$ parameters.

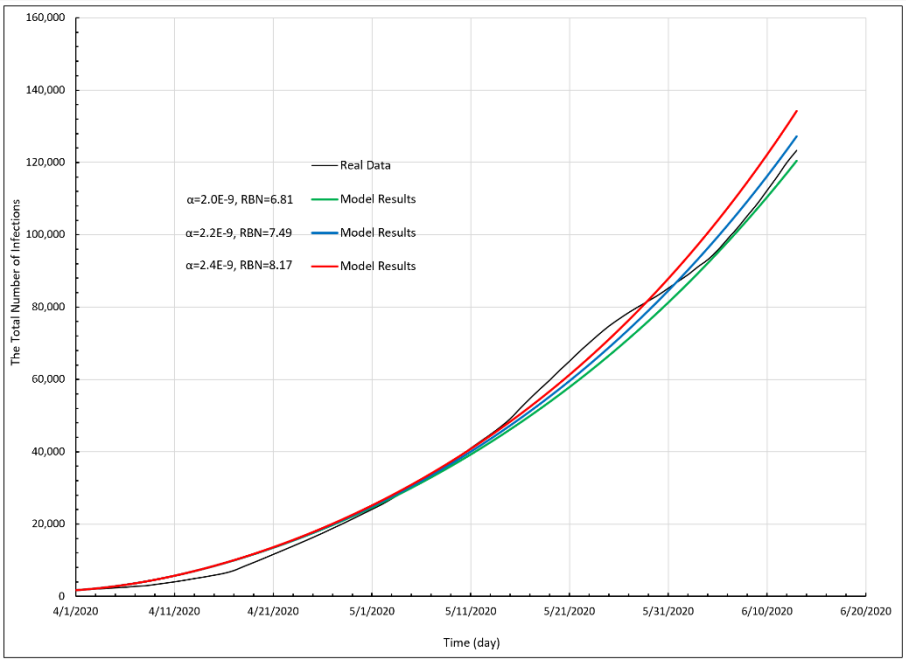

Figure 5. The total number of infections based on the SEIRQ model against the real data in Saudi Arabia between 4/1/2020 and 6/13/2020

Now, we will predict the spread of COVID-19 in Saudi Arabia based on the current data and parameters with the same rates without any change in the procedures and considering that everything will continue as it is. We will illustrate the results of the total number of infections by applying the SEIRQ 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 will continue to

be unstable. The curves have been established by using the same three values of the two parameters α and $\Re_0$.

The figure 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 very high numbers.

Thus, we will later describe the best practices for this situation (best protocol) to control the spread of the COVID-19.

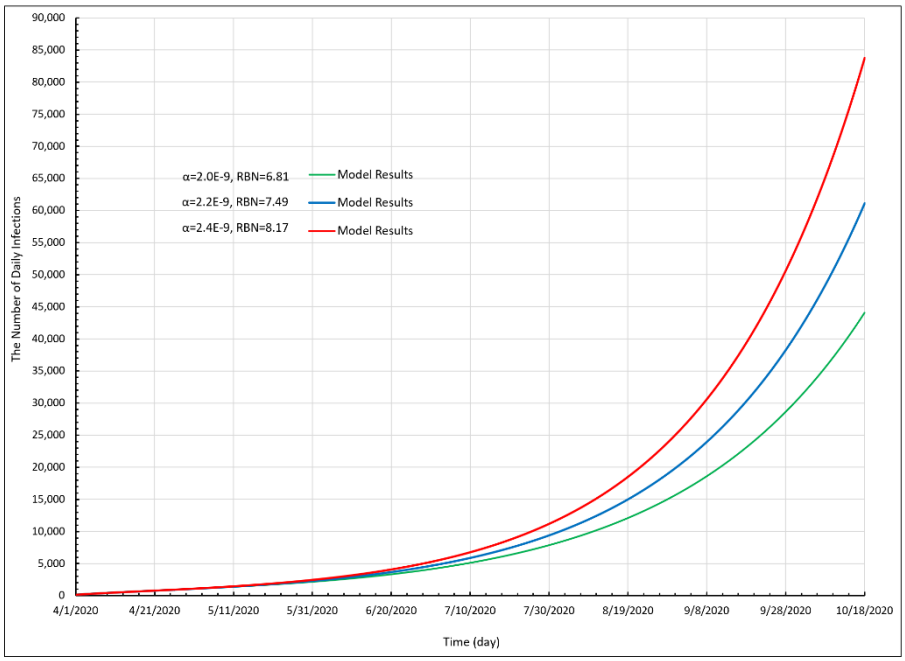

Figure 6. The number of daily infections based on the SEIRQ model in Saudi Arabia between 4/1/2020 and 10/18/2020

3.2 Study of the sensitivity of the RBN $(\Re_0)$ based on the current data of Saudi Arabia

To study the sensitivity of the critical parameters against the reproduction number $(\Re_0)$, we use the equations (52)-(59) and represent Fig. 7, which shows the increment of the value of RBN $(\Re_0)$ concerning the parameters $\alpha, r, \beta_1, \sigma_3, \sigma_2$, and β_2, respectively. For the parameters d_1 and d_2, we do not need to study its effects where we cannot change its values (no one can

control the death rate in for the population). Therefore, we will use the values of that parameter in this study.

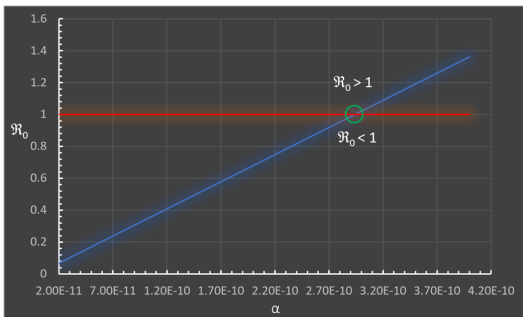

Figure 7a. $\Re_0$ against α

$\left(\alpha \le 2.8\times10^{-10} \rightarrow \Re_0 \le 1\right)$

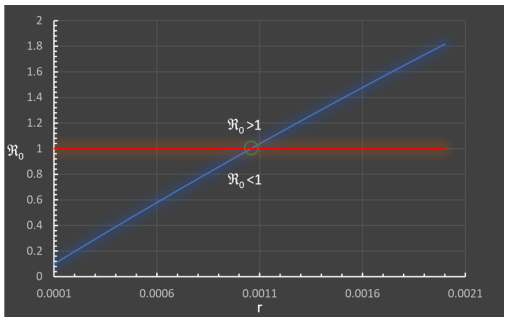

Figure 7b. $\Re_0$ against r $\left(r \le 0.001 \rightarrow \Re_0 \le 1\right)$

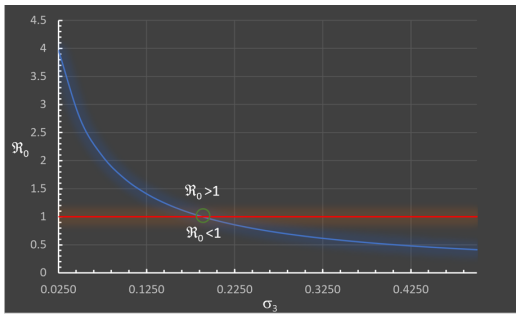

Figure 7c. $\Re_0$ against σ_3 $\left(\sigma_3 \ge 0.18 \rightarrow \Re_0 \le 1\right)$

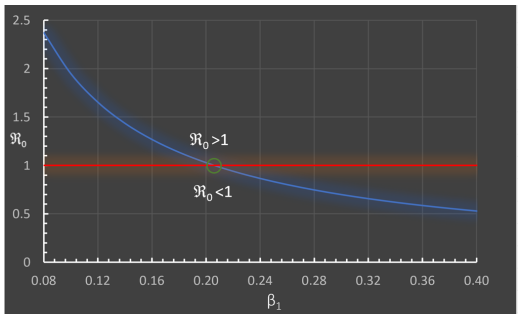

Figure 7d. $\Re_0$ against β_1 $\left(\beta_1 \ge 0.2 \rightarrow \Re_0 \le 1\right)$

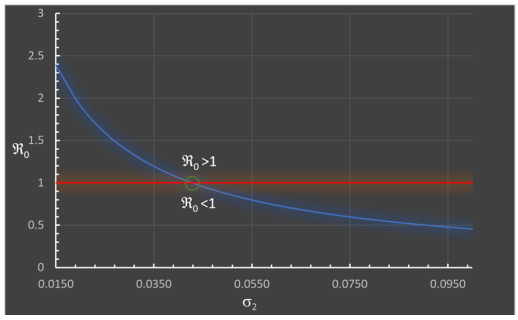

Figure 7e. $\Re_0$ against σ_2 $\left(\sigma_2 \ge 0.04 \rightarrow \Re_0 \le 1\right)$

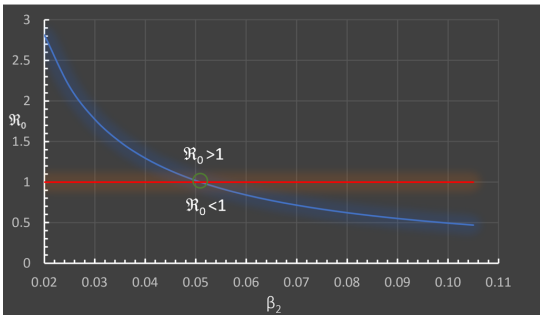

Figure 7f. $\Re_0$ against β_2 $\left(\beta_2 \ge 0.045 \rightarrow \Re_0 \le 1\right)$

Figure 7. The sensitivity of the parameters on the value of the RBN $\left(\Re_0\right)$

Fig. 7a shows that the parameter α has a significant effect on the value of the reproduction number $\Re_0$, where an increase of the parameter α leads to an increase in the value of the reproduction number $\Re_0$. The Saudi Arabia data indicate that for a stable epidemic spreading of COVID-19 $\Re_0 < 1$, the value of the parameter α must be smaller than or equal to the value 2.8×10^{-10}, which is not the situation in the studied time interval.

Fig. 7b-7f shows that the values of the other parameters have significant effects on the reproduction number $\Re_0$. The value of each parameter that gives a stable reproduction number $(\Re_0 < 1)$ individually, when the other parameters remain constant, is provided as follows

$$r \le 0.001,\ d_1 > 0.002,\ \beta_1 > 0.2,\ \sigma_3 \ge 0.18,\ d_2 \ge 0.4,\ \sigma_2 \ge 0.04,\ \beta_2 \ge 0.045 \qquad (67):$$

The other parameters change within its suitable range, making all its significant private effects, even the value of the reproduction number $\Re_0$ higher or smaller than one.

4. Discussions

4.1 The current state 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 SEIRQ 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 the fresh start, and we will renew all the initial conditions in Table I. The number of infections on this day was $I(0) = 4223$[27-29]. 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:

Table 3: The new values of parameters in SEIRQ that give an ideal situation

Parameter	Value	Background
β_1	0.2	Assumed
β_2	0.01	Assumed
σ_1	0.01	Calculated
σ_2	0.01	Estimated
σ_3	0.02	Estimated
r	0.003	Calculated
d_1	3.0×10^{-5}	Calculated
d_2	3.5×10^{-7}	Calculated
α	2.0×10^{-10}	Assumed

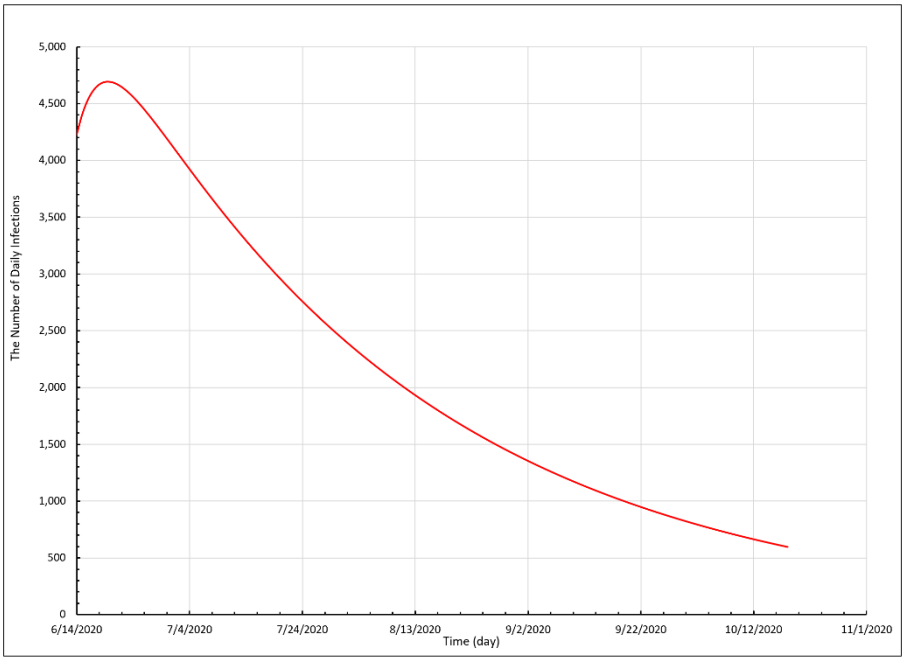

Figure 8. The number of daily infections based on the SEIRQ model in Saudi Arabia was between 6/14/2020 and 10/18/2020 if the values of the parameters, as in Table 3.

Figure 8 shows how the current state of spreading COVID-19; moreover, it offers an estimation for the situation in Saudi Arabia up to October 18, 2020.

It is noted in figure 8 that the spreading of COVID-19 in Saudi Arabia passed through its peak point on 16-18 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 $\Re_0 = 0.1 < 1$ which means the situation is stable

According to this curve, we can also see that the number of daily infections on October 18, 2020, will be approximately 600 persons/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 the spread Covid-19 in Saudi Arabia

To obtain the ideal situation, which can help us break the spread COVID-19 in Saudi Arabia, we must start implementing the following protocols and procedures (see figure 9):

1. Decrease the value of the transmission rate from the susceptible population to infected but not detected by testing the population to be in the following interval $\alpha \leq 2.8 \times 10^{-10}$.

2. Increase the value of the transmission coefficient from an infected population but not detected by testing to a quarantine population β_1 to be $\beta_1 \geq 0.2$, which means expanding the detection work and the need to isolate infected people in compulsory quarantine areas as an example.

3. Increase the value of the transmission coefficient from the confirmed detected population by testing to a quarantine population β_2 to be $\beta_2 \geq 0.01$, which means we must help the confirmed infected population, which they need to be in the quarantine zone.

4. Increase the value of the transmission rate from the quarantine population to the recovery zone σ_1 to be $\sigma_1 \geq 0.001$, which means we must apply a successful treatment on the quarantine area and help them recover.

5. Increase the value of the transmission rate from the confirmed detected population to the recovery population σ_2 to be $\sigma_2 \geq 0.01$ 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 σ_3 from infected and undetected populations to the recovery zone directly to be $\sigma_3 \geq 0.02$ by using a successful treatment and supplying with vitamins, health awareness, social spacing, and applying the principle of prevention are better than curing.

7. Increase the value of infected but not detected individuals by checking population to infected population for treatment r to be $r_1 \geq 0.001$, 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.

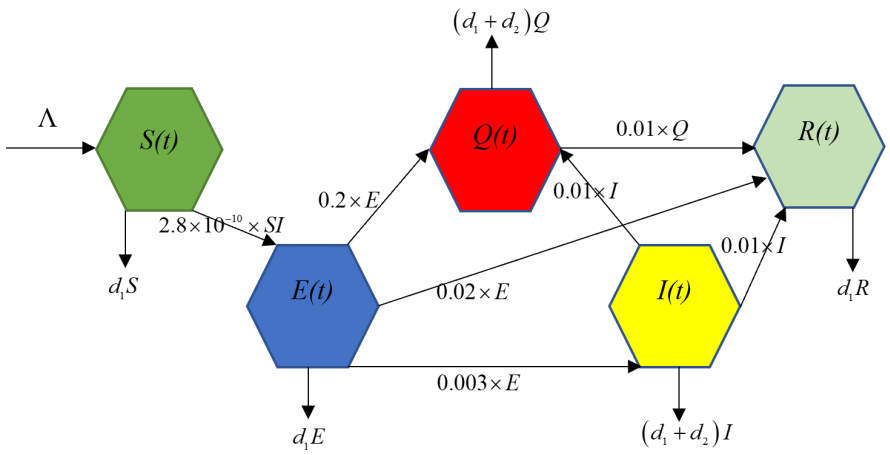

Figure 9. The flowchart of the ideal protocol based on the SEIRQ model

5. Conclusion

For this analysis, a new statistical outbreak (SEIRQ) 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 SEIRQ 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 approach to slowing down the transmission of COVID-19 is to remain home and to put sick individuals in a distant location or a protected place as far as possible.

Ultimately, efficient and appropriate care of sick patients must be given, and medicines, tones, and nutrients must be distributed to non-infected individuals to prevent them.

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AUTHOR CONTRIBUTIONS

H.Y., M.E., and N.A. conceived the original idea and led the overall study. A.E. and A.S. wrote the paper and carefully revised the manuscript. H. Y, M. E, N.A., A.E., and A.S. collected and analyzed all data. All the authors read and approved the final manuscript.

COMPETING INTERESTS

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