Analysis the Dynamics of SIHR Model: Covid-19 case in Djibouti

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Abstract. The COVID-19 epidemic is an emerging infectious disease of the viral zoonosis type caused by the corona-virus strain SARS-CoV-2, is classified as a human-to-human communicable disease and is currently a pandemic worldwide. In this paper, we propose conceptual mathematical models the epidemic dynamics of four compartments. We have collected data from the Djibouti health ministry. We define the positivity, boundedness of solutions and basic reproduction number. Then, we study local and global stability and bifurcation analysis of equilibrium to examine its epidemiological relevance. Finally, we analyze the fit of the data in comparison with the result of our mathematical results, to validate the model and estimating the important model parameters and prediction about the disease, we consider the real cases of Djibouti from 23th March to 10th June 2020.

Keywords: SIHR model; COVID-19; Basic reproduction number; stability analysis; model validation.

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1 Introduction

Corona-viruses are a large family of viruses that can be pathogenic in humans and animals. We know that, in humans, several corona-viruses can cause respiratory infections whose manifestations range from a simple cold to more serious illnesses such as Middle East respiratory syndrome (MERS) where dromedary camels were thought to be the intermediate source for the transmission of the virus [9, 10, 13].

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Small genomic sequence analysis of bat acknowledged bat as the natural reservoir of MERS [14]. Severe acute respiratory syndrome (SARS), for the first time in China in November 2002. It was in December 2019 that a new epidemic of Covid-19, emerged in Wuhan, in the Chinese province of Hubei, spread around the world and turning into a pandemic. The World Health Organization (WHO) declared the disease as a pandemic and was named SARS-CoV-2 virus (March 11, 2020) [3]. The latter has decimated throughout the world, particularly the countries most affected are the USA, Italy, France and Spain by this increase in mortality. On the other hand, it is since March 23 that the Republic of Djibouti declared its first case of COVID-19 and recorded a very low mortality rate. The authorities imposed general confinement, with the exception of essential services. Traffic has been kept to a minimum, and requires administrative clearance.

Disease models play an important role in understanding and managing the transmission dynamics of various pathogens. We can use them to describe the spatial and temporal patterns of disease prevalence, as well as to explore or better understand the factors that influence infection incidence. Modeling is a key step in understanding what treatments and interventions can be most effective, how cost-effective these approaches may be, and what specific factors need to be considered when trying to eradicate disease. Some recent studies provided different guidelines by introducing basic reproduction number, education and socio-economic index and lock-down strategies [5, 6, 8, 11, 12]. To understand the complex dynamics underlying disease transmission, epidemiologists often use a set of models called compartmental models. Developed in the early 20th century, these models stratify a population into groups, generally based on their risk or infection status. Underlying these models is a system of differential equations that track the number of people in each category over time.

The simplest way to model epidemic spread in populations is to classify people into different population groups or compartments. Compartmental models are governed by a system of differential equations that track the population as a function of time, stratifying it into a different groups based on risk or infection status. The models track the number of people in each of the following categories:

Susceptible: Individual is able to become infected.
Exposed: Individual has been infected with a pathogen, but due to the pathogen's incubation period, is not yet infectious.
Infectious: Individual is infected with a pathogen and is capable of transmitting to others.
Recovered: Individual is either no longer infectious or removed from the population.

Compartmental models are deterministic, that is, given the same inputs, they produce the same results every time. They are able to predict the various properties of pathogen spread, can estimate the duration of epidemics, and can be used to understand how different situations or interventions can impact the outcome of pathogen spread. The Kermack-Mckendric SIR model is a very well established model and

used widely for various epidemics [15]. To do this, the SIR, SIRS and SEIR models have been developed which highlight (in particular) the crucial role played by the R_0 parameter, describing the average number of new infections due to a sick individual. As one can imagine, if this number is less than 1 then the epidemic will tend to die out, while it may persist or even spread to the whole population if $R_0 > 1$ [16, 17].

Therefore, the model with multiple compartments is the useful tool to predict the nature of recent most dangerous disease, COVID-19. In this paper, we study a model of four compartments SIHR (Susceptible-Infected-Hospitalized-Recovered). The key objectives of this study are as follows:

1. We analyze the stability of the equilibrium of the model using the basic reproduction number to understand the severity.

2. Theoretical results are established using local and global analysis of the model.

3. Numerical demonstrations validated the analytic outcomes.

The paper is organized as follows: Mathematical Model is elaborately discussed in section 2. Positivity and boundedness of solution including auxiliary results are described in section 3. Then, in section 4, we study the basic reproduction number DFE and EEP. Local-global stability analysis are prescribed in section 5. Finally, Section 6 is accomplished the data analysis in comparison with model solution with further prediction to control the epidemic, as a case study in Djibouti.

In the following section, we will discuss our mathematical model and formulation of the model elaborately.

2 Model

To study the epidemic of COVID-19 spread at Djibouti, we extend the classical deterministic susceptible-infectious-removed (SIR) epidemic model by adding a hospitalized compartment. In the proposed model, let the total population is divided into four compartment those are the susceptible population (S), infected population (I), hospitalized population (H) and recovered population (R).
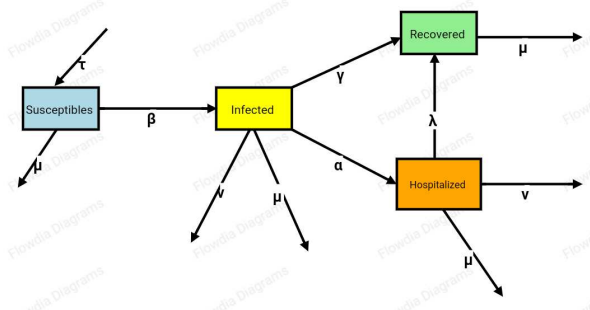

Figure 1: Diagram the transmission of the SIHR model.

Table 1: Model parameters and their descriptions.

Notation	Interpretations
τ	Recruitment rate of S class
μ	Natural death rate
ν	Death rate due to infection
β	Transmission rate
γ	Recovery rate of I class
λ	Recovery rate of H class
α	Hospitalized rate

The flow diagram of the proposed model is given in Figure 1 below and the corresponding mathematical equations are given in (1).

$$
\begin{cases}
\frac{dS}{dt} = \tau - \mu S - \beta SI \\[2mm]
\frac{dI}{dt} = \beta SI - (\nu + \mu + \gamma + \alpha)I \\[2mm]
\frac{dH}{dt} = \alpha I - (\nu + \mu + \lambda)H \\[2mm]
\frac{dR}{dt} = \gamma I + \lambda H - \mu R.
\end{cases}
\tag{1}
$$

with the initial conditions $S(0) > 0, I(0) > 0, H(0) \geq 0, R(0) \geq 0$ where the interpretation of parameters is presented in Table 1.

3 Positivity and Boundedness of Solution

The population (N) is then divided into four classes; the susceptible (S), the infected (I), the hospitalized (H), and the recovered (R) at any time $t \geq 0$,

$$
N(t) = S(t) + I(t) + H(t) + R(t)
$$

with the initial conditions $S(0) > 0, I(0) > 0, H(0) \geq 0, R(0) \geq 0$.

Now we use the model (1) we have

$$
\begin{aligned}
\frac{dN}{dt} &= \frac{dS}{dt} + \frac{dI}{dt} + \frac{dH}{dt} + \frac{dR}{dt} \\
&= \tau - \mu N - \nu I - \nu H
\end{aligned}
$$

Which give

$$
\frac{dN}{dt} \leq \tau - \mu N
\tag{2}
$$

Integrating the inequality (2), using initial condition, we obtain

$$
N(t) \leq N(0)e^{-\mu t} + \frac{\tau}{\mu}\left(1 - e^{-\mu t}\right)
$$

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Letting t tends to infnity, asymptotically we get $N(t) < \frac{\tau}{\mu}$.

Thus we can summarize the above results in the following theorem

Theorem 3.1 . *The closed region* $\Omega = \{(S, I, H, R) \in \mathbb{R}_+^4 : \quad 0 < N < \frac{\tau}{\mu}\}$ *is positively invariant set for the system (1).*

4   Basic reproduction number DFE and EEP

Compartmental models are deterministic, that is, given the same inputs, they produce the same results every time. They are able to predict the various properties of the spread of the virus, can estimate the duration of epidemics and can be used to understand how different situations or interventions can affect the results of the spread. To do this, the R_0 parameter, describing the average number of new infections due to a sick individual, plays a crucial role. As you can imagine, if this number is less than 1 then the epidemic will tend to die out. In this case, the disease-free equilibrium (DFE) will be locally asymptotically stable and the disease cannot persist in the population. While it may persist or even spread to the whole population if $R_0 > 1$. This implies that the disease-free equilibrium (DFE) is unstable. Using next generation matrix [4, 7] the basic reproduction of (1) is found here. Since the DFE is $E_0 = (\frac{\tau}{\mu}, 0, 0, 0)^t$ and hence the basic reproduction number can be found using the analytical approach.

Let $\mathcal{F} = \begin{pmatrix} \tau \\ \beta\,SI \end{pmatrix}$ represents the rate of new infection matrix and

$\mathcal{V} = \begin{pmatrix} \mu\,S + \beta\,S\,I \\ (\nu + \mu + \gamma + \alpha)I \end{pmatrix}$ denotes the transfer rate matrix of the individuals.

Let us we define $F = \frac{\partial \mathcal{F}}{\partial x_j}(E_0)$ and $V = \frac{\partial \mathcal{V}}{\partial x_j}(E_0)$, the reproduction number for the COVID-19 model given by (1) can be calculated from the relation $R_0 = \rho(FV^{-1})$, the spectral radius of FV^{-1} is given below

$$R_0 = \frac{\beta\,\tau}{\mu(\nu + \mu + \gamma + \alpha)} \tag{3}$$

To find the endemic equilibrium state of the model we set

$$\frac{dS}{dt} = 0, \quad \frac{dI}{dt} = 0, \quad \frac{dH}{dt} = 0, \quad \frac{dR}{dt} = 0$$

Solving the above system, we get the epidemic equilibrium (EEF) state

$$E_1 = (S_1, I_1, H_1, R_1)$$

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where

$$S_1 = \frac{\nu + \mu + \gamma + \alpha}{\beta}, \quad I_1 = \frac{\tau\beta - \mu(\nu + \mu + \gamma + \alpha)}{\beta(\nu + \mu + \gamma + \alpha)}, \quad H_1 = \frac{\alpha\tau\beta - \alpha\mu(\nu + \mu + \gamma + \alpha)}{\beta(\nu + \mu + \lambda)(\nu + \mu + \gamma + \alpha)}$$

$$R_1 = \frac{(\gamma(\nu + \mu + \lambda) + \lambda\alpha)(\tau\beta - \mu(\nu + \mu + \gamma + \alpha))}{\beta\mu(\nu + \mu + \lambda)(\nu + \mu + \gamma + \alpha)}$$

5   Stability and bifurcation the equilibrium states

In this section we shall establish the stability and bifurcation condition if the equilibrium points. In Theorem 5.1, we shall establish nature of the E_0 and in Theorem 5.3 nature of E_1.

5.1   Stability and bifurcation of disease-free equilibrium state (E_0)

Theorem 5.1 *The DFE will be locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.*

Proof 5.2 *The Jacobian matrix corresponding to the system (1) at DFE point $E_0 = (\frac{\tau}{\mu}, 0, 0, 0)$*

$$J(E_0) = \begin{pmatrix} -\mu & -\frac{\beta\tau}{\mu} & 0 & 0 \\ 0 & \frac{\beta\tau}{\mu} - (\nu + \mu + \gamma + \alpha) & 0 & 0 \\ 0 & \alpha & -(\nu + \mu + \lambda) & 0 \\ 0 & \gamma & \lambda & -\mu \end{pmatrix}$$

The characteristic roots of the Jacobian matrix at $J(E_0)$ are $-\mu$, $-\lambda - \nu - \mu$, $-\mu$ and $(\nu + \mu + \gamma + \alpha)(R_0 - 1)$. Since first three roots are negative and other will be negative if $R_0 < 1$ and positive if $R_0 > 1$. Therefore, the disease-free equilibrium state (E_0) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Since when $R_0 = 1$ i.e when

$$\beta = \tilde{\beta} = \frac{\mu(\nu + \mu + \gamma + \alpha)}{\tau}$$

then one of the eigenvalues of the Jacobin matrix corresponding to the system (1) at DFE is zero. Using the Theorem by Castillo-Chavez and Song [18, 19, 20] to

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investigate the nature of the disease free equilibrium points. Let V_d and V_g be the eigenvector corresponding to the zero eigenvalue of $J(E_0)$ and $[J(E_0)]^T$ respectively then

$$V_d = \begin{pmatrix} \frac{-(\nu+\mu+\gamma+\alpha)}{\mu}) \\ 1 \\ \frac{\alpha}{\nu+\mu+\lambda} \\ \frac{\alpha\lambda+\gamma(\nu+\mu+\lambda)}{\mu(\nu+\mu+\lambda)} \end{pmatrix} \qquad \text{and} \qquad V_g = \begin{pmatrix} 0 \\ 1 \\ 0 \\ 0 \end{pmatrix}$$

and

$$\text{let} \quad F = \begin{pmatrix} \tau - \mu S - \beta SI \\ \beta SI - (\nu+\mu+\gamma+\alpha)I \\ \alpha I - (\nu+\mu+\lambda)H \\ \gamma I + \lambda H - \mu R. \end{pmatrix} \quad \text{then}$$

$$V_g^T F_\beta|_{E_0, \beta=\tilde{\beta}} = 0, \qquad V_g^T DF_\beta|_{E_0, \beta=\tilde{\beta}} V_d = \frac{\tau}{\mu} \neq 0$$

$$V_g^T D^2 F|_{E_0, \beta=\tilde{\beta}}(V_d, V_d) = \frac{-2(\nu+\mu+\gamma+\alpha)^2}{\tau} \neq 0$$

Hence the system experiences transcritical bifurcation when the rate of infection crosses the critical value $\beta = \tilde{\beta}$. Thus to spreading the disease the rate of transmission plays important role. There is critical values of the rate of infection which the disease easy to control but above of which the society will experience endemic disease spreading.

5.2 Stability of endemic equilibrium state (E_1)

Theorem 5.3 *The endemic equilibrium state $E_1 = (S_1, I_1, H_1, R_1)$ is stable if $R_0 > 1$.*

Proof 5.4 *The Jacobian corresponding to the endemic equilibrium point E_1 is $J(E_1)$ is given below*

$$J(E_1) = \begin{pmatrix} -\mu - \beta I_1 & -\beta S_1 & 0 & 0 \\ \beta I_1 & \beta S_1 - (\nu+\mu+\gamma+\alpha) & 0 & 0 \\ 0 & \alpha & -(\nu+\mu+\lambda) & 0 \\ 0 & \gamma & \lambda & -\mu \end{pmatrix}$$

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The characteristic roots of the Jacobian matrix at $J(E_1)$ are

$$\det(J(E_1) - X\,I_4) = \left(-\mu - X\right)\left(-\nu - \mu - \lambda - X\right)\left(X^2 - aX + b\right)$$

The roots of the characteristic equations are $X_1 = -\mu < 0, X_2 = -\nu - \mu - \lambda < 0$ and other two satisfies the following quadratic equation

$$X^2 - aX + b = 0, \tag{4}$$

Since the two roots of (4) are negative because

$$a = \frac{-\tau\beta}{\nu + \mu + \gamma + \alpha} < 0$$

and

$$b = \left(\mu(\nu + \mu + \gamma + \alpha)(R_0 - 1)\right) > 0$$

if $R_0 > 1$.

6   Parameter Estimation, Model Validation and Prediction

In this study, we considered the country Djibouti less infected with the COVID-19 virus and collected the data available online in chronological order from Worldometer [1, 3].

6.1   Parameter Estimation

Using Matlab minimization technique and fminsearch software package, we have estimated the important model parameters using the Djibouti infection cases from 23th March to 10th June, 2020 (total days 80) which are given in Table 2. To estimate the important model parameters we consider the cumulative number of infected persons from the real data source and the model predicted cumulative number of infected persons. The fitness of the model with the real can be verified computing the residual. The residuals are defined as

$$\text{residuals} = \left\{ Y_j - I(t_j) \quad |j = 1, 2, 3, ..., n \right\}$$

where Y_j is the jth day cumulative infection data and $I(t_j)$ model predicted cumulative infected data of same day. If the residuals are randomly distributed then we can say that the fitness is reasonably good [18].

Table 2: Parameters estimation for Djibouti.

Parameter	value: 23 March to 1 May	value: 1 May to 10 June	References
τ	0.03332	0.03332	[2]
μ	0.0444	0.0444	[2]
ν	0.0033	0.0568	[1]
β	0.99	1.82	Estimated
γ	0.276	0.19260	Estimated
λ	0.0026	0.0013	Estimated
α	0.0037	0.018523	Estimated

6.2 Model Validation and Prediction

To study the particular case: the spreading of COVID-19 in Djibouti we have considered the real cases in cumulative number of infection (from March 23 to June 10, 2020) and using the above described formula we have estimated the model parameters, using the global sensitivity index method we found the sensitivity index of the parameters. To execute the Matlab package, we have considered the initial population size as

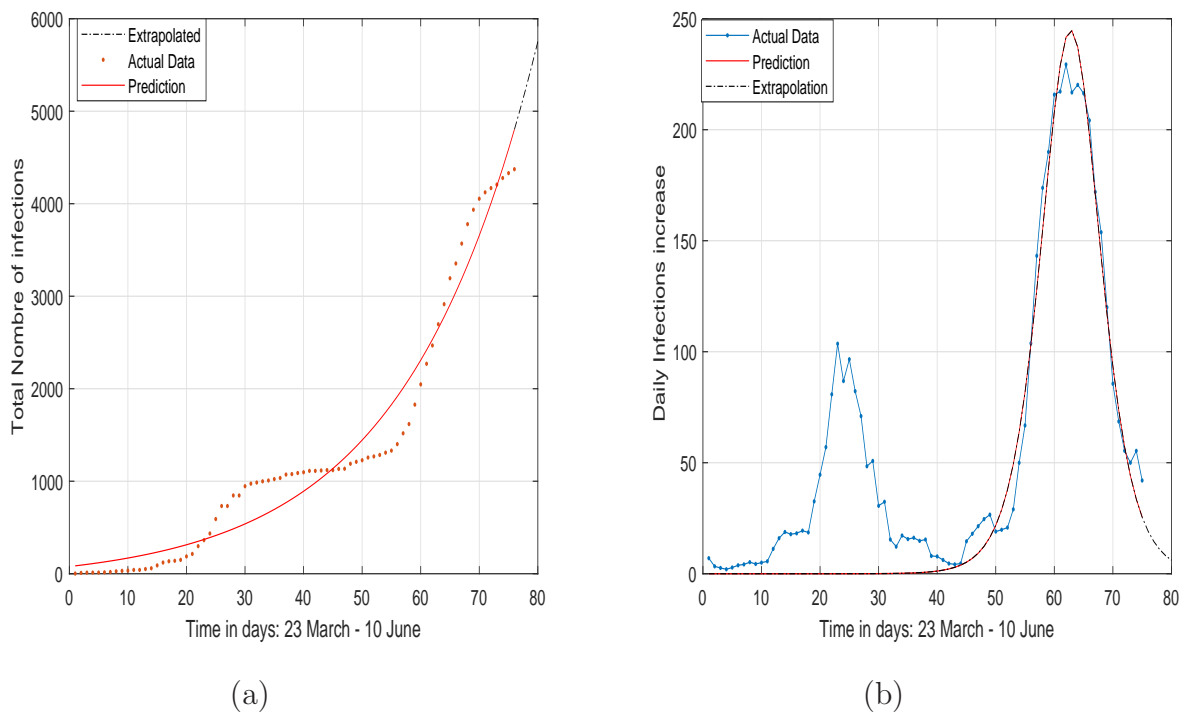$$S(0) = 986363, \quad I(0) = 2, \quad H(0) = 0, \quad \text{and} \quad R(0) = 0$$

(a)   (b)

Figure 2: (a) Fitting model to cumulative cases in Djibouti, (b) The time series of new cases of COVID-19 in Djibouti in 23 March to 10 June, 2020

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The estimated model parameters and their sensitivity indices are given in Table 2. To validate the model we consider the real case of COVID-19 infection of Djibouti from 23 March to 10 June, 2020 i.e. the real cases for 80 days. In Figure 2(a and b) respectively we have presented the best fitted cumulative infected cases and the curves represent of the per day new infection of real cases and the model predictions.
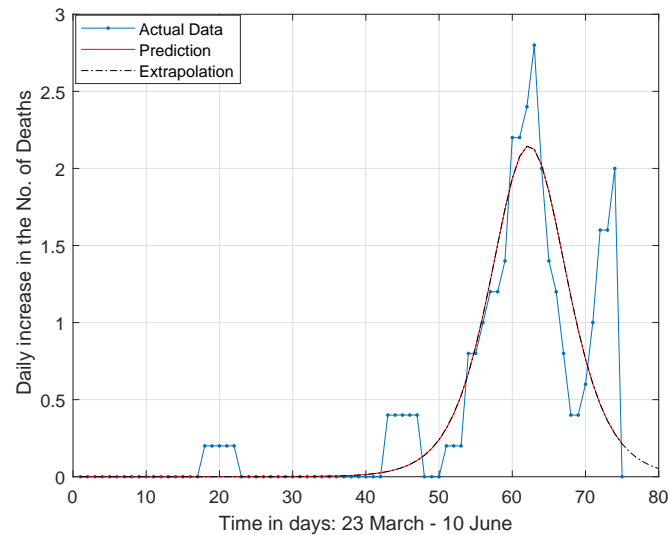

Figure 3: Number of death cases in Djibouti.

FIG 3 shows that the peak of death corresponding to the peak of number of confirmed cases in FIG. 2 (b). As a result, the more the COVID-19 epidemic spreads, the more the number increases.
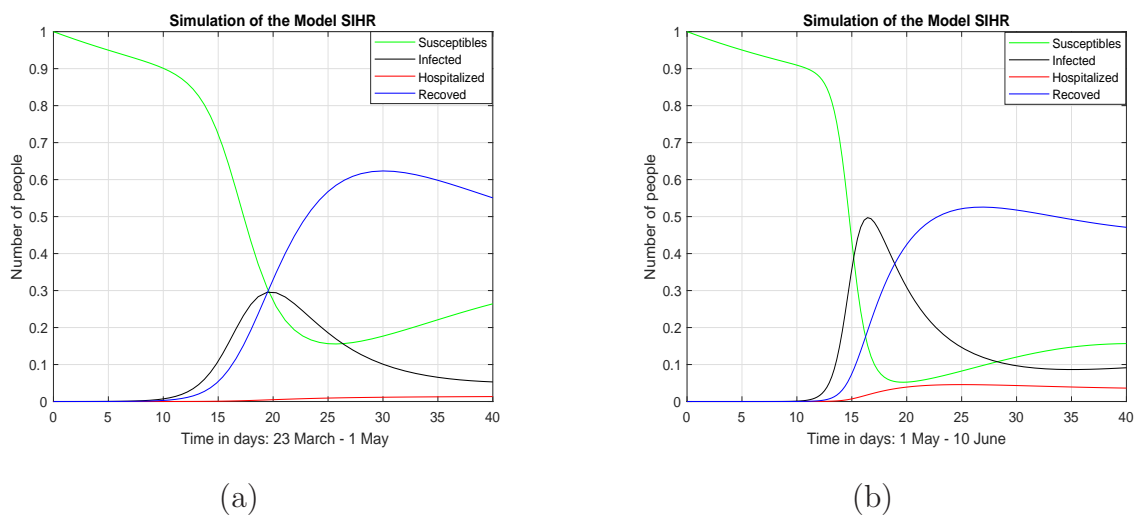

(a)   (b)

Figure 4: (a)Validation of the SIHR model from March 23 to May 1, 2020 (b) Validation of the SIHR model from May 1 to June 10, 2020

We observe in figure 4(a-b) that the susceptible population is decreasing with time, which means more and more people are getting exposed. Since infected population is increasing, therefore they are getting large number of infected individuals over time which can lead to an outbreak in a very short time. If we analyze the rest of the population dynamics, we see that the infected population grew faster over the last 40 days, which shows that the spread of the epidemic over time. we also see in figure 4(a) a lower rate infected initially meanwhile the recovered population is not growing as much as infected population in figure 4(b). Using the parameters that are estimated in Table 2, we can determine the value of the basic reproduction number in equation (3), with $R_0 = 2.62525$ and $R_0 = 5.0978$ of figure 4(a-b) respectively. Finally, the more the hospitalized population increases the more the number of deaths over the last 40 days, which corresponds to the period of containment.

7   Conclusion

In this study, we have formulated a SIHR epidemic model for pandemic COVID-19. All the properties necessary for epidemiological relevance have also been proved. Theoretically it is proven that the dynamics depends on the basic reproduction number to examine the stability of the system. All the properties necessary for epidemiological relevance have also been proved. We have estimated the parametric values for Djibouti using on the data of the ministry of health. The maximum number of reported cases was observed on 28 May-2020; which means that the number of infections was on an upward quickly trend for the next 9 days. After that day, the number of daily reported cases was observed to decrease asymptotically. Our proposed model approximates that the disease in Djibouti could be fully under control by after September 2020.

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