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Article

SEIHCRD Model for COVID-19 Spread Scenarios, Disease Predictions and Estimates the Basic Reproduction Number, Case Fatality Rate, Hospital, and ICU Beds Requirement

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Abstract: We have proposed a new mathematical method, the SEIHCRD model, which has an excellent potential to predict the incidence of COVID-19 diseases. Our proposed SEIHCRD model is an extension of the SEIR model. Three-compartments have added death, hospitalized, and critical, which improves the basic understanding of disease spread and results. We have studied COVID-19 cases of six countries, where the impact of this disease in the highest are Brazil, India, Italy, Spain, the United Kingdom, and the United States. After estimating model parameters based on available clinical data, the model will propagate and forecast dynamic evolution. The model calculates the Basic reproduction number over time using logistic regression and the Case fatality rate based on the selected countries' age-category scenario. The model calculates two types of Case fatality rate one is CFR daily, and the other is total CFR. The proposed model estimates the approximate time when the disease is at its peak and the approximate time when death cases rarely occur and calculate how much hospital beds and ICU beds will be needed in the peak days of infection. The SEIHCRD model outperforms the classic ARX model and the ARIMA model. RMSE, MAPE, and R squared matrices are used to evaluate results and are graphically represented using Taylor and Target diagrams. The result shows RMSE has improved by 56%–74%, and MAPE has a 53%–89% improvement in prediction accuracy.

Keywords: COVID-19; coronavirus; SIER model; SEIHCRD model; parameter estimation; mathematical model; India; Brazil; United Kingdom; United States; Spain; Italy; hospital beds; ICU beds; basic reproduction number; case fatality rate

1 Introduction

The world is fighting against a new enemy these days, which is the COVID-19 virus. The COVID-19 disease, known as coronavirus disease in 2019. We all are fighting every day against all the economic and social implications because of this virus, and most of the countries are facing this new enemy in the western countries.

The main motivation of our work is, as we know that many countries have suffered a lot from this COVID-19. Some countries suffer from loss of beds and ICU beds. Due to triage conditions, doctors have to select critical conditioned people for treatment, and some patients have not been treated due to the lack of hospital beds and ICU beds. It is regrettable to us that someone dies without treatment. Perhaps if they were treated, then save their lives. If the government has prior knowledge of how much beds are needed at a particular time, then the arrangement can be made, and it can save many lives for those who have died of lack of facility.

China reported a pneumonia outbreak in Wuhan in December 2019 [1]. This outbreak was linked to a novel strain of Coronavirus on 31 December 2019 [2], which has given the tentative name 2019-nCoV by the World Health Organization (WHO) [3–5], later renamed SARS-CoV-2 by the International Committee on Taxonomy of Viruses. WHO first describe Coronavirus in 1966 [6]. The World Health Organization announced these outbreaks as a public health emergency of international on 30 January and a pandemic on 11 March 2020 [7,8].

This pandemic has reported more than 5.59 million cases of COVID-19 have been reported in more than 188 countries, and territories and more than 2.28 million people have recovered from the virus and more than 350,000 deaths as of 27 May 2020 [9]. World Health Organization has not yet given official validity to any of the vaccines for COVID-19 [10]. United States has permitted to use antiviral remdesivir for severe patients of COVID-19 [11]. COVID-19 has transmitted among people through close contact, small droplets via coughing, talking, and sneezing [10–13]. The droplets usually not stay in the air more time; hence it falls on to the ground instead of travelling in the air [10]. People have also be infected by contacting the infected substance and then contacting their faces with unwashed hands [10,12].

COVID-19, the most common symptoms are fever, including cough, fatigue, shortness of breath, and loss of sense of smell [10,14]. In some cases, pneumonia and acute respiratory distress syndrome symptoms find in COVID-19 [15]. Lungs are the most affected part of the body by COVID-19 [16]. Around one out of every six people who get COVID-19 becomes seriously ill and develops difficulty breathing [17]. World Health Organization suggested some preventive measures that include hand washing maintain distance from other people (social distancing), covering one's mouth while coughing, always use a face mask in a public place, and follow self-isolation when anyone feels infected [10,18]. Many countries follow lockdown, restrictions on travel, work from home, and facility closure control to spread the virus. We have to follow staying at home, avoid public places, keep the distance from others, sanitize your hand regularly and wash your hand for at least 20 s, avoid touching the face, eyes, hairs, nose, and mouth with unwashed hands control to spread this virus [19–21].

COVID-19 has caused the global recession, and it affects social life [22]. COVID-19 has affected many sporting activities; financial, religious, and political activities have been rescheduled or cancelled [23,24]. This tragedy also has some good consequences; the emission of pollutants and greenhouse gases are reduced [25,26]. China has reported around 80 percent of deaths in those over 60 years of age and 75 percent in chronic health conditions, including heart disease and diabetes, as of 5 February [27]. Wuhan is the city where the first death case has reported on 9 January 2020 [28]. The Philippines is the country where the first confirmed case death outside China has reported on 1 February [29], and the first confirmed case reported outside of Asia on 14 February in France [30]. The WHO and Chinese officials have reported human to human transmission by 20 January 2020 [31,32]. Johns Hopkins University estimates that global death to the case ratio is 6.3 percent (350,458 fatalities per 5,591,067 cases) as of 27 May 2020 [33].

Many smartphone applications have been developed for voluntary use. These application uses Bluetooth to log a user's proximity to other smartphones. Users get a warning message when they have been directly touched with someone who has recently tested positive for COVID-19 [32]. Italy has reported its first confirmed case on 31 January 2020; two visitors come from China [34]. WHO declared Europe as the active hub of a pandemic on 13 March 2020 [35]. Italy has surpassed China with the most number of fatalities on 19 March 2020 [36]. The United States become the most number of cases reported in the world by 26 March [37]. European travellers are the main source of spreaders in New York [38]. Nearly 3.9 billion people had under some form of lockdown by the first week of April [39].

COVID-19 has a profound impact on the economy of all countries. Global stock markets fell on 24 February 2020 because of the rapid increase in the number of cases of COVID-19 across mainland China [40,41]. The world has seen the financial crisis first-time a huge decline in stock markets after 2008, and it crashed in March 2020 [42–44], and because of this pandemic, many financial deals are being cancelled postponed [45].

This paper proposed a new mathematical model to study the dynamics of transmission and control of the COVID-19 pandemic in most affected countries. The SEIR model is a widely used epidemiological model based on the SIR model given by Kermack et al. [46]. Brauer et al. [47] epidemic model has been very effective in forecasting outbreak behaviour quite close to several reported epidemics. After Kermack and Mckendrick's manuscript, many epidemic mathematical models have been developed stochastic models, discrete-time models, continuous-time models, and diffusion models. Compartmental models primarily depend on differential equations. These models are normally subdivided into many compartments (i.e., Susceptible, Infected, Recovered, Critical, Death, etc.). Compartmental models focused on basic law defining the transition of people from one compartment to another. These Models use mathematics to find the different parameters to estimate the effect of different interventions. Modelling can help determine which intervention to stop and which to continue and predict the future [48]. The model can predict how disease spreads, what will be the lifetime of any epidemic, how much people infected, recovered, and deceased. It can also estimate many parameters like reproduction numbers etc. These models are used in many applications nowadays, mostly in epidemiology, and many other fields like economics, politics, social science, and in the medical field. Epidemiological models such as SEIR provide a valuable computational approach to understanding the microscopic view of the spread of disease. These models play an important role in measuring possible strategies for the control and mitigation of infectious diseases [48–50]. These models are useful in cases where disease dynamics are not unclear. It estimates the number of cases in worst and best-case scenarios. Mathematical models are also helpful in understanding the scenario for spreading the disease [51–53].

The SEIR model failed to estimate the spread where preventive measures are adopted, such as social distancing, different age groups, the number of ICU beds, number of hospital beds, and mortality rate. The mathematical model helps predict the disease outbreak of COVID-19, and the SIR model and SEIR model have been widely used for prediction. SEIHCRD model is the modification of the SEIR model. The present manuscript encompasses a new modified SEIR model, which estimates the spread of COVID-19 spread, including all the parameters mentioned above.

The proposed SEIHCRD model is a novel approach and consists of many new features. Our proposed SEIHCRD model is a new mathematical method that extends the SEIR model by adding death, hospitalized, and critical compartments. The hospitalized compartment and critical

compartment are to a new compartment added in this model to enhance the disease transmission visibility. No one has used these two compartments in any model of my knowledge until that time. The model also calculates how many hospital beds and ICU beds are needed in peak time. The proposed model also calculates the case fatality rate and the basic reproduction rate.

The calculation process for requiring beds and ICU beds by this method is new. We calculate the basic reproduction number using the logistic regression over time; its unique idea is used in this model. We also consider age groups for case fatality rate analysis; if any country's elderly population is more, then the fatality rate will be higher in that country.

The basic reproduction number for COVID-19 in January was between 1.4 and 2.5 [54], but later analysis showed that this could vary from 3.8–8.9 [55]. As of last May 2020, the spread of disease in most countries is either stable or decreasing [56]. The summary of the proposed model results for the selected countries is shown in Tab. 1.

Table 1: Summary of the proposed model results for the selected countries

Description	Brazil	India	Italy	Spain	United Kingdom	United States
Approximate time when the disease is on peak	180–200	190–210	70–90	105–125	130–150	130–150
The approximate time when cases of death rarely occur	290	295	220	210	240	310
Basic reproduction number (highest)	4.4	2	5	6.8	4.2	4.4
Case fatality rate (highest)	7.2	2.8	7.3	7.9	7.5	7.6
Overall case fatality rate	3.2	2.3	3.3	2.5	3	2.9
Approximately needed hospital beds while the disease is at a peak	800	110	580	450	200	75
Approximately the needed ICU beds when the disease is at a peak	430	260	90	250	500	350
Highest number of people dead in a single day	1800	560	850	700	1100	1250

The structure of this paper is as follows; Section 1 introduces COVID-19 and explains the significance of this research. The SEIHCRD model for COVID-19 spread estimation; predictive modelling has been presented in Section 2. Section 3 has discussed the data analysis and parameter estimation used for validating proposed mathematical models. Results and discussions of the

proposed model have been discussed in Section 4. Finally, the conclusion and some future works have been discussed in Section 5.

2 Proposed Methodology

The SIR and SEIR compartmental models are the most commonly used mathematical method for infectious disease. SEIHCRD-Model is a new mathematical method extending the SEIR-Model adding death, hospitalized, and critical compartments. The proposed method and some basic compartmental models have been described below.

2.1 SIR Model

Mathematical modelling of infectious disease, specially Coronavirus disease (COVID-19), has been a trending topic for many epidemiologists and data scientists in the last some weeks. Coronavirus disease (COVID-19) is an infectious disease; hence it can spread from one member of the population to another member of the population. Kermack et al. [46] has proposed the SIR (susceptible, infected, recovered) model in 1927. SIR model is separated into three population-wise compartments of Susceptible (S), Infectious (I), and Recovered (R). SIR model describes the transition of people from Susceptible to Infected and then Infected to Recovered based on underlying parameters, which controls disease dynamics in the population. Deceased cases come under the Recovered compartment in the SIR model. The SIR model is shown in Fig. 1.

Figure 1: SIR model

Differential Equations for Traditional SIR Model

We write the model equations that are independent of the population of the country by considering the fraction of the people in each category. The rates of transfer from one category to another are the model parameters, and a set of differential equations are formed. The SIR model has been described below using the coupled ordinary differential equations:

$$\frac{dS}{dt} = -\eta \cdot \beta \cdot I \cdot \frac{S}{N}, \tag{1}$$

$$\frac{dI}{dt} = \eta \cdot \beta \cdot I \cdot \frac{S}{N} - \gamma \cdot I, \tag{2}$$

$$\frac{dR}{dt} = \gamma \cdot I, \tag{3}$$

$$N = S(t) + I(t) + R(t), \tag{4}$$

where,

N—Total population

S—A proportion of the entire population that is healthy and have never been infected

I—A proportion of the entire population that is infected by the virus

R—A proportion of the entire population that has recovered from the infection

where initial conditions (S(0), I(0), R(0)) are not exactly known, and these systems of ordinary differential equations are extremely sensitive to the initial parameters. Description of some parameters are given below:

η—Social distancing factor

β—The rate of transmission of infection from susceptible to infected

γ—The rate of recovery

R_0—Basic reproduction number

X—Number of days an infected person has and can spread the diseases $\left(X = \frac{1}{\gamma}\right)$

Basic reproduction number $R_0 = \beta \cdot X$,

Therefore, from above, we can write it as $R_0 = \frac{\beta}{\gamma}$.

2.2 *SEIR Model*

Kermack et al. [46], Beretta et al. [57] have further developed their theories and proposed a time delay SIR model. Cooke et al. [58] investigated the incubation period in the spread of infectious diseases, introduced the "Exposed, E," compartment, and proposed a time delay model. SEIR model is separated into four population-wise compartments of Susceptible (S), Exposed (E), Infectious (I), and Recovered (R). SEIR model describes the transition of people from Susceptible to Exposed, then Exposed to Infected and then Infected to Recovered based on underlying parameters, which controls disease dynamics in the population. The SEIR model is shown in Fig. 2.

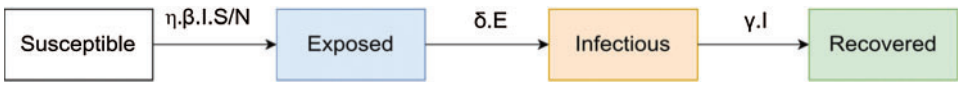


Figure 2: SEIR model

Deceased cases come under the recovered compartment in the SEIR model. Deceased cases play an essential role in infectious modelling; hence, we have to make it a separate compartment. The extension of the SEIR model is the SEIRD model in which the Dead compartment is added. SEIR model is separated into four population-wise compartments of Susceptible (S), Exposed (E), Infectious (I), Recovered (R), and Dead (D). SEIRD model describes the transition of people from Susceptible to Exposed, then Exposed to Infected, then Infected to Recovered and Infected to Dead. The SEIRD model is shown in Fig. 3.

Differential Equations for SEIR Model and SEIRD Model

After adding the exposed compartment, ordinary differential equations are changing accordingly, Eqs. (2), and (4) are being modified and some ordinary equations are added. Hence, updated coupled ordinary differential equations of the SEIR Model are given below:

$$\frac{dE}{dt} = \eta \cdot \beta \cdot I \cdot \frac{S}{N} - \delta \cdot E, \tag{5}$$

$$\frac{dI}{dt} = \delta \cdot E - \gamma \cdot I, \tag{6}$$

$$N = S + E + I + R, \tag{7}$$

Eqs. (1) and (3) remains the same as explained in the SIR model.

where

E—A proportion of the entire population that is exposed to infection, transmit the infection and turn into either Symptomatic or purely Asymptomatic, and not detected

Description of some parameters used in the SEIR model is given below:

δ—the rate of transmission of infection from exposed to infectious and the rest of the parameters are the same as the SIR model.

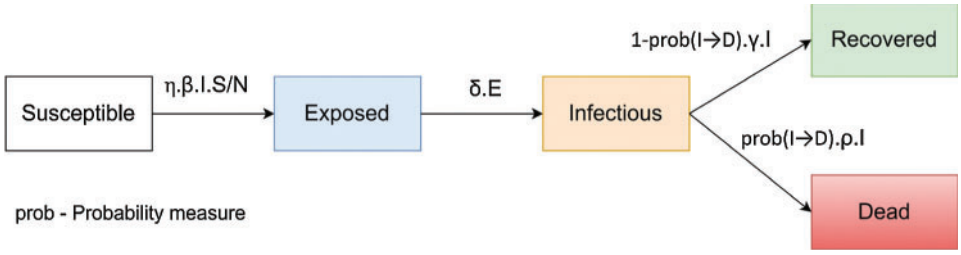


Figure 3: SEIRD model

After adding the dead compartment, ordinary differential equations are changing accordingly, Eqs. (3), (6), and (7) are being modified and some ordinary equations are added. Hence, updated coupled ordinary differential equations of the SEIRD Model are given below:

$$\frac{dI}{dt} = \delta \cdot E - (1 - prob\,(I \to D)) \cdot \gamma \cdot I - prob(I \to D) \cdot \rho \cdot I, \tag{8}$$

$$\frac{dR}{dt} = (1 - prob\,(I \to D)) \cdot \gamma \cdot I, \tag{9}$$

$$\frac{dD}{dt} = prob(I \to D) \cdot \rho \cdot I, \tag{10}$$

$$N = S + E + I + R + D, \tag{11}$$

Eqs. (1) and (5) remains the same as explained previously.

Here, D—A proportion of the entire population that is dead because of the infection.

Description of some parameters used in the SEIRD model is given below:

ρ—Median time from Infected to Death and the rest of the parameters are the same as the SEIR model.

2.3 SEIHCRD Model

The present manuscript encompasses two new compartments added for more accurate analysis is the Hospitalized compartment and the Critical compartment. This model allows overflowing hospitals. SEIHCRD model is separated into seven population-wise compartments of Susceptible (S), Exposed (E), Infectious (I), Hospitalized (H), Critical (C), Recovered (R), and Dead (D). SEIRD model describes the transition of people from Susceptible to Exposed, then Exposed to Infected, and then from Infected, they can either Hospitalized or Recovered compartment. Of course, only infected individuals can enter the hospitalized compartment and critical compartment. From hospitalized, they can either Critical or Recover, and from the Critical compartment, they can either die or recover. The SEIHCRD model is shown in Fig. 4.

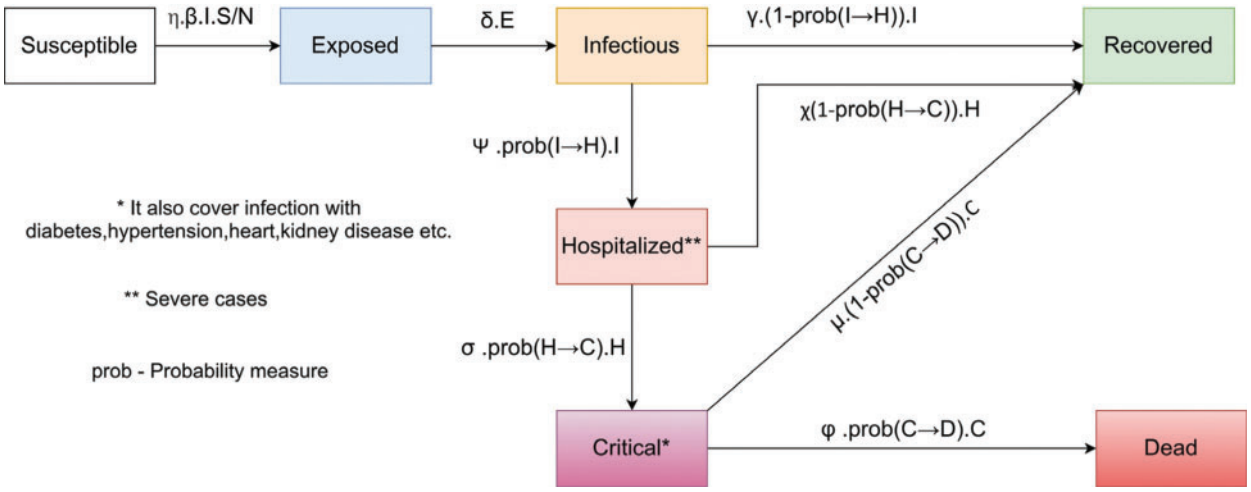


Figure 4: SEIHCRD Model

Some infections are mild like fever, cough, and may even have mild pneumonia but do not require hospitalization. These individuals may recover, or in the future, they go to the hospitalized compartment.

People with severe infections suffer from severe pneumonia and need hospitalization. These individuals may either recover or progress to the critical compartment. People with critical infection experience multi-organ failure, and multiple disorders require treatment in an ICU. These people either recover from the disease or die from it.

Differential Equations for SEIHCRD Model

After adding hospitalized and critical compartments, ordinary differential equations are changing accordingly, Eqs. (8)–(11) are being modified and some ordinary equations are added. Hence, updated coupled ordinary differential equations of SEIHCRD Model are given below:

$$\frac{dI}{dt} = \delta \cdot E - \Psi \cdot prob\,(I \to H) \cdot I - \gamma \cdot (1 - prob\,(I \to H)) \cdot I, \tag{12}$$

$$\frac{dH}{dt} = \Psi \cdot prob\,(I \to H) \cdot I - \sigma \cdot prob\,(H \to C) \cdot H - \chi\,(1 - prob\,(H \to C)) \cdot H, \tag{13}$$

$$\frac{dC}{dt} = \sigma \cdot prob\,(H \to C) \cdot H - \varphi \cdot prob\,(C \to D) \cdot C - \mu \cdot (1 - prob(C \to D)) \cdot C, \tag{14}$$

$$\frac{dR}{dt} = \gamma \cdot (1 - prob(I \to H)) \cdot I + \mu \cdot (1 - prob(C \to D)) \cdot C + \chi\,(1 - prob(H \to C)) \cdot H, \tag{15}$$

$$\frac{dD}{dt} = \varphi \cdot prob\,(C \to D) \cdot C, \tag{16}$$

$$N = S + E + I + H + C + R + D, \tag{17}$$

Eqs. (1) and (5) remains the same as explained previously.

Here

H—A proportion of the entire population that is found positive in the test and hospitalized

C—A proportion of the whole population those are seriously ill and who need ICU

Also, the description of some parameters used in the SEIR model is given below:

Ψ—Median time to development of pneumonia and other symptoms for hospitalization

σ—Median time from hospital to ICU admission

φ—Median intensive care units (ICUs) length of stay

χ—Median hospital stay

μ—The recovery time of critical conditioned people

We know that every country has limited resourced of hospital beds and ICUs. Sometimes the number of critical cases is more than the number of ICUs; in this condition, doctors have to choose who gets treated with the limited number of resources. This manuscript accepts all these conditions as follows:

If there is a B number of ICUs and C number of critical cases, then the following condition occurs:

1. If the number of ICUs is more than critical cases, then all patients get treated.
2. But if the number of ICUs is less than the number of critical cases (C > B), then B number of patients treated and rest (C − B) die because of shortage.

The SEIHCRD Model, with critical case analysis, is shown in Fig. 5.

The SEIHCRD model with critical case analysis is modifying the ordinary differential Eqs. (14)–(16). Updated equations are as follows:

$$\frac{dC}{dt} = \sigma \cdot prob\,(H \to C) \cdot H - \varphi \cdot prob\,(C \to D) \cdot \min\,(Beds\,(t)\,, C) - \max\,(0, C - Beds\,(t)) - \mu \cdot (1 - prob\,(C \to D)) \cdot \min\,(Beds\,(t)\,, C)\,, \tag{18}$$

$$\frac{dR}{dt} = \gamma \cdot (1 - prob(I \to H)) \cdot I + \mu \cdot (1 - prob(C \to D)) \cdot \min(Beds(t), C) + \chi\,(1 - prob(H \to C)) \cdot H, \tag{19}$$

$$\frac{dD}{dt} = \varphi \cdot prob\,(C \to D) \cdot \min\,(Beds\,(t)\,, C) + \max(0, C - Beds\,(t)), \tag{20}$$

Here, Beds—Number of available ICU beds.

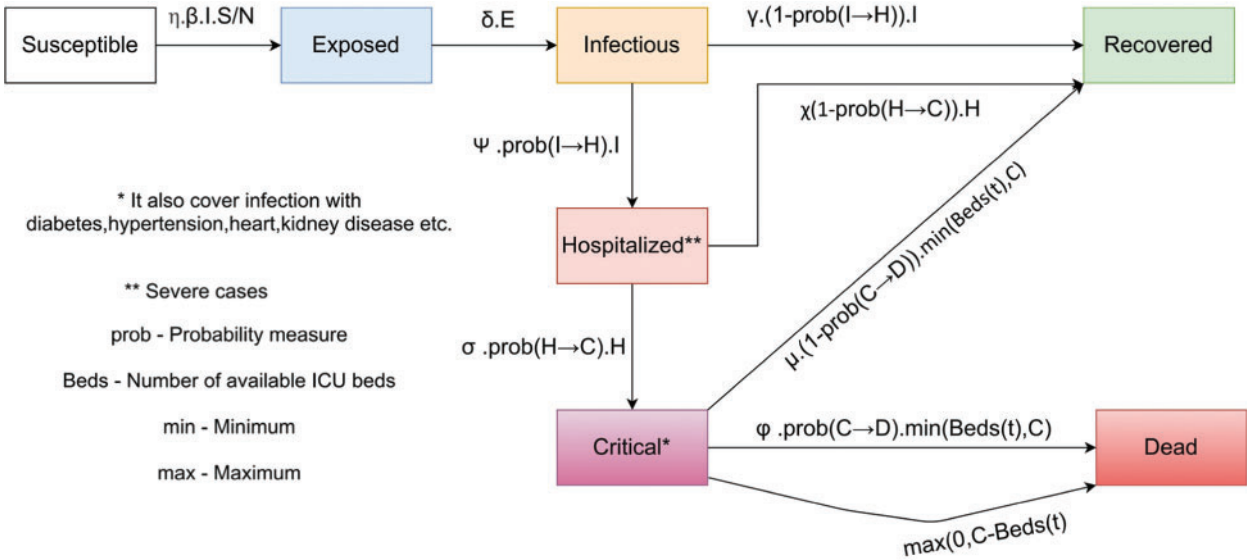


Figure 5: SEIHCRD model with critical case analysis

3 Data Analysis and Parameter Estimation

Compartmental models are ordinary differential equations. These ordinary differential equations have required some initial conditions and parameters to solve and characterize ODE. The prevalence of COVID-19 in the compartment, the population, has been influenced by the complexities of many factors. Preliminary estimation of parameters helps solve important parameters such as fatality rate and basic reproduction rate, which will help us better understand the transmission trend of COVID-19. In the present manuscript, we first collect data for a specific period, then estimate the basic reproduction number, infection rate, and recovery rate of COVID-19, and based on these estimates. We analyze the spread and endpoint of COVID-19.

η is the social distancing parameter. The social distancing parameter includes avoiding social gatherings and physical contact to prevent the spread of infectious disease. Its value lies in between zero to one. Everyone is quarantined if a lockdown is implemented, and then its value is zero, and they follow the routine without restriction, then its value is one.

R(0) and R_0 are different quantities; R(0) describes the number of recovered at $t = 0$, whereas R_0 is the basic reproduction number that is the ratio between the rate of contacts to the rate of recovery. The basic reproduction number is the expected number spread by infected people in a population where all peoples are susceptible to infected.

3.1 R_0 Change with Time

R_0 value is change with time; whenever any country implements lockdown, the value of R_0 decreases, and when that country removes lockdown, its value starts increasing again. R_0 value has decreased when any country puts strict lockdown, and after some time, it goes below one. R_0 is the ratio of β and γ in the compartmental models; hence we can say that $\beta = R_0 \cdot \gamma$. The value of R_0 is R_{0_start} before the lockdown, and if the lockdown is imposed on day L, then the value of R_0 is decreased up to R_{0_end}, and the value of β is change accordingly.

Basic reproduction number R_0 is not constant in real life; it changes with time. The basic reproduction number value has changed accordingly if social distancing is imposed. The model shows the initial impact of social distancing on the reproduction number. This model uses the logistic function because it changes very slowly; initially, its speed increase when the lockdown is imposed, and then it slows down in the end. The reproduction number is

$$R_0(t) = \frac{R_{0_{Start}} - R_{0_{End}}}{1 + e^{-\eta(-t+x_0)}} + R_{0_{End}}, \tag{21}$$

Description of parameters are given below:

$R_{0_{Start}}$—Value of R_0 on the first day

$R_{0_{End}}$—The value of R_0 on the last day

x_0 is the value of inflection point (i.e., the day when the value of R_0 decline drastically)

η is the social distancing parameter.

According to the value of the social distancing parameter, it changes drastically.

3.2 Age-Dependent Fatality Rate

The fatality rate is not stable; it depends on many things. The fatality rate affects most by one of the common reasons is the Age factor, some fatal disease, the number of ICU beds available, etc. The fatality rate is more when the most number of people are infected, and the fatality rate and is less when infected people are less. The base fatality rate is there when fewer people are infected.

Infected people become very much sometimes; at that time, we need more medical equipment for treatment, sometimes everyone is not treated due to lack of medical facility. We should know what proportion of people are currently infected; hence we describe fatality rate φ as

$$\varphi(t) = s \cdot \frac{I(t)}{N} + \varphi_{opt}, \tag{22}$$

Description of parameters are given below:

s—It is arbitrary but the fixed value that controls the influence of infection (it chooses freely once and then stay constant over time)

φ_{opt}—It is the optimal fatality rate

I(t) are infected people at time t, and N is the total population. The value of s controls the above equation. Therefore, carefully give the value of s.

Analysis of case fatality depends on Age group is complex. We separate different age groups (e.g., people aged 0–9, aged 10–19, . . . aged 90–100). for age group analysis, we need two things.

1. Fatality rates by age group,
2. The proportion of the total population is in that age group.

The fatality rate is high if the population of older people is more, and if the proportion of young people is more, then the fatality rate is low. The fatality rate has calculated by:

$$\begin{aligned} \textit{fatality rate (with out comorbidity cases)} &= \textit{age group fatality rate for all cases} \\ &\quad * \textit{proportion of population in that age group,} \end{aligned} \tag{23}$$

$$\begin{aligned} \textit{fatality rate (with comorbidity cases)} &= \textit{age group fatality rate for comorbidity cases} \\ &\quad * \textit{proportion of population in that age group,} \end{aligned} \tag{24}$$

So the overall fatality rate is a combination of the above two cases then,

$$\textit{over all fatality rate} = \textit{with out comorbidity cases} + \textit{with comorbidty cases,} \tag{25}$$

In the present manuscript, all the comorbidity cases are considered as critical cases. The fatality rate for all cases is shown in Tab. 7, and the proportion of age groups is shown in Fig. 16.

3.3 Hospitalized and Critical Cases Analysis

Every country has limited resourced of hospital beds and ICUs. Sometimes the number of Critical cases are more than the number of ICUs in this condition; doctors have to choose who gets treated with a limited number of resources. This manuscript accepts all these conditions as follows. If there is a B number of ICUs and C number of critical cases, then the following condition occurs:

1. People with a severe infection suffer from severe pneumonia and need hospitalization, and hospital beds are available; then, they are treated in the hospital, but sometimes beds are not available due to shortage, then they have to wait till the hospital bed is empty or self-quarantine in their home.
2. If the number of ICUs is more than critical cases, then all patients are treated.
3. However, if the number of ICUs is less than the number of critical cases (C > B), then B number of patients treated and rest (C-B) die because of a shortage.

The premise for hospital beds and ICUs is that countries respond and start constructing clinics and opening the rooms, etc., while the virus spreads. Hence, over time, the number of hospital beds and ICUs is increasing. We can model the number of beds as:

$$Beds_{hosp}(t) = Beds_{hosp0} + s.t.Beds_{hosp0}, \tag{26}$$

Description of parameters are given below:

$Beds_{hosp0}$—The total amount of Hospital beds available

s—Some scaling factor,

Sometimes infected people are massive at that time, patients not treated because of a lack of medical facility. To overcome this situation, every country's government improve the medical facility over time. Critical condition persons require ICU for treatment; hence, a sufficient number of ICU beds are needed for critical patients. We calculate the number of ICU beds over time, as given below:

$$Beds(t) = Beds_0 + s.t.Beds_0, \tag{27}$$

Description of parameters are given below:

$Beds_0$—The total amount of ICU beds available

s—Some scaling factor

Eq. (27) explain how much the number of ICU beds increases per day. It mainly depends on s, which is some scaling factor. The number of beds increases s times per day; scaling factor s plays a vital role in calculating how many numbers of beds increase daily according to this patient's serve in the hospitals.

3.4 Fitting the Model to Find Some Important Parameters Value

In this manuscript, we are focus on fitting the SEIHCRD Model with time-dependent basic reproduction number and age group based fatality rate, Hospital beds and ICUs with real COVID-19 data that come close to the real data to find the parameters for our model that produce the possible prediction which is helpful in the future development.

All the experimental studies have been performed on the PYTHON platform using some important libraries, i.e., pandas, NumPy, LMfit, ode, etc. The machine used for performing simulation work has Processor Intel(R) Core(TM) i7-5500U CPU@2.40 GHz, 2401 MHz, 2 Core(s), and 4 Logical Processor(s), 12 GB RAM hardware configuration.

The curve-fitting model required some value initially for parameters. Initial guesses for parameters are very crucial. We need to know what parameters have been learned and what we have to get out of it. The proposed model has been used in many parameters. We have computed some parameters and considered some according to the present study and data. We do not need to fit N; just put the population of the place we have to model, and similarly, no need to calculate $Beds_0$; just put the number of ICUs of the place we have to model. We have to give value to some parameters based on real data and analysis, i.e., Social distancing parameter η lies in the range zero and one, where zero indicates everyone is locked down and quarantined while one is for everyday life.

A Chinese study has shown the incubation period to be 5.2 days on average, but it varies among different peoples [59]. The Chinese team study found 14 days of medical observation is necessary for those people who are exposed to pathogens.

Median Hospital stay ($\chi = 1/10$) and recovery period ($\gamma = 1/10$)

The JANA study has found that the median hospital stay is ten days, and all those are discharged alive, and research showed the basic recovery period of the patient is ten days [60,61].

The median time to develop pneumonia and other hospitalization ($\Psi = 1/5$) and hospital to ICU admission ($\sigma = 1/7$). The median time from symptom onset to the development of pneumonia is approximately five days, [62,63]. The median time from symptom onset to severe hypoxemia and ICU admission is about 7–12 days [63–67]. Median intensive care units (ICUs) length of stay ($\varphi = 1/8$).

The median intensive care units (ICUs) length of stay for COVID-19 patients was approximately 8–13 days of respiratory support in a Chinese report [62,67]. Hence the recovery time from critical is the same as ICU's length of stay that is eight days ($\mu = 1/8$).

First, we fit the available clinical data, and then we estimate the model parameters values from it. We used the least square method and the Levenberg-Marquardt model to calculate the parameters R_0_start, R_0_end, k, x_0, s, $P(I \to H)$, $P(C \to D)$, and $P(H \to C)$ for the proposed model. To estimate the final value of any parameter, we first set the range of the parameter

means the maximum value and the minimum value. Then we have to set the initial value of the parameter to fit the model and get the final fitted value. We do not need to fit some parameter, for example, η, δ, Ψ, γ, σ, φ, χ, μ etc. need not to fit. We have to get these parameter values from the review of research papers and reports of trusted organizations. We calculate the disease transmission rate β using R_0_start, R_0_end, η, x_0, and γ. We know $\beta = R_0 \times \gamma$, and it changes over time. Tabs. 2 and 3 show the numerical values of the model parameters for selected countries.

Table 2: The numerical values of the model parameters for selected countries

Country	Values	R_0start	R_0end	k	x_0	s	P(I → H)	P(C → D)	P(H → C)
Brazil	Maximum	8	3.5	5	250	0.1000	1	1	1
	Minimum	2	0.3	0.01	25	0.00001	0	0	0
	Initial value	3	1	2.5	100	0.001	0.2	0.6	0.5
	Fitted value	4.4	0.9	2.3	180	0.008	0.18	0.48	0.3
India	Maximum	8	3.5	5	250	0.1	1	1	1
	Minimum	2	0.3	0.01	25	0.00001	0	0	0
	Initial value	3	1	2.5	100	0.001	0.2	0.6	0.5
	Fitted value	2	0.9	0.1	178	0.003	0.15	0.41	0.22
Italy	Maximum	8	3.5	5	250	0.1	1	1	1
	Minimum	2	0.3	0.01	25	0.00001	0	0	0
	Initial value	3	1	2.5	100	0.001	0.2	0.6	0.5
	Fitted value	5	0.9	0.04	90	0.009	0.26	0.66	0.33
Spain	Maximum	8	3.5	5	250	0.1	1	1	1
	Minimum	2	0.3	0.01	25	0.00001	0	0	0
	Initial value	3	1	2.5	100	0.001	0.2	0.6	0.5
	Fitted value	6.8	0.9	0.45	110	0.0067	0.27	0.62	0.31
United Kingdom	Maximum	8	3.5	5	250	0.1	1	1	1
	Minimum	2	0.3	0.01	25	0.00001	0	0	0
	Initial value	3	1	2.5	100	0.001	0.2	0.6	0.5
	Fitted value	4.2	0.9	0.38	130	0.004	0.23	0.55	0.35
United States	Maximum	8	3.5	5	250	0.1	1	1	1
	Minimum	2	0.3	0.01	25	0.00001	0	0	0
	Initial value	3	1	2.5	100	0.001	0.2	0.6	0.5
	Fitted value	4.4	0.9	0.337	190	0.005	0.21	0.45	0.27

Table 3: Numerical values of non-fitted model parameters for selected countries

Parameters	Value
η	1
δ	1/5.2
Ψ	1/5.0
γ	1/10.0
σ	1/7.0
φ	1/8.0
χ	1/10.0
μ	1/8.0

The case fatality rate (CFR) represents the proportion of cases that eventually die from the disease [68]. The basic formula of the case fatality rate is $= \frac{Deaths}{Cases}$, and sometimes this formula is corrected then $CFR = \frac{Death\ at\ day\ x}{cases\ at\ day\ (x-T)}$, where T = average time from case confirmation to death.

We know that $\beta(t)$ can be calculated by basic reproduction number $R_0(t)$ and γ hence, no need to find any separate parameter for β. The beds scaling factor s can be fitted; it does not affect much in the result because the amount of people who are treated because of lack of facility is significantly less as compared to the number of death. The proposed model has three probability estimates $P(I \to H)$, $P(H \to C)$ and $P(C \to D)$ split up by age groups and weighted by the proportion of per age group. We will try to fit all the above probabilities, which exceptionally close to the prediction obtained of special risk group such as diabetics, high blood pressure, heart disease, etc., now we have to fit all the probabilities $P(I \to H)$, $P(H \to C)$ and $P(C \to D)$ and $R_{0_{Start}}$, $R_{0_{End}}$, x_0 and η are the parameters of $R_0(t)$.

Johns Hopkins University Center for Systems Science and Engineering is the primary source of data [69]. We have collected and cleaned data for age groups, probabilities, and ICU beds from UN Data [70].

A total number of Hospital beds and ICUs as per one lack peoples for topmost affected countries. The number of people per age group for top affected countries. Probabilities for $P(I \to H)$, $P(H \to C)$, and $P(C \to D)$ per age groups, but we use fitted probabilities and collect the data of the number of fatalities day wise from 22 January 2020 onwards.

We only use the data of the number of fatalities, not total cases or active cases, because the number of reported cases is not much accurate; it depends on many factors like the number of test cases, etc., but the number of fatalities reported is more accurate.

We have to collect all the data and parameters that we already know, then define some initial guesses and set the upper and lower bounds for those we do not know. We can change the upper and lower bound and initial suppose according to the situation. We set Levenberg–Marquardt as a fit model after defining all parameters. Levenberg–Marquardt algorithm is the most important algorithm in data fitting [71,72]. LMfit library provides a high-level interface to non-linear optimization and curve-fitting problems for Python [73]. R-squared value is a measure of how close the data are to the fitted line. R-squared value is always between zero and one. In general, the higher the R-squared value, the better the model fits your data. Curve fitting of death cases of India and Brazil is shown in Fig. 6. R-squared value of curve fitting for Brazil, India, Italy, Spain, the United Kingdom, and the United States are shown in Tab. 4.

"Curve fitting for death cases of Brazil, India, Italy, Spain, the United Kingdom and the United States has been added and shown in the manuscript. Updated figures are included here for your kind perusal."

A Chinese study has found, 80% of cases are mild. Based on all 72,314 cases of COVID-19 confirmed, suspected, and asymptomatic cases in China as of February 11, a paper by the Chinese CCDC released on February 17 and published in the Chinese Journal of Epidemiology [61,64,65, 74,75] has found that:

1. 80.9% of infections are mild and can recover at home.
2. 13.8% are severe, developing severe diseases including pneumonia and shortness of breath.

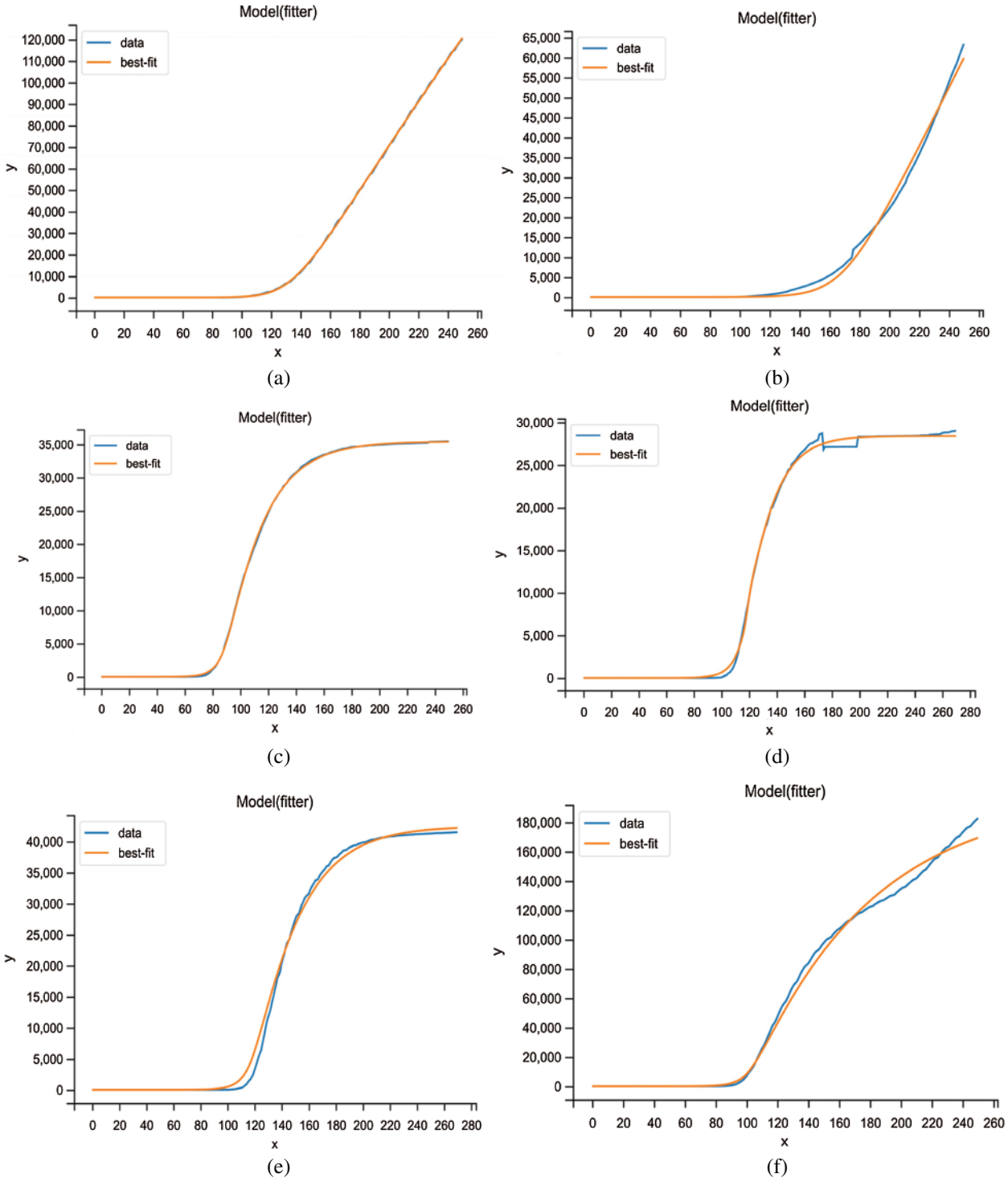


Figure 6: Curve fitting of death cases of (a) Brazil, (b) India, (c) Italy, (d) Spain, (e) the United Kingdom and (f) the United States

Table 4: R-squared value of curve fitting for Brazil, India, Italy, Spain, United Kingdom, and the United States

Country	R-squared value (death cases)
Brazil	0.999
India	0.986
Italy	0.997
Spain	0.996
United Kingdom	0.988
United States	0.982

3. 4.7% as critical and can include respiratory failure, septic shock, and multi-organ failure.
4. In about 2% of reported cases, the virus is fatal.
5. The risk of death increases the older you are.
6. Relatively few cases are seen among children.

Pre-existing illnesses that put patients at higher risk:

1. cardiovascular disease
2. diabetes
3. chronic respiratory disease
4. hypertension

We have collected and analyzed data from all US States. In Tab. 5, we have shown the data provided by New York City Health as of May 13, 2020 [68,76]:

Table 5: Age-wise rate of hospitalization from infected cases, critical cases from infected cases, and deceased cases from ICUs

AGE	Rate of hospitalization from infected cases (%)	Rate of critical cases from infected cases (%)	Rate of deceased cases from ICUs (%)
80+ years old	18.4	0.16	0.98
70–79 years old	16.6	0.10	0.86
60–69 years old	11.8	0.07	0.57
50–59 years old	8.2	0.05	0.26
40–49 years old	4.3	0.03	0.10
30–39 years old	3.4	0.025	0.06
20–29 years old	1.0	0.009	0.05
10–19 years old	0.1	0.003	0
0–9 years old	0.01	0.001	0

3.5 COVID-19 Fatality Rate by AGE

We know Death Rate = (number of deaths/number of cases) can be written as the probability of dying if infected by the virus (in percentage), and it depends on the different age groups.

In Tab. 6, percentages represent, for a person in a given age group, the risk of dying if infected with COVID-19 [77].

Table 6: Age-wise death rate of all cases and comorbidity cases

Age	Death rateof all cases (%)	The death rate of comorbidity cases (%)
80+ years old	14.8	0.98
70–79 years old	8.0	0.86
60–69 years old	3.6	0.57
50–59 years old	1.3	0.26
40–49 years old	0.4	0.10
30–39 years old	0.2	0.06
20–29 years old	0.2	0.05
10–19 years old	0.2	0
0–9 years old	(no fatalities) 0	0

3.6 COVID-19 Fatality Rate by COMORBIDITY

The comorbidity fatality rate for all the cases has shown in Tab. 7, and the percentage showed that for a patient with a given pre-existing condition, the risk of dying if infected by COVID-19 [78].

Table 7: For all top comorbidity cases death rate

PRE-existing condition	Death rate all cases (%)
Cardiovascular disease	10.5
Diabetes	7.3
Chronic respiratory disease	6.3
Hypertension	6.0
Cancer	5.6
No pre-existing conditions	0.9

We have used the publicly available dataset of COVID-19 provided by the Johns Hopkins University [79]. This dataset includes many countries' daily count of confirmed cases, recovered cases, and deaths. This time series dataset is available from 22 January 2020. We also gathered and crosschecked data in Worldometer, Coronavirus cases [76], a website providing real-time data of COVID-19. These data are collected through public health authorities' announcements and are directly reported public and unidentified patient data; hence ethical approval is not required.

3.7 Distribution of Total Cases Worldwide

WHO has reported that 216 countries are affected by COVID-19. Fig. 7 shows that 35% of cases are from six countries only. The United States of America has the highest number of cases, which alone is 19% worldwide.

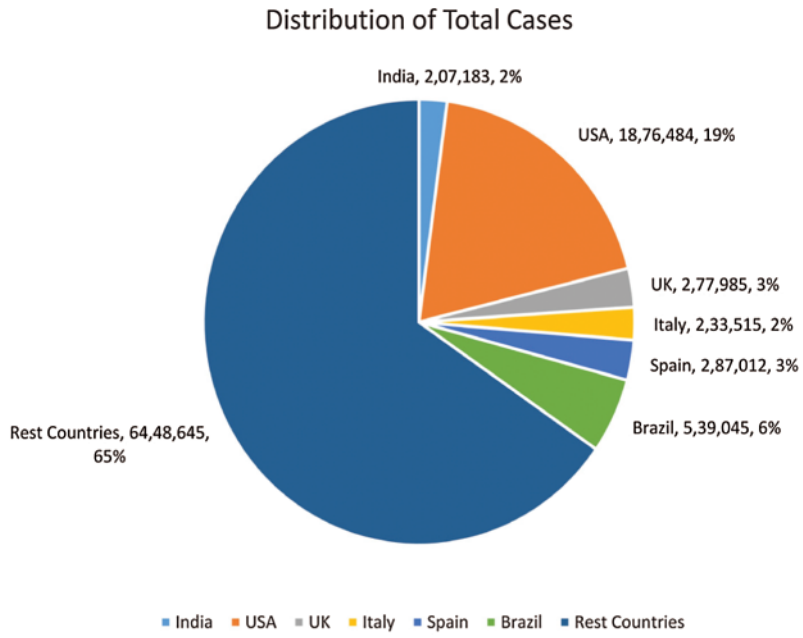


Figure 7: Distribution of total cases worldwide

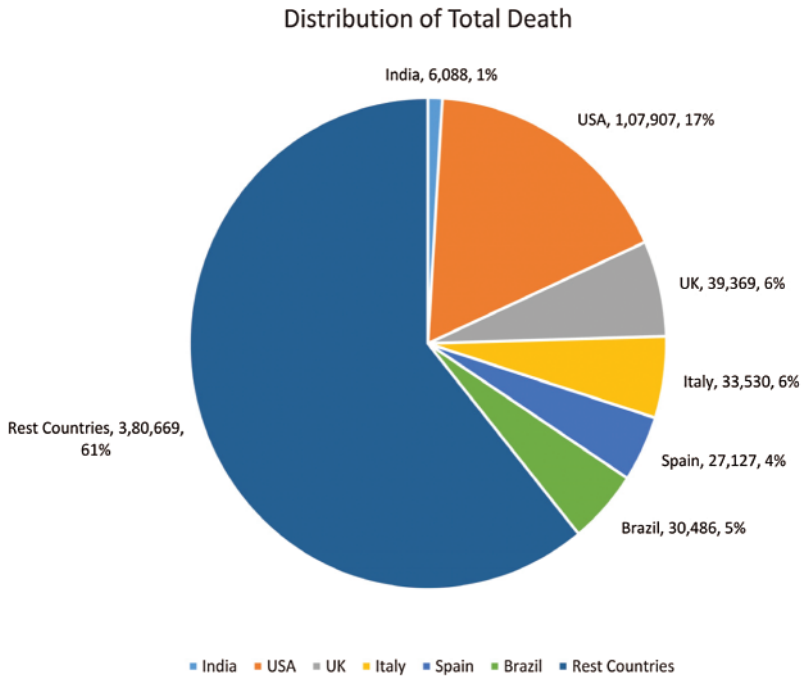


Figure 8: Distribution of death cases worldwide

3.8 Distribution of Death Cases Worldwide

Death cases are more accurate because rarely any case from COVID-19, which has not been registered. Fig. 8 shows that 39% of cases are from six countries only. The United States of America has the highest number of cases, 17% of the world.

Total cases: Fig. 9 shows the Country wise total cases from 22 January 2020–06 September 2020 of COVID-19.

Total death: Fig. 10 shows the Country wise total death from 22 January 2020–06 September 2020 of COVID-19.

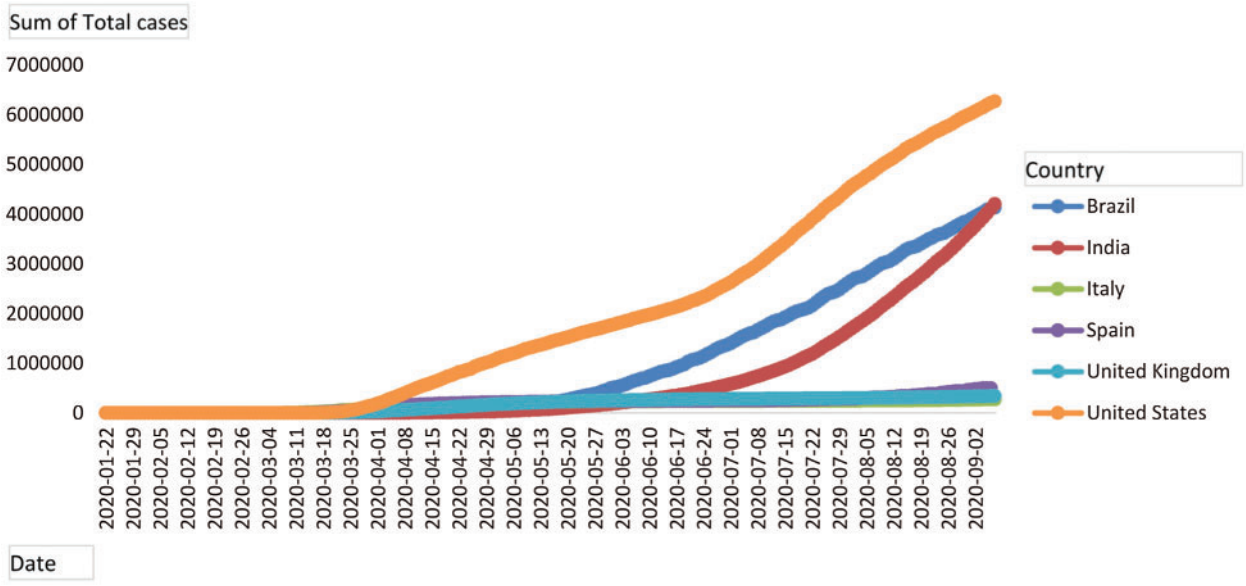


Figure 9: Day-wise total cases of Brazil, India, Italy, Spain, United Kingdom, and the United States

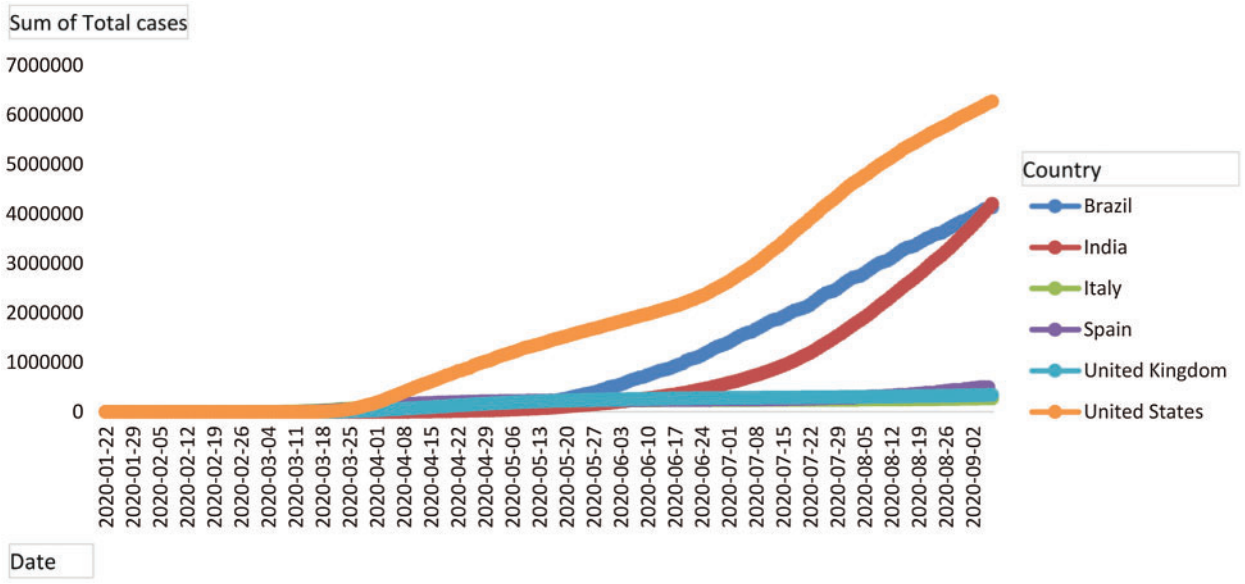


Figure 10: Day-wise total death of Brazil, India, Italy, Spain, United Kingdom, and the United States

The proposed method mainly focused on death cases because death cases hardly go undetected. The proposed methods result shows the predicted outcome is very closed to the real scenario. Total death cases and predicted total cases of Italy, Spain and the United Kingdom are shown in Fig. 11.

Total death cases and predicted total cases of Brazil, India and the United States are shown in Fig. 12.

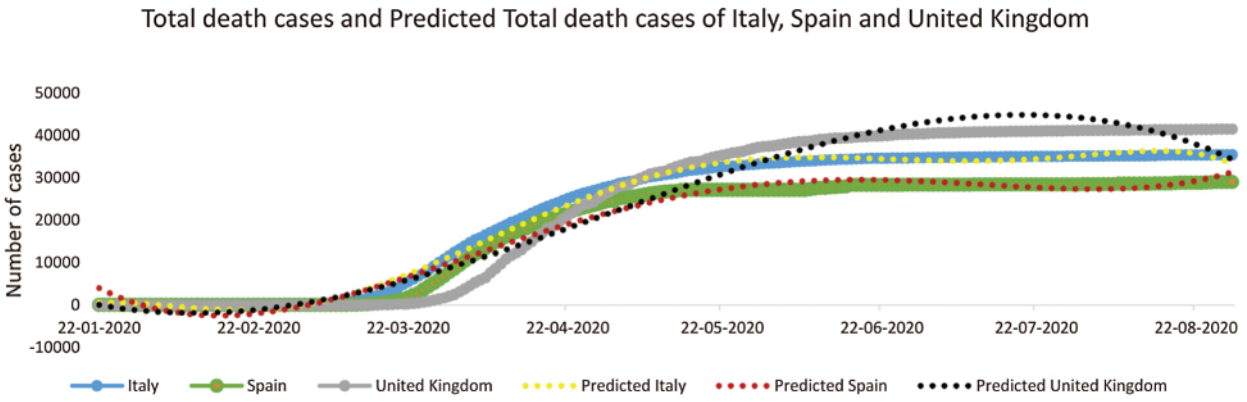


Figure 11: Real data and predicted total death cases of Italy, Spain and the United Kingdom

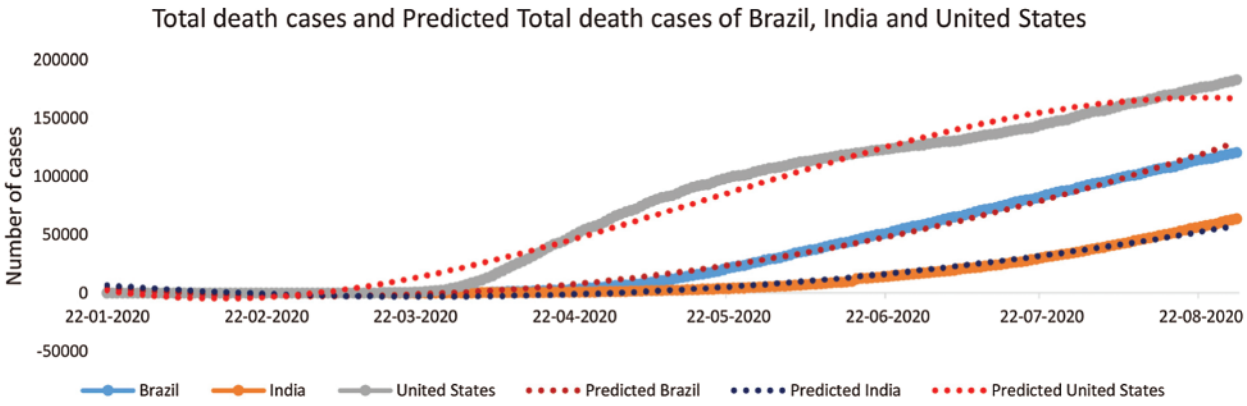


Figure 12: Real data and predicted total death cases of Brazil, India and the United States

Daily new cases: Fig. 13 shows the Country wise daily new cases from 22 January 2020–06 September 2020 of COVID-19.

Daily new death: Fig. 14 shows the Country wise daily new death cases from 22 January 2020–06 September 2020 of COVID-19.

Case fatality rate: It is difficult to estimate the overall case fatality rate of an ongoing pandemic, but we can calculate the daily fatality rate. Fig. 15 shows the Country wise daily case fatality rate from 01 March–03 June 2020 of COVID-19.

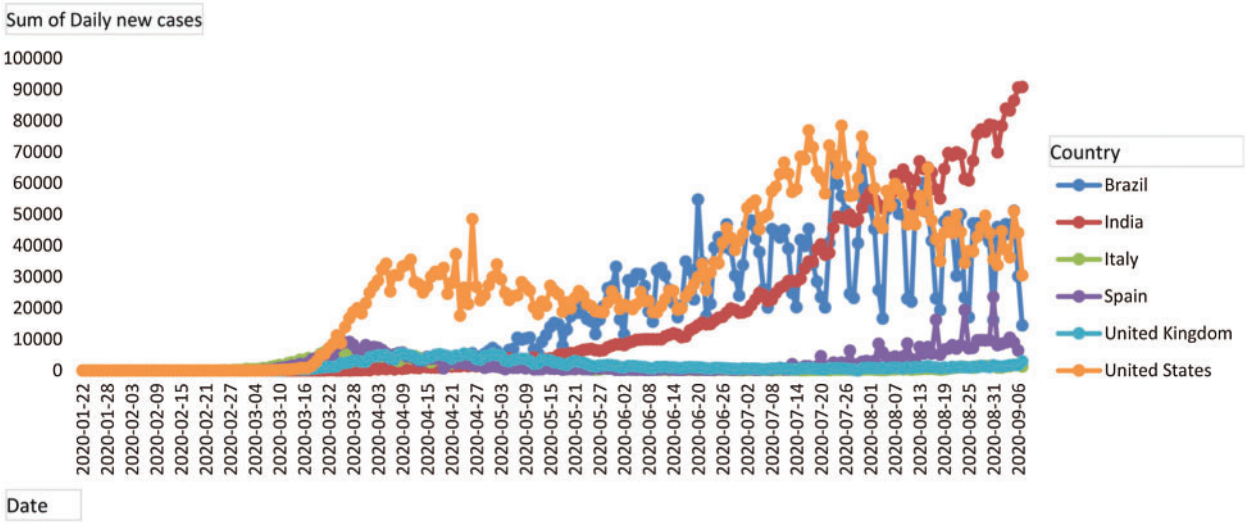


Figure 13: Daily new cases of Brazil, India, Italy, Spain, United Kingdom, and the United States

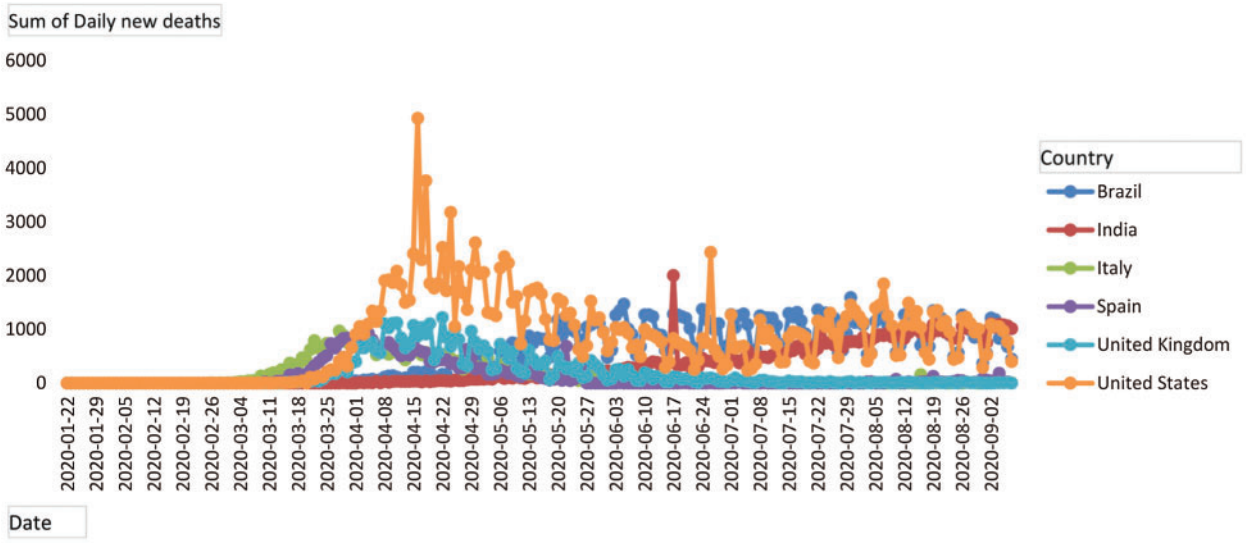


Figure 14: Daily new death cases of Brazil, India, Italy, Spain, United Kingdom, and the United States

3.9 Age-Wise Population

Italy and Spain in the 70 plus year-wise age category population is more percentage-wise, according to World Bank data. India and Brazil's population is higher in the age category of 0–20 years. Brazil, India, Italy, Spain, the United Kingdom, and the United States, the distribution of the population are almost equal between 20 and 70 age groups in all these countries. The population has distributed according to age category is shown in Fig. 16.

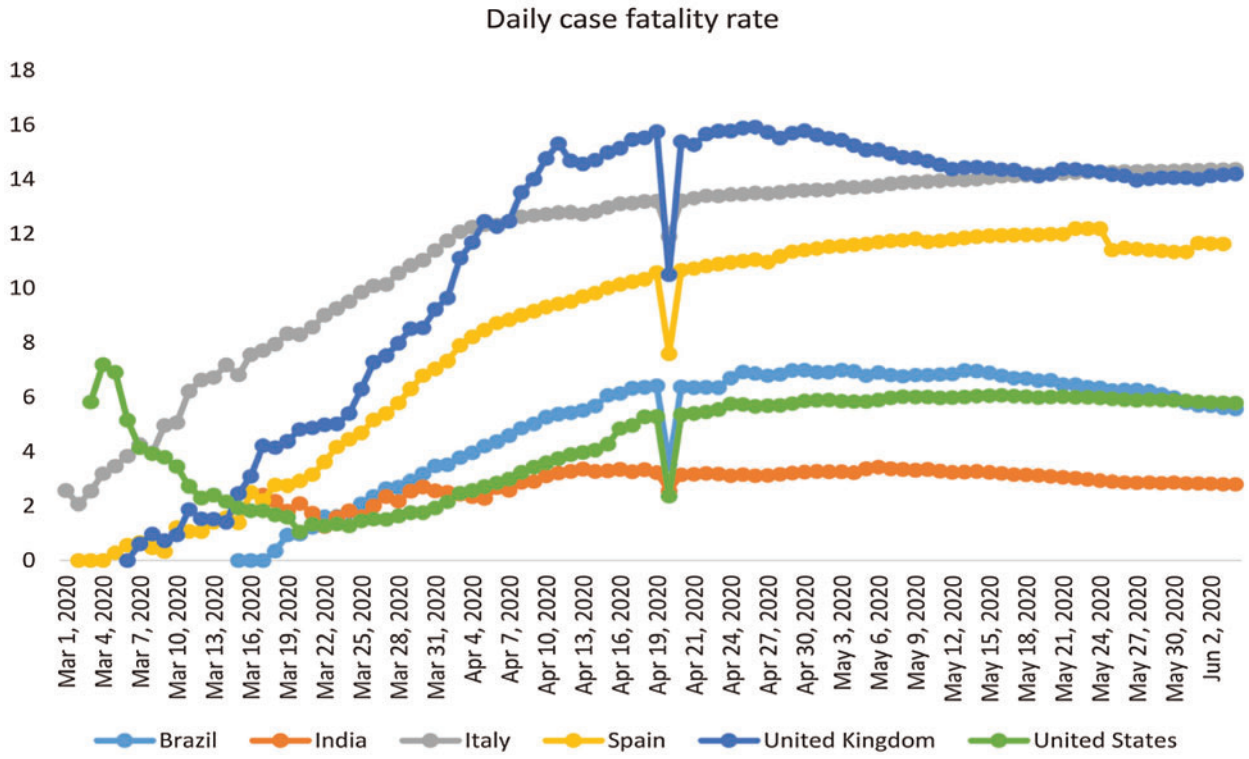


Figure 15: Daily case fatality rate of Brazil, India, Italy, Spain, United Kingdom, and the United States

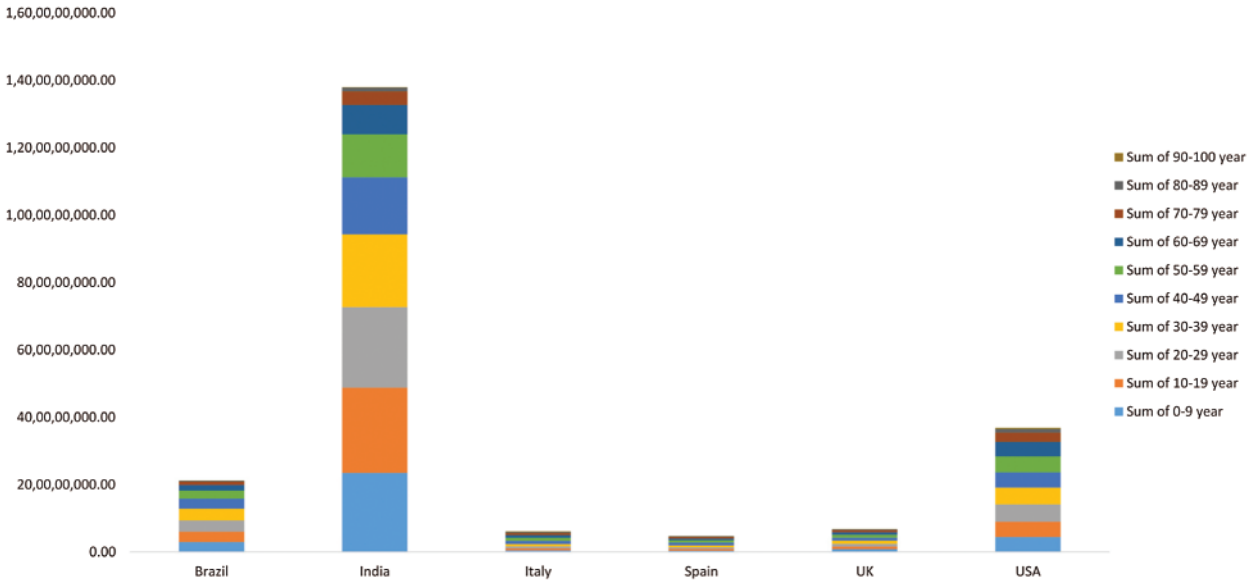


Figure 16: The distribution of the population according to the age category of Brazil, India, Italy, Spain, United Kingdom, and the United States

3.10 Number of Hospital Beds per 100k

Hospital beds or curative beds are counting unit beds per 100,000 population or 100k population according to WHO and OECD. The basic measures focus on all the hospital beds, which are occupied or empty. The Country-wise number of hospital beds has shown in Fig. 17.

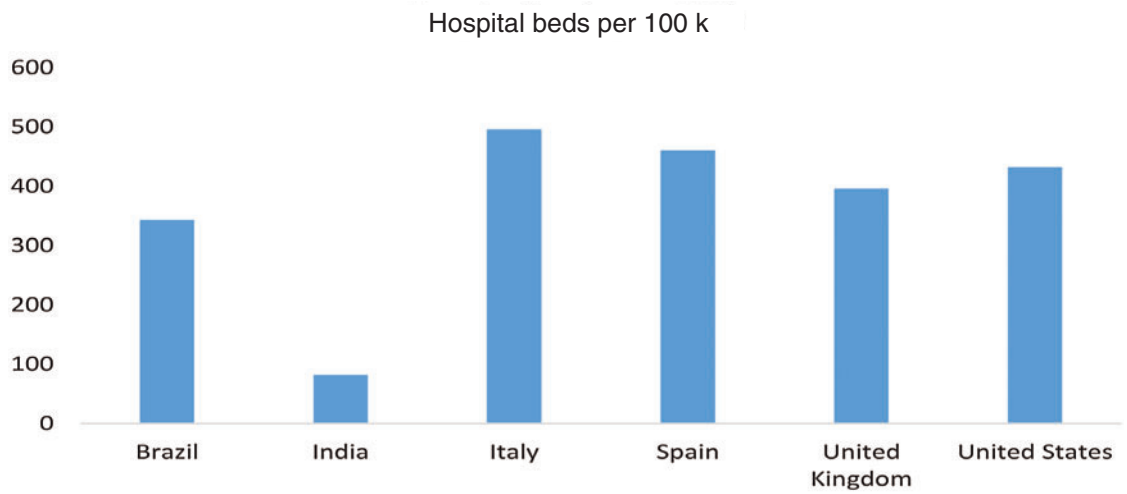


Figure 17: The Country-wise number of hospital beds of Brazil, India, Italy, Spain, United Kingdom, and the United States

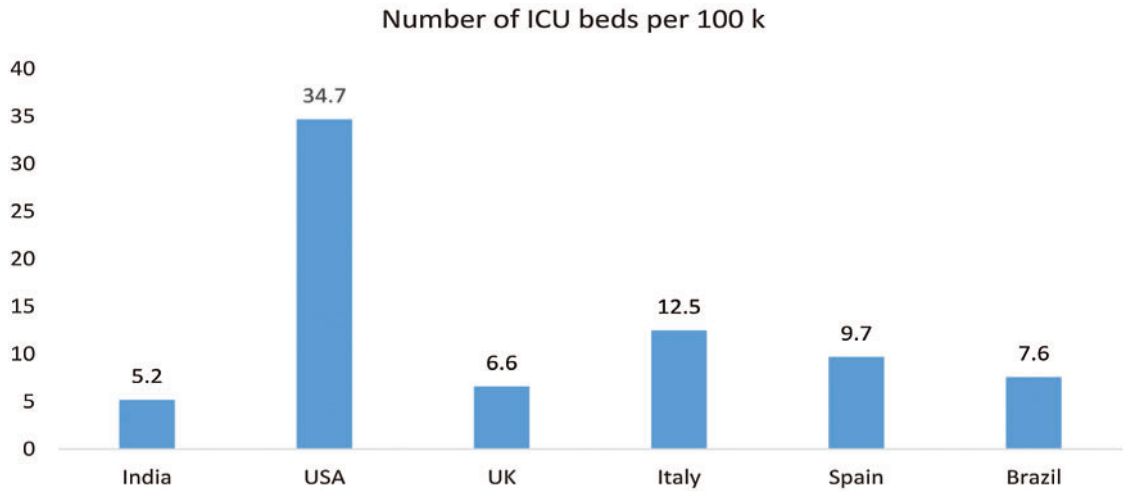


Figure 18: The Country-wise number of ICU beds of Brazil, India, Italy, Spain, United Kingdom, and the United States

3.11 Number of ICU Beds per 100 k

ICU beds counting unit is beds per 100,000 population or 100k population according to WHO and OECD. ICU beds have provided to all the cases with severe conditions. The Country-wise number of ICU beds is shown in Fig. 18.

4 Results and Discussion

We have analyzed and predict the COVID-19 trend among the top affected countries of the world using our proposed SEIHCRD model in this section. Our proposed methods outcome shows Italy, Spain, the United Kingdom, the United stated of America have seen their worst time; now, their conditions are improving. The peak of Brazil and India is yet to come in June and July month. Brazil will need hospital beds and ICU beds when the number of cases will become very high in the middle and last of June. Disease distribution in India is very random; e.g. Number of cases in Maharashtra and Delhi is very high compared to other states, some beds needed in June, especially in Delhi state. Our method shows that Italy already suffers its peak now they shuttle down. The proposed model has been demonstrated that the endpoint of USA cases in September and UK cases will shuttle down in July. We have compared our proposed method results with real-world data; then, it is mostly the same.

4.1 SEIHCRD Model for Brazil

Brazil has the second-highest in COVID-19 cases, just behind the USA as of the starting of June 2020. COVID-19 cases will be at a peak in Brazil according to our proposed method in June and July. The basic reproduction number in nearly 4.5 in initial days, after some days, decreases, and after 220 days, it becomes one or even less. The case fatality rate has ups and down daily, but it goes higher and higher up to 7.5 in our model and then slow down, and total CFR is nearly 3.0 overall. The result of our proposed method shows that in Brazil, the number of cases will increase; hence Brazil will need some Hospital beds and ICU beds in June, July, and August. A daily number of death cases on top of nearly 190th day and goes up to 1800 die per day, then slow down and shuttle down in October. The model has shown almost 15–20 days, 700 hospital beds, and 400 ICU beds required on-peak time. SEIHCRD Model results for Brazil has shown in Fig. 19.

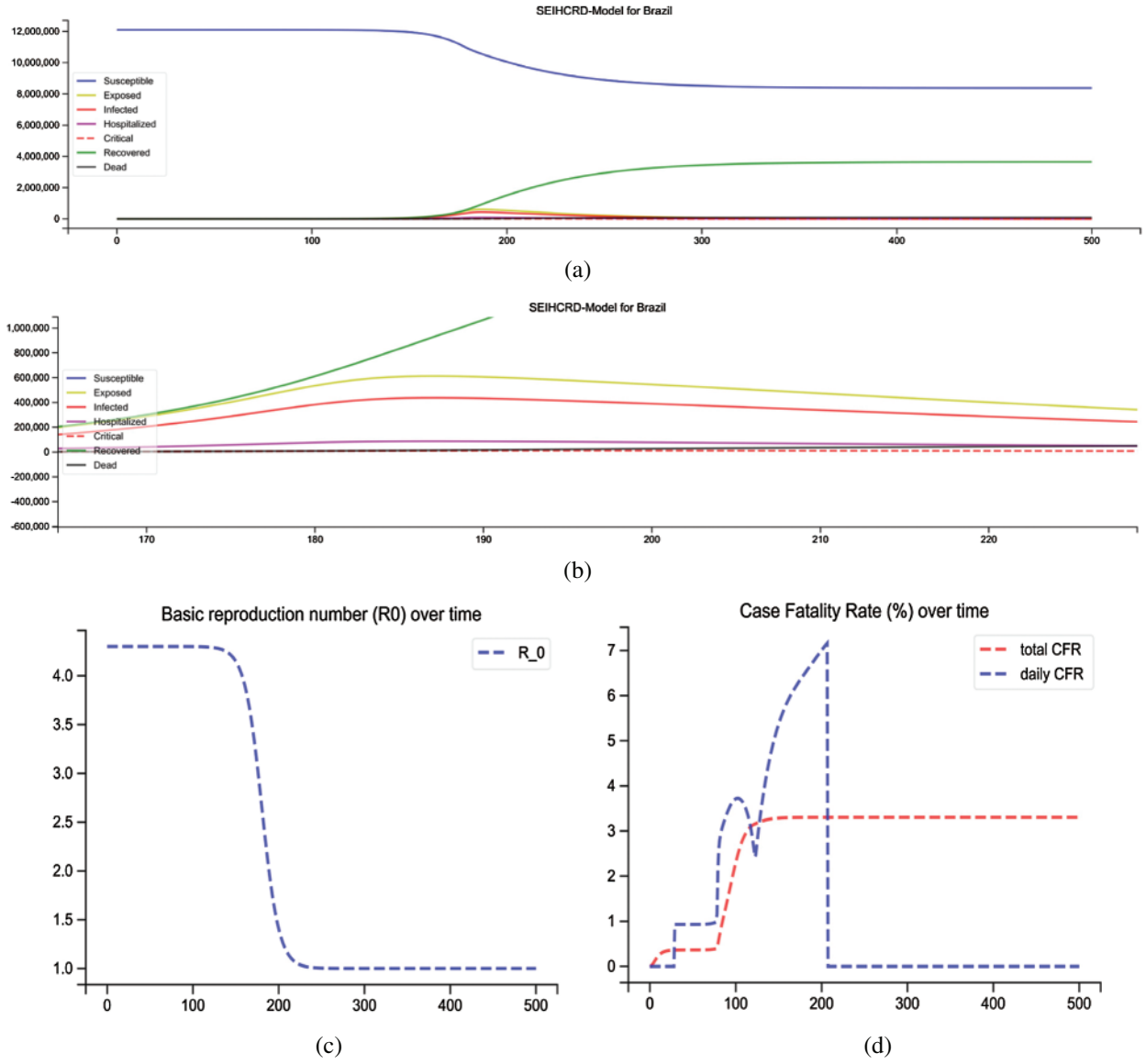
4.2 SEIHCRD Model for India

The SEIHCRD model results show COVID-19 cases are on the peak in India around 200th day (June last or July month), and there will rarely dead cases come in November month. SEIHCRD-Model for India shows that the case fatality rate of COVID-19 in India is meagre. Basic reproduction number R_0 is nearly 2.0 in starting, it decreases after some time and falls slowly, and after 170 days, it is 1.3 that is almost equal to the real scenario, and it goes down than one or even lower in the next 50–60 days. The daily Case fatality rate varies between 1.5, 3.0, and the overall case-fatality rate very steady after 200 days of nearly 2.0. India's geographical condition is entirely different from the rest of the countries. The spread of COVID-19 disease is random in India. Maharashtra, Delhi, Tamil Nadu, and Gujrat are the most disease-affected states. According to the proposed model, June last and July starting the number of patients admitted to the hospital on the peak. Hospital beds and ICU beds have been needed in June in India, especially in Delhi states. Around the 200th day, when the cases are at peak, then the number of death cases reaches 550 and the need of nearly 250 Hospital beds and ICU beds. SEIHCRD Model results for India are shown in Fig. 20.

4.3 SEIHCRD Model for Italy

SEIHCRD model result shows, Italy has seen its lousy phase and now in a state of improvement and is trying to recover from that disastrous pandemic. Italy's healthcare system is the second-best in the world, according to WHO. COVID-19 cases on a peak between 70 and 90th days in Italy, and after 220 days, its death cases are sporadic, and its death cases almost stop

coming in August. The basic reproduction number R_0 starts from 5.0, and after about 100 days, the value of R_0 starts decreasing visually. The number of death decrease drastically in the next few days after peak days. The proposed model for Italy showed that around 100th day, the number of hospital beds and the number of ICU beds are required. That time the number of death cases is 800 per day, and daily-hospitalized cases are nearly 2500. The Case fatality rate value reached 7.0; after that, its value is reduced drastically in Italy. SEIHCRD Model results for Italy has shown in Fig. 21.



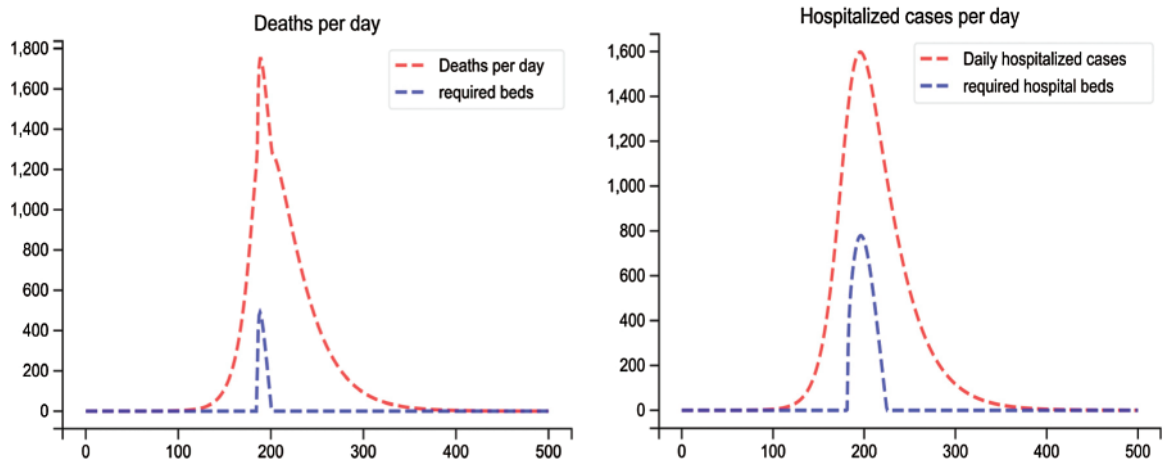
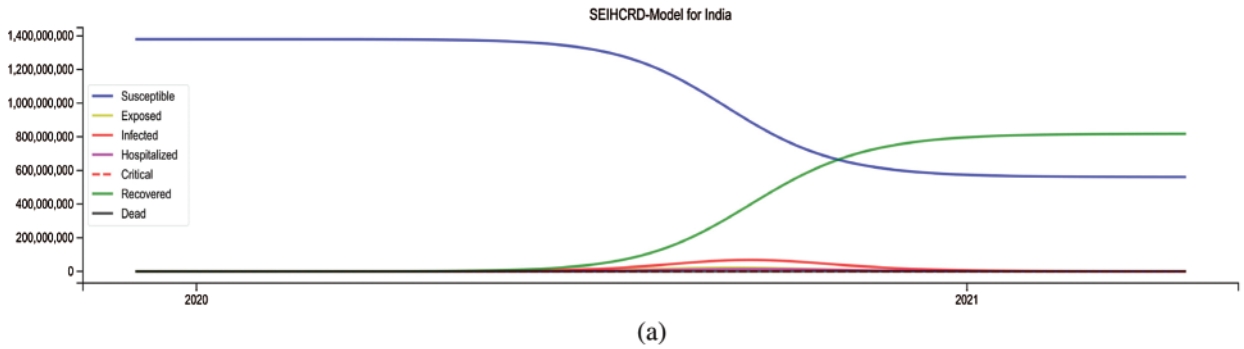


Figure 19: SEIHCRD model for Brazil (a) Spread scenario of SEIHCRD Model for Brazil. A 500-day analysis has been done by the proposed model, which starts from 22 January. (b) In this, the peak point of the model has shown by zooming for cases. (c) The basic reproduction number of Brazil over time (d) The case fatality rate of Brazil over time. (e) Redline shows the number of deaths per day, and the blue line shows how much ICU beds are required in peak days. (f) The Red line indicates the number of cases hospitalized per day, and the blue line shows how much hospital beds are required in peak days

4.4 SEIHCRD Model for Spain

Spain has also gone through its worst phase. COVID-19 cases are on the peak in Spain around the 110th day according to the SEIHCRD model, and after that, Spain recovered by this disaster rapidly in the next few days. The result shows that COVID-19 cases will not come in June last or July. The basic reproduction number is 7.0; after some time, it reduces, and around 170th day, it goes to one and below. The Case fatality rate goes up to 7.0; after that, its value decreased drastically, and it gets one and below around 170th day. In the proposed model for Spain, they are showing that between 110 and 130th days, some hospital beds and ICU beds are required. At that, the number of deaths is nearly 700 per day, and daily-hospitalized cases are almost 1250. SEIHCRD Model results for Spain has shown in Fig. 22.



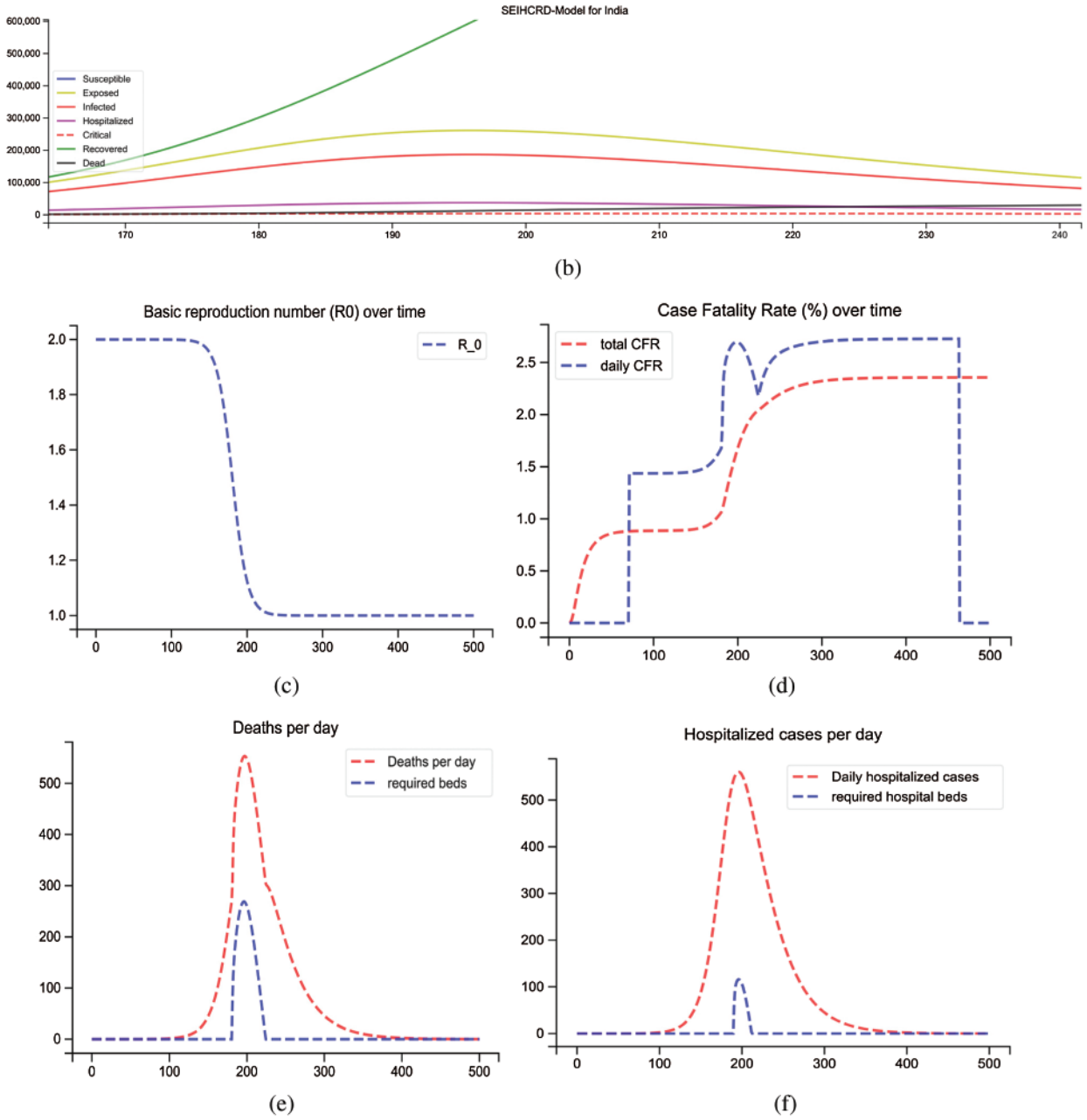


Figure 20: SEIHCRD Model for India (a) Spread scenario of SEIHCRD Model for India. A 500-day analysis has been done by the proposed model, which starts from 22 January. (b) In this, the peak point of the model is shown by zooming for cases. (c) The basic reproduction number of India over time (d) The case fatality rate of India over time. (e) Redline shows the number of deaths per day, and the blue line shows how much ICU beds are required in peak days. (f) The Red line indicates the number of cases hospitalized per day, and the blue line shows how much hospital beds are required in peak days

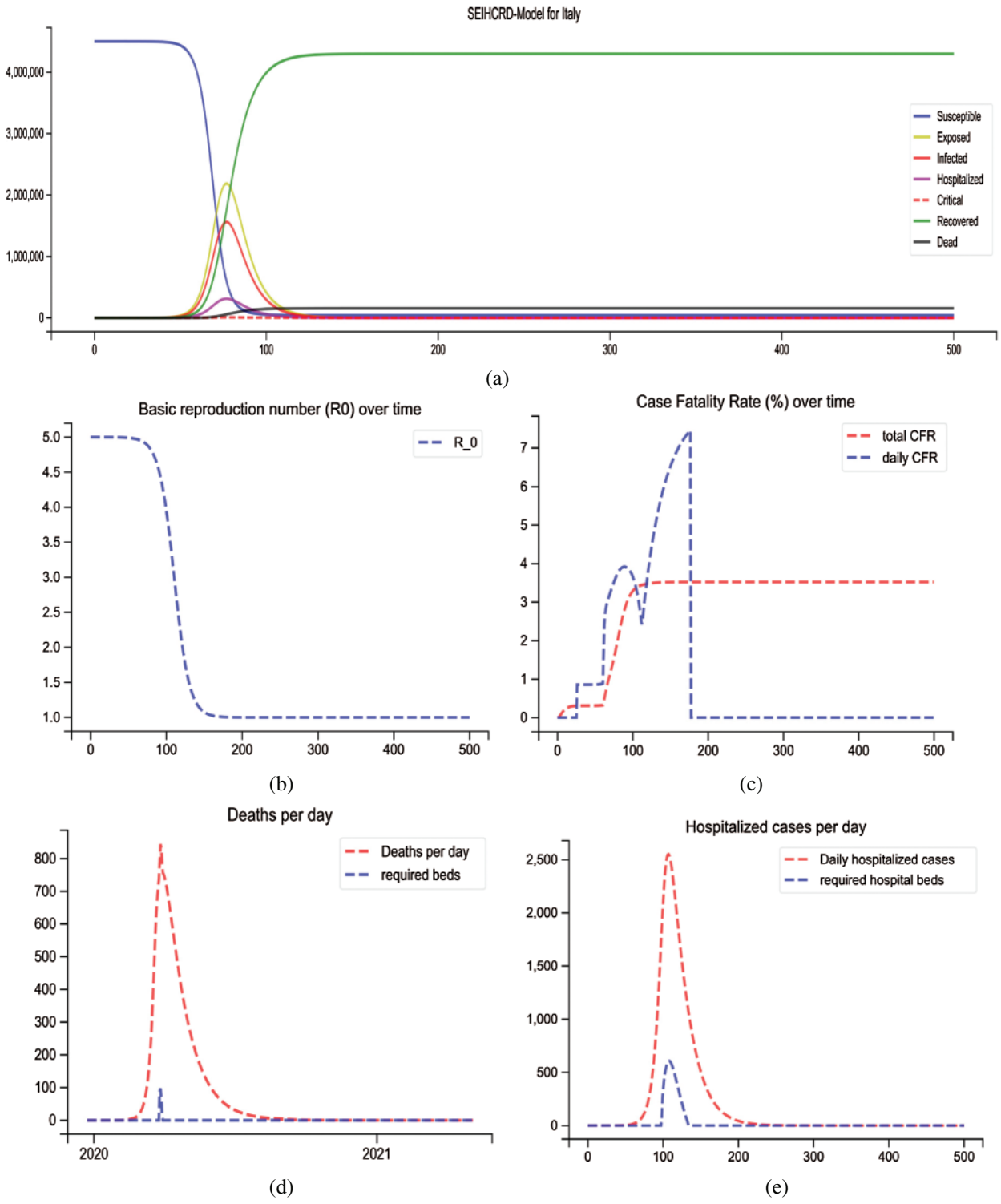
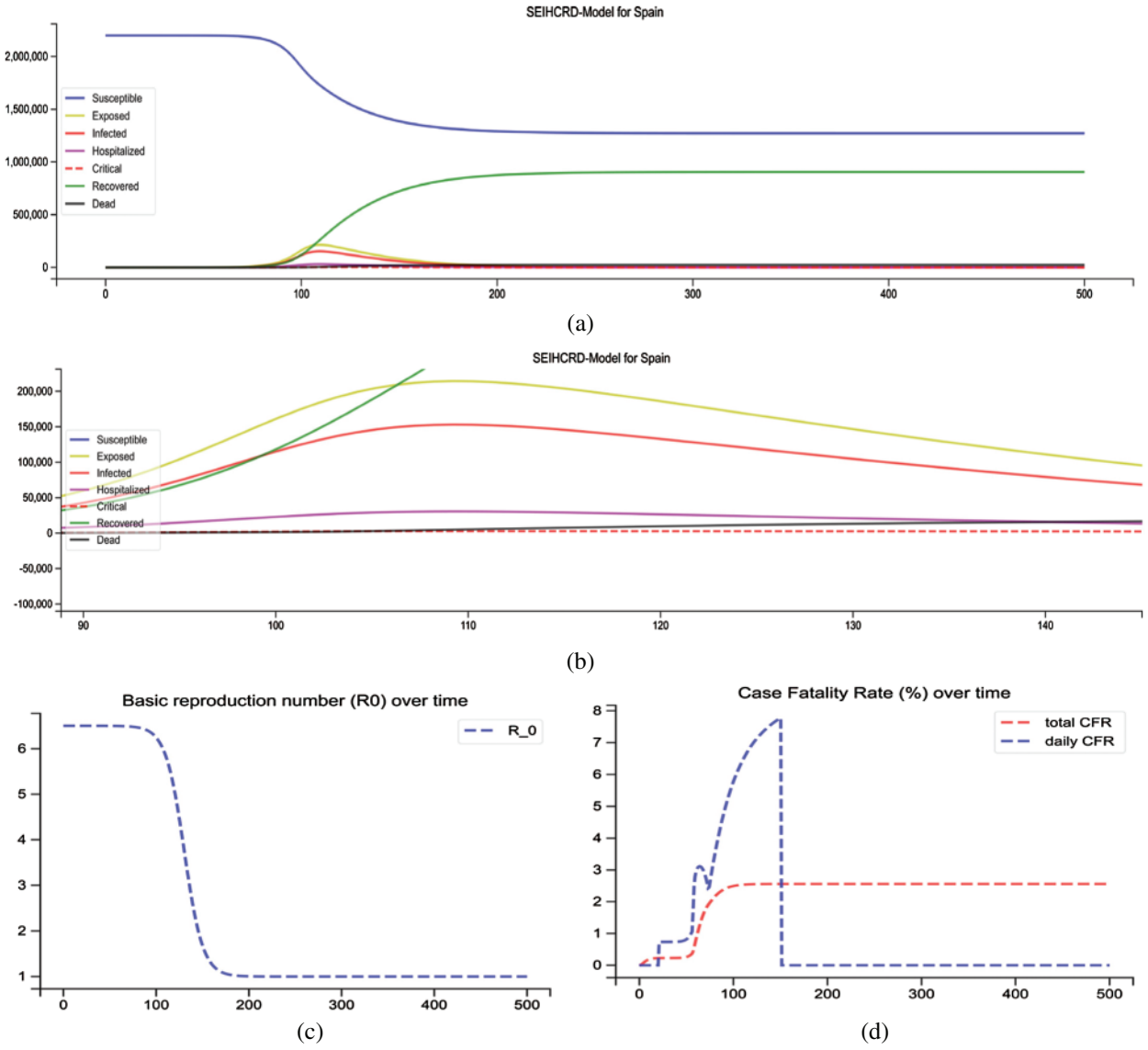
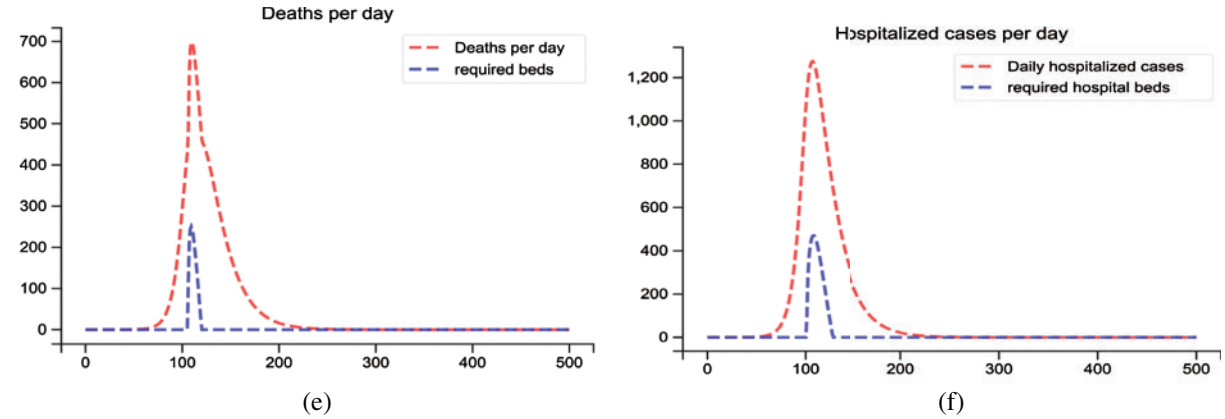


Figure 21: SEIHCRD Model for Italy (a) Spread scenario of SEIHCRD Model for Italy. A 500-day analysis has been done by the proposed model, which starts from 22 January (b) The basic reproduction number of Italy over time (c) The case fatality rate of Italy over time. (d) Redline shows the number of deaths per day, and the blue line shows how much ICU beds are required in peak days. (e) The Red line indicates the number of cases hospitalized per day, and the blue line shows how much hospital beds are required in peak days

4.5 SEIHCRD Model for the United Kingdom

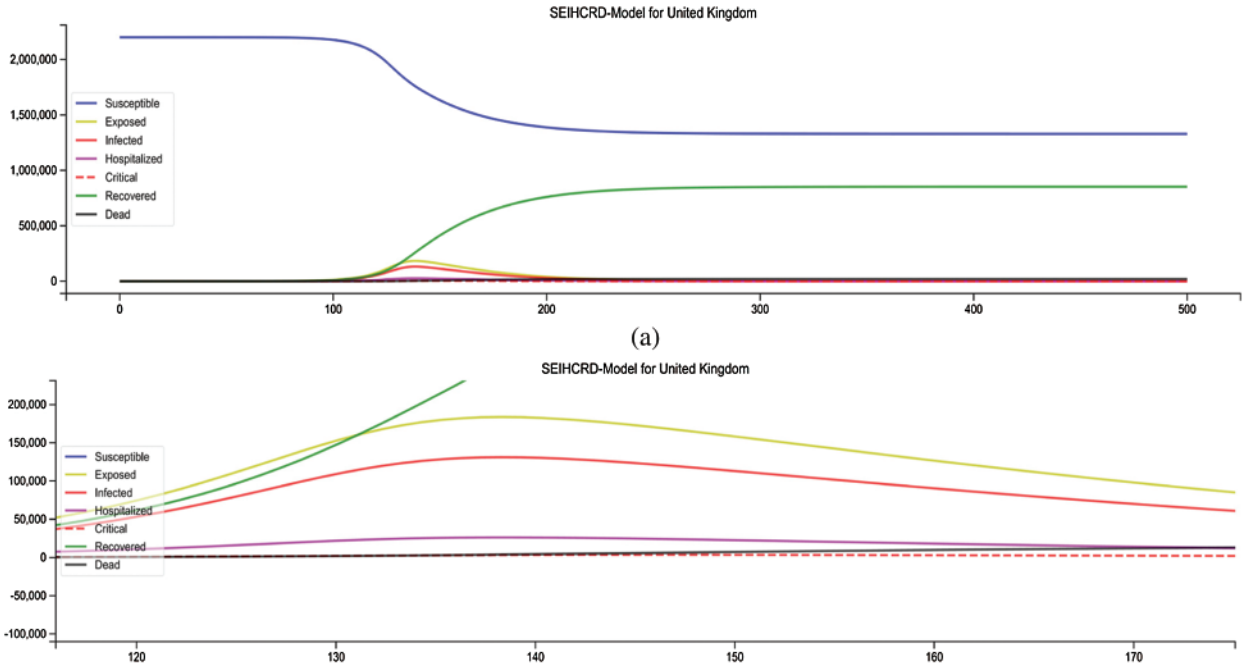
SEIHCRD-Model for the United Kingdom shows that COVID-19 cases peak around 140th day, and after that, the United Kingdom has recovered by this disaster very fast in the next few days. After 240 days, its deceased cases are sporadic, and it almost stops in September. The basic reproduction number R_0 starts from 4.5, and after about 120th day, the value of R_0 starts decreasing visually. There are many ups and downs in the daily case fatality rate, but it goes higher and higher up to 7.5 in our model and then slows down, and total CFR is nearly 3.0 overall. SEIHCRD model has shown that some hospital beds and ICU beds have been required between the 100th and 120th days. That time the number of death is 1100 per day, and daily-hospitalized cases are nearly 800. The population of old age people is more in the United Kingdom; it has been shown in the previous section. SEIHCRD Model results for the United Kingdom has shown in Fig. 23.





(e) (f)

Figure 22: SEIHCRD Model for Spain (a) Spread scenario of SEIHCRD Model for Spain. A 500-day analysis has been done by the proposed model, which starts from 22 January. (b) In this, the peak point of the model is shown by zooming for cases. (c) The basic reproduction number of Spain over time (d) The case fatality rate of Spain over time. (e) Redline shows the number of deaths per day, and the blue line shows how much ICU beds are required in peak days. (f) The Red line indicates the number of cases hospitalized per day, and the blue line shows how much hospital beds are required in peak days



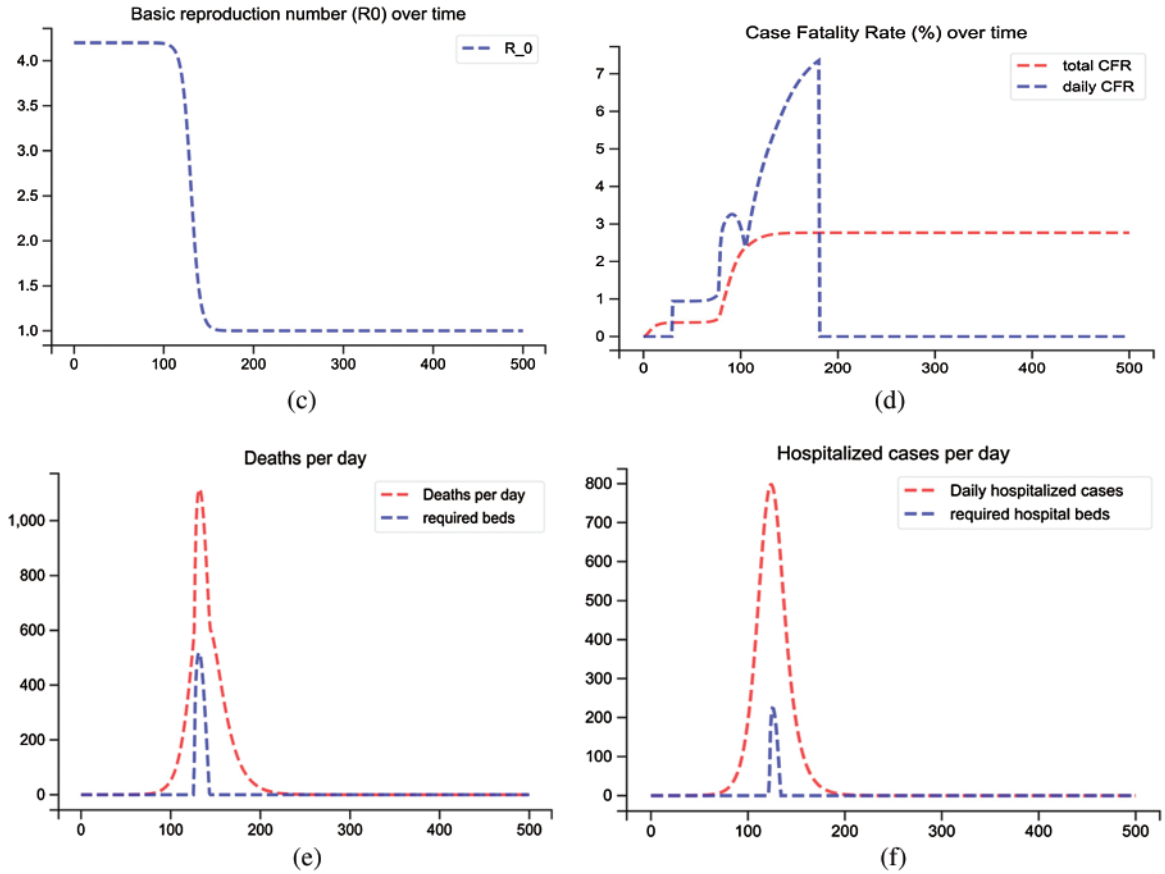
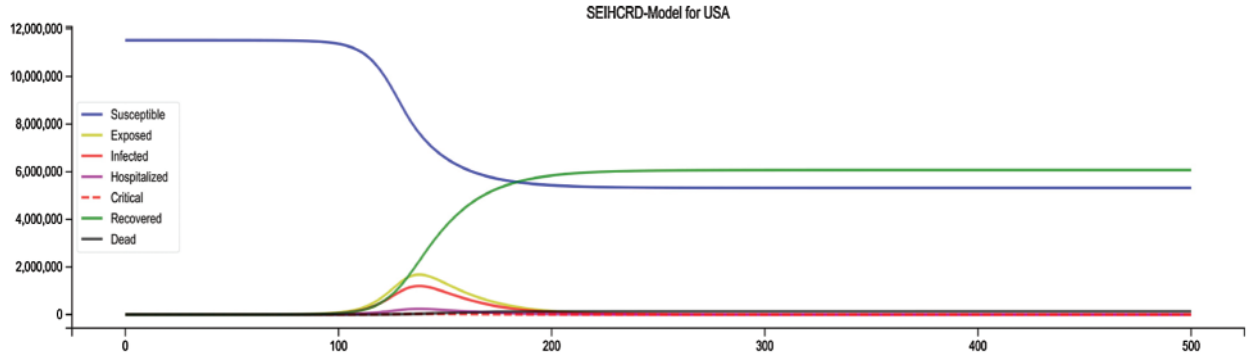


Figure 23: SEIHCRD Model for the United Kingdom (a) Spread scenario of SEIHCRD Model for the United Kingdom. A 500-day analysis has been done by the proposed model, which starts from 22 January. (b) In this, the peak point of the model is shown by zooming for cases. (c) The basic reproduction number of the United Kingdom over time (d) The case fatality rate of the United Kingdom over time. (e) Redline shows the number of deaths per day, and the blue line shows how much ICU beds are required in peak days. (f) The Red line indicates the number of cases hospitalized per day, and the blue line shows how much hospital beds are required in peak days

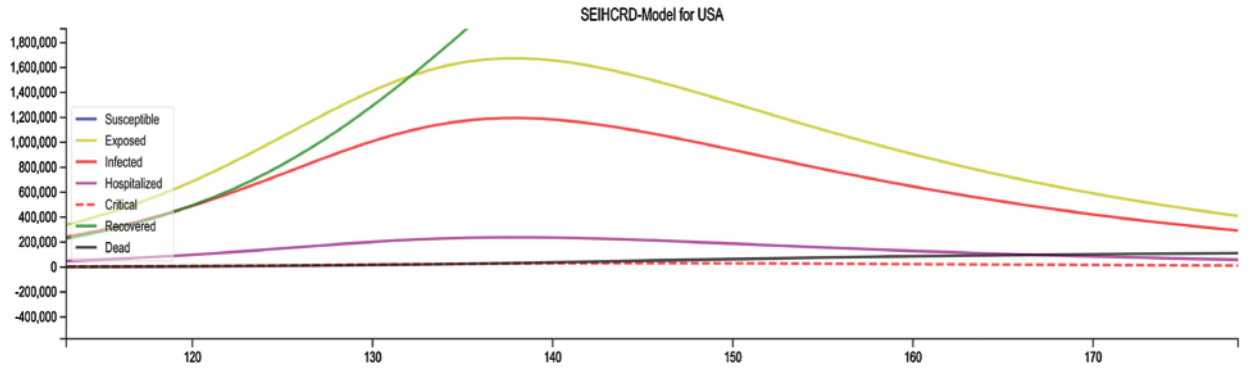
4.6 SEIHCRD Model for the United States

The WHO health has reported that the medical facility of the USA is good, and they have more hospital beds and ICU beds for people in comparison to other countries by ratio. United States has the highest number of COVID-19 cases in the world. According to the SEIHCRD model for the United States of America COVID-19, cases are on a peak between 130 and 145 days after that it is improving, its speed is plodding but steady, and cases stop in October. New York, California, Illinois, and New Jersey have the most affected states of the USA. The proposed model for the USA has shown that between 120 and 180 days, the number of hospital beds and the number of ICU beds required, but its count is meagre. That time the number of death has 1200 per day, and daily-hospitalized cases have nearly 1400. The result shows the basic reproduction rate is 4.5 in starting after some time, it decreases and goes up to one and even

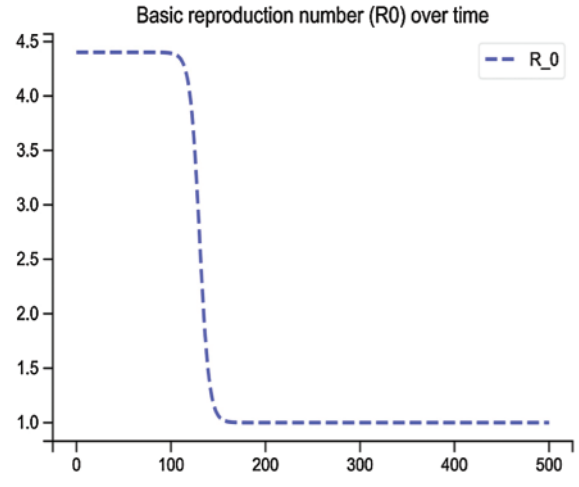
lower. The case fatality rate goes up to 8.0; after 200 days, it drastically fell. Our proposed method shows that the USA has the highest number of cases; therefore, it takes more time in recovery. SEIHCRD Model results for the United States has shown in Fig. 24.



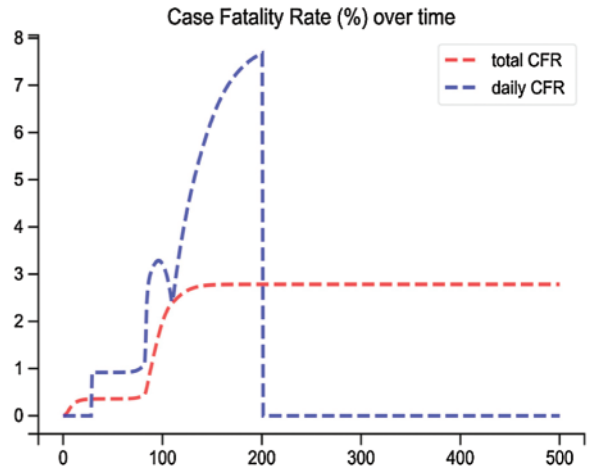
(a)



(b)



(c)



(d)

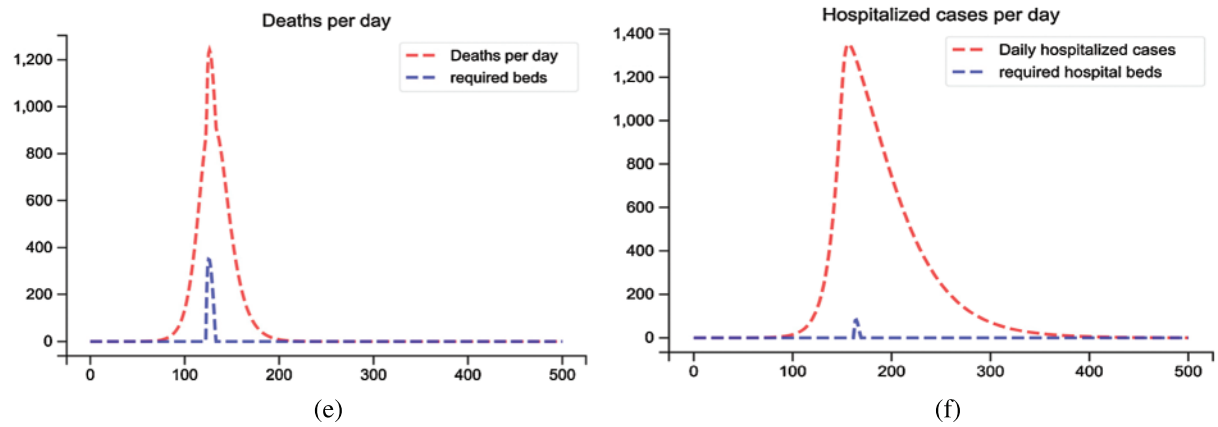


Figure 24: SEIHCRD Model for the United States (a) Spread scenario of SEIHCRD Model for the United States. A 500-day analysis has been done by the proposed model, which starts from 22 January. (b) In this, the peak point of the model has shown by zooming for cases. (c) The basic reproduction number of the United States over time (d) The case fatality rate of the United States over time. (e) Redline shows the number of deaths per day, and the blue line shows how much ICU beds are required in peak days. (f) The Red line indicates the number of cases hospitalized per day, and the blue line shows how much hospital beds are required in peak days

5 Evaluation Criteria

The prediction performance of the proposed system is evaluated using the following metrics.

5.1 Mean Absolute Percentage Error (MAPE)

Analyze the efficiency of the forecasting model of our method, we use the mean absolute percentage error (MAPE) [80] or Mean Absolute Percentage Deviation (MADE) as the criteria standard. Its formula is express as the following equation

$$MAPE = \frac{1}{n}\sum_{i=1}^{n}\left|\frac{y_i - x_i}{y_i}\right| \times 100 \tag{28}$$

where y_i denotes the ith actual value, and x_i represents the ith predicted value. If the value of MAPE is low, the accuracy of the method is high.

5.2 Root Mean Square Error (RMSE)

Root Mean Square Error (RMSE) or Root-Mean-Square Deviation (RMSD) is a measure of the average magnitude of the errors [81]. Specifically, it is the square root of the average squared differences between the prediction and actual observations. Therefore, the RMSE will be more useful when large errors are particularly undesirable. If the value of RMSE is low, the accuracy of the method is high. RMSE formula is express as the following equation

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i^{obs} - y_i^{pred})^2} \tag{29}$$

where y_i^{obs} and y_i^{pred} are the actual and predicted observations, respectively.

ARX[1]—Autoregressive with Exogenous inputs model

ARIMA[2]—Autoregressive Integrated Moving Average model

Proposed[3]—SEIHCRD model

The results are evaluated using a variety of metrics (RMSE, MAPE) as well as graphically illustrated using Taylor and Target diagrams [82–84]. Taylor diagram (Fig. 25, left) is used to perform the comparative assessment of several different models and to quantify the degree of correspondence between the modelled and observed behaviour in terms of three statistics: Pearson correlation, RMSD (Root Mean Square Deviation), and the standard deviation. The model that is located lower on the diagram is considered to represent reality better. Note that the proposed model is lower than the ARX model.

The target diagram (Fig. 25, right) summarizes and visualizes information regarding the bias and the error between a model and real observations. The Y-axis corresponds to the normalized bias (Bias), and the X-axis corresponds to the normalized unbiased RMSD (uRMSD). The model overestimates variables located in the upper part of the diagram ($Y > 0$). The standard deviation of a model is larger than the standard deviation for the observations when variables are located in the right part of the target diagram ($X > 0$). The distance between any point and the origin is the value of the total RMSD. Note that while the proposed model performs better than the ARX model and ARIMA model in terms of uRMSD and total RSMD, it has a more considerable bias than the ARX model and ARIMA model. The results are summarized in Tab. 8.

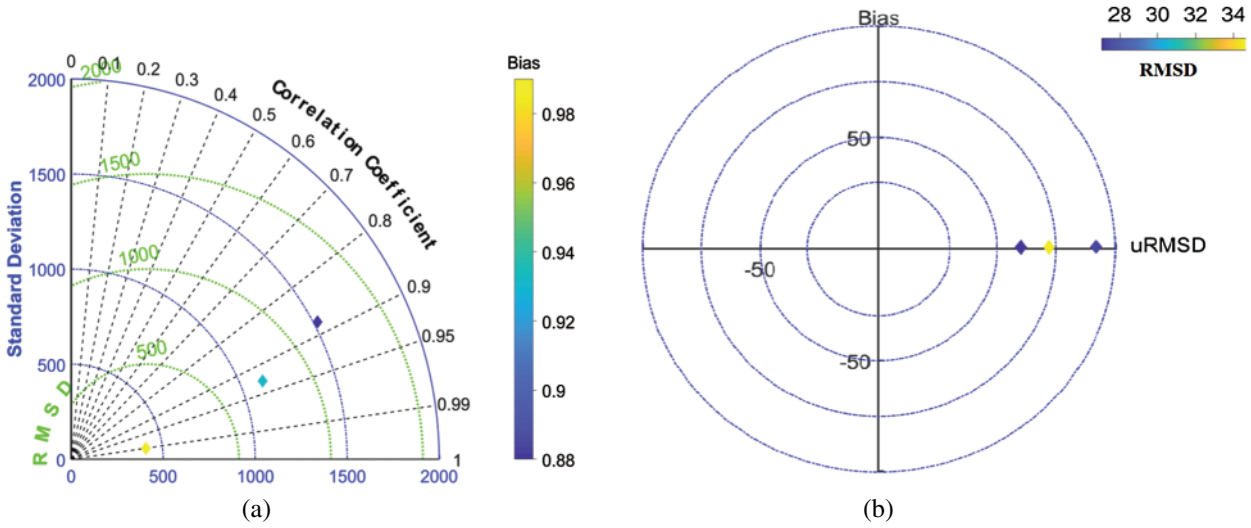


Figure 25: (a) Taylor diagram, (b) Target diagram

Table 8: MAPE and RMSE results of the prediction models for the selected countries

Countries	Prediction models	Root mean square error (RMSE)	Improvement, % (RMSE)	Mean absolute percentage error (MAPE)	Improvement, % (MAPE)
Brazil	ARX[1]	1712.1192	70.07647014	0.823	83.11057108
	ARIMA[2]	1160.8206	55.86514402	0.401	65.33665835
	Proposed[3]	**512.3265**	–	**0.139**	–
India	ARX	1632.4289	73.65129961	0.923	88.94907909
	ARIMA	1280.4388	66.40809385	0.321	68.22429907
	Proposed	**430.1238**	–	**0.102**	–
Italy	ARX	1321.7734	71.19529717	0.793	77.17528373
	ARIMA	988.2355	61.47346457	0.382	52.61780105
	Proposed	**380.7329**	–	**0.181**	–
Spain	ARX	1488.9956	72.4067687	0.812	87.93103448
	ARIMA	980.2128	58.08440779	0.219	55.25114155
	Proposed	**410.862**	–	**0.098**	–
United Kingdom	ARX	1529.6228	69.90575716	0.8421	87.17491984
	ARIMA	1069.9999	56.97865018	0.301	64.11960133
	Proposed	**460.3284**	–	**0.108**	–
United States	ARX	1536.2227	68.7390116	0.855	86.66666667
	ARIMA	1230.8774	60.98405901	0.346	67.05202312
	Proposed	**480.2384**	–	**0.114**	–

6 Discussion

Results from the SEIHCRD model suggest that this model has excellent potential for predicting the incidence of COVID-19 diseases in time series. The central aspect of our proposed model is the addition of hospitalized and critical compartments, which improves the basic understanding of disease spread and results. We have the number of hospital beds and the number of ICU beds of the selected countries; based on that, we have calculated the number of beds required in the peak days of infection. Basic reproduction number and case fatality rate are the basic measures for any epidemic that we have also calculated. Sometimes conditions get worse because of a massive number of infected people at the same time, and the country does not have facilities to treat all critical cases when triage conditions occur. The SEIHCRD model can solve the problem of triage.

After estimating the model parameters based on available clinical data, the model will propagate and predict dynamic evolution. First, we fit the data, and then we get some important parameter values from it. We used the least square method and the Levenberg–Marquardt model to calculate the parameters R_0_start, R_0_end, k, x_0, s, P(I $\rightarrow$ H), P(C $\rightarrow$ D), and P(H $\rightarrow$ C) for the proposed model. The proposed model is very sensitive to the initial conditions and values of the parameters. A small change in the parameter can make a massive difference to the result. Hence be careful to select the initial parameter of the model. For example, if change the value of P(H $\rightarrow$ C), from .23–43, then changes the overall spread scenario of infection. We do not need to fit some parameter, for example, η, δ, Ψ, γ, σ, φ, χ, μ etc. We have to get these parameter values from the review of research papers and reports of trusted organizations. We calculate the disease transmission rate β using R_0_start, R_0_end, η, x_0, and γ. The proposed model estimates the case-fatality rate based on the age-category scenario of the selected countries and includes comorbidity cases that improve the results. Comorbidity cases make a huge difference in the outcome because the fatality rate of comorbidity cases is very high compared to normal infected people.

We used three accuracy measures, MAPE, RMSE and R-squared value, for model validation. The SEIHCRD model outperforms the classic Autoregressive with the Exogenous Inputs model (ARX) and the Auto-Regressive Integrated Moving Average model (ARIMA). The Taylor diagram and target diagram are included in the result to show the performance of the proposed model compared to the ARX and ARIMA models. The result shows that the RMSE accuracy of the proposed model has improved by 68%–74% as compared to the ARX model, and it improved by 56%–66% as compared to the ARIMA model. MAPE accuracy has also improved the proposed model; it enhanced by 77%–89% as compared to the ARX model, and 53%–68% enhanced by 53-68% as compared to the ARIMA model.

7 Limitations

Models are always simplifications of the real world. No models are perfect; there are some shortcomings in it. SEIHCRD Model also has some limitations, which are as follows:

Our system of differential equations is very sensitive to initial parameters. We have to very careful while given the initial parameters. Small changes in parameters can cause a massive difference in results. Our present manuscript has especially focused on severe cases and death cases. We have consented the severe cases that do not get treatment in the critical compartment. We have considered recovered cases not infected again in the future. R_0 value cannot be increased; it either decreases or remain constant.

8 Conclusion

Results from the SEIHCRD model suggest that this model has excellent potential for predicting the incidence of COVID-19 diseases in time series. Our proposed SEIHCRD model is an extension of the SEIR model. Three-compartments have added death, hospitalized, and critical, which improves the basic understanding of disease spread and results. The addition of the hospitalized and critical compartment is the key feature of the model, which shows the spread of disease and calculates how much hospital beds and ICU beds will be needed in the peak days of infection. The proposed model estimates the case-fatality rate based on the age-category scenario of the selected countries. The model calculates two types of Case fatality rate: One is CFR daily, and the other is total CFR. The model calculates the basic reproduction number over time using logistic regression because it is impossible to have a constant basic reproduction number in real life throughout the pandemic. The proposed model calculates the approximate time when the disease is at its peak and the approximate time when cases of death rarely occur.

After estimating model parameters based on available clinical data, the model will propagate and predict dynamic evolution. The model proposed is highly sensitive to the initial parameter conditions and values. We focus mainly on cases of death because instances of death are rarely undetected.

For model validation, we have used three precision measures, MAPE, RMSE and R-squared. The SEIHCRD model outperforms the classic ARX model and the ARIMA model. To show the performance of the proposed model compared to the ARX and ARIMA models, and the Taylor chart and the Target chart are included in the result section. The result shows that the RMSE accuracy of the proposed model has improved by 68%–74% as compared to the ARX model, and it improved by 56%–66% as compared to the ARIMA model. MAPE accuracy has also improved the proposed model; it enhanced by 77%–89% as compared to the ARX model, and 53-68% enhanced by 53-68% as compared to the ARIMA model.

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Conflicts of Interest: The authors have no conflicts of interest to report regarding the present study.

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