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Dynamical Transmission of Coronavirus Model with Analysis and Simulation

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ABSTRACT

COVID-19 acts as a serious challenge to the whole world. Epidemiological data of COVID-19 is collected through media and web sources to analyze and investigate a system of nonlinear ordinary differential equation to understand the outbreaks of this epidemic disease. We analyze the diseases free and endemic equilibrium point including stability of the model. The certain threshold value of the basic reproduction number R_0 is found to observe whether population is in disease free state or endemic state. Moreover, the epidemic peak has been obtained and we expect a considerable number of cases. Finally, some numerical results are presented which show the effect of parameters estimation and different step size on our obtained solutions at the real data of some countries to check the actual behavior of the COVID-19 at different countries.

KEYWORDS

Epidemic model; COVID-19; parameter estimation; reproductive number; stability analysis

1 Introduction

Epidemiological research plays a significant role in understanding the effects of community-based infectious disease. In mathematical modeling, we investigate model building models, perform parameter estimation, test model sensitivity by varying parameters and compute their numerical simulations. Such research helps to understand the ratio of disease spread within the population and infection of disease [1]. These types of diseased models are often called infectious diseases (i.e., the disease which transferred from one person to another person). Measles, rubella, chicken pox, mumps, aids and gonorrhea syphilis are the examples of infectious disease [2].



Severe Acute Respiratory Syndrome (SARS) is caused by a coronavirus and plays important role for its investigation [3]. According to the group of investigators that has been working since 30 years on the coronavirus family investigated that SARS and coronavirus has many similar features like biology and pathogenesis [4]. RNA enveloped viruses known as coronavirus are spread among humans, mammals and birds. Many respiratory, enteric, hepatic and neurological diseases are caused by coronavirus [5,6]. Human disease is caused by six types of coronavirus [7]. The symptom of the common cold in immune-compromised individuals is caused by 229E, OC43, NL63 and HKU1 coronaviruses. The other 2 coronavirus types are zoonotic in origin. These are severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV). SARS-CoV and MERS-CoV are fatal illnesses [8]. In 2002 and 2003, Guangdong (The Province of China) faced major outbreaks of acute respiratory syndrome which has a caustic agent of SARS-CoV. The Middle East suffered from severe respiratory disease outbreaks which have a caustic agent of MERS-CoV in 2012. Considering the high occurrence and wide dispersal of coronaviruses, the vast inherent diversity and frequent recombination of their genomes, and the interface between human and animal activity, new coronaviruses are likely to occur frequently in humans due to recurrent cross-species infections and occasional spillover events [9,10].

In 2019, China faced a major outbreak of coronavirus disease 2019 (COVID-19) and this outbreak has the potential to become a worldwide pandemic [11]. Interventions and real-time data is needed for the control on this outbreak of coronavirus [12]. In previous studies, the transfer of the virus from one person to another person, its severity and history of the pathogen in the first week of the outbreak has been explained with the help of real-time analyses [13]. In December 2019, a group of people in Wuhan admitted to the hospital that all were suffering from pneumonia and the cause of pneumonia was idiopathic. Most of the people linked cause of pneumonia with the eating of wet markets meet and seafood. Investigation on etiology and epidemiology of disease was conducted on 31 December 2019 by Chinese Center for Disease Control and Prevention (China CDC) with the help of Wuhan city health authorities [10]. Epidemical changing was measured by time-delay distributions including date of admission to hospital and death. According to the clinical study on the COVID-19, symptoms of coronavirus appear after 7 days of onset of illness [14]. The time from hospital admission to death is also important to prevent undervaluing when measuring the risk of death [15]. COVID-19 epidemiological data and incubation period was measured through public data on known cases [16]. For more details, see [16–28]. The *SIR* epidemic model with delay in the context of the fractional derivative with Mittag–Leffler kernel has been considered. The Atangana–Baleanu fractional derivative is a non-singular fractional derivative with Mittag–Leffler kernel. The deterministic model of the coronavirus the terms of the stochastic perturbations [29,30].

The goal of this article is to expand on mathematical ways of obtaining R_0 for ODE disease models in a population, taking into account the epidemiological significance of R_0 , and to show how this reproduction numbers can be utilized to direct control strategies that address disease rates and impacts in different countries. Stability and qualitative analysis of the model are discussed in Section 2. In Sections 3 and 4 actual data of different countries are formulated, also find the infected, death and recovered rate. At the end numerical simulation design which support the result and predict the disease stage in society.

2 SIR Mathematical Models

Kermack et al. [17] are those persons who are inventor of the diseases models and played an important role in Mathematical epidemiology. A deterministic, compartmental mathematical model is formulated for describing the transmission dynamics of the measles. The population is increasingly fraternizing and replicates a traditional developing country's dynamics as it explores an exponentially growing trend [17,18]. To continue with a basic model, suppose that each member of a population is either susceptible, contagious (infected with the disease) or life-long resistant from the disease. If the illness is short lived relative to the lifespan of the population, so infection is overlooked in various ways. Such a model could fit COVID 19 as a very simple model. Let S , I and R define the number of susceptible, infectious, recovered individuals at time t . Transmission of coronavirus is human, social life and some others ways are responsible for enhance the disease, so this is often modeled by mass action, namely a term τSI , where τ is the disease transmission rate constant and τI is the force of infection. Thus δ is the recovery rate, and let h define the fraction of infectious individuals who recover from the disease. The total population (A) is divided into three classes S , I and R , respectively, which are susceptible, infected and recovered to describe the coronavirus model in the following equations:

$$\frac{dS}{dt} = -\tau S(t) I(t) \quad (1)$$

$$\frac{dI}{dt} = \tau S(t) I(t) - \delta I(t) \quad (2)$$

$$\frac{dR}{dt} = \delta h I(t) \quad (3)$$

With initial condition $S(0) \geq 0$, $I(0) \geq 0$, $R \geq 0$, Since τ and δ ρ are interpreted rates, their ranges are $0 \leq \tau \leq 1$ and $0 \leq \delta \leq 1$. This leads to the definition of $R_0 = \frac{\tau S_0}{\delta}$, with the DFE locally asymptotically stable (LAS) if $R_0 < 1$, but unstable if $R_0 > 1$. Moreover, we assume that $S(0) + I(0) + R(0) = 1$ for all $t > 0$.

Here hard immunity and precaution level is more important at endemic stage to control the virus. The modified form of coronavirus model after adding new parakeets in the model which is given as

$$\frac{dS}{dt} = \delta A - \sigma S(t) I(t) - \delta S(t) \quad (4)$$

$$\frac{dI}{dt} = \sigma S(t) I(t) - (\rho + \delta) I(t) \quad (5)$$

$$\frac{dR}{dt} = \rho I(t) - \delta R(t) \quad (6)$$

where δ is per capita death rate, σ is infected rate, ρ is per capita recovery rate. Since δ , σ and ρ are interpreted rates, their ranges are $0 \leq \delta \leq 1$, $0 \leq \sigma \leq 1$ and $0 \leq \rho \leq 1$.

2.1 Quantitative Analysis

To evaluate the equilibrium point, we take left hand side equal to zero of Eqs. (4)–(6). Therefore the disease free equilibrium is $(S, I, R) = E = (A, 0, 0)$. The equilibrium which is not disease free, i.e., Endemic Equilibrium Witch tells that the disease persists in a population and never dies out. If $I \neq 0$ then $S = \frac{(\rho + \delta)}{\sigma}$, $I = \frac{\sigma\delta - \delta(\rho + \delta)}{\sigma(\rho + \mu)}$, $R = \frac{\sigma\rho A - \rho(\rho + \delta)}{\sigma(\rho + \delta)}$.

Thus the endemic equilibrium state is given as $(S, I, R) = E_0 = \left(\frac{(\rho + \delta)}{\sigma}, \frac{\sigma\delta A - \delta(\rho + \delta)}{\sigma(\rho + \delta)}, \frac{\sigma\rho A - \rho(\rho + \delta)}{\sigma(\rho + \delta)} \right)$.

Theorem 1: The endemic equilibrium E_0 is locally asymptotically stable if $R_0 > 1$ and otherwise unstable

Proof: In this system the threshold result of this equilibrium is $R_0 > 1$, so this is in endemic state. Consider the Jacobean matrix (J) as

$$J = \begin{bmatrix} -(\sigma i + \delta) & -\sigma s & 0 \\ \sigma i & \sigma s - (\rho + \delta) & 0 \\ 0 & \rho & -\delta \end{bmatrix}$$

$$J = F - V$$

$$\text{Were } F = \begin{bmatrix} -\sigma i & -\sigma s & 0 \\ \sigma i & \sigma s & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \delta & 0 & 0 \\ 0 & (\rho + \delta) & 0 \\ 0 & -\rho & \delta \end{bmatrix}$$

By using the relation $|K - \lambda I| = 0$ where $K = FV^{-1}$ and got the Eigen value $\lambda = \frac{\sigma(\delta S)}{\delta(\rho + \delta)}$ which represents the reproductive number

$$R_0 = \frac{\sigma(\delta S)}{\delta(\rho + \delta)}$$

Theorem 2: E_0 is locally asymptotically stable if $\text{Re}(\lambda) < 0$.

Proof: For the system (4)–(6) the $|J - \lambda I| = 0$, then we get

$$\begin{vmatrix} -(\sigma I + \delta + \lambda) & -\sigma s & 0 \\ \sigma i & \sigma s - (\gamma + \delta) - \lambda & 0 \\ 0 & \rho & -(\delta + \lambda) \end{vmatrix} = 0$$

$$\text{i.e., } (\sigma I + \delta + \lambda)[\sigma S - (\rho + \delta + \lambda)](\delta + \lambda) + \sigma^2 S[I(\delta + \lambda)] = 0 \quad (7)$$

The equation which is given above is called characteristic equation. But recall that E is given as

$$(S, I, R) = \left(\frac{(\rho + \delta)}{\sigma}, \frac{\sigma \delta A - \delta (\rho + \delta)}{\sigma (\rho + \delta)}, \frac{\sigma \rho A - \rho (\rho + \delta)}{\sigma (\rho + \delta)} \right)$$

$$(\delta + \lambda) \left[(\sigma i + \delta + \lambda) [\sigma s - (\rho + \delta + \lambda)] - \sigma^2 si \right] = 0$$

$$\text{either } (\delta + \lambda) = 0 \text{ or } \left[(\sigma I + \delta + \lambda) [\sigma S - (\rho + \delta + \lambda)] - \sigma^2 SI \right] = 0$$

i.e.,

$$\left. \begin{aligned} \lambda_1 &= -\delta \\ \lambda_2 &= \frac{-\delta}{2} + \frac{\sqrt{\delta(4\rho + 9\delta - 4\sigma N)}}{2} \\ \lambda_3 &= \frac{-\delta}{2} - \frac{\sqrt{\delta(4\rho + 9\delta - 4\sigma N)}}{2} \end{aligned} \right\} \tag{8}$$

if $\lambda_i < 0$ or if λ_i is complex with negative real parts then system is stable.

Therefore, $Re(\lambda) < 0$, since all the parameters are non-negative. So E_0 is locally asymptotically stable. This proves the proposition.

3 Result and Discussion

Many COVID-19-patients are adults. Of the 44,672 confirmed infection patients in China, 2.1% were below the age of 20. Fever, dry cough, and shortness of breath were the most commonly reported symptoms, and most patients (80%) experienced mild illness. Approximately 14% experienced severe disease and 5% were critically ill. The latest outbreak of coronavirus 2019 noted 12 March 12, 2020, as noted in [20], Coronavirus Cases are 126,369, death is 4,633 and recovered population is 68,304. Active cases are 53428 in the mild condition is 89% and critical is 11%, closed cases recovered is 94% and death is 6% with this disease. The data given in Tab. 1 for study are taken from literature and some website [19–24]. Tab. 1 shows COVID-19 population of different countries which are taken from these sources [20–24] till 23rd March 2020. China is the most populated area. According to our data the most affected area from COVID-19 is USA, which has 449555 total COVID-19 cases. Italy has maximum death rate and the Pakistan has minimum death rate as well as affected cases. Tab. 1 shows direct relation of deaths with the cases of COVID-19. Tab. 2 shows death, infected, recovered and suspected cases in different countries. Death rate, infected rate, recovered rate and suspected cases are in a country depends on how many citizens of that country are taking precautionary measures. Spain had maximum death rate from COVID-19 at the end of the march because they skip to take precautionary measures. Now-a-days, china has downfall of COVID-19 because they took precautionary measures. Iran has maximum suspected cases. The value of h is the fraction between infected and recovered cases of COVID-19. The parameter of h tells about reproductive rate of COVID-19 which ultimately gives data about disease existence or absence. Endemic equilibrium means disease is spreading in specific area and disease free equilibrium is antonym of endemic equilibrium. According to our data china, Russia and Pakistan are the disease free areas. USA, Italy and many other countries are in danger zone of COVID-19. Data is at end of December 2020, Figs. 1, 8, 9 and

12, 14–16 show data of USA, Belgium, Switzerland, Portugal, South Korea, Russia and Pakistan respectively. These countries have more infected population than recovered rate. It means the latent period of above mentioned countries are just started. Figs. 2–7, 10, 11, 13 show data of different countries with initial conditions $(N, 0, 0)$ where N is total population regarding their country. These countries have more recovered data as compared to infected population which means the citizens of these countries took precautionary measures. Circles are just pointing the time scale and solid line represents the actual behavior of the infected and recovered at different step sizes for different countries. Mathematical modeling plays important role in determining of parameters of disease like quantities of disease survival and different control strategies of disease. Basic reproduction number is important condition. The different names for basic reproduction number are basic reproductive number or reproductive ratio where we decide whether population is in disease free state or endemic state. Control methods and magnitude of reproduction can be used to describe severity of a disease. For example, seasonal influenza in a specific area can be described by estimating reproductive number of the disease.

Table 1: Table of population and disease data

Country	Population	Total cases	Total death	Total recovered
USA	330370141	18473716	326772	10802496
Italy	60461826	1964054	69214	1281258
Germany	83969900	1534116	27297	1115400
France	65273511	2479151	60900	184464
China	1438070898	86899	4634	81950
Iran	83639890	1164535	53816	894366
Turkey	84130947	2043704	18351	1834705
Belgium	11578239	632321	18939	43513
Switzerland	8640059	428197	7067	311500
Canada	37665739	528354	14597	438452
Brazil	212216052	7366677	189264	6405356
Portugal	10203379	383258	6343	308446
Austria	8994761	347204	5745	315952
South Korea	51259193	53533	756	37425
Russia	145920447	2963688	53096	2370857
Pakistan	219887256	465070	9668	417134

Before the migration to and from Wuhan was cut off, the basic reproduction number in China was 5.6015. From 23 January to 26 January 2020, the basic reproduction number in China was 6.6037. From 27 January to 11 February 2020, the basic reproduction number outside Hubei province dropped below 1, but that in Hubei province remained 3.7732. Because of stricter controlling measures, especially after the initiation of the large-scale case-screening, the epidemic rampancy in Hubei has also been contained. The average basic reproduction number in Hubei province was 3.4094 as of 25 February 2020. The two uses of the R_0 are, to assess the ability of an infectious disease to invade the community (when the R_0 of a disease is greater than 1, the infection will spread, as it indicates that one infected individual will spread the disease to more

than one individual) and to determine the fraction of the community which should be vaccinated in order to prevent the growth of the epidemic [31,32].

Table 2: Table of infected, death and recovered rated according to collected data

Country	Death rate	Infected rate	Recovered rate
USA	0.017688482	0.055918237	0.584749489
Italy	0.035240375	0.032484199	0.652353754
Germany	0.017793309	0.018269832	0.727063664
France	0.024564861	0.037980966	0.074406117
China	0.053326275	6.04275E-05	0.943048827
Iran	0.046212437	0.013923201	0.768002679
Turkey	0.008979285	0.024291941	0.897735191
Belgium	0.029951559	0.054612882	0.068814732
Switzerland	0.016504086	0.0495595	0.727468899
Canada	0.02762731	0.014027443	0.829845142
Brazil	0.02569191	0.0347131	0.86950412
Portugal	0.016550209	0.03756187	0.8047999
Austria	0.016546468	0.038600692	0.909989516
South Korea	0.01412213	0.001044359	0.699101489
Russia	0.017915516	0.0203103	0.799968485
Pakistan	0.020788268	0.002115038	0.896927344

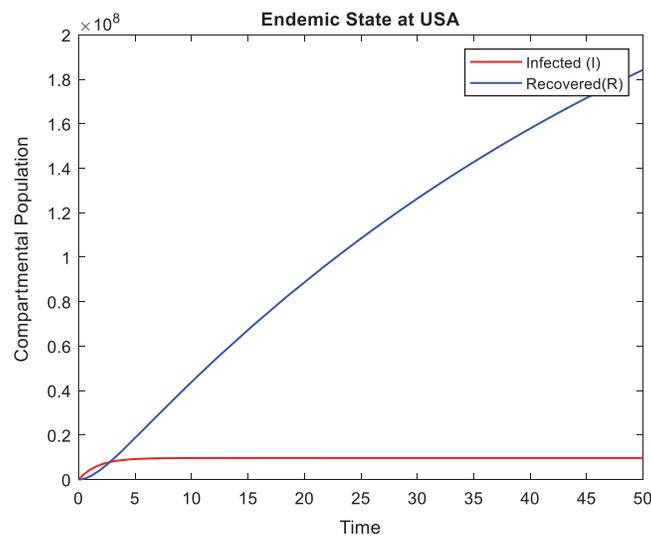


Figure 1: Actual behavior of Coronavirus at USA in a time t

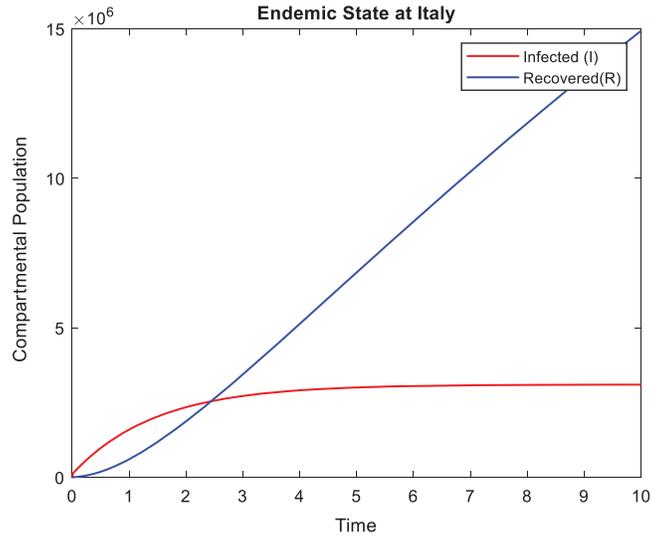


Figure 2: Actual behavior of Coronavirus at Italy in a time t

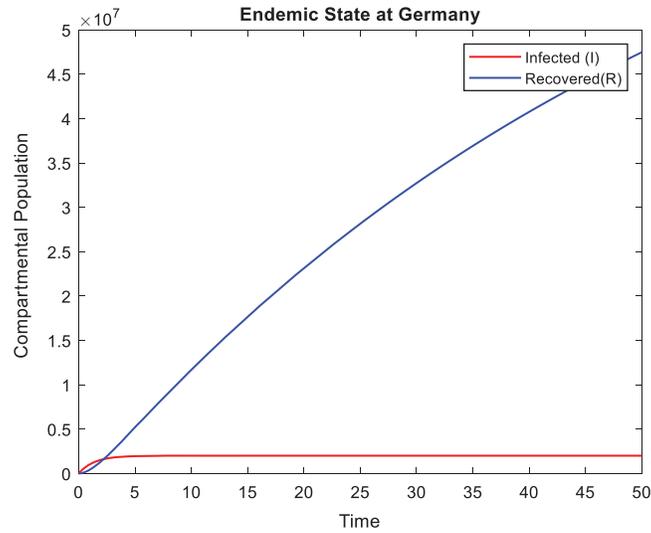


Figure 3: Actual behavior of Coronavirus at Germany in a time t

4 Numerical Simulations

The above results are based on some data collected by the 24th December 2020, but our results are expected by different countries to increase or decrease the rate of infection and recover which help to study the outbreak of COVID-19. Countries properly follow the precautionary measure and operate on it. They are many countries which contain the coronavirus, but most

of countries increased the recovered rate efficiently but the risk of infection either fluctuates or stable after some period. The model chosen is easy but it gives the ton of valuable disease-related knowledge that will help prepare and handle the disease in society to reduce the risk of death.

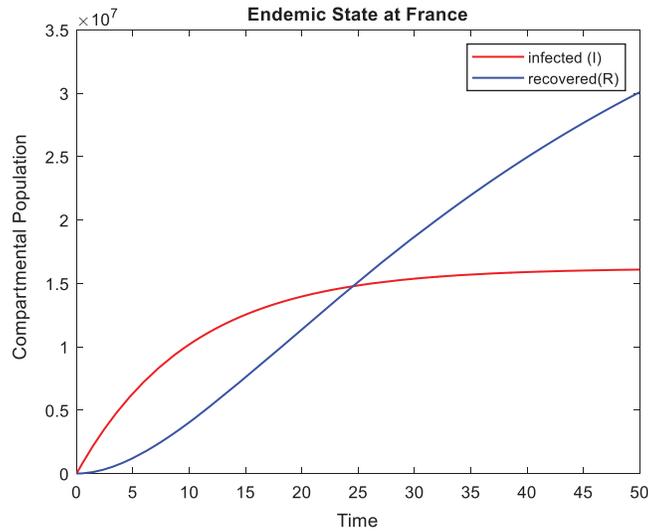


Figure 4: Actual behavior of Coronavirus at France in a time t

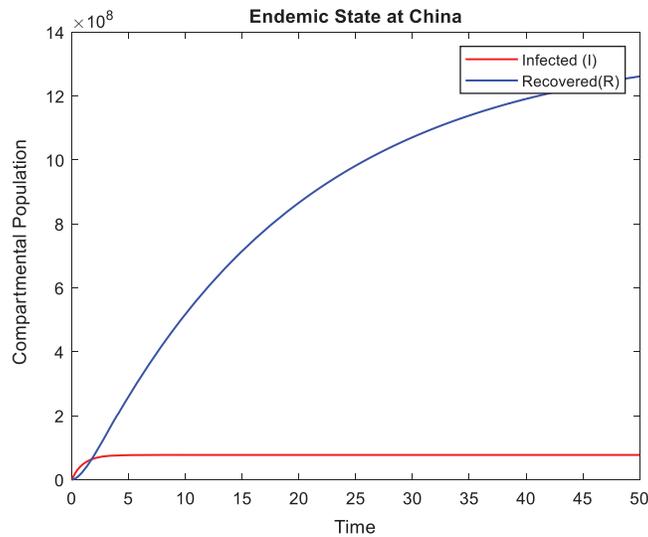


Figure 5: Actual behavior of Coronavirus at China in a time t

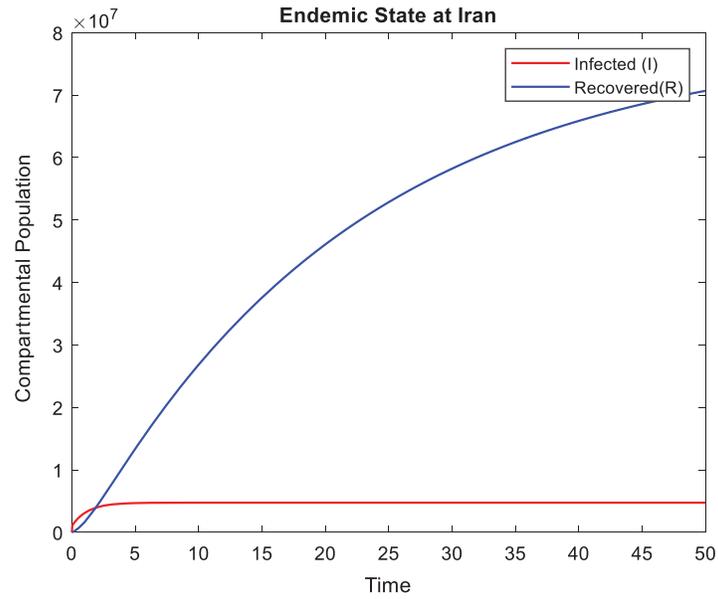


Figure 6: Actual behavior of Coronavirus at Iran in a time t

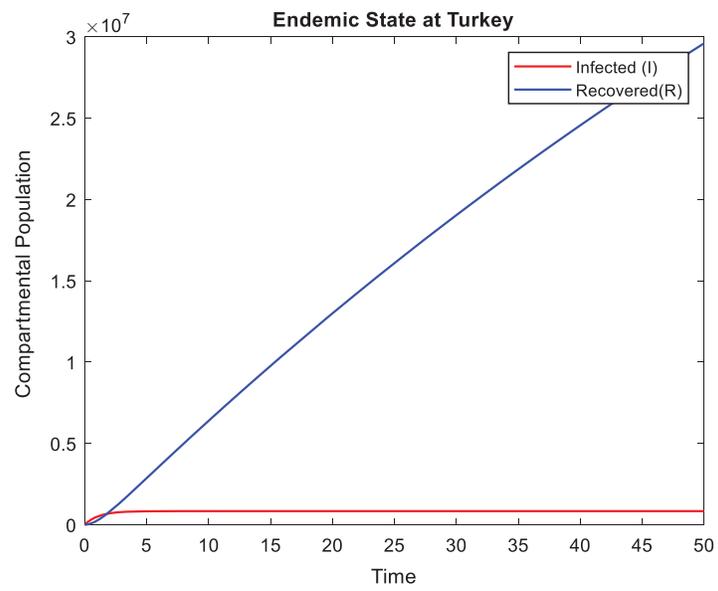


Figure 7: Actual behavior of Coronavirus at Turkey in a time t

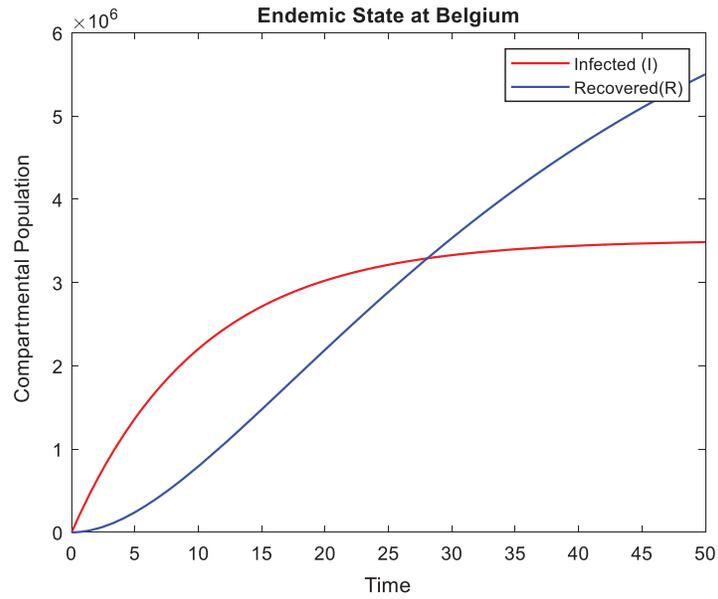


Figure 8: Actual behavior of Coronavirus at Belgium in a time t

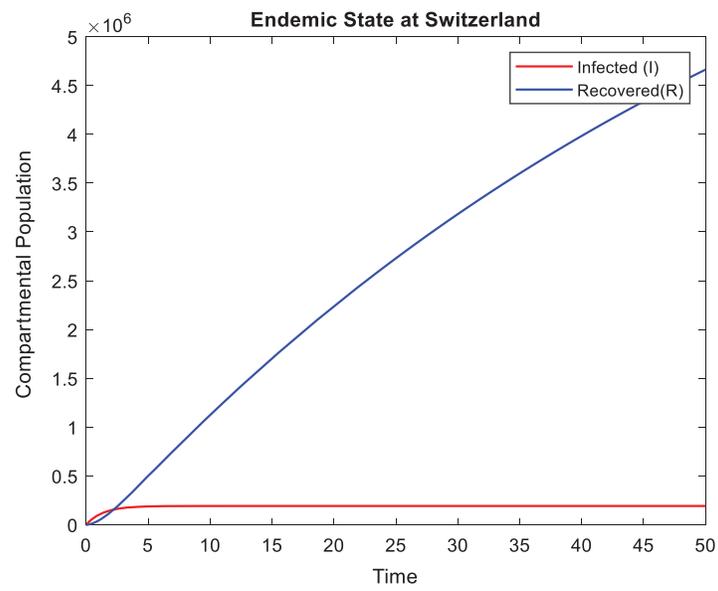


Figure 9: Actual behavior of Coronavirus at Switzerland in a time t

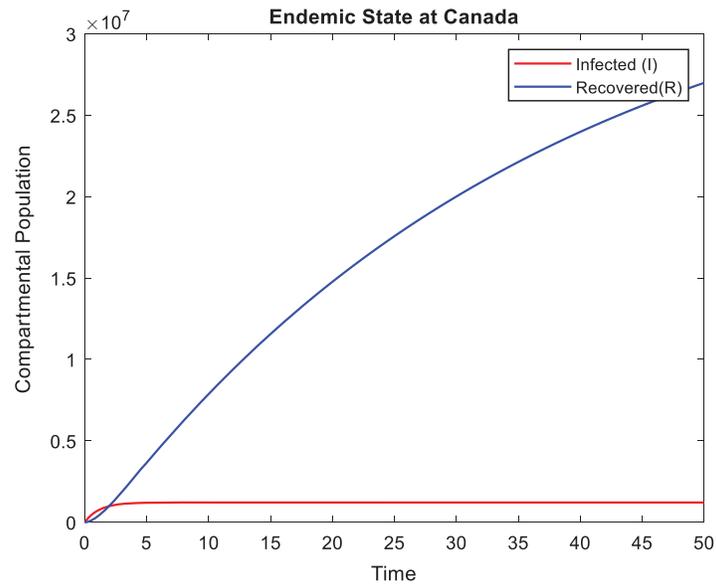


Figure 10: Actual behavior of Coronavirus at Canada in a time t

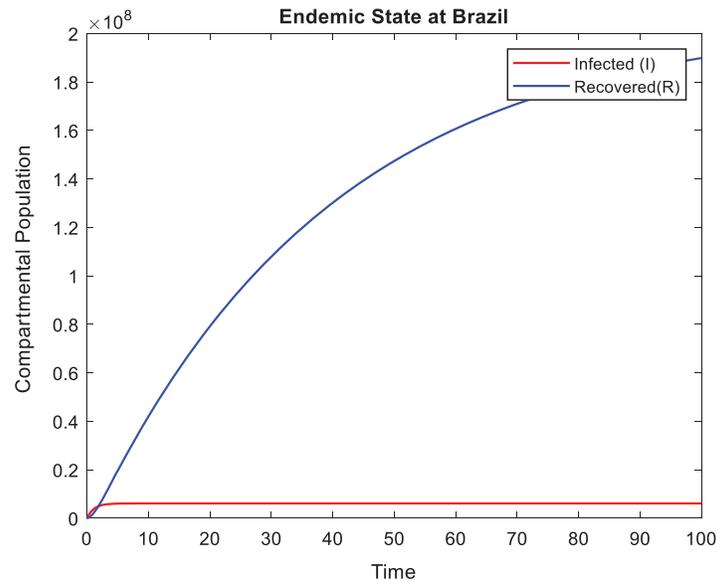


Figure 11: Actual behavior of Coronavirus at Brazil in a time t

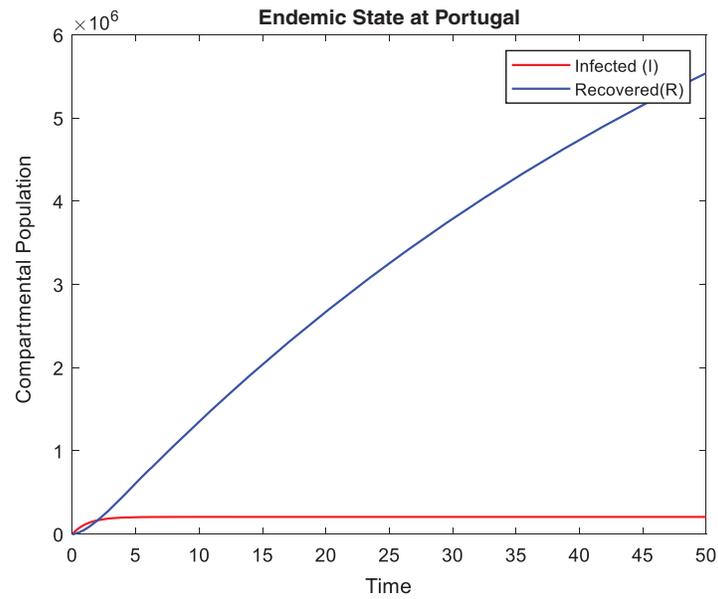


Figure 12: Actual behavior of Coronavirus at Portugal in a time t

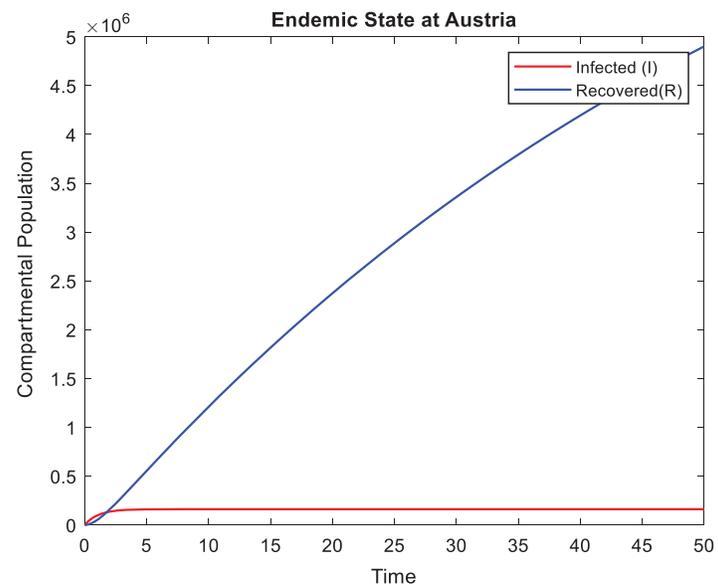


Figure 13: Actual behavior of Coronavirus at Austria in a time t

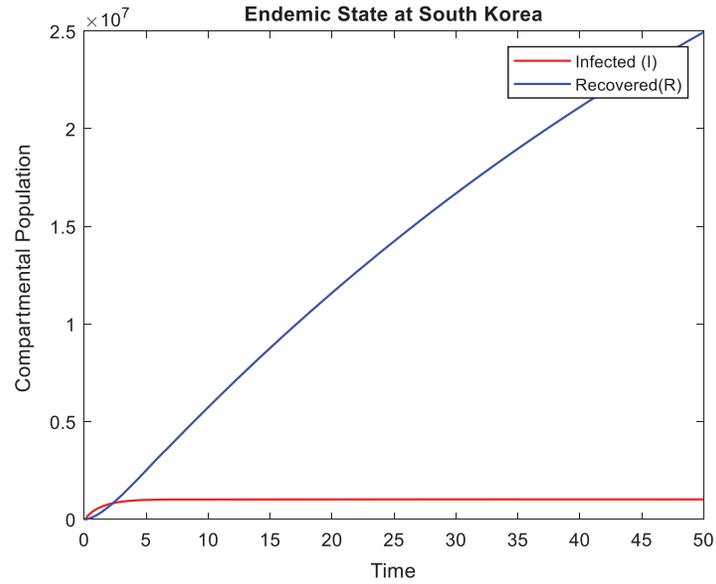


Figure 14: Actual behavior of Coronavirus at South Korea in a time t

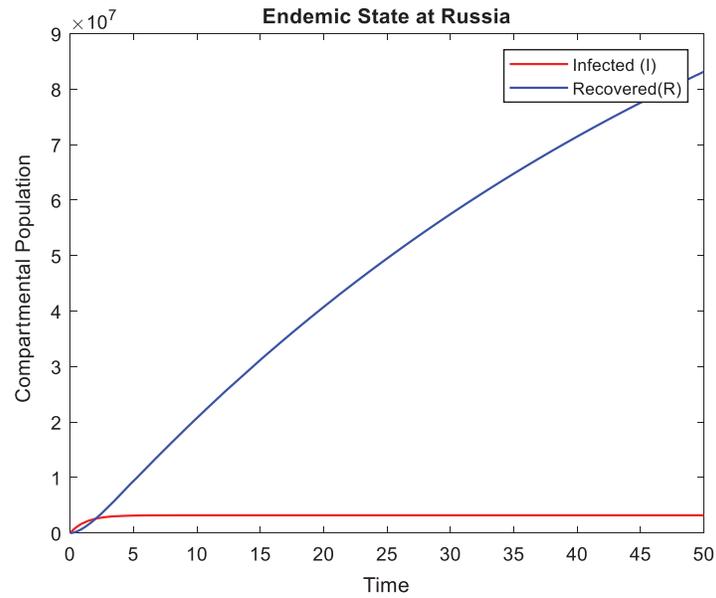


Figure 15: Actual behavior of Coronavirus at Russia in a time t

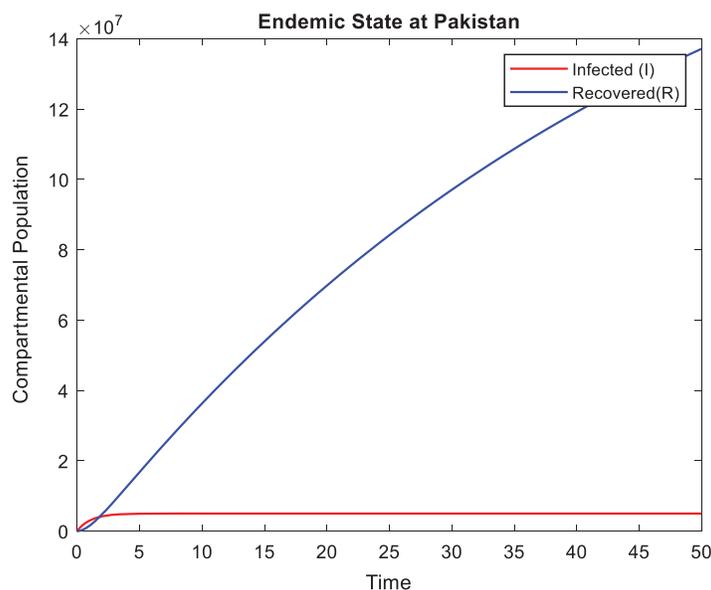


Figure 16: Actual behavior of Coronavirus at Pakistan in a time t

5 Conclusion

In this paper, we developed an epidemic model analytical solution scheme and formulated the reproductive number in order to observe the state of the coronavirus. The well-known Susceptible-Infected-Recovered (SIR) epidemic model is considered with and without demographic results. It is found that infection and recovered rate play a key role for an epidemic to occur, and that vaccination will regulate the epidemic. The effect of parameter estimation on our obtained solutions is expressed by figures. The numerical simulations show the actual behavior of the COVID-19 in a time t which will be helpful to analyze and control this pandemic disease. This model will assist the public health planar in framing a COVID-19 control policy. In addition, we will expand the model incorporating deterministic and stochastic model comparisons with fractional technique, as well as using optimal control theory for new outcomes.

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

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