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DYNAMICS OF COVID-19 PANDEMIC IN NEPAL: A MATHEMATICAL PERSPECTIVE

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Abstract

In this paper, transmission dynamics of coronavirus disease (COVID-19) outbreak in Nepal is studied by using the SIR compartmental mathematical model. The total population in this model was sub-divided into three compartments, namely Susceptible S (t), Infected I (t) and Recovered R (t). The qualitative analysis of the model was done analytically. The qualitative behaviour of the model like conditions for positivity of solutions, invariant region of the solution, the existence of the equilibrium points of the model and their stability, and also sensitivity analysis of the were analysed. The model is analysed by deriving some important expressions such as basic reproduction ratio, disease-free and endemic equilibrium points. The study examines the applicability of the SIR model for the study of the COVID-19 pandemic and other similar communicable diseases. The main objective the study is to analyse and forecast transmission dynamics of the COVID-19 pandemic in Nepal for the future. The estimation of the parameters of the model is based upon data from January 20, January 2020 to July 28, 2020. The actual time-series data of the corona virus disease 2019 for Nepal seem to good fit the proposed SIR model. The findings suggest that the quick detection of cases, sufficient implementation of quarantine and public self-protection behaviour are the best measures to reduce the transmission rate of the COVID-19.

Keywords

compartmental model; basic reproduction number; numerical simulations; disease-free equilibrium; endemic equilibrium

Introduction

Since December 2019, many unexplained cases of pneumonia with cough, dyspnea, fatigue and fever as the main symptoms have occurred in Wuhan, China in a short period of time (Shen, Peng, Xiao, 2020). China's health authorities and Centre for Disease Control (CDC) quickly identified the pathogen of such cases as one of the type of coronavirus, which the World Health Organization (WHO) named the re-emerged coronavirus disease as the COVID-19 (WHO, 2020). On January 22, 2020, the Information Office of the State Council of the People's Republic of China held a press conference, introduced the relevant situation of pneumonia and control of new coronavirus infection to the world. On the same day, the People's Republic of China's CDC released a plan for the prevention and control of pneuemonitis of new coronavirus infection, including the COVID-19 epidemic research, specimen collection and testing, tracking and management of close contacts, education and communication to the public (National Health Commission of China, 2020).

An outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a zoonotic coronavirus has seemed to severe acute respiratory syndrome coronavirus (SAR-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) has rapidly spread across China and various regions of the world. As of July 28, 2020, the cumulative number of confirmed cases has reached 19063 in Nepal and 16341920 globally (World Health Organization, 2020). The scientific community has tried to understand the nature and behaviour of coronavirus disease 2019 (COVID-19) which is caused by SARS-CoV-2. The scientists have established many statistical and mathematical modelling approaches. The value of R_0 for the virus transmissibility has been evaluated through stochastic Markov chain Monte Carlo (MCMC) methods (Liu, et al.,2020), a mathematical incidence decay and exponential growth model adopting the serial interval from severe acute respiratory syndrome (SARS) (Zhao et al., 2020). Researchers have also utilized several methods to generate short-term forecasts for cumulative case counts (Roosa et al., 2020), and have developed a 'susceptible, un-quarantined infected, quarantined infected, confirmed infected' (SUQC) model to characterize the dynamics of outbreaks (Zhao and Chen, 2020). Ivorra et al. have developed a mathematical model for the spread of the corona virus disease 2019 (COVID-19) and studied a particular case of China, country spreading the disease, and use its reported data to identify the model parameters, which can be of interest for estimating the spread of COVID-19 in other countries (Ivorra et al., 2020).

The emerging and re-emerging disease have led to a revived interest in the mathematical modelling on the disease.

One of the primary reasons for studying infectious disease is to improve control disease and ultimately to eradicate the infectious from the population. Models can be a power tool in this approach, allowing us to optimize the use of limited resources to target control measures more efficiently. A considerable number of recent studies have contended to estimate the scale the severity of COVID-19, and several mathematical models and predicting approaches have attempted to explain the transmission of COVID-19. The majority of the studies have estimated the basic reproductive number, a key parameter to evaluate the potential for COVID-19 transmission. However, different models often yield different conclusions in terms of differences in model structure and input parameters. It is imperative and crucial to improve the early predictive and warning capabilities of potential models for the pandemic.

In this work we discuss the stability analysis of a general Susceptible-Infected-Recovered (SIR) epidemic model of infectious disease (Siettos & Russo, 2013). The local dynamics of a general SIR is determined by the value of the basic reproductive number R_0 which depends on the parameter values. Detailed derivations are presented considering non-mathematicians working in the field of Biological sciences and non-availability of these derivations in the literature.

Methods

Data were collected on the epidemic situation of COVID-19 in Nepal and its neighbouring countries- India and China and compared the results with those of the SIR model with different parameter setting scenarios. The number of positive novel corona virus (COVID-19) cases in Nepal, India and China from 20 January 2020 to 28 July 2020 were recorded. The data source was based on the daily reports of WHO situation analysis of COVID-19. These three countries were selected because of their significance difference in the disease spread patterns. The initial 26 days were considered for the estimation the values of the parameters such as disease transmission rate (β), recovery rate of the infected people(γ), fatality rate (μ) and basic reproduction ratio (R_0) etc. for the model. The modelling and the visualizations were carried out using the software named *COVID-19. Analytic version 1.1.1* package developed in the *R-program 3.6.1 version*. Also the time series and Histogram diagram were plotted for the Nepal and its neighbouring countries using *R program.*

Mathematical modelling of the Disease

The SIR Mode

To study the transmission dynamics of the disease the total population is divided into three mutually disjoint classes, susceptible class (S), the infectious class (I), and the class of recovered (R)

populations. The susceptible individuals are those who are healthy and can contract disease under appropriate conditions. Infected individuals are those who have contracted the disease and are now infected with the COVID-19. These individuals are capable transferring the disease to the susceptible individuals via contacts. As time progress, infected individuals lose infectivity and move to the recovered compartment. These recovered individuals are immune to infectious microbes and thus do not acquire the disease again.

Some simplifying assumptions of the model are following:

1. The population is considered to be closed. The model is implemented for short period so grand total population of the whole system remains constant.
2. The population is uniform and homogenously mixing.
3. The disease transmission occurs only by the contract of susceptible and coronavirus infected individuals.
4. All the infected beings have an equal chance to be recovered.
5. Secondary waves of infections and any other outbreak of the infection are not considered in these models.
6. The movements out of one compartment into the next one are governed by constant rate (Anderson amd May, 1992).

The transmission dynamics of the disease is describes by the following non-linear ordinary differential equations.

$$\frac{dS(t)}{dt} = \mu N - \lambda S(t)I(t) - \mu S(t) \quad \text{.....3.1}$$

$$\frac{dI(t)}{dt} = \lambda S(t)I(t) - \gamma I(t) - \mu I(t) \quad \text{.....3.2}$$

$$\frac{dR(t)}{dt} = \gamma I(t) - \mu R(t) \quad \text{.....3.3}$$

S (t), I (t) and R (t) are number of susceptible, invectives and recovered people respectively at time *t*. With the initial conditions,

$$S(t=0) = S_0, I(t=0) = I_0, R(t=0) = R_0 \geq 0$$
$$S(t=0) = S_0, I(t=0) = I_0, R(t=0) = R_0 \geq 0.$$

μ: the recruitment rate and natural death rate.

β : the effective contact rate between the contact between the susceptible and infected individuals (disease transmission rate).

γ: the mean recovery rate of the infective individuals.

$\gamma=\frac{1}{D}$: the average rate of recovery in infected population,

D: the duration of infection or average infection period.

β is the product of the population exposed to the infected population and the probability of transmission. The model is developed for the short period of time so the total population is assumed to be constant N. So we have

$$S+I+R=N$$
$$\Rightarrow \frac{dS}{dt}+\frac{dI}{dt}+\frac{dR}{dt}=\frac{dN}{dt}$$
$$\Rightarrow \frac{dS}{dt}+\frac{dI}{dt}+\frac{dR}{dt}=0$$

Writing *s (t), i (t)* and *r (t)* for the fractions of the population in the respective classes we have

$$s(t)+i(t)+r(t)=1$$
$$or, r(t)=1-s(t)-i(t)$$

Hence the equations of the SIR model reduce as follows:

$$\frac{ds}{dt}=\mu-\beta is-\mu s \quad \text{.....3.4}$$
$$\frac{di}{dt}=\beta is-\gamma i-\mu i \quad \text{.....3.5}$$
$$\frac{dr}{dt}=\gamma i-\mu r \quad \text{.....3.6}$$

With initial conditions,

$$s(0)=s_0\geq 0$$
$$i(0)=i_0\geq 0$$

By setting *r (t) =1-s (t)-i (t)* and using this expression in the equations, we can obtain the following equivalent system:

$$\frac{ds}{dt}=\mu-\beta si-\mu s$$
$$\frac{di}{dt}=\beta si-\gamma i-\mu i \quad \text{.....3.7}$$

The feasible region for the above system is

$$\Omega = \{(s(t), i(t)) \in R_+^2, s(t) + i(t) \leq 1\}.$$

Here,

$$s(t) = 0 \Rightarrow \frac{ds}{dt} = \mu > 0,$$

$$i(t) = 0 \Rightarrow \frac{di(t)}{dt} = 0,$$

$$\frac{ds(t)}{dt} + \frac{di(t)}{dt} = -\gamma i(t) \leq 0.$$

Thus the feasible region Ω is positively invariant.

Basic Reproduction Number (R_0) as a Threshold Parameter

Basic reproduction number is one of the most fundamental quantities used by epidemiologists. It is defined as the expected number of secondary cases following the introduction of one infectious individual into a fully susceptible population (Anderson & May, 1992). In the equation (3.5), the negative term $(\gamma + \mu)$ *i* in the equation tell us that each infectious individual spends an average $1/(\gamma + \mu)$ time units in this class. Therefore, if we assume the entire population is susceptible *(s=1)*, then the average number of newly infected per infectious individual is determined by the transmission rate multiplied by the infectious period, which is termed as the basic reproduction number and denoted by R_0.

We have, $R_0 = \frac{\beta}{\gamma + \mu}$.

The basic reproduction number controls the dynamical behaviour of the system in the feasible region Ω. The basic reproduction number is a threshold quantity that helps to determine whether an outbreak of infectious disease dies out or spreads in a community in the long run. When R_0 is less than or equal to 1, the disease vanishes without the need of any medical strategies. Similarly, when R_0 is greater 1, the disease becomes endemic and requires some forms of control strategies to come into place (Hethcode, 2000).

Dynamical Properties of the Model

The Equilibrium State

At the disease-free equilibrium (DFE), the number of population in each compartment will be constant i.e.

$$\frac{ds}{dt}=\frac{di}{dt}=\frac{dr}{dt}=0$$

Solving the corresponding equations we get the disease-free equilibrium point as $E_0=\left(s^0,i^0,r^0\right)=(1,0,0,)$

Again, for the Endemic Equilibrium point *E* = (s*, i*, r*)*, the equation for the infective is equated to zero and we get

$$\begin{aligned}&\beta si-(\gamma+\mu)=0\\&\Rightarrow i\left(\beta s-(\gamma+\mu)\right)=0\\&\Rightarrow i=0 \text{ or } s=\frac{\gamma+\mu}{\beta}\end{aligned}$$

The first solution $i^*=0$ represents the disease free equilibrium, so we concentrate on the second solution, $s^*=\frac{\gamma+\mu}{\beta}$, The reciprocal of the quantity is the basic reproduction number $R_{0.}$ This leads us to an important result for our model: *In the SIR mathematical model with birth and deaths, the endemic equilibrium is characterized by the fraction of susceptible in the population being the inverse of* R_0.

Substituting this into equation (3.4) and solving for i^*.

$$\frac{ds}{dt}=\mu-(\beta i+\mu)s^*$$

$$\begin{aligned}&0=\mu-\left(\beta i^*+\mu\right)s^*\\&\Rightarrow 0=\mu-\left(\beta i^*+\mu\right)\left(\frac{\gamma+\mu}{\beta}\right)\\&\Rightarrow 0=\mu-\beta i^*\left(\frac{\gamma+\mu}{\beta}\right)-\mu\left(\frac{\gamma+\mu}{\beta}\right)\end{aligned}$$

$$\Rightarrow i^*(\gamma+\mu)=\mu-\mu\left(\frac{\gamma+\mu}{\beta}\right)$$

$$\Rightarrow i^*=\frac{\mu}{(\gamma+\mu)}\left[1-\frac{1}{\left(\frac{\beta}{\gamma+\mu}\right)}\right]$$

$$=\frac{\mu}{\beta}\left(\frac{\beta}{\gamma+\mu}\right)\left[1-\frac{1}{R_0}\right]$$

$$=\frac{\mu}{\beta}R_0\left[1-\frac{1}{R_0}\right]$$

$$\therefore i^*=\frac{\mu}{\beta}(R_0-1)$$

Population variables can never be negative. Hence the endemic equilibrium is biologically feasible only if $R_0 > 1$, which agree with our earlier ideas about when an endemic is possible. Now applying the result, $s^* + i^* + r^* = 1$, we can obtain an expression for r^*.

$$r^*=1-s^*-i^*$$

$$=1-\frac{\gamma+\mu}{\beta}-\frac{\mu}{\beta}(R_0-1)$$

$$=1-\frac{1}{R_0}-\frac{\mu}{\beta}(R_0-1)$$

Hence the endemic equilibrium is given by

$$E^*=(s^*, i^*, r^*)=\left(\frac{1}{R_0}, \frac{\mu}{\beta}(R_0-1), \left(1-\frac{1}{R_0}-\frac{\mu}{\beta}(R_0-1)\right)\right)$$

Stability Properties

Definition 3.1. *$E^* = (s^*, i^*)$ is a globally asymptotically stable solution of the system (3.4)-(3.5), if $E^* = (s^*, i^*)$ is a bounded positive solution and for any other solution E=(s(t),i(t)) the following relation for large t holds:*

$$\lim_{t\to\infty}\left(\left|s(t)-s^*(t)\right|+\left|i(t)-i^*(t)\right|\right)=0.$$

Theorem 3.1. *If $R_0 \leq 1$, then the disease-free equilibrium E_0 of the system is globally asymptotically stable on the feasible region* **Ω**.

Proof. We use the Lyapunov function theory to show that the proposed system is globally asymptotically stable for the disease free-equilibrium E_0. For this, we construct the following Lyapunov function $V: \Omega \to R$ as

$$V(s,i)=i(t)$$

Calculating the time derivative of V along the solution of the proposed system, we obtain

$$V'(t)=\beta s(t)i(t)-(\gamma+\mu)i(t),$$

$$=(\gamma+\mu)(R_0 s(t)-1)i(t).$$

It is observed that $V'(t)\leq 0$ when $R_0 < 1$.

If $R_0 < 1$ then $V'(t)=0 \Leftrightarrow i(t)=0.$

Also if $R_0 = 1$ then $V'(t)=0 \Leftrightarrow s(t)=1.$

Hence, according to LaSalle's invariance principle the disease-free equilibrium point E_0 is globally asymptotically stable on Ω (La Salle, 1987).

Theorem 3.2. The endemic equilibrium $E^* = (s^*, i^*)$ of the system is globally asymptotically stable on feasible region Ω.

Proof. For the establishment of the global stability of the endemic equilibrium E^*, we construct the Lyapunov function $L: \Omega_+ \to R$, where $\Omega_+ = \{(s(t), i(t)) \in \Omega \mid s(t) > 0, i(t) > 0\}$ defined as given

$$L(s,i) = W_1\left[s - s^* \ln\left(\frac{s}{s^*}\right)\right] + W_2\left[i - i^* \ln\left(\frac{i}{i^*}\right)\right]$$

Here, W_1 and W_2 are positive constant to be chosen latter. By taking the derivative of the above function with respect to time *(t)*, we get

$$\frac{dL(s,i)}{dt} = W_1\left(s - s^*\right)\left(-\beta i - \mu + \frac{\mu}{s}\right) + W_2\left(i - i^*\right)\left(\beta s - \left(\gamma + \mu\right)\right)$$

This above expression implies that for the equilibrium point we must have

$$\mu = -\beta i^* + \frac{\mu}{s}$$

$$\& \ \left(\gamma + \mu\right) = \beta s^*$$

So the above equation reduces to the form

$$\frac{dL(s,i)}{dt} = \beta\left(W_2 - W_1\right)\left(s - s^*\right)\left(i - i^*\right) - W_1\mu\left(s - s^*\right)^2.$$

For $W_1=W_2=1$, we get

$$\frac{dL(s,i)}{dt} = -\mu\frac{\left(s - s^*\right)^2}{ss^*} \leq 0.$$

This further implies that

$$\frac{dL(s,i)}{dt} = 0 \Leftrightarrow s = s^*.$$

Hence according to the LaSalle's invariance principle the endemic equilibrium point E^* is globally asymptotically stable on the feasible region Ω (La Salle, 1976).

Numerical Simulations

Numerical simulations are performed to investigate the dynamics of the system and to support the findings of the theoretical findings. To carry out the numerical simulations on the epidemic SIR model we need to make a specific choice of the values of the parameters and the initial conditions. We use the *covid19.analytic* package of *R* library for the numerical solution of the model. We take particular values of the parameter β=0.5428596 and γ=0.4571404 and observe the graphical presentation of number of susceptible, infected and

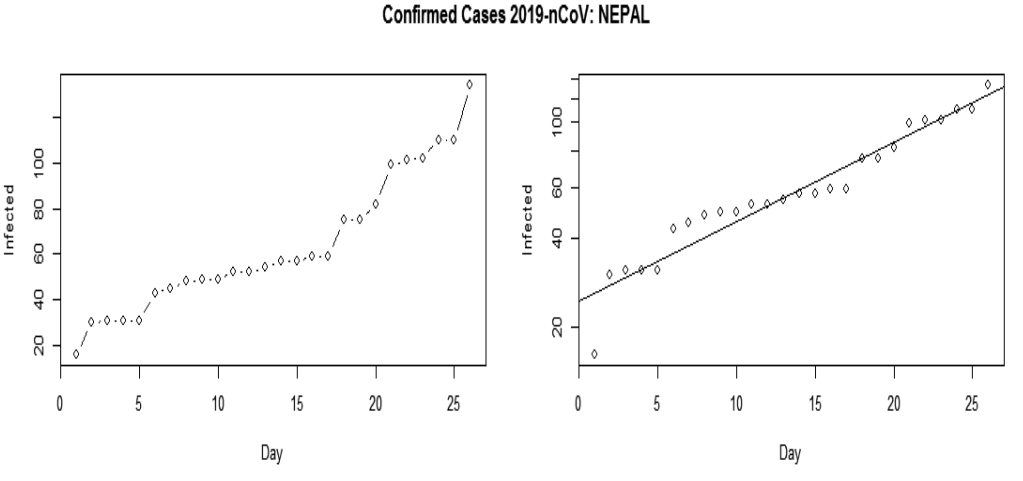
recovered against the time (day) for the solution of the SIR model are as shown in the fgure1.

All the simulations are performed by R-program. The parameter values are stablished by using the offficially reported data of 26 days from the first cases on COVID-19 found in Nepal provided by WHO coronavirus situation in Nepal. WHO, 2020) We take the total population of the region (Nepal) as 28090000 for the simulation of the SIR model.

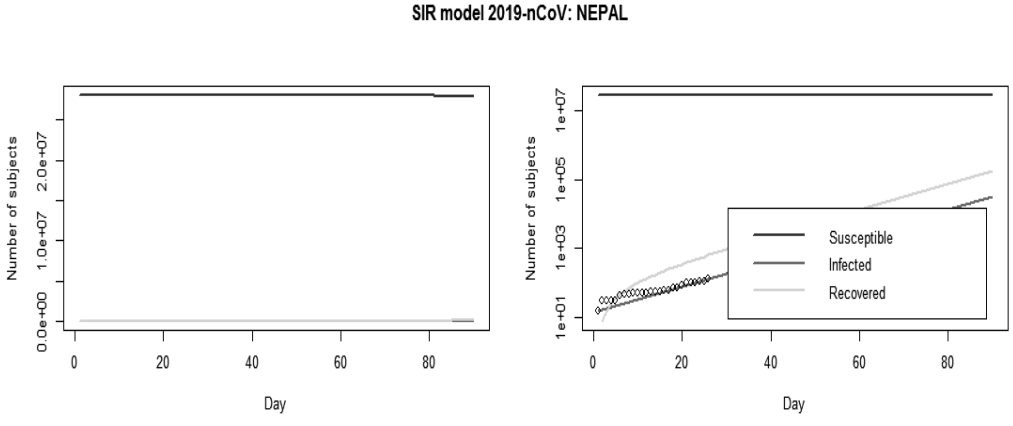
Table1. The parameter values used for the simulation.

Parameter	Value	Source
Fatality Rate	0.02	Medically Estimated
R_0	1.18751159	Estimated from the record of reported data of Covid-19 for 26 days from the first case found in Nepal. (using covid19. analytic package in R)
β	0.5428596	
γ	0.4571404	
μ	0.000000292	

The expected maximum number of infected people is 31426 (0.11%) and the epidemic may hit its peaked at 90 (2020:07:16). Also, the maximum number of casualities will be 629 assuming 2% fatality rate. The ploting of the simulated number of population is in the figure 1.



(a)



(b)

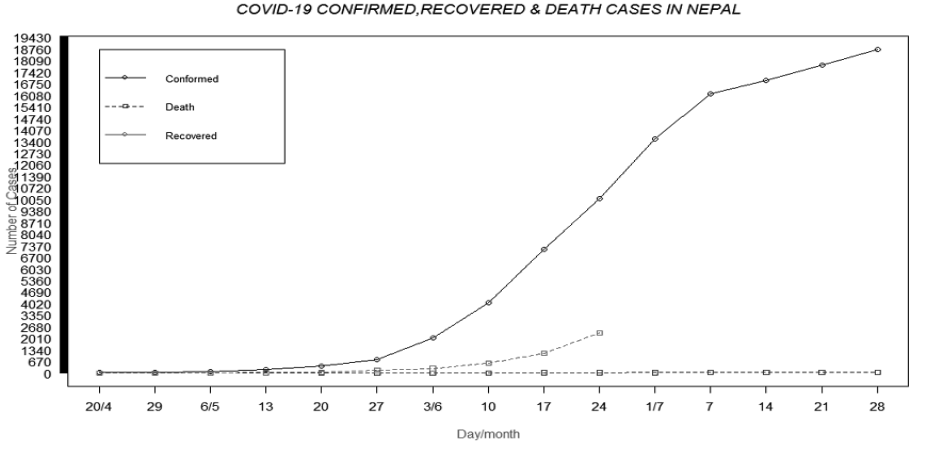
Figure 1. (a) The plot shows the infected population in Nepal for 26 days of the first reported case found. Estimated values of the parameter, R_0= 1.18751159 and the fatality rate= 0.02, are obtained using the data of initial 26 days. **(b)** SIR model for the total population of Nepal as 28090000. The graph contains solutions of the SIR system simulating the coronavirus disease.

COVID-19 Situation in Nepal

Nepal recorded its first case of COVID-19 on 25 January 2020 (WHO, 2020). Both the infected are the imported cases. Moreover, at the initial stage of the outbreak Nepalese data followed closely the exponential growth trend with very low growth rate. Till date, Nepal is one of the countries that have faced grievous consequences of COVID-19. Till 28th July 2020, Nepal has 19063 recorded cases through polymersase chain reaction (RT-PCR) and 49 death have been reported associated with COVID-19 PCR positive status. The male to female ratio of death cases is 85.4% to 14.6%. Although over all case fatality ratio (CFR) across all age is less than 1%, the CFR progressively increases above 1% beyond 55 years of age. All 7 provinces and 77 districts of Nepal are now affected and in five out of seven provinces where 71% of the population reside, there are cluster of cases. Around 84% cases are reported from province 2, province 5, Farwestern and Karnali province combined (WHO Nepal situation updates on COVID-19, 2020).

Considering the removable rate (γ) as a constant factor, R_0 may be considered as the product of the transmissibility, mean contact rate and the duration of the infection. Current estimates of the incubation period of the corona virus ranges from 2-10 days, and these estimates will be refined as more data become available. The transmission rate is a very important factor to control epidemics. The reduction of the transmissibility is

the only measure to control the epidemics in the present context unless the success of the clinical attempt to develop the vaccine against the coronavirus. The best method to reduce the transmissibility is to develop vaccines for the coronavirus, which is under continuous effort by the scientists of the almost all countries. At present, there are no specific vaccines or treatments for COVID-19. However, there are many ongoing clinical trials evaluating potential treatments. WHO will continue to provide updated information as soon as clinical findings become available. The best measures to prevent and slow down transmission are to be well informed about the COVID-19 virus, the disease it causes and how it spreads. Protecting yourself and others from infection by washing your hands or using an alcohol based rub frequently and not touching face are the ways of reducing the transmission rate. At the time period of the study, use of sanitizers and frequently hand washing with soap is under the practices to decrease the transmission. Also, second effective way is to reduce the contact rate. The mean contact rate is decreased effectively by putting the COVID-19 positive person in quarantine and keeping them in isolation. Also the health education programme should be conducted in national and international media about the social distancing and awareness about the disease



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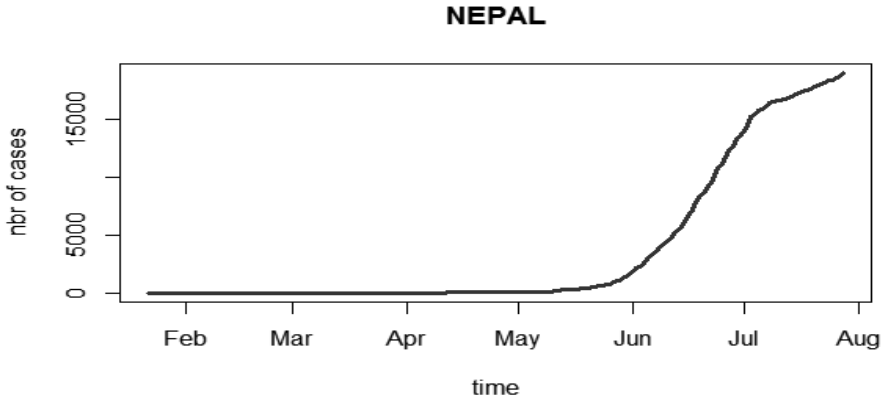

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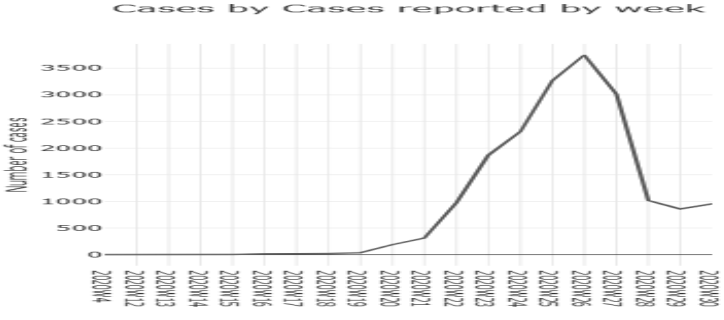

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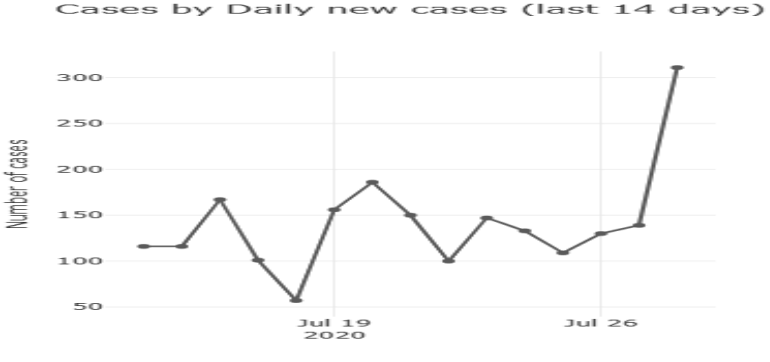

(d)

Figure 2. (a) The total number of cumulative confirmed death and recovered cases of Nepal up to 28 July, 2020. The data is plotted for every 7 days records. **(b)** Plot showing daily total cumulative confirmed cases reported daily in Nepal. **(c)** Line chart

showing number of cases reported weekly in Nepal **(d)** line chart of COVID-19 cases reported daily new cases for last 14 days.

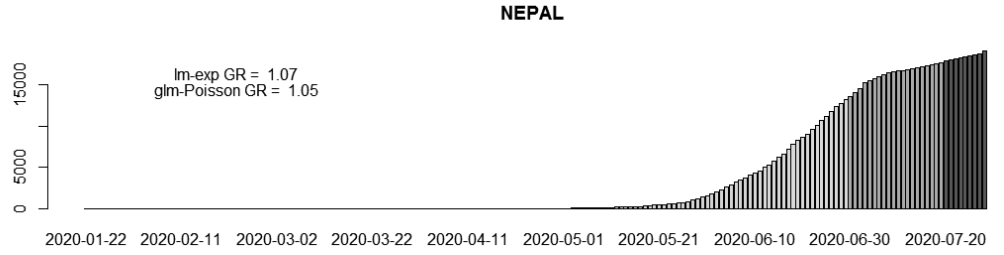

Figure 3. The Histogram of the number of coronavirus cases found in Nepal from the day of first case found in Nepal to 28th July 2020. Bar diagram indiates the positive exponential growth with low growth rate.

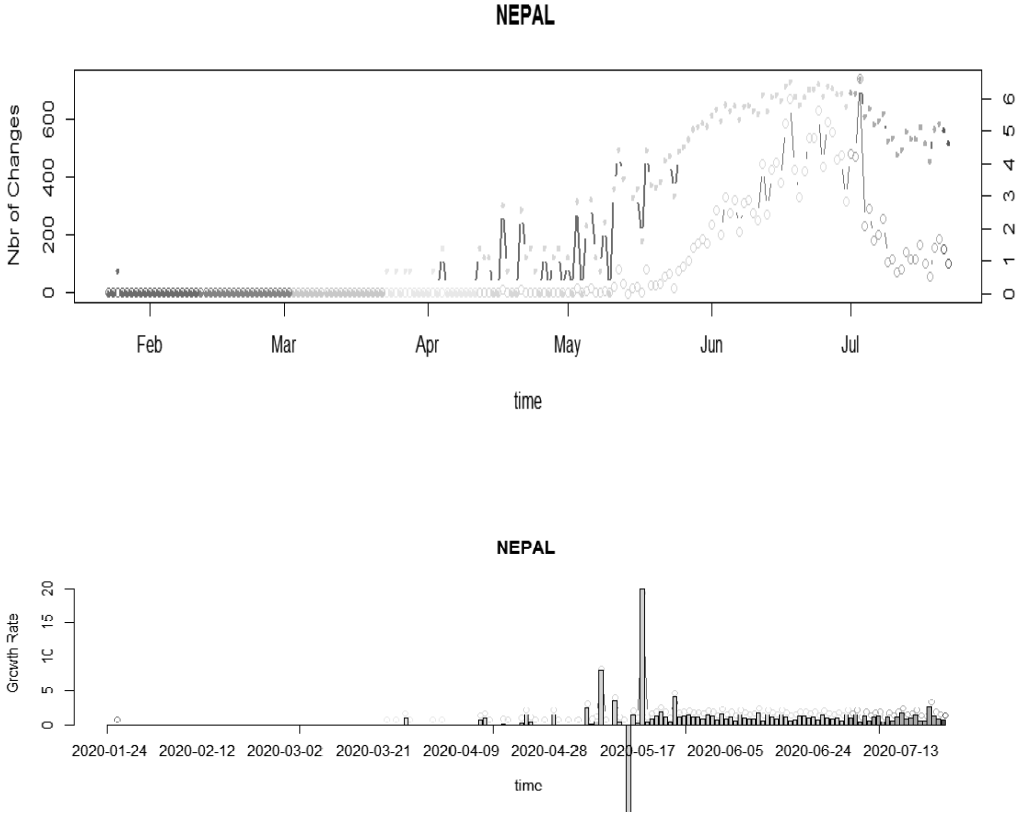

Figure 4. The growth rate of the COVID-19 active cases in Nepal

Figure 2 displays the plots for confirmed cases in Nepal from 30 January 2020 to 28 July 2020 staring from the first case in Nepal. The model has been fitted for the COVID-19 outbreak in Nepal for the recorded period. Figure 2 (c) amd (d) represents the line chart of the new cases of weekly reported cases and daily new cases respectively. The line chart analysis presents the meaningful statistics for confirmed COVID-19 data. It is clear from the plot that the time series is not stationary. An increasing trend is displayed by the time series suggesting a high rise in COVID-19 cases. Trends for number of recovery and death cases with respect to time due to COVID-19 infection in Nepal depicted in figure 2. It is observed that the number of recoveries as well as deaths increase with time, however the rate of recovery is higher than the rate of death. This indicates a low mortality rate is expected from the disease.

It is obvious as Nepal is the last amongst these countries to get infected. However, the plot also reflects that China has been able to control the pandemic and is now presenting very new cases. Thus, it follows that if strict prevention measures such as quarantine and sanitization are continued for some days, the situation could be controlled in coming days.

Conclusions

The COVID-19 outbreak in Nepal is analysed using deterministic compartmental SIR mathematical model. Although the SIR model is one of the simplest epidemiological models, it is still one of the most useful to study viral infections like COVID-19. From the qualitative analysis of the model, dynamical properties is analysed by establishing the stability condition of the disease-free and endemic equilibrium points. As our model involves various parameters, we have shown the sensitivity of these parameters via numerical simulations. It is also explained how the reproduction number can be minimized by reducing other parameters. The model can assist in the decision making by making projections regarding important issues such as intervention induced changes in the spread of disease. Till now, the Nepal is in the beginning or in the first half of the epidemic; a continuity of the study on the topic is essential for reanalysis of the updated dataset. However, the transmission model is based on the current understanding of the available data and natural as well as medical history of the infection can alert us to the deficiencies in our current understanding of the COVID-19 pandemic and suggest crucial questions for investigation and information to be collected. Findings from this study provide timely data that can inform public health decision-making and policies designed to end the epidemic. Based on the model forecast, the COVID-19 confirmed cases are expected to rise in coming days. At present, Nepal is at the position of exponentially rising cases of

the disease. The number will hit peak and then gradually decreases. Further study can be conducted by considering other parameters and the introducing the more compartments for isolated and hospitalized individuals.

Limitations

The obtained biological parameters for SARS-CoV-2 are based on the current reported data, but these values might be refined as more comprehensive data become available. In this model, we have assumed that individual become infectious and symptomatic at the same time and all infected individuals will eventually becomes symptomatic. Additional work is required to improve the accuracy of the parameter values and estimation.

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