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Mathematical Modelling of Transmission Dynamics of COVID-19: A Case Study of Nepal

Laxman Bahadur Kunwar, Lecturer
Department of Mathematics, Tribhuvan University
Thakur Ram Multiple Campus, Birgunj, Nepal

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ABSTRACT

In this study, the SIR compartmental mathematical model has been proposed to predict the transmission dynamics of COVID-19 in Nepal. The model is analysed by deriving some important expressions such as the basic reproduction ratio and possible maximum number of infectives in the future. This study examines the applicability of the SIR model for the study of the COVID-19 pandemic and other similar infectious diseases. The prime objective of the study is to analyse and forecast the COVID-19 pandemic in Nepal for the upcoming time. The estimation of the parameters of the model is based upon data from January 20, 2020 to July 14, 2020. The model presented in the paper fitted to the time-series data well for the whole Nepal and its neighbouring countries such as India and China. The findings suggest that there is a potential for this model to contribute to better public health policy in combating COVID-19.

KEYWORDS: Basic reproduction number, compartmental model, mathematical modelling of COVID-19, numerical simulations, pandemic

INTRODUCTION

Mathematical modelling has become a powerful tool that can be used to understand the dynamics of infectious disease and to support the development of control strategies. One of the primary reasons for studying infectious disease is to improve control disease and ultimately to eradicate the infection 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 study, I 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. For R_0 less than or equal to 1 the disease-free equilibrium is locally asymptotically stable while for R_0 greater than 1 the endemic equilibrium exists.

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 CDC quickly identified the pathogen of such cases as a type of coronavirus, which the World Health Organization (WHO) named COVID-19 on January 10, 2020 (WHO, 2020). On January 22, 2020, the Information Office of the State Council of the People's Republic of China held a press conference, introducing the relevant situation of pneumonia and control of new coronavirus infection. On the same day, the People's Republic of China's CDC released a plan for the prevention and control of pneumonitis of new coronavirus infection, including the COVID-19 epidemic Research, specimen collection and testing, tracking and management of close contacts, and propaganda, education and communication to the public (National Health Commission of China, 2020).

An outbreak of severe acute respiratory syndrome coronavirus2 (SARS-CoV-2), named as COVID-19, a zoonotic coronavirus seems to be similar to the serve acute respiratory syndrome coronavirus (SARS-CoV) and MERS-COV those with rather high lethality rate (Zhang Y, 2020). A mathematical model for simulating the phase-based transmissibility of novel coronavirus has showed the transmissibility of SARS-COV-2 was higher than the Middle East respiratory syndrome in the Middle East countries, similar to severe acute respiratory syndrome, but lower than MERS in the Republic of Korea (Chen et al., 2020). Recently, a mathematical model has been developed including individual behavioural response, governmental actions, zoonotic transmission, and emigration of a large proportion of the population in a short time period (Qianying, 2020). As of July 14, 2020, the cumulative number of confirmed cases has reached 16801 in Nepal and 12964809 globally. Also 570288 deaths have been declared by WHO worldwide till now (World Health Organization, 2020).

The prime objective of the study is to analyse and forecast the COVID-19 pandemic situation in Nepal for the upcoming time such that the findings of the study will contribute to build better health policy in combating COVID-19 for the upcoming days in Nepal.

METHODS

The study area of the research is Nepal and its neighbouring countries. The study is based on the secondary data, which is publicly available on the website of the WHO. The data were collected on the epidemic situation of COVID-19 in Nepal and its neighbouring countries like India and China and compared the results with those of the SIR model with different parameters setting the scenarios. The number of positive novel coronavirus (COVID-19) cases in Nepal, India, and China from 20 January 2020 to 14th 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. These data were used to estimate the values of the parameters such as effective contact rate, recovery rate of the infected people, basic reproduction ratio, etc. for the SIR model. The model and the visualizations were done using the software package named *COVID-19.analytic version 1.1.1* package developed with the *R-program 3.6.1 version.* In addition, the time series plotting and Histogram diagram were done for Nepal and its neighbouring countries using *R program.* The epidemic has not saturated in Nepal yet, it seems to be in its first half in

most locations. Those datasets cannot be used to derive some reliability criteria for the found parameters; some additional investigations with the inclusion of the datasets of upcoming duration are necessary.

THE MATHEMATICAL MODEL

The SIR Model

I have used the compartmental model to describe the dynamics of the population in which the entire population is divided into three classes: (a) the group of susceptible individual (S), (b) the group of infected individuals (I), and (c) the group of recovered (R) individuals. 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 as follows:

(i) The population is considered to be closed. The model is implemented for short period so the change in populations due to migration and natural death and birth are neglected.
(ii) The population spatial is homogeneity.
(iii) The disease transmission occurs only by the contract of susceptible and coronavirus infected individuals.
(iv) All the infected beings have an equal chance to be recovered.
(v) Secondary waves of infections and any other outbreak of the infection are not considered in these models.
(vi) The real time data of the officially reported positive cases are used for the model.

The model consists of a system of three nonlinear ODEs as:

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

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

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

S (t), I (t) and R (t) are the number of susceptible, invectives, and recovered people respectively at time *t*. The initial conditions are $S(t=0) = S_0, I(t=0) = I_0, R(t=0) = R_0 \geq 0$.

β: Disease transmission rate by the contact between the susceptible and infected individuals.

γ: The mean recovery rate .

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

D: the duration of infection or average infection period.

β: The product of the population exposed to the infected population (κ) and the probability of transmission (b). 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:

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

With initial conditions,

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

Qualitative Analysis of the Model

Existence of the long term limits: Since $\beta, \gamma \geq 0$ we must have $\frac{dS}{dt} = -\beta SI \leq 0$ and $\frac{dR}{dt} = \gamma R \geq 0$

Also, $0 \leq S(t) \leq S(0) \leq N$ and $0 \leq R(0) \leq R(t) \leq N$. These inequalities implies that the limits

$$S(\infty) = \lim_{t \to \infty} S(t),$$
$$R(\infty) = \lim_{t \to \infty} R(t),$$
$$I(\infty) = \lim_{t \to \infty} I(t) = N - S(\infty) - R(\infty)$$

All values exist.

The Disease always dies out: We have the initial conditions, $S(0) = S_0, I(0) = I_0, R(0) = 0$

It is easy to show that the disease always die out i.e. I (0) = 0 for all initial conditions.

$$\left[\frac{dI}{dt}\right]_{t=0} = \beta I_0 S_0 - \gamma I_0$$
$$= I_0(\beta S_0 - \gamma)$$

Clearly, $S_0 > \frac{\gamma}{\beta} \Rightarrow \frac{dI}{dt} = I_0(\beta S_0 - \gamma) > 0$

And $S_0 < \frac{\gamma}{\beta} \Rightarrow \frac{dI}{dt} = I_0(\beta S_0 - \gamma) < 0$

By equation (3.1)

$\frac{dS}{dt} = -\beta IS \le 0 \Rightarrow S \le S_0$ for any time t ≥ 0.

There are two possible cases.

Case I: If $S_0 < \frac{\gamma}{\beta}$, then $\frac{dI}{dt} = I(\beta S - \gamma) \le 0$ for all $t \ge 0$. In such case, $I_0 > I(t) \to 0$ as $t \to \infty$

So the infection dies out i.e. no epidemic can occur.

Case II: If $S_0 > \frac{\gamma}{\beta}$, then $\frac{dI}{dt} = I(\beta S - \gamma) > 0$ for all t ≥ 0. In such case I (t) initially increase and we will have an epidemic.

This is a famous result due to Kermack and McKendrick (1927) and referred as the threshold phenomenon. The initial population of susceptible must exceed this critical threshold for an infection to invade. Alternatively, we can interpret this result as acquiring $\frac{\gamma}{\beta}$, the relative removable rate, to be small enough to permit the disease spread. The inverse (reciprocal) of the relative removable rate is called the *basic reproductive ratio.* It is universally represented by the symbol R_0 and it is one of the most important quantities in epidemiology. The basic reproductive ratio represents the average number of secondary cases arising from an average primary case in an entirely susceptible population and essentially measures the maximum reproduction potential for an infection (Diekman & Heesterbeek, 2000). An infection can only invade if $R_0 > 1$. This seems very realistic in simple interpretation as pandemic occurs only when one host transmits more than one new host on the average.

The Basic Reproduction Number: Hethcote (2000) defined the *contact number* (σ) as the multiplication of the contact rate (β) per unit time by the average infection period $1/\gamma$. So it is interpreted as the average number of adequate contacts of a typical infective during infectious period. In general, $R_0 \ge \sigma \ge R$. Here, R denotes the reproduction number at some time other than the outset of the epidemic.

We estimated the early transmission R_0 for Nepal using available reported data by WHO coronavorus situation in Nepal. The epidemic growth potential is control by the

parameter R_0 We used the next generation matrix to derive a formula for the R_0 (Diekmann , Heesterbeek, & Roberts, 2010). When we use the model of fractions of infected individuals in a closed population (i.e. $I = \frac{I}{N}$ instead of *I)*

$$R_0 = \sigma = \beta / \gamma$$

$$= \frac{\kappa.b}{1/D}$$

But when we use the model with the infected population I as the whole, then

$$R_0 = \frac{\beta N}{\gamma}$$

In terms of related studies for the COVID-19 infection assumption, we set D=14 to estimate the R_0 . Mathematically, the value of R_0 can be calculated by multiplying the rate at which new cases are produced by an infectious individual i.e. transmission rate (β) (when the entire population is susceptible) and the average infection period $\left(1/\gamma\right)$.

Epidemic Burn Out: The long term or asymptotic state can be also interpreted from the model. Taking equations

$$\frac{dS}{dt} = -\beta IS \text{ and } \frac{dR}{dt} = \gamma I$$

$$\because \frac{dS}{dR} = \frac{\frac{dS}{dt}}{\frac{dR}{dt}}$$

$$\frac{dS}{dR} = \frac{-\beta SI}{\gamma I}$$

$$\frac{dS}{dR} = -\frac{\beta}{\gamma} S$$

$$\frac{dS}{dR} = -SR_0$$

Integrating with respect to R, we get

$$\int dS = \int -SR_0 dR$$

$$S(t) = S(0)e^{-R(t)R_0} \text{.....3.7}$$

Assuming *R (0) = 0*

The equation (3.7) shows that as the epidemics develops, the number of susceptible declines and, with a delay to take the infectious period into account, the number of recovered increases. Since e^{-RR_0} is always positive *S (t)* always remains above zero for

any value of *t*. Therefore, there will always be some susceptible in the population who escape any infection.

The Possible Maximum number of Infected Individuals:

$$\because \frac{dI}{dS} = \frac{\frac{dI}{dt}}{\frac{dS}{dt}}$$

$$= \frac{\beta IS - \gamma I}{-\beta IS}$$

$$= \frac{\beta IS}{-\beta IS} - \frac{\gamma I}{-\beta IS}$$

$$= -1 + \frac{\gamma}{\beta S}$$

$$= \frac{\gamma}{\beta S} - 1$$

$$dI = \left(\frac{\gamma}{\beta S} - 1 \right) dS$$

Integrating we get

$$\int dI = \int \left(\frac{\gamma}{\beta S} - 1 \right) dS$$

$$I = \frac{\gamma}{\beta} \int \frac{1}{S} ds - \int dS$$

$$I = \frac{\gamma}{\beta} \log S - S + C$$

Here, C is the constant of integration. Using initial condition

$I(0) \approx 0, S(0) \approx N,$ we get

$$0 \approx \frac{\gamma}{\beta} \log N - N + C$$

$$\Rightarrow C \approx N - \frac{\gamma}{\beta} \log N$$

Hence, $I = \frac{\gamma}{\beta} \log S - S + N - \frac{\gamma}{\beta} \log N$.....3.8

From this equation, we can compute the instantaneous maximum number of infective. For maximum value of I, $\frac{dI}{dS} = 0$

$$\Rightarrow \frac{\gamma}{\beta S} - 1 = 0$$

$$\Rightarrow \frac{\gamma}{\beta S} = 1$$

$$\Rightarrow S = \frac{\gamma}{\beta}$$

At $S = \frac{\gamma}{\beta}$

$$\frac{d^2 I}{dt^2} = -\frac{\gamma}{\beta\left(\frac{\gamma}{\beta}\right)^2}$$

$$= -\frac{\beta}{\gamma} < 0$$

So the maximum number of infective population *(I)* occurs at $S = \frac{\gamma}{\beta}$. Using the equation (3.8), the maximum number of infective is given by

$$I_{\max.} = \frac{\gamma}{\beta}\log\frac{\gamma}{\beta} - \frac{\gamma}{\beta} + N - \frac{\gamma}{\beta}\log N$$

$$= \frac{N}{R_0}\log\frac{N}{R_0} - \frac{N}{R_0} + N - \frac{N}{R_0}\log N$$

$$= \frac{N}{R_0}[\log\frac{N}{R_0} - \log N] - \frac{N}{R_0} + N$$

$$= \frac{N}{R_0}\log\left(\frac{1}{R_0}\right) - \frac{N}{R_0} + N$$

$$= N - \frac{N}{R_0}(\log R_0 + 1)$$

$$\therefore I_{\max.} = N\left(1 - \frac{1+\log R_0}{R_0}\right) \text{.....3.9}$$

This is the instantaneous maximum number of infective. The equation (3.8) can be used to determine the value of S for which the number of infective vanish i.e. I=0.

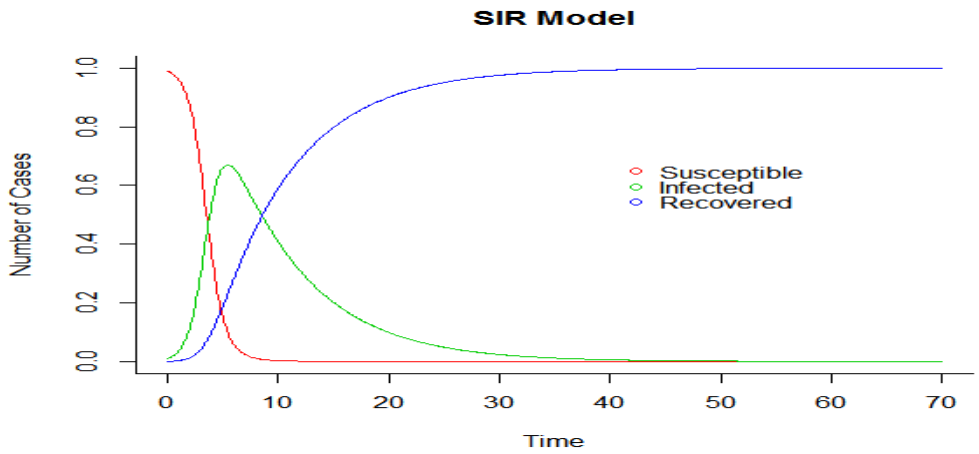
$$I = \frac{\gamma}{\beta}\log S - S + N - \frac{\gamma}{\beta}\log N$$

Since the logarithm is defined only for some positive value, the above expression shows that value of $S=N$ for the number of infective vanish i.e. $I=0$. Therefore, the epidemic terminates before all susceptible have become infected and some individuals escape the disease entirely.

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 package deSolve of *R* library for the numerical solution of the model. We take particular values of the parameter β=1.4 and γ=0.14 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 figure 1.

Figure 1

SIR System Simulating the Infectious Disease



Note: The graph contains solutions of the SIR system simulating the infectious disease. Numerical Simulation of the SIR model presenting the number of susceptible(S), infective (I), and recovered (R) against time for initial situation S(0)=1, I(0)=0 and R(0)=0 and taking β=1.4 and γ=0.14.

COVID-19 IN NEPAL

Nepal recorded its first case of COVID-19 on 25 January 2020. The infected cases increased to 2 on 24 March 2020 (WHO, 2020). Both the infected are the imported cases. Moreover, at the initial stage of the outbreak the data followed closely the exponential growth trend with a very low growth rate. Till date, Nepal is one of the countries that have faced grievous consequences of COVID-19. Till 14th July 2020, Nepal has 16,166 recorded cases through polymersase chain reaction (RT-PCR) and 35 deaths have been reported associated with COVID-19 PCR positive status. The male to female ratio of death is 6:1. 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. The age sex distribution is highly skewed towards young males, who constitute 86% (13,944/16,166) of the confirmed cases. Of the males, 92% (12,893/13,944) are in 15-54 year age group (WHO, coronavirus situation in Nepal, 2020).

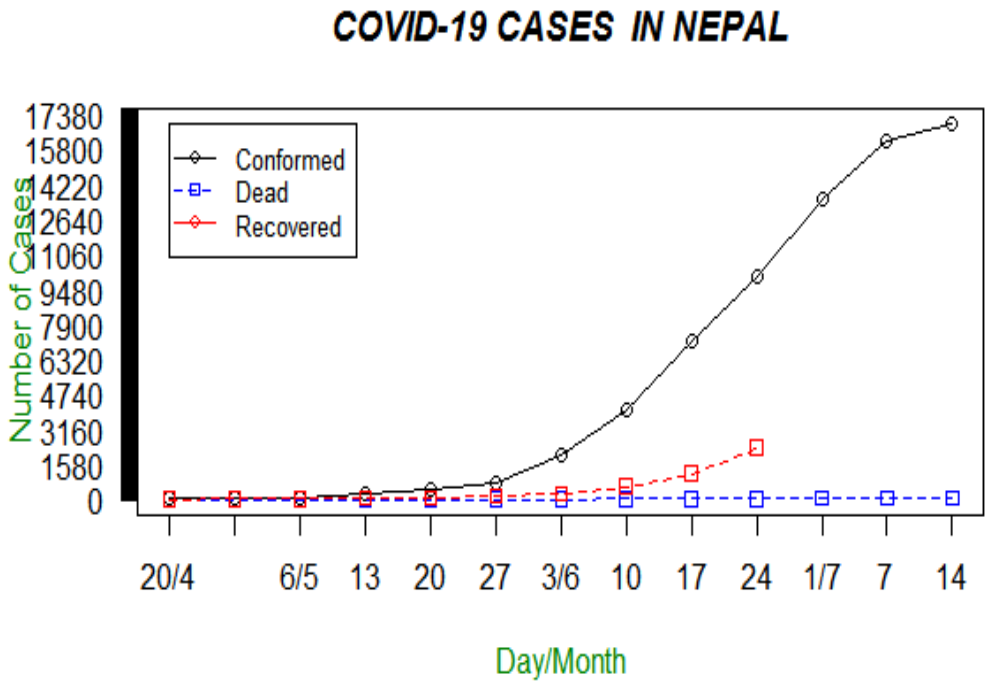
The effective contact rate is the per capita rate of infection given contact and it depends on the two factors: (i) the transmissibility of the virus (pathogen) (τ) and (ii) the frequency of the contact (f) .We assumed removable rate (γ) as a constant factor. So the expected time to removal (D) will be $\frac{1}{\gamma}$. We have $R_0 = \beta/\gamma = \frac{\tau.b}{1/D}$

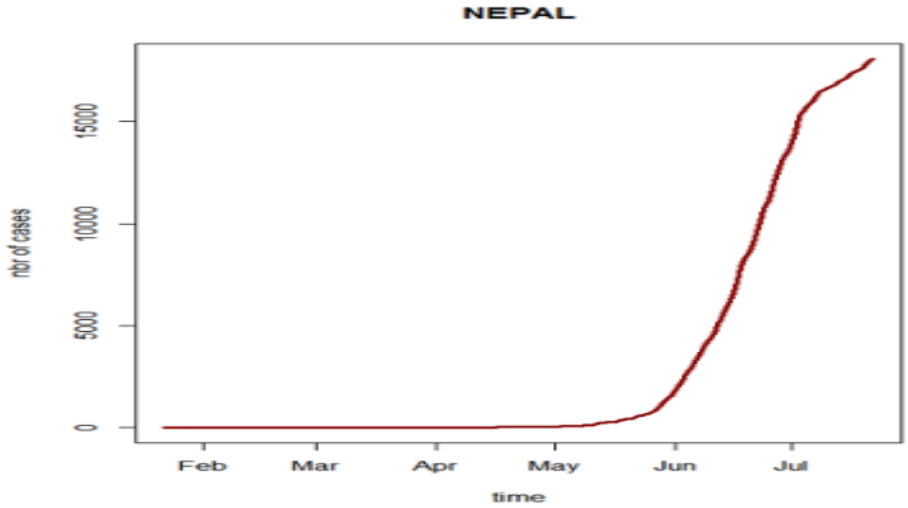
$$\therefore R_0 = \tau f D \ldots\ldots\ldots\ldots\ldots\ldots 4.1$$

Hence, R_0 is simply the product of the transmissibility (τ), mean contact rate (f) and the duration of the infection (D).The current estimates of the incubation period of the virus ranges from 2 -10 days, and these estimates will be refined as more data become available. This is a very important result because it tells us how to control epidemics. The transmissibility should be reduced to control the epidemics. The best method to reduce the transmissibility (τ) is to develop vaccines for the coronavirus, which is under continuous effort by the scientists of the almost all countries. At the time period of the study, the 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 (f). The mean contact rate is decreased effectively the quarantine the COVID-19 positive people and keeping them in isolation. Additionally, the health education programme should be conducted in national and international media about the social distancing and awareness about the disease.

Figure 2

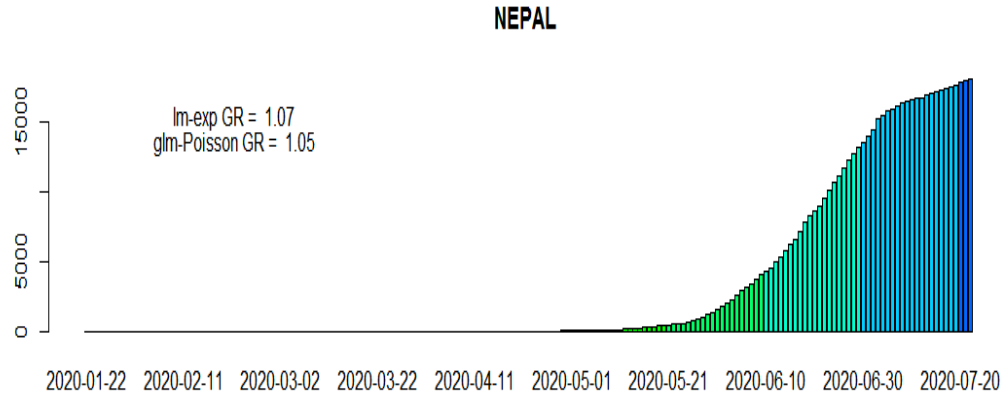
The total number of cumulative confirmed cases, death cases and recovered cases of Nepal



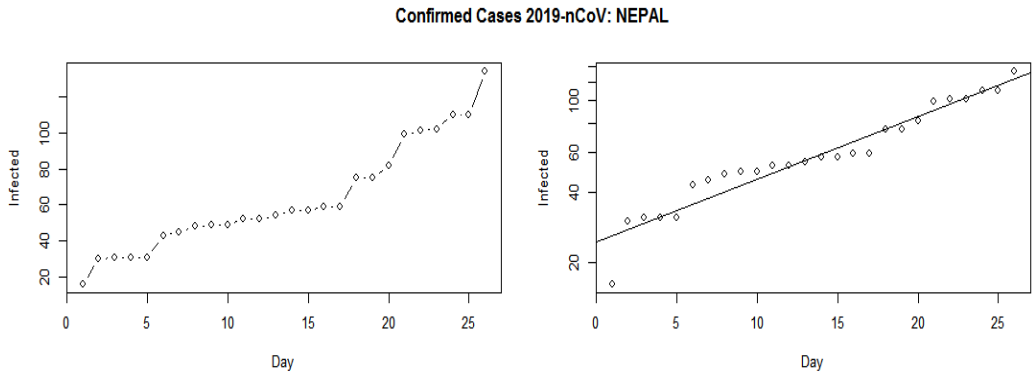


Note: The data is plotted for every 7 days records.

Figure 3
The Histogram of the Number of Coronavirus Cases in Nepal



Note: The Histogram of the number of coronavirus cases found in Nepal from the day of first case found to 20th July 2020. The bar diagram indicates the positive exponential growth with low growth rate.



(a) Variation of number of 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.

Figure 4

SIR Model for the Total Population of Nepal as 280 90000

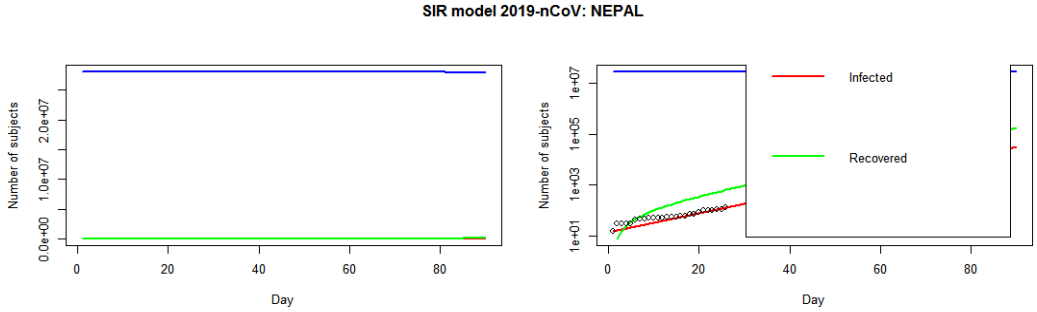


Figure 5

The Growth Rate of the COVID-19 Active Cases in Nepal

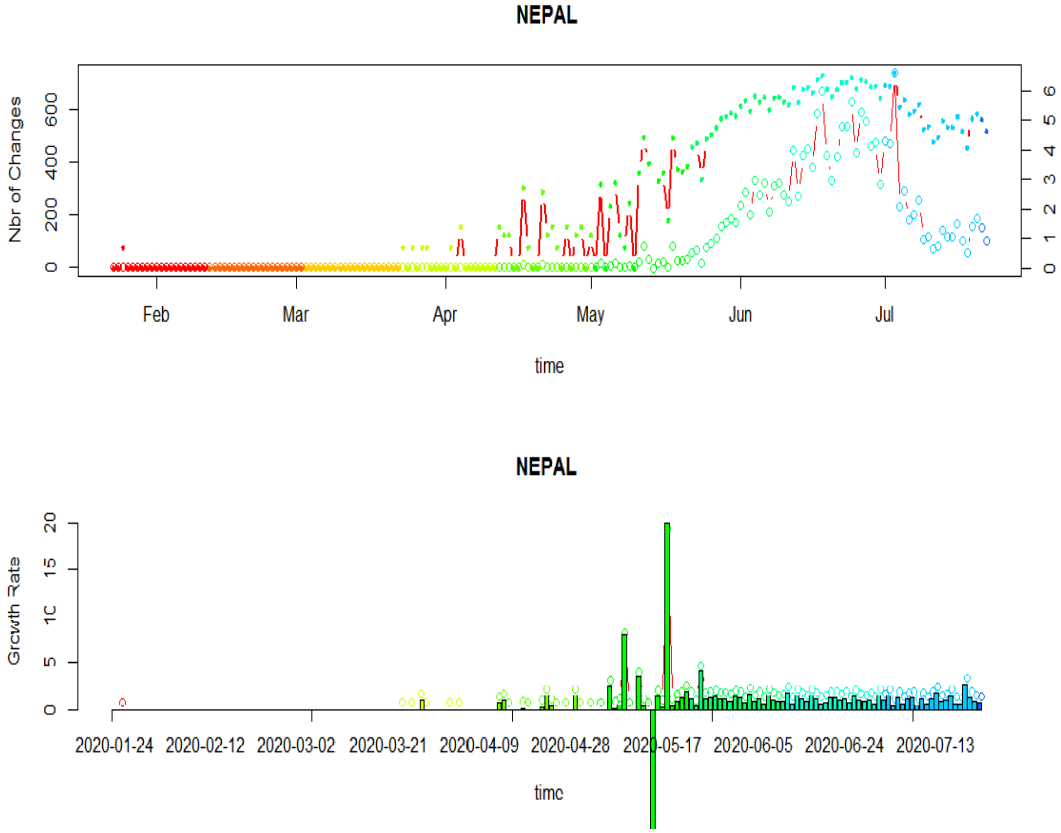


Figure 2 displays the plots for confirmed cases in Nepal from 30 January 2020 to 20 July 2020 staring from the first case in Nepal. The model has been fitted for the COVID-19 outbreak in Nepal for the recorded period. A slight deviation of residual from the straight line can be observed from the plot. Time series analysis presents the meaningful statistics for confirmed COVID-19 data. Figure 3 presents the time series graph of the active infected COVID-19 cases from 10 January to 20 July 2020. 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 a number of recovery and death cases with respect to time due to the 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.

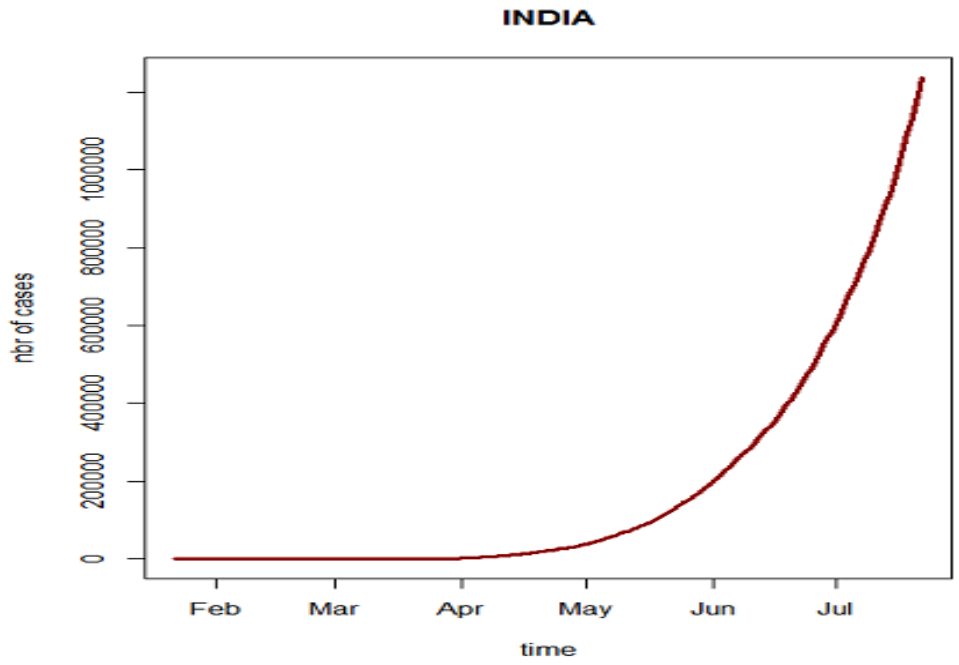
We perform rigorous numerical simulations to an insight of the epidemic in Nepal. All the simulations are performed by R-program. The parameter values are established by using the offficially reported data of 26 days from the first cases on COVID-19 found in Nepal provided by the WHO coronavirus situation in Nepal (WHO, 2020). We take the total population of the region (Nepal) as 28090000 for the simulation of the SIR model. The parameter values used for the simulation is in Table 1.

Table 1
Parameter Values Used for the Model

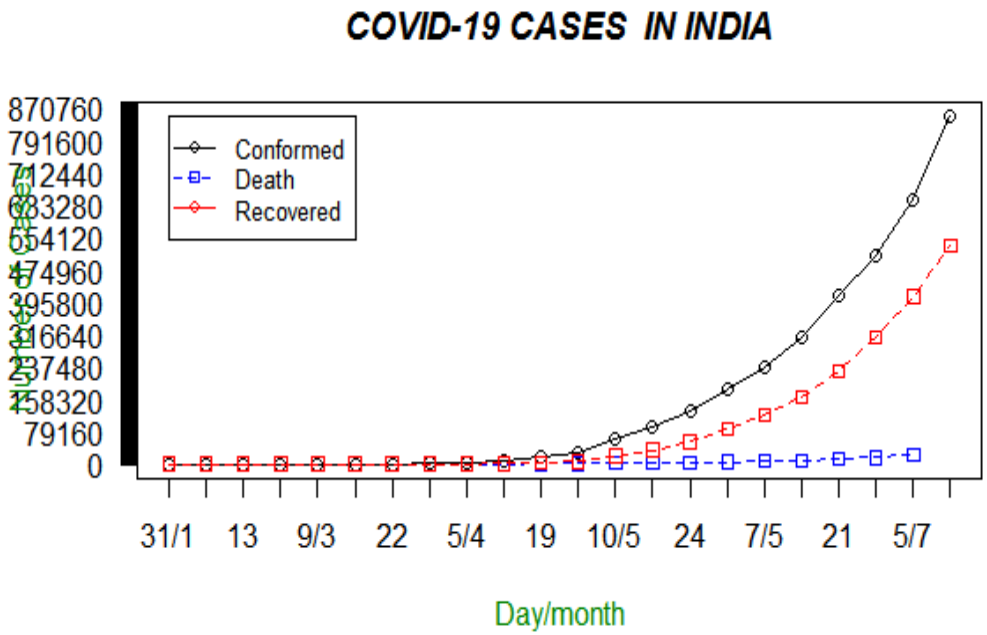
Parameter	Value	Source
Fatality Rate	0.02	Estimated from the record of reported data of Covid-19 for 26 days from the first case found in Nepal as it is mentioned in the section Methods
R_0	1.18751159	
β	0.5428596	
γ	0.4571404	

The expected maximum number of infected people is 31426 (0.11%) and the epidemic may hit its peaked at 90 (2020:07:16). In addition, the maximum number of casualities will be 629 assuming 2% fatality rate. The ploting of the simulated number of population is in the figure 4.

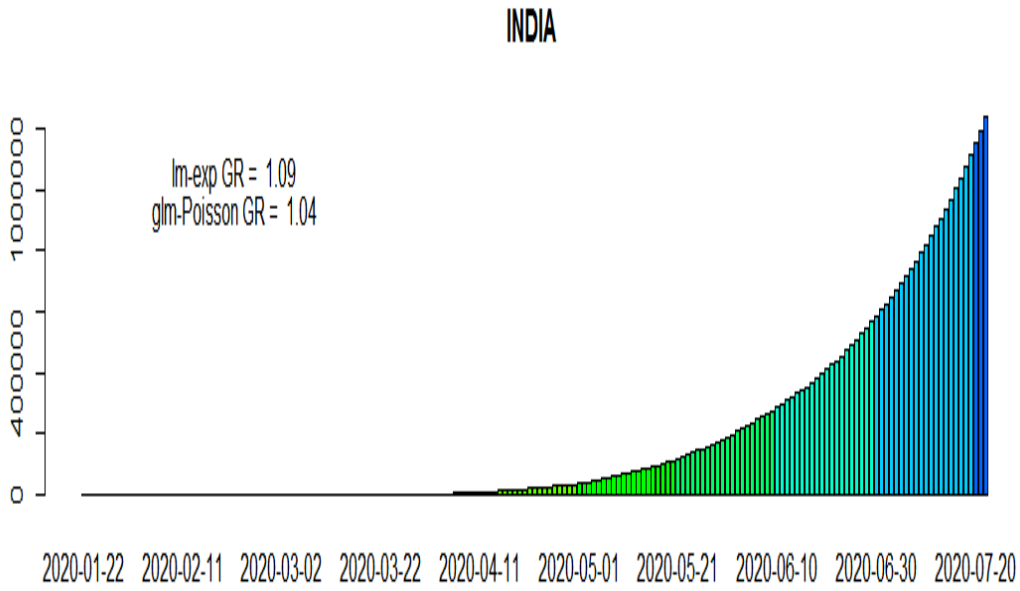
Figure 6
COVID-19 Cases in India



(a)



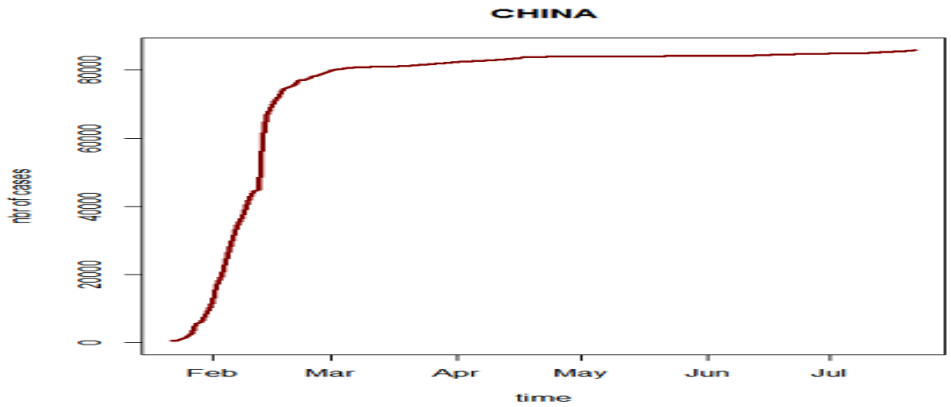
(b)



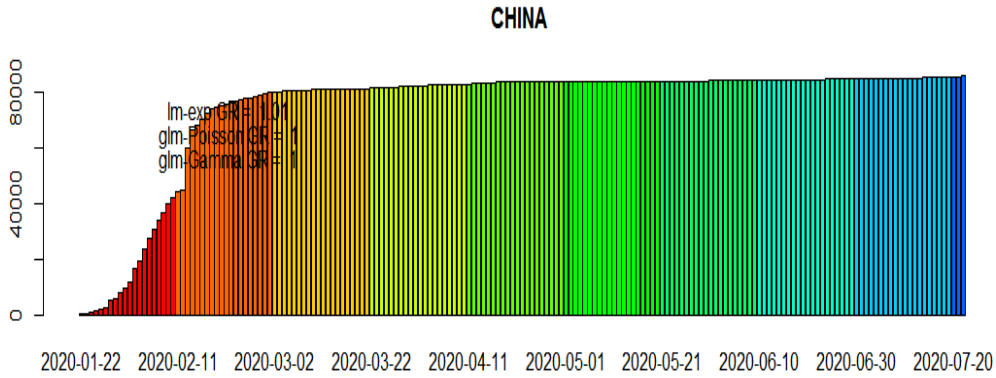
(c)

Note: COVID-19 situation in India. (a), (b) Cumulative number of confirmed, recovered and death cases from the first case found in India, and (c) Bar diagram of the confirmed cases. Bar diagram shows the exponential growth with moderate positive rate.

Figure 7
COVID-19 Situation in China



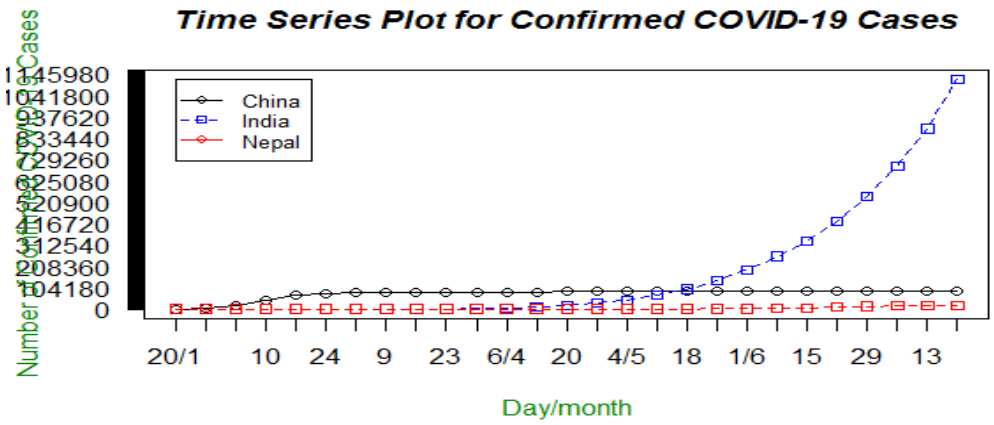
(a)



(b)

Note: COVID-19 situation in China. (a) Cumulative number of confirmed cases, from the first case found in China, and (b) Bar diagram of the confirmed cases. Bar diagram shows early stable condition from 4th March, 2020.

Figure 8
A Comparative Plot of Confirmed COVID-19 Infection Cases in Nepal



Note: A comparative plot of confirmed COVID-19 infection cases for Nepal and its neighbour countries- India and China from 20 January 2020 to 20 July 2020.

Figure 8 shows the comparative study of confirmed COVID-19 infection cases of Nepal with respect to those of its neighbouring countries such as India and China. According to the plot, India is most infected while Nepal the least infected of the selected countries (Nepal, India, and China). It is obvious that 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.

DISCUSSION AND CONCLUSIONS

Analysing and curbing the COVOD-19 epidemic in Nepal is an essential part of fighting the pandemic globally. The COVID-19 outbreak in Nepal is analysed using the deterministic compartmental SIR mathematical model. Although the SIR model is one of the simplest epidemiological models, it is still one of the most useful tools to study viral infections like COVID-19. I have explored the SIR model to study the coronavirus epidemic disease. From the qualitative analysis of the model, it is found that the long term limits of the susceptible, recovered, and infected population exist; we also derive the condition for the no epidemic case or epidemic burn out. As this model involves various parameters, I 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 world is in the middle or in the first half of the epidemic; the author is planning to continue the study on the topic with 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, the study 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. Therefore, when the model fails to predict, this failure can provide us with important clues for further research. The research can be extended in various ways. One can introduce new compartments so that the epidemic can be explained more precisely. Finally, it is suggested that new directions for further research to compare our results with other models in the near future.

LIMITATIONS

The paper will inevitably make some assumptions when building the model. When we build a dynamic model for a certain period of time for COVID-19, we ignore the impact of factors like population birth rate, and natural mortality. For simple calculations, it is also assumed that the latent population of COVID-19 and the infected but not yet isolated population have the same range of activities and capabilities.

ETHICS APPROVAL

In the study, the need for ethical approval or individual consent was not applicable because no individual patient's data was collected. All the data and materials used in the study are publicly available.

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APPENDICES

[1] R codes: Numerical Solution of the SIR model .

```
Library<-(deSolve)
 sir<-function(time,state,parameters){
 with(as.list(c(state,parameters)),{
 dS<--beta*S*I
 dI<-beta*S*I-gamma*I
 dR<-  gamma*I
 return(list(c(dS,dI,dR))) })}
init<-c(S=1-0.01,I=0.01,R=0)
parameters<-c(beta=1.4247,gamma=0.14286)
times<-seq(0,70,by=0.1)
out<- ode(y=init,times=times,func = sir,parms=parameters)
out<-as.data.frame(out)
out$time<-NULL
head(out,10)
matplot(x=times,y=out,type = "l",xlab ="Time",ylab = "Number of Cases",main="SIR Model",lwd = 2,lty = 2,bty="l",col = 2:4)
legend(40,0.7,c("Susceptible","Infected","Recovered"),pch=1,col=2:4,bty="n")
```

[2] **R Codes: COVID-19 cases in Nepal**

```
conf<-c(31,54,82,217,402,772,2036,4075,7173,10096,13562,16166,16945)
death<-c(0,0,0,0,2,4,8,15,20,24,29,35,38)
recov<-c(4,16,16,33,37,155,266,584,1158,2338)
g_range<-range(0,conf,death,recov)
plot(conf,type="o",col="black",ylim=g_range,axes=FALSE,ann=FALSE)
axis(1,at=1:13,lab=c("20/4","29","6/5","13","20","27","3/6","10","17","24","1/7","7","14")
axis(2,las=1,at=10*0:g_range[2])
box()
lines(death,type="o",pch=22,lty=2,col="blue")
lines(recov,type="o",pch=22,lty=2,col="red")
title(main="COVID-19 CASES IN NEPAL",col.main="black",font.main=4)
title(xlab="Time",col.lab=rgb(0,0.5,0))
title(ylab="Number of Cases",col.lab=rgb(0,0.5,0))
legend(1,g_range[2],c("Conformed","Dead","Recovered"),cex=0.8,col=c("black","blue","red"),pch=21:22,lty=1:2)
```

[3] R codes: SIR model simulation of Nepal

```
Libyary<-(covid19.analytics)
ag<-covid19.data(case='aggregated')
tsc<-covid19.data(case='ts-confirmed')
report.summary(geo.loc = 'Nepal',graphical.output = F)
#Total per Location
```

```
tots.per.location(tsc,geo.loc='Nepal')
tots.per.location(tsc,geo.loc='India')
tots.per.location(tsc,geo.loc='China')
#Growth Rate
growth.rate(tsc,geo.loc='Nepal')
growth.rate(tsc,geo.loc='India')
growth.rate(tsc,geo.loc='China')
#Total Plot
totals.plt(tsc,geo.loc0='Nepal',one.plt.per.page=TRUE,log.plt=FALSE,fileName=TRUE)
totals.plt(tsc,geo.loc0= 'india',one.plt.per.page =TRUE,log.plt=FALSE,fileName=TRUE)
totals.plt(tsc,geo.loc0='China',one.plt.per.page=TRUE,log.plt=FALSE,fileName=TRUE)
totals.plt(tsa,c('India'))
totals.plt(tsa,c('Nepal'))
totals.plt(tsa,c('China'))
generate.SIR.model(tsc,'Nepal',tot.population=28090000)
```

[4] R codes: COVID-19 Cases of India.

```
conf<-c(1,3,3,3,44,84,360,909,3577,8447,16116,26917,62939,90927,131686,
182142, 235657,308993,410461,508953,648315,849553)
death<-c(0,0,0,0,0,2,7,19,83,273,519,826,2109,2872,3867,5164,6642,8884,13254,
15685,22674)
recov<-(0,0,0,3,3,3,3,80,274,765,2301,5913,19357,34109,54440,86983,119292,162378,
227755,309712,409082,534629)
g_range<-range(0,conf,death,recov)
plot(conf,type="o",col="black",ylim=g_range,axes=FALSE,ann=FALSE)
axis(1,at=1:22,lab=c("31/1","6/2 ","13","28","9/3","14","22","28","5 /4","12", "19","26",
"10 /5","17","24","31","7 /6","14","21","28","5 /7","12"))
axis(2,las=1,at=10*0:g_range[2])
box()
lines(death,type="o",pch=22,lty=2,col="blue")
lines(recov,type="o",pch=22,lty=2,col="red")
title(main="COVID-19 CASES IN INDIA",col.main="black",font.main=4)
title(xlab="Day/Month",col.lab=rgb(0,0.5,0))
title(ylab="Number of Cases",col.lab=rgb(0,0.5,0))
legend(1,g_range[2],c("Conformed","Dead","Recovered"),cex=0.8,col=c("black","blue",
"red"),pch=21:22,lty=1:2)
```

[5] **R codes: A comparative plot of confirmed COVID-19 infection cases for Nepal and its neighbour countries.**

```
chi<-c(278,2798,17238,40235,70635,77262,80174,80904,81077,81601,82447,
83005,83597,84237,84341,84400,84450,84494,84530,84588, 84634,84778,85018,
85204,85320,85568,86068)
ind<-c(0,0,3,3,3,3,3,43,114,415,1071,4067,9152,17265,27892,42533,67152,96169,
138845,190535,256611,332424,425282,548318,697413, 878254,1118043)
nep<-c(0,0,1,1,1,1,1,1,1,5,9,12,31,51,75,120,304,673,1572,3448,5760,9026,12772,15784,
16801,17658)
g_range<-range(0,chi,ind,nep)
plot(chi,type="o",col="black",ylim=g_range,axes=FALSE,ann=FALSE)
axis(1,at=1:27,lab=c("20/1","27","3/2","10","17","24","2/3","9","16","23","30","6/4","13",
  "20","27","4/5","11","18","25","1/6","8","15","22","29","6/7","13","20"))
```

```
axis(2,las=1,at=10*0:g_range[2])
box()
lines(ind,type="o",pch=22,lty=2,col="blue")
lines(nep,type="o",pch=22,lty=2,col="red")
title(main="Time Series Plot for Confirmed COVID-19 Cases",col.main="black", font.main=4)
title(xlab="Day/month",col.lab=rgb(0,0.5,0))
title(ylab="Number of Confirmed COVID-19 Cases",col.lab=rgb(0,0.5,0))
legend(1,g_range[2],c("China","India","Nepal"),cex=0.8,col=c("black","blue","red"),pch=21:22,lty=1:2)
```