

International Journal of Graduate Research and Review

ISSN: 2467-9283



Indexing and Abstracting

InfoBase Index, Cosmos, Open Academic Journals Index (OAJI), InfoBase Index, Cosmos, ResearchGate, CiteFactor, Scholar Stear, JourInfo, ISRA: Journal-Impact-Factor (JIF), Root Indexing etc

Impact Factors*

IBI factor: 3 Impact factor (OAJI): 0.201

> Vol-7, Issue-1 February 2021





Research Article

Mathematical Modelling of COVID-19 Pandemic in Nepal Using Logistic Growth Model

Laxman Bahadur Kunwar¹, Vijai Shanker Verma^{2*}

¹Department of Mathematics, Tribhuvan University, TRM Campus, Birgunj, Nepal ^{2*}Department of Mathematics & Statistics, DeenDayal Upadhyaya Gorakhpur University, Gorakhpur, India

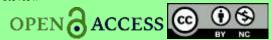
Article Information

Received: 26 November 2020 Revised version received: 30 December 2020 Accepted: 05 January 2021 Published: 25 February 2021

Cite this article as: L.B. Kunwar and V.S. Verma (2021) Int. J. Grad. Res. Rev. Vol 7(1): 17-24.

*Corresponding author Vijai Shanker Verma, Department of Mathematics & Statistics, DeenDayal Upadhyaya Gorakhpur University, Gorakhpur, India. Email: drvsverma01@gmail.com

Peer reviewed under authority of IJGRR © 2021 International Journal of Graduate Research and Review



Abstract

In this study, coronavirus disease (COVID-19) outbreak in Nepal is studied by using exponential and logistic mathematical models. The model is analysed by deriving some important expressions such as growth rate of epidemic, maximum possible number of infected people and corresponding time of epidemic peak, relationship between number of cases per day and the total number of cases. The main objective of the study is to examine the applicability of the logistic model for the study of the COVID-19 pandemic and other similar communicable diseases in the future. The estimation of the parameters of the model is based upon COVID-19 pandemic data from January 20, 2020 to October 14, 2020. The actual time-series data of the coronavirus disease 2019 for Nepal seem to good fit the proposed 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. The detailed derivations of the expressions are presented regarding the working situation of non-mathematics researchers in the field of Biological Sciences.

Keywords: logistic equation; exponential growth; growth rate; mathematical modelling; coronavirus COVID-19; pandemic.

This is an open access article & it is licensed under a <u>Creative Commons Attribution Non-Commercial 4.0 International</u> (<u>https://creativecommons.org/licenses/by-nc/4.0/</u>)</u>

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 et al., 2020). China's health authorities and Centers for Disease Control and Prevention (CDC) quickly identified the pathogen of such cases as one of the type of coronavirus, which on January 10, 2020, the World Health Organization (WHO) named the reemerged 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 to explain the relevant situation of pneumonia and possible way to control 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 pneumonitis of new coronavirus infection. The plan had included the COVID-19 epidemic research, specimen collection and testing method, tracking and management of close contacts, and propaganda, education and communication to the public etc. (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 October 14, 2020, the cumulative number of confirmed cases has reached 115357 in Nepal and 37109851 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 basic reproduction number (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, unquarantined infected, quarantined infected, confirmed infected' (SUQC) model to characterize the dynamics of outbreaks (Zhao and Chen, 2020). Ivorra et al. (2020) have developed a mathematical model for the spread of the coronavirus 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). Recently, transmission dynamics of coronavirus in the context of Nepal has been studied mathematically by applying the SIR model with the determination of the related parameters (Kunwar, 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 (Hethcote, 2000). 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 key parameter basic reproductive number (R_0) 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.

The spread of COVID-19 is described using logistic equation and the parameters of the model for Nepal are determined. Detailed derivations are presented considering non-mathematicians working in the field of biological sciences and non-availability of these derivations in the literature.

Method

Data were collected on the epidemic situation of COVID-19 in Nepal and compared the results with those of the logistic model with different parameter setting scenarios. The numbers of positive novel corona virus (COVID-19) cases in Nepal from January 20, 2020 to October 14, 2020 were recorded. The data source was based on the daily reports of WHO situation analysis of COVID-19. The initial 100 days were considered for the estimation of the values of the parameters. The modelling and the visualizations were carried out using the MATLAB software and COVID-19. analytic version 1.1.1 package developed in the *R*-program 3.6.1 version.

Mathematical Modelling

Malthusian Growth Model

Thomas R. Malthus, in 1798 proposed the mathematical model for the population growth, called Malthusian law of population growth which is widely regarded as the first principle of population dynamics in the field of population ecology (Malthus, 1798). The law is also called the exponential population growth model.

Let N(t) is the total population of a species at time t. Then the rate of change of the population is proportional to the population at that time so that we have

$$\frac{dN}{dt} = (b-d)N(t)$$

or, $\frac{dN}{dt} = rN(t)$

Here, r = b - d is called growth rate. The above ODE is separable so for $N \neq 0$, we can write

$$\int \frac{1}{N} dN = r \int dt$$

or, log N = rt + C

Here, C is an arbitrary constant which is determined using initial condition, $N(0) = N_0$ i.e. taking the initial population size as N_0 . Thus we have

$$\log N_0 = 0 + C$$

or, $C = \log N_0$
 $\therefore \log N = rt + \log N_0$
or, $\log \left(\frac{N}{N_0}\right) = rt$
or, $\frac{N}{N_0} = e^{rt}$
or, $N = N_0 e^{rt}$

0.0

Thus, we have

This model indicates that the population at any time depends on two parameters; the growth rate r and the initial population size N_0 . The dependence on parameter of the solution of the exponential model is shown in Fig' 1.

Logistic Growth Model

The logistic equation in differential form was suggested by the Belgian Mathematician Pierre Verhulst in 1845 to model population growth (Verhulst, 1845). It can be considered as the modification on the existing exponential growth model. The logistic growth model for the population N of any species is written in the ODE form as

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right).$$
(2)

Here, N(t) represents the total number of people affected by the epidemic.

K: Maximum number of infected people during the whole epidemic period.

r: growth rate of the epidemic.

t: time from the beginning of the epidemic.

The two particular solutions are N(t) = 0 and N(t) = K for all *t* corresponding to equilibrium points, and for $N(t) \neq 0$, we have

$$\int \frac{K}{(K-N)N} dN = \int r dt$$

or, $\int \frac{(K-N)+N}{(K-N)N} dN = rt + C$
or, $\int \left[\frac{1}{N} + \frac{1}{(K-N)}\right] dN = rt + C$
or, $\log |N| - \log |K-N| = rt + C$
or, $\log \left|\frac{N}{K-N}\right| = rt + C$

$$or, \left|\frac{N}{K-N}\right| = e^{rt} \cdot e^{C}$$

Using initial condition $N(0) = N_0$, we get

$$\left|\frac{N}{K-N}\right| = e^{C}$$

or, $\left|\frac{N}{K-N}\right| = \left|\frac{N_{0}}{K-N_{0}}\right| \cdot e^{rt}$

The orbit of any $N_{0}\neq 0$ or *K* cannot include 0 or *K*. So, neither *N* nor *K*-*N* can change sign on an orbit and hence the sign of $\frac{N}{K-N}$ is the same for all *t*. Thus, we have

$$\frac{N}{K-N} = \frac{N_0}{K-N_0} e^{rt}$$

$$or, N = \frac{K \frac{N_0}{K-N_0} e^{rt}}{1 + \frac{N_0}{K-N_0} e^{rt}}$$

$$or, N = \frac{K N_0 e^{rt}}{K-N_0 + N_0 e^{rt}}$$

Thus, we have

The solution depends on two parameters, the initial population N_0 and the linear growth rate r. At the initial stage of the epidemic, t = 0, and the model also shows the same growth as the Malthusian model and the population of infectives is governed by following exponential equation.

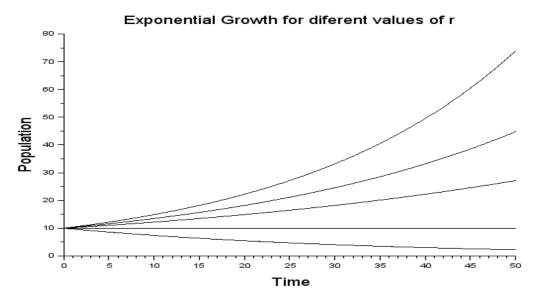


Fig. 1: The dependence on parameters of solution of the exponential model with initial population size $N_0 = 10$ and the different growth rates (*r*).





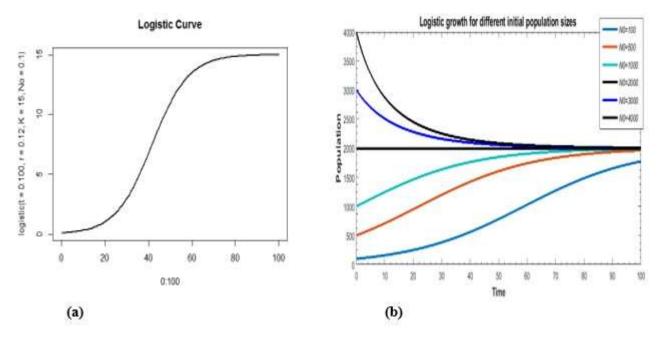


Fig. 2: (a) Growth of population in Logistic model. Population cannot grow to infinity but bounded by an upper limit (carrying capacity). (b) Logistic curves, varying the initial population with the fixed *K*=2000 and constant growth rate (r=0.05).

The logistic model is characterized by an increasing growth rate at the beginning of the epidemic, however, as the population size increases and approaches the maximum limit, the growth starts to decrease until reaches to zero and the curve change from a convex to concave. The maximum limit is called the carrying capacity (K).

For the medical point of view, the expression for the optimal rate of the infected population has a great importance. The equation (3) is differentiable and by differentiating it, we get

$$\frac{dN}{dt} = \frac{N_0 K (K - N_0) r e^{rt}}{\left(K + N_0 \left[e^{rt} - 1\right]\right)^2}....(5)$$

The curve has non-monotonic characteristic and it yields the maximum rate of infected population as,

$$Max.\left(\frac{dN}{dt}\right) = \frac{rK}{4}....(6)$$

For the corresponding epidemic peak time, substituting $\frac{dN}{dt} = \frac{rK}{4}$ in the equation (2), we get

$$\frac{rK}{4} = rN\left(1 - \frac{N}{K}\right)$$

or, $4N^2 - 4KN + K^2 = 0$
or, $(2N - K)^2 = 0$
 $\therefore N = \frac{K}{2}$

Now, substituting in equation (3), we obtain

$$\frac{K}{2} = \frac{N_0 K}{N_0 + (K - N_0)e^{-rt}}$$

$$or, 2N_0 = N_0 + (K - N_0)e^{-rt}$$

$$or, \frac{1}{e^{-rt}} = \frac{K - N_0}{N_0}$$

$$or, e^{rt} = \frac{K - N_0}{N_0}$$

$$or, \ln e^{rt} = \ln\left(\frac{K - N_0}{N_0}\right)$$

$$or, rt = \ln\left(\frac{K - N_0}{N_0}\right)$$

$$or, t = \frac{1}{r}\ln\left(\frac{K - N_0}{N_0}\right)$$

Hence, the time of the epidemic peak is given by

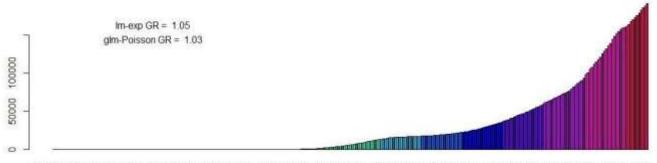
$$T_{p} = \frac{1}{r} \ln \frac{K - N_{0}}{N_{0}}....(7)$$

As it can be seen, these characteristics equations (6) and (7) can be estimated when the data are no longer described by an exponential curve and both model parameters r and K are found or known.

The time dependences by relations (3) and (5) are smooth functions as shown in the histogram in Fig. 3 and reported daily active cases by days. The variation of the Fig.4 shows that dependence (5) must be non-smooth and irregular.







2020-01-22 2020-02-19 2020-03-18 2020-04-15 2020-05-13 2020-06-10 2020-07-08 2020-08-05 2020-09-02 2020-09-30 2020-10-28

Fig. 3: Histogram of the total infected cases versus time from day zero for Nepal.

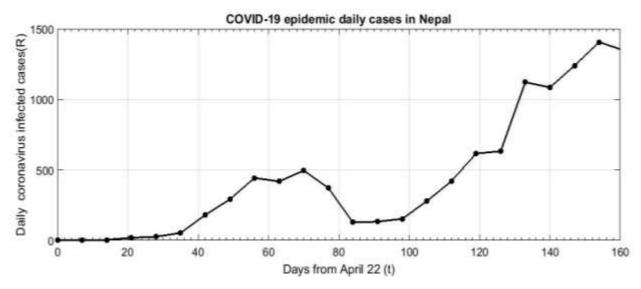


Fig. 4: Graph showing the daily infected cases versus time from day zero.

The number of infected cases per day is required for much further analysis in the medical statistical operation. The expression for the rate of the infected population can be determined by solving the difference logistic equation

$$R_n = N_{n+1} - N_n = rN_n \left(1 - \frac{N_n}{K}\right)$$
.....(8)

After removing the index, we obtain a simple relationship between the number of cases per day (R) and the total number of cases (N)

$$R = rN\left(1 - \frac{N}{K}\right).$$
(9)

This is an equation of a parabola in terms of the variables R and N. In the Figure 8 the solid lines are the plotting of

R versus N, and curves are parabolic. The dots are the actual data and they good fit the predicted path.

We can say that one active phase is over the distribution of the data of Nepal clearly follows the equation (9). The graph shows the Parabolic approximations (the solid line) arising from equation (9) which represents the relationship between the number of cases per day (R) and the total number of cases (N) for Nepal. The observed data for the period of April 22, 2020 to October 14, 2020 are also presented in the same plot. Eventually, the parabolic approximation of the available data is good enough for the country. So the logistic model is suitable for the population dynamics of the coronavirus disease epidemic in Nepal.



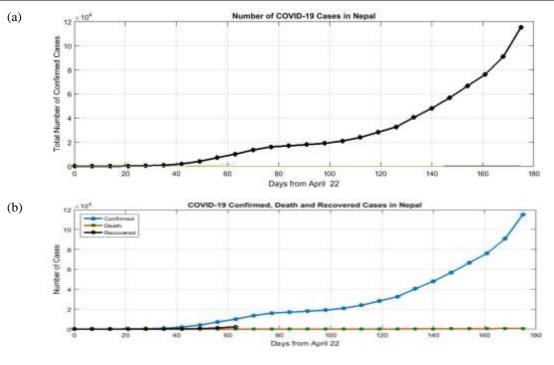


Fig. 5: (a) Graph of the cumulative number of novel coronavirus cases versus number of days starting from April 22 in Nepal (Data is recorded weekly). (b) Comparative graph showing infected cases, death cases and recovered cases of COVID-19.

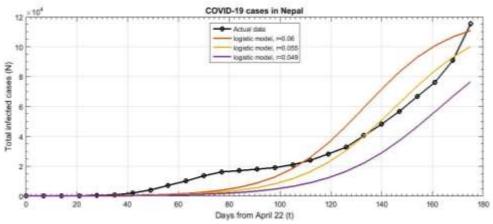
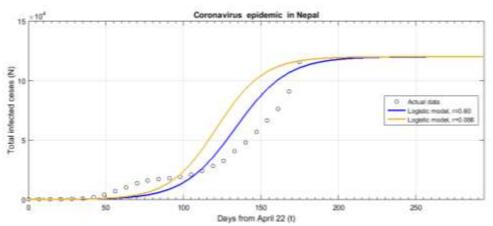
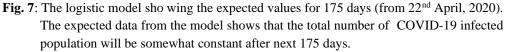


Fig. 6: Curves of the actual total infected cases with COVID-19 coronavirus and the logistic model estimated numbers in Nepal from April 22, 2020 to October 14, 2020.







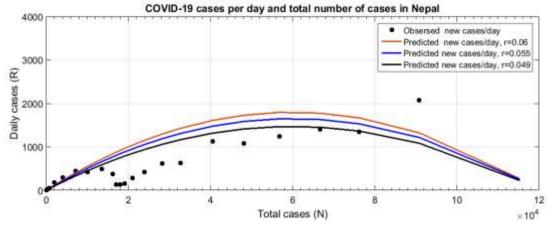


Fig. 8: The relationship between the number of cases per days (R) and the total number of cases (N) in the framework of the logistic model: approximation from Equation (9) is given by lines. The lines show the parabolic curves in the framework of the logistic model and the observed data (represented by dots) of Nepal are closely around the curve.

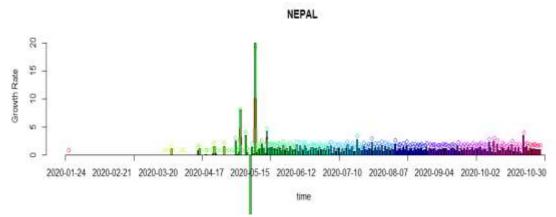


Fig. 9: Graph showing the growth rate of the infected cases with respect to previous day.

Results and Discussion

At the initial stage of the epidemic, the exponential curve good fits the actual number of cases. Graph in the Figure 7 shows the data of first 140 days good fits the logistic model. In the graph, x-axis is the number of days starting from April 22 whereas y-axis is the number of cumulative cases. The black line is the model fitted to the data. The first 70 days follows the exponential growth model but after 70 days the curve slightly flattened and begins to follow the logistic growth model. The Figures (6) and (7) illustrate the good correspondence between the logistic model fitted and real data for Nepal.

Using the exponential growth model for initial phase (100 days) we determine the value of the growth rate for Nepal as r = 0.0616. If the actual data would not have fit the exponential expected values, we would reject the logistic growth model at the same stage. At the same time, the most important characteristic for prediction, the maximum possible number of infected population *K*, is estimated only at the stage the noticeable difference between the data

and the exponential curve, when the number of infected people is already not small. We have used the maximum possible number of infected population (K) as 120000 taking 100 days from 22nd April 2020 period and we also determine the value of the growth rate (r) using the logistic growth equation (3) and its value is found to be r = 0.063, which is approximately same as obtained from the exponential growth model for the same period of 100 days. On the basis of the equation (6) the maximum rate for the Nepal is $max.\left(\frac{dN}{dt}\right) = 1890$ people per day. Nepal must have peak of confirmed cases on October first week of 2020 (after128 days from April 22, 2020) on the basis of the model. Nepal has its peaks of confirmed cases and deaths on September last week 2020 on the basis of the reported data, but the Nepal has not completed the complete one phase of the pandemic till now. According to the WHO database, Nepal has a total of 1, 15,357 cumulative confirmed cases due to COVID-19 with 562 deaths as of October 14, 2020. As the country had passed

the peaked of the pandemic, the official publishing data on the peaks was compared to the forecast obtained using the model.

Conclusion

Mathematical modelling of the dynamics of the spread of COVID-19 infection in Nepal is carried out. The simplest non-linear equation describing logistic model is selected as the model. This model contains only two parameters that are chosen based on statistical data at the initial stage (first 100 days) of the epidemic. The logistic model captures the observed trend that initially confirmed cases increased slowly, and then increased rapidly before it slowed down again. The first parameter is the rate of increase in confirmed cases and seconds the maximum possible population resident who can potentially be infected with K(Normalization factor). The values of the parameter depend on a number factors, such as the population size, crowding (population density), resistance to disease, disciple of the population during quarantine measure etc. The findings suggest that the quick detection of cases, sufficient implementation of quarantine and public selfprotection behaviour are the best measures to reduce the transmission rate of the COVID-19.

Limitations

The obtained biological parameters for COVID-19 are based on the current reported data, but these values might be refined as more comprehensive data become available. Additional work is required to improve the accuracy of the parameter values and estimation.

Acknowledgement

I would like to thank Professor Dr. Manju Agarwal, Former Head of Department of Mathematics & Astronomy, Lucknow University, Lucknow, India, for her encouragement, critical reviews and suggestions that improved the quality and presentation of the paper.

Conflict of Interest

The authors declare that there is no conflict of interest with present publication.

Authors' Contributions

First author led the literature survey, data collection, modelling, plotting graphs using MATLAB & R-programming and prepared the first draft of the manuscript. Both the authors worked on the analysis, interpretation of findings, reviewed the manuscript and made the final draft. Both the authors read and approved the final manuscript.

References

- Hethcote HW (2000) The mathematics of infectious diseases. *SIAM review*. **42(4):** 599-653.
- Ivorra B, Ferrández MR, Vela-Pérez M & Ramos AM (2020) Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections. The case of China. *Communications in nonlinear science and numerical simulation*. 105303.
- Kunwar LB (2020) Mathematical Modelling of Transmission Dynamics of COVID-19: A Case Study of Nepal. *Prithvi Academic Journal*. 19-38. DOI: https://doi.org//10.3126/paj.v3il.31283
- Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, & et al. (2020) Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. *New England Journal* of Medicine. **382:** 1199-1207.
- Liu Y, Gayle AA, Wilder-Smith A & Rocklöv J (2020) The reproductive number of COVID-19 is higher compared to SARS coronavirus. *Journal of travel medicine* 27(2): taaa021. DOI: https://doi.org/10.1093/jtm/taaa021
- Malthus TR, Winch D & James P (1992) Malthus': An Essay on the Principle of Population'. Cambridge University Press.
- National Health Commission of the People's Republic of China (2020, July) *Daily Briefing on novel coronavirus cases in China*. China Daily. Retrieved from http://en.nhc.gov.cn/
- Roosa K, Lee Y, Luo R, Kirpich A, Rothenberg R, Hyman JM, Yan P & Chowell G (2020) Real-time forecasts of the COVID-19 epidemic in China from February 5th to February 24th, 2020. *Infectious Disease Modelling*. 5: 256–263. DOI: https://doi.org/10.1016/j.idm.2020.02.002.
- Shen M, Peng Z & Xiao Y (2020) Modeling the epidemic trend of the 2019 novel coronavirus outbreak in China. *bioRxiv*. DOI: https://doi.org/10.1101/2020.01.23.916726.
- Verhulst PF (1838) Notice sur la loi que la population suit dans son accroissement. *Corresp. Math. Phys.* **10:** 113-126.
- Verhulst PF (1845) Recherches mathématiques sur la loi d'accroissement de la population. *Journal des économistes* **12**: 276.
- World Health Organization (2020, October) Situation Reports on Coronavirus Disease (COVID-19) Pandemic. WHO COVID-19 Dashboard.
- Zhao S & Chen H (2020) Modeling the epidemic dynamics and control of COVID-19 outbreak in China. *Quantitative Biology*. 1-9.
- Zhao S, Lin Q, Ran J, Musa SS, Yang G, Wang W, Lou Y, Gao D, Yang L, He D, Wang MH. (2020) Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak. *International journal of infectious diseases* 92: 214-217

