

## Probabilistic Approach of Growth of Coronavirus

Mobin Ahmad

*Department of Mathematics, Faculty of Science, Jazan University, Jazan 45192, Saudi Arabia*

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### **ABSTRACT**

A new coronavirus was detected on a wholesale market for seafood in Wuhan, China in December 2019. This coronavirus was officially named COVID-19 by WHO. China had registered a total of 78 824 COVID-19 cases and 2,788 deaths as of 28 February 2020 since the first patient was admitted to hospital on 12 December 2019. Wuhan's confirmed combined cases and deaths made up 61.1% of the total China mainland and 76.5% of it a priority region for the preventing and control of epidemics. In the meantime 4.879 confirmed cases, and 79 deaths as of Feb 28, 2020, had been registered by 51 countries and regions outside of China. The outbreak COVID-19 affects the day-to-day life and the economic development of the country greatly. This paper uses three types of math model: logistic model, model of Bertalanffy, and model of Gompertz. In order to prove the validity of current mathematical models, epidemia patterns of SARS were first adapted and analyzed. The findings were used to modify and evaluate the COVID-19 situation. For different parameters and locations, the prediction outcomes of three mathematical trends are different. In general, among the three models tested, the fitting effect of the Logistic Model could be the best while the fitting effect of the Gompertz model might be better than the Bertalanffy model. Based on current trends, the number of people in non-Hubei and 80261-85140 in China, respectively, estimated to be infected by Wuhan is 49852-57447, 12972-13405. The total number of deaths in Wuhan is between 2502-5108, NonHubei 107-125 and China 3150-6286. COVID-19 is expected to be reached in other regions by the end of April 2020, in Wuhan and by the end of March 2020.

**KEYWORDS:** Probabilistic, Growth, coronavirus, infection management and control, travel restriction, mathematical model.

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### **I. INTRODUCTION**

In China since December 2019 a number of unidentified cases of respiratory infectious diseases caused by the novel coronavirus have successively been discovered. Since mid-December 2019, the outbreak of COVID-19 has experienced 3 phases: local outbreak, population transmission and wide transmission. Local outbreak stage: This phase is primarily an outbreak in local populations exposed to the demand for seafood before the end of December 2019. The exposure of the seafood market was mainly related at this point. The stage of transmission to the community: the virus spreads through the early infected populations and forms the community's transmission due to the spread of the epidemic. In many communities and families in Wuhan, interpersonal and cluster transmission has occurred. The process of the wider transmission of the epidemic: Due to the high mobility of staff during the Chinese Lunar New Year, the epidemic quickly grew and spread from Hubei Province to other areas in China and the number of COVID-19 cases in other countries increased gradually.

At 24:00, the total number of confirmed cases of COVID-19 and 2870 deaths was announced by China on 29 February 2020 in 79,824. 61,5 percent, and 76,5 percent, of the region, which is the focus area for disease prevention and control, were the total number of confirmed cases and deaths at Wuhan. Simultaneously, 7,661 confirmed cases and a total of 121 deaths were recorded in countries and regions outside China. Infectious diseases are a serious threat to human life and health, a serious threat to economic and social development and a risk to national security and stability. The diseases are a serious threat to human society. The results of economic globalization, foreign trade, better transport and faster movements of people and goods have produced favorable conditions for the broad spread of infectious diseases, thereby increasing and widening the spread of infectious conditions. Many infective diseases, including COVID-19, SARS (2003), influenza H1N1, H5N1, etc., which have arisen in recent years have a major impact on human health and social life. Whether infectious diseases can be controlled and the transmission of infectious diseases can be eased is an urgent problem that society is currently facing. For the prediction of various infectious diseases, theoretical analysis, quantitative analysis and simulation are required. The above analysis can not be carried out without models established for various infectious diseases.

### **Risk of the 2019-Covid for Public Health**

Coronaviruses are single-strand RNA-viruses that are part of the Coronaviridae family. They usually cause mild breathing infections, even if they are often deadly. The pneumonia epidemic has received considerable international attention since 31 December 2019, when the Wuhan Municipal Health Commission confirmed 27 viral pneumonia cases, including 7 severely diseased cases. On 7 January 2020 the Chinese authorities identified a novel coronavirus as the causative agent and on 10 January 2020 the same coronavirus was identified by the World Health Organization (WHO). On the same day the WHO released a wide range of interim recommendations for all countries, including how to monitor potential infection, collect and check patients, track and reduce the burden of infection in health centers, maintain good drug supply and interact effectively with the lay people. By the morning of 23 January 2020, in other parts of China as well as in various countries such as South Korea, Japan, Thailand, Singapore, Mexico and the Philippines and the United States of America, more than 571 confirmed cases with 17 deaths had been recorded. 28,276 incidents, 3863 of which were serious and 565 had been registered as of 6 February 2020 (02:45 GMT). In the current and evolving intervention measures, the transmission capacity, mostly determined by simple reproductive number, time and value, and length of outbreak, remains unclear and needs further research. The government of China revised the regulations on infectious diseases on 20 January 2020 in order to include the 2019-nCoV as a Class B agent (an epidemic-causing pathogen). The same day officials in public health announced that the new virus should be listed as a class A (pathogen which may trigger an outbreak within a short period) agent. Several non-pharmaceutical (NPIs) measures have been introduced, including extensive monitoring contacts accompanied by quarantine of people who may be exposed and isolation of contaminated, symptomatic subjects, but their effectiveness is uncertain at an early stage. In order to prepare Wuhan and other cities and respond rapidly to the importation of infected cases, it is necessary to measure the effectiveness of those actions. With the advent of the Spring Festival, a large section of the population will be mobilizing mass movement, which will usually reseed the new coronavirus. Radical measures have been taken without precedent. As an example, China's authorities placed travel restrictions on five cities on 23 January 2020, effectively shutting down the movement of over 40 million people (Wuhan, Huanggang, Ezhou, Chibi, and Zhijiang). Nevertheless, it remains to be determined whether such expensive and resource consuming steps will contribute to preventing and controlling infections and how long travel restrictions will be enforced in those towns and other parts of the country. The estimation of the fundamental breeding number of a new coronavirus affecting a naive population is important to determine the potential and severity of an outbreak and to provide critical information for the design and implementation of disease outbreak responses in the identification of the best possible, evidence-based interventions, mitigation measures and determination measures. The WHO recognizes that mathematical models, especially timely ones, play an important role in advising health decision-makers on evidence-based decisions. As far as we know, only a few mathematical models have been publicly released, including a transmission network model of the Bats-Hosts-Reservoir-People system and a repeated traveller trial to assess undervalued cases of coronavirus.

### **TRADITIONAL MODEL FOR PREDICTION OF INFECTIOUS DISEASES**

Traditional models for the prediction of infectious diseases primarily include differential prediction and time series models based on statistics and random processes. The Differential Equation Prediction Models create a differential equivalent, which can represent the infectious disease's dynamic characteristics according to population growth characteristics, disease occurrences and population-wide transmission rules. The frequency of diseases can be demonstrated, the transmission laws are known, the improvements and development patterns are predicted, the causes and key factor for the transmission of diseases are analyzed, optimal methods for prevention and control and the theoretical and quantitative bases are established, and the model dynamics are simulated numerically and qualitatively. Popular models for the prediction of dynamic infectious diseases differential equations have ordinary differential systems, directly representing the relation between each compartment's immediate rate of change and the corresponding time for each compartment. A that model system is a partial differential system in the light of the age structure. Delay differential system is a type of differential system which is used when a stage structure is considered (such as the diseased person has a certain infectious duration, the latent person has a certain incubator period, the immune person has a certain immune period, and so on). The classical model of differential equating prediction assumes that there is a clear total population in a certain region that can speed the natural infectious disease transmission cycle, explain the evolution of different node types in relation to the time, and reveal the overall information transmission law. The population, however, is changing over time in practice. In terms of food, services and living areas, there will toujours be some sort of contact with other populations. The relation between people is random and the difference between spreads is ignored which limits the model's scope of application. Time-Series Models predict infectious diseases by study of one-dimensional time series of occurrence of infectious diseases based on statistical data and random processes. Usually Autoregressive Integrated Moving Average Model (ARIMA),

Exponential Smoothing Method (ES), Gray Model (GM), Markov chain method, etc. ARIMA Prediction Model, which allows a stationary set of differences and is used as a combination auto reverse of the sequence to some degree in the past, is the commonly used model of time series. The infectious disease prediction model developed by this approach is based on an approximation of the parameters of available time series data and the use of a large number of irregular data is therefore difficult.

### **INTERNET MONITORING OF INFECTIOUS DISEASES**

Work on Internet-based infectious disease surveillance has begun to grow since the mid-1990s. It can provide public health institutions, medical workers and the public with information services. It can provide early warning and situational awareness information for consumers of infectious diseases following detection and processing. The key source of data was the traditional web page details (e.g. related news articles, authoritative bodies, etc.). Nevertheless, in recent years, work has started with the development of the Internet, expanding social media data sources (e.g. Twitter, Facebook, micro blog, etc.) and media. Due to the global expansion of the internet, people are using search engines, online social networks and map tools to monitor the frequency and location of query keyword information, to improve the integration of financial, public and hot problem data, to conduct search engine and social media disease surveillance, and to predict the impact of infectious diseases. Internet search is theoretically successful and can represent infectious diseases' real-time status. Thus, Internet and search engine application infectious disease prediction models are a good addition to the traditional models for the prediction of infectious diseases. U.S. scientists compared the flu predictions for different countries and regions with official flu monitoring data from 2004 to 2009 and found that the Google search engine projections were similar to the actual influenza epidemic. Jiwei et al. have filtered the Twitter data stream, maintained fluoride information, and tagged geographically located information to indicate from which Twitter fluoride information came and how the information changed over a certain time period. It has shown that there is an extremely positive link between Twitter influenza details and influenza outbreak data from the US, with some 1 million users publishing messages around 3,6 million Twitter flu-relating from June 2008-June 2010. Disease Control and Prevention Centers 14. Centres. Google launched Google's Dengue Trends (GDT) in 2011 and, according to the Google Search Patterns, Google Flu Trends (GFT) and other resources for quantitatively monitoring the pattern of infectious disorders such as dengue fever and influenza in many regions of the world<sup>15</sup>. The Internet model of prediction of infectious diseases has the benefits of being fast and in real time as compared with conventional predictive models which can forecast the infectious disease trend as soon as possible and are ideal for a large number of people's data analyses. Nevertheless, its sensitivity, spatial resolution and prediction accuracy must be further improved. Therefore, models based on the Internet for infectious disease predictions cannot replace the conventional models and can only be used to extend the traditional model for forecasting infectious disease. This paper is to utilize 2003 SARS data to verify the 3 mathematical models (logistic model, Bertalanffy model, and model Gompertz) to determine the virus' development trend. These three models are then utilized to fit and analyze COVID-19 epidemic trends in Wuhan, mainland China and non-Hubei regions.

### **EARLY DETECTION OF MACHINE LEARNING INFECTIOUS DISEASES**

In short, machine learning is to learn more useful knowledge for particular problems across a wide variety of data using its own algorithms model. Machine learning encompasses a variety of areas, including medicine, computer science, mathematics, engineering, psychology, etc. For instance, neural networks, a very advanced algorithm for machine learning, can simulate high-dimensional, optimal mapping between input and output by simulating the processing mechanism of the nervous system of the biological brain. In the face of complex relationships of data, the conventional statistical method is not so successful that reliable results can not be obtained as the neural network<sup>18</sup>. Since the majority of new human infectious diseases (animal infectious diseases) are of animal origin, it is successful preconditions for the prevision of diseases by defining the specific intrinsic features of species and environmental conditions leading to an influx of new infections. New reservoirs (mammals) and carriers (insects) of zoonotic disease can be precisely predicted by studying the intrinsic characteristics of wild species by machine-learning. The main objective of computer-based learning is to extend theory of the causality of inferences and machine learning to define, measure and produce visual tools to explain the dynamic causal relationships and associations between animal infectious diseases and the zoonotic diseases. The extremely non-linear and complex problems to be analyzed in the early prediction model of machine learning-infectious diseases usually lead to local minima and foreign minima, which lead to some restrictions in the machine learning model.

**Mathematical model**

Infectious disease forecasting models include primarily dynamic and time series prediction models based on statistics and random processes, the Internet-based infectious disease prediction model, and machine learning. Some of the models are too complex, and too many variables are taken into account. The logistic model, models Bertalanffy and GOMPERZ are chosen in this paper to forecast the epidemic situation of the COVID19, which are relatively simple but in compliance with the statistical law of epidemiology. The least square approach for curve fitting is used after the pattern is chosen. Mathematical optimization is the least square form. It finds the best data function by reducing the number of square errors. The least square approach is used to rapidly collect unknown data and minimize the amount of error squares between these data and actual data.

**1. Model Selection**

**(1) Logistic model:** Logistic model is mainly used in epidemiology. It is commonly to explore the risk factors of a certain disease, and predict the probability of occurrence of a certain disease according to the risk factors. We can roughly predict the development and transmission law of epidemiology through logistic regression analysis,

$$Q_t = \frac{a}{1 + e^{b-c(t-t_0)}} \tag{1}$$

$Q_t$  is the cumulative confirmed cases (deaths);  $a$  is the predicted maximum of confirmed cases (deaths).  $b$  and  $c$  are fitting coefficients.  $t$  is the number of days since the first case.  $t_0$  is the time when the first case occurred.

**(2) Bertalanffy model:** The model of Bertalanffy is often used as a model of growth. It is used primarily to analyze factors that influence growth and power. The growth features of fish are described. Species of animals such as pigs, horses, cattle, sheep and other infectious diseases can also be identified by other species. Infectious disease production is related to the growth of people and communities. The Bertalanffy model is chosen in this paper to explain the propagation law of infectious diseases and to study the factors influencing and affecting COVID-19 spread.

$$Q_t = a(1 - e^{-b(t-t_0)})^c \tag{2}$$

$Q_t$  is the cumulative confirmed cases (deaths);  $a$  is the predicted maximum of confirmed cases (deaths).  $b$  and  $c$  are fitting coefficients.  $t$  is the number of days since the first case.  $t_0$  is the time when the first case occurred.

**Fitting and analysis of COVID-19 epidemic**

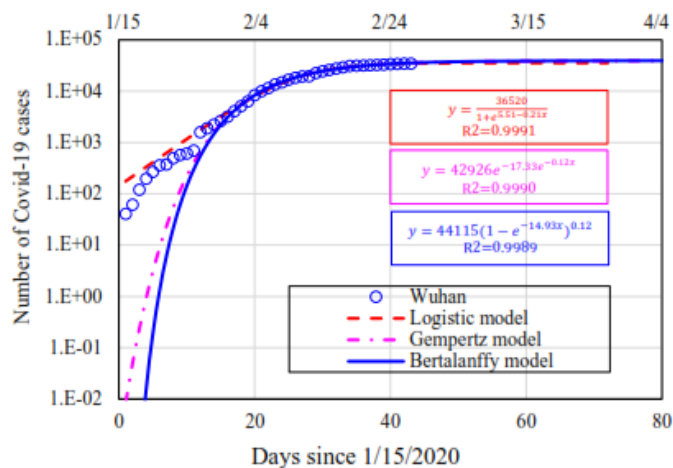
As COVID-19 and SARS virus are both coronaviruses, the infection pattern may be similar. Firstly, we used SARS data to verify the rationality of our model.

**1. Number of Confirmed Cases**

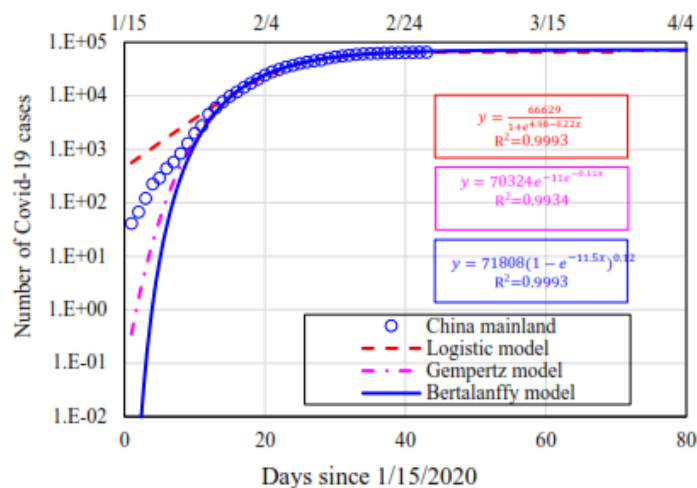
Figure 1 indicates the total number of confirmed new coronavirus cases (hereinafter COVID-19). Since the first case was confirmed, the number of confirmed cases in China has increased dramatically. With Wuhan as their base, the epidemic is spreading throughout the Hubei and throughout the world. Since Wuhan was the main confirmed case, development patterns are essentially the same as Wuhan for new confirmed cases throughout the world. Based on the prediction results, in the later stage of the epidemic the three models can well predict the epidemic situation of COVID-19. Amongst these is the Logistic model, which fits all Wuhan data, rather than the two other models, while the Gompertz model fits the data outside Wuhan better. It should be remembered that on 12 February 2020, the number of confirmed cases suddenly increased by 13,332. Of course, the change of that data did not come from the virus process, but our treatment method is to remove the effect of this aspect of a data mutation (13,332 people). Based on regular real-time COVID-19 updates, the above three Models (Logistical model, Bertalanffy model and Gompertz model) have been used for the evaluation of fitting analysis of the COVID-19 epidemic. In Table 1, where the cumulation of confirmation (final cumulative number = + 13332) is estimated, the results of the prediction are shown;  $b$  and  $c$  suit coefficients;  $t$  corresponds to the number of days since the first event.  $R^2(C)$  means a cumulative confirmed case fitting property;  $R^2(N)$  refers to a new confirmed case fitting goodness. The final total number of confirmed cases of COVID-19 in Wuhan is projected to be 49852-57447, as determined from the results of the three models. Areas: Non-Hubei: 12972-13405. China maritime, respectively: 80261-85140.

Table 1- The prediction epidemic results of COVID-19 in Logistic Model, Bertalanffy Model and Gompertz Model

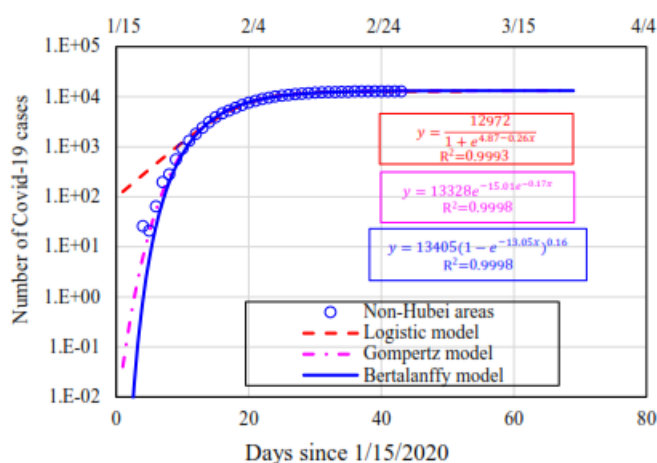
| Model             | Parameter                  | Wuhan  | China mianland | Non-Hubei areas |
|-------------------|----------------------------|--------|----------------|-----------------|
| Logistic model    | a                          | 36520  | 66929          | 12972           |
|                   | b                          | 5.51   | 4.98           | 4.87            |
|                   | c                          | 0.21   | 0.22           | 0.26            |
|                   | Cumulative number of cases | 49852  | 80261          | 12972           |
|                   | R <sup>2</sup> (C)         | 0.9991 | 0.9993         | 0.9993          |
|                   | R <sup>2</sup> (N)         | 0.8124 | 0.9183         | 0.9648          |
| Gompertz model    | a                          | 42926  | 70324          | 1332            |
|                   | b                          | 17.33  | 10.98          | 15.01           |
|                   | c                          | 0.12   | 0.11           | 0.17            |
|                   | Cumulative number of cases | 56258  | 83656          | 13328           |
|                   | R <sup>2</sup> (C)         | 0.999  | 0.9934         | 0.9998          |
|                   | R <sup>2</sup> (N)         | 0.813  | 0.3372         | 0.9804          |
| Bertalanffy model | a                          | 44115  | 71808          | 13405           |
|                   | b                          | 14.93  | 11.5           | 13.05           |
|                   | c                          | 0.12   | 0.12           | 0.16            |
|                   | Cumulative number of cases | 57447  | 85140          | 13405           |
|                   | R <sup>2</sup> (C)         | 0.9989 | 0.9993         | 0.9998          |
|                   | R <sup>2</sup> (N)         | 0.8105 | 0.895          | 0.978           |



(a) Three models for predicting COVID-19 cases in Wuhan since January 15, 2020



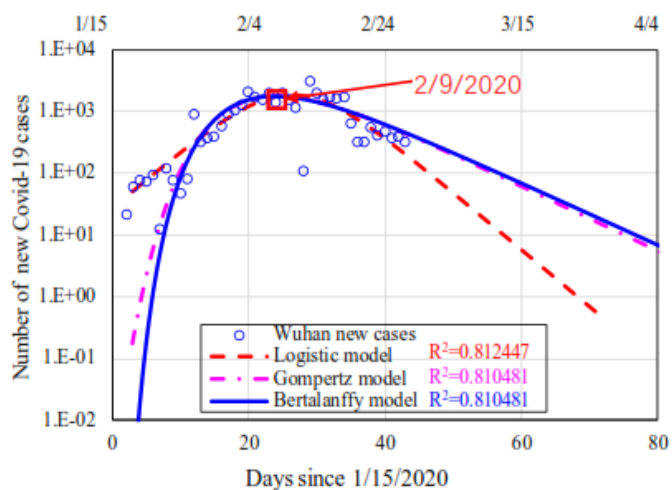
(b) Three models for predicting COVID-19 cases in China mainland since January 15,2020



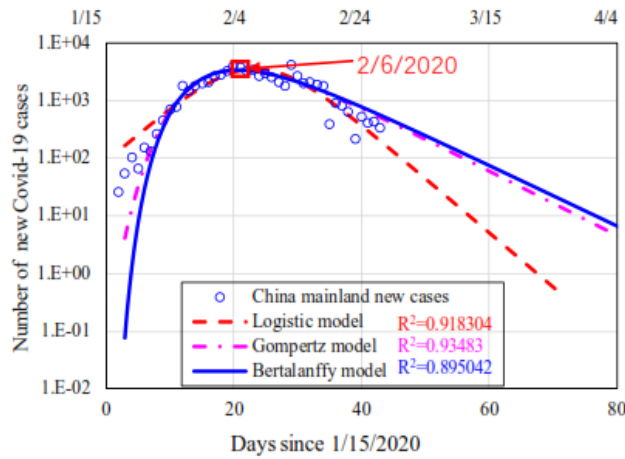
(c) Three models for predicting COVID-19 cases in non-Hubei areas since January 15,2020

Figure 1- The prediction of cumulative number of COVID-19 cases fitted by Gompertz, Logistic and Bertalanffy models

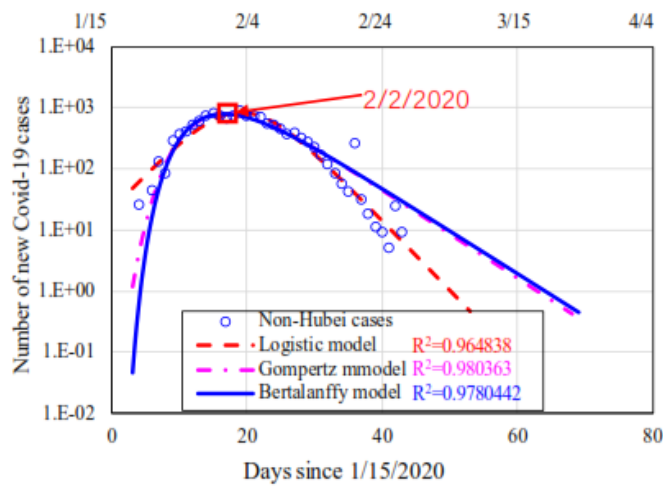
To anticipate the turning point, in Wuhan, mainland China and non- Hubei regions, we use the above three models to compare new confirmed cases. As shown in Figure 2, the turning-points are 9 February, 6 February and 2 February 2020 in WWuhan, China continental and non-Hubei regions. The results allow the three models to predict well the COVID-19 epidemic at an early and late stage of the epidemic to be used for the prediction of newly confirmed cases. In particular, the Logistic model matches all data better than the other two.



(a) Three Models for predicting new COVID-19 Cases in Wuhan since January 15, 2020

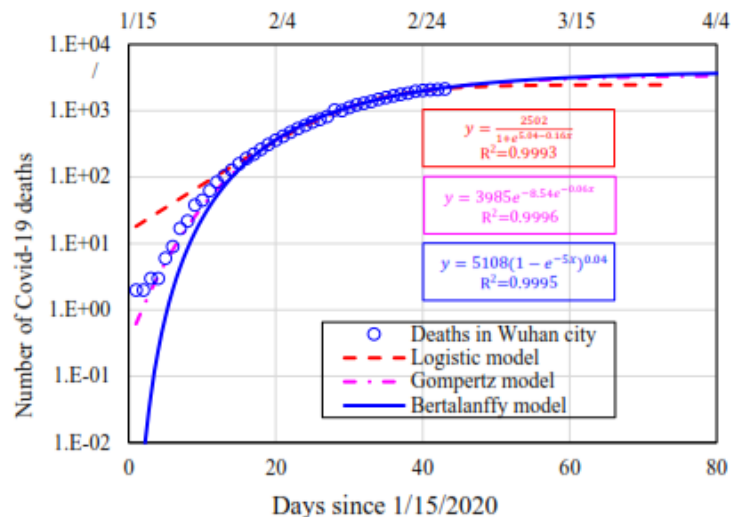


(b) Three Models for Predicting new COVID-19 Cases in China mainland since January 15,2020

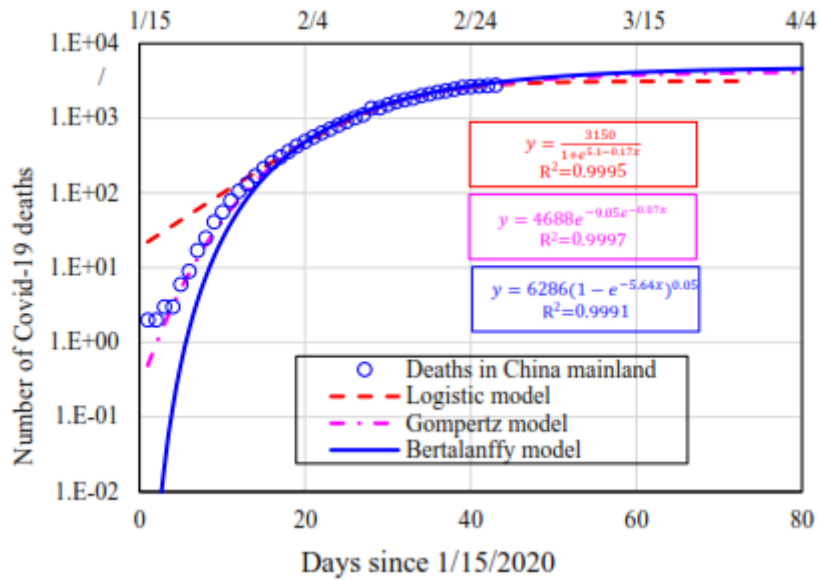


(c) Three Models for Predicting new COVID-19 Cases in non-Hubei areas since January 15,2020  
 Figure 2 The prediction of new COVID-19 cases fitted by Gompertz, Logistic and Bertalanffy models

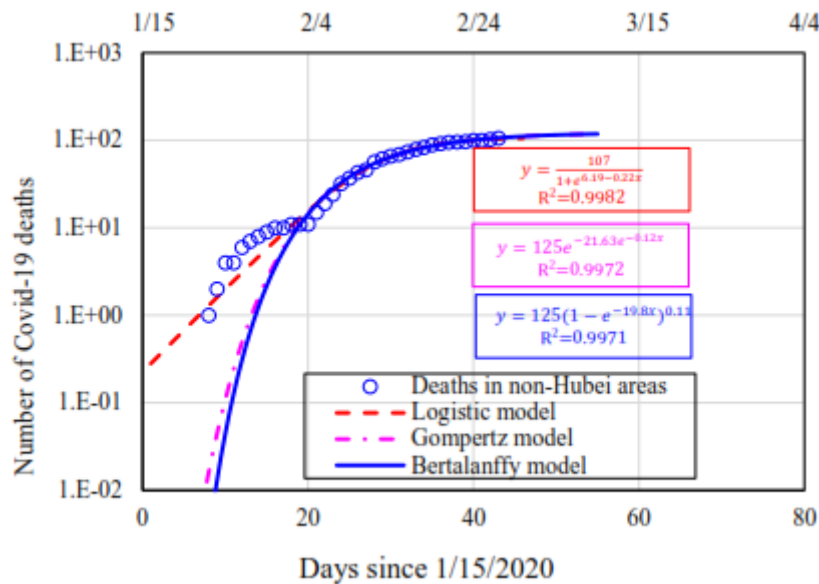
**2 Death Toll:**The death toll of COVID-19 in China is mainly concentrated in Wuhan, Hubei province, so the trends of the death toll in China are basically the same with Wuhan. Similarly, Gompertz, Logistic and Bertalanffy models were used to predict the final death toll of COVID-19. The results are shown in Figure 3.



(a) Three Models for Predicting COVID-19 death toll in Wuhan since January 15,2020



(b) Three Models for Predicting COVID-19 death toll in China mainland since January 15,2020



(c) Three Models for Predicting COVID-19 death toll in non-Hubei areas since January 15,2020

Figure 3 Three Models for Predicting COVID-19 death toll

In Table 2, where the estimate of the death toll; b and c are appropriate coefficients; t is a number of days from the first case, each model has its correct parameter. R2(DC) means cumulative death suit. R2(DC) According to the figures available, the death toll expected by the three models in question is Wuhan: 2502-5108; non-Hubei areas: 107-125; main country of China: 3150-6286. It could be due to the fact that the factors that affect the influenza death rate outweigh the amount reported and newly confirmed by the combined, for example, continuous improvement of the level of treatment, emergencies and steps. However, the Logistic model is clearly better than the two other ones, despite the appropriate precision of the ones in Figure 4. As later fit results of the mathematical model are more relevant than previous fit results, the correct results of the Logistic model can be more reliable, that is, the total death rate of COVID-19 in Wuhan is approximately 2502, 107 in non-Hubei regions and 2150, respectively, in China continental.



**Table 2 Logistic Model, Bertalanffy Model and Gompertz Model for predicting the COVID-19 death toll**

| Model             | Parameter             | Wuhan  | China mainland | Non-Hubei areas |
|-------------------|-----------------------|--------|----------------|-----------------|
| Logistic model    | a                     | 2502   | 3150           | 107             |
|                   | b                     | 5.04   | 5.1            | 6.19            |
|                   | c                     | 0.16   | 0.17           | 0.22            |
|                   | Cumulative death toll | 2502   | 3150           | 107             |
|                   | R <sup>2</sup> (DC)   | 0.9993 | 0.9995         | 0.9982          |
| Gompertz model    | a                     | 3985   | 4688           | 125             |
|                   | b                     | 8.54   | 9.05           | 21.63           |
|                   | c                     | 0.06   | 0.07           | 0.12            |
|                   | Cumulative death toll | 3985   | 4688           | 125             |
|                   | R <sup>2</sup> (DC)   | 0.9996 | 0.9997         | 0.9972          |
|                   | R <sup>2</sup> (DN)   | 0.7529 | 0.8178         | 0.7679          |
| Bertalanffy model | b                     | 4.99   | 5.64           | 19.8            |
|                   | c                     | 0.04   | 0.05           | 0.11            |
|                   | Cumulative death toll | 5108   | 6286           | 125             |
|                   | R <sup>2</sup> (DC)   | 0.9995 | 0.9991         | 0.9971          |

## II. CONCLUSION

The conceptual model, Gompertz model and Bertalanffy model prediction methods are similar, but the mathematical models are different. From these findings, the three model models will better predict the progression of the COVID-19 outbreak later in the epidemic by estimating the total number of confirmed diagnoses. Among them is the logistic model, whereas the model Gompertz fits in with the data in non-Hubei areas better than the other two models. The three model types can all forecast the COVID-19 disease situation in the early and late stages of the outbreak in the estimation of newly confirmed cases. The logistic model's correct results are better than the other two for all data in Wuhan and Non-Hubei regions. The fitting coefficients of the three models are relatively strong for the estimation of the total death toll and can be well predicted in the later stage of the epidemic. The capacity of medical personnel in several ways is strengthening, supporting various services across the country is strengthening and the ability to improve care and treatment is strengthening. Different resources are becoming more available during the later period. The mortality rate for COVID-19 will be reduced rapidly with these factors. The above factors can also influence the cumulative number of confirmed instances, but because of the large number of confirmed cases, the cumulative number of confirmed cases can be influenced by these favorable human factors.

- (1) It is estimated that COVID-19 will be over probably in late-April, 2020 in Wuhan and before late-March, 2020 in other areas respectively;
- (2) The cumulative number of confirmed COVID-19 cases is 49852-57447 in Wuhan, 12972-13405 in non-Hubei areas and 80261-85140 in China mainland;
- (3) According to the current trend, the cumulative death toll predicted by the three models are: 2502-5108 in Wuhan, 107-125 in non-Hubei areas, and 3150-6286 in China mainland;
- (4) According to the fitting analysis of the existing data by the three mathematical models, the inflection points of the COVID-19 epidemic in Wuhan, non-Hubei areas and China mainland is basically in the middle of February 2020;

(5) The prediction results of three different mathematical models are different for different parameters and in different regions. In general, the fitting effect of Logistic model may be the best among the three models studied in this paper, while the fitting effect of Gompertz model may be better than Bertalanffy model.

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