Global dynamics of a SUIR model with predicting COVID-19

Jingyuan Wang  
Beihang University  
Beijing, China  
jywang@buaa.edu.cn

Xin Lin  
Beihang University  
Beijing, China  
sweeneylin@buaa.edu.cn

Yuxi Liu  
Flinders University  
Adelaide, Australia  
liv1356@flinders.edu.au

Qilegeri  
Beihang University  
Beijing, China  
qlgr@buaa.edu.cn

Hui Lin  
China Electronics Technology Group Corporation  
Beijing, China

Manqing Wu  
China Electronics Technology Group Corporation  
Beijing, China

Abstract—Since December 2019, a novel coronavirus (2019-nCoV) has been breaking out in China, which can cause respiratory diseases and severe pneumonia. Epidemic models relying on the incidence rate of new cases for forecasting epidemic outbreaks have received increasing attention. However, many prior works in this area mostly focus on the application of the traditional SIR model and disregard the transmission characteristics of 2019-nCoV, exceptionally the infectious of undiagnosed cases. Here, we propose a SUIR model based on the classical SIR model object to supervise the effective prediction, prevention, and control of infectious diseases. SUIR model adds a unique \( U \) (Undiagnosed) state of the epidemic and divides the population into four states: \( S \) (Susceptible), \( U \) (Undiagnosed), \( I \) (Infectious and Uninfectious), and \( R \) (Recovered). This approach enables us to predict the incidence of 2019-nCoV effectively and the clear advantage of the model accuracy more reliable than the traditional SIR model.

Index Terms—2019-nCoV, COVID-19, SARS-CoV-2, SIR model, SUIR model

I. INTRODUCTION

In late December 2019, several local health institutions reported that the South China seafood wholesale market in Wuhan, one of the central cities of China, was epidemiologically related to the group of patients with unexplained pneumonia, and the global attention shifted to China. Local health authorities identified a novel coronavirus, tentatively named 2019-nCoV, which is the third human cross-infection of coronavirus in 30 years, causing global health concerns. Chinese government took extraordinary measures, first in Wuhan and then in 12 other Chinese cities, to control the epidemic by closing markets and imposing blockades [1]. The disease has now spread globally, including cases confirmed in 187 Countries [2]. Depending on the statistics of the World Health Organization, by the end of March 2020, the global region was 750890 confirmed cases, and 36405 cases died [3]. Global countries are issue policies to control the 2019-nCoV spread and provide financial support and health rescue. Therefore, predicting the future growth trend of the epidemic situation performs a vital function in measuring the large scale epidemic situation [4].

Mathematical and Empirical models have been widely adopted in the field of the epidemic, which adequately illustrates the transmission speed, spatial range, transmission path, and dynamic mechanism of infectious diseases [5]. Depending on the categories of infectious diseases, conventional infectious disease models divide into SIR, time delay SIR, and SEIR model [6, 7, 8]. Subsequently, there are many applications based on the epidemic model. Huo and Zhao considered birth and death rates on heterogeneous complex networks, which proposed a fractional SIR model and obtain results that when the disease-free equilibrium is globally asymptotically stable, the disease can disappear [9]. A detailed study of the T-SIR (Time-series Susceptible-Infected-Recovered) model by Ottar et al. [10] exposed the epidemic cycle and the outbreak of measles. A significant SIR model on the subject was presented by Jiang and Wei [11], which established the existence of Hopf bifurcations at the endemic equilibrium. Analysis of the SIR model involved with nonlinear incidence rate and time delay was proved that the underlying reproductive number \( R_0 > 1 \), the system is permanent [12]. McCluskey further developed a SIR model of disease transmission with delay and nonlinear incidence on [12], which used a Lyapunov functional shown the global dynamics are fully determined [13]. A qualitative study by Li et al. [14] identified a threshold \( \sigma \) to determines the outcome of the disease on the SEIR model of infectious disease transmission. Smith et al. applied a latent period, excess death of the infected, and a standard incidence on the SEIR epidemic model to identify the reproduction number \( \vartheta \) [15]. However, these techniques not considered the transmission characteristics of epidemics, such as undiagnosed infectiousness. It is thus critical to assess the effects of undiagnosed states on the epidemic progression for the benefit of global expectation. This paper proposes a Susceptible-Undiagnosed-Infected-Removed (SUIR) Model and applies the simplex algorithm on the historical 14-day incidence data to fit \( \beta \) and \( \gamma \) of parameters, and predict the number of infected and removed (including cured and dead) in the next t (per day). We also confirmed our model prediction combining with a pretraining \( R_0 \) and Wuhan \( R_0 \) approaches that was addressed the challenging to initialize the susceptible population of the traditional infectious disease.
model.

This paper is organized as follows. In Section 2, the SUIR epidemic model is formulated. In Section 3, the properties of the database are studied, the basic Hyperparameters are given, the reliability of the analytic solution and prediction error are illustrated. In Section 4, some statistical inferences and model results are discussed. Some conclusions are summarized in Section 5.

II. METHODOLOGY

A. Mathematical and Empirical Models

Kermack-McKendrick [6] proposed the system dynamic (Susceptive-Infective-Removal, SIR) model, which describes the transmission process of infectious diseases through a quantitative relationship to the transmission mechanism of general infectious diseases, analyzed the change rule of the number of infected cases and reveals the growth trend of infectious diseases. SIR model divided into three categories population, which include Susceptible (S), Infectious (I), and Removed (R). Based on the research of Kermack and McKendrick [6], Beretta and Takeuchi [7] further developed their theories and proposed a time delay SIR model. Cooke and Driessche [8] investigated the incubation period in the spread of infectious diseases, introduced "Exposed, E," and proposed a time delay model. Depending on the above SIR model of infectious diseases, which were similar to the 2019-nCoV epidemic. This paper focuses on applying the SIR model as a fundamental hypothesis.

The traditional SIR model is based on the SI model [17] to consider the recovery process of patients further and incorporates two critical parameters, including the infection rate (\( \beta \)) and the proportion coefficient (\( \gamma \)). Due to the characteristics of the 2019-nCoV, the traditional SIR model without including a unique U state (undiagnosed). Therefore, we inject the state of U (undiagnosed) into the SIR model and propose the SUIR model to effectively track the spread trend of the epidemic situation and predict the future infection population.

B. Differential Equations for Traditional SIR Model

Based on the differential equation of SIR model provided by [17] and prerequisite (considering the recovery process of patients):

\[
\frac{dS}{dt} = -\beta IS, \quad (1)
\]

\[
\frac{dI}{dt} = \beta IS - \gamma I, \quad (2)
\]

\[
\frac{dR}{dt} = \gamma I, \quad (3)
\]

\[
S(t) + I(t) + R(t) = M. \quad (4)
\]

\( M \) represents the total population. Kermack-McKendrick [6] assumed that the patient obtains permanent immunity from recovery. Therefore, recovery patients can be removed from the system. In fatal infectious diseases, death cases were classified into the R category.

C. Structure and Hypothesis for SUIR model

The SUIR model was divided the population into four states: S, U, I and R. Conceptually, the chain of the state transition is shown as Figure 1:

1) S, susceptible;
2) U, undiagnosed, refers to the patients who have been infected with diseases but have not classified as confirmed;
3) I, (the confirmed cases not quarantined, infectious) and \( IS \) (confirmed and quarantined, uninfected), refers to the infected individual and was regarded as the confirmed patient;
4) R, removed, refers to the patient who recovers with immunity or dies.

The model first applied the historical data of S, I, and R states to fit the transfer proportion parameters among population estimates and then adopted the fitted parameters to predict the future disease state. The above model is similar to SIR, but the state of I was divided into two sections in practical application, including the state of I (Confirmed but not quarantined, infectious) and the state of \( IS \) (Confirmed and quarantined, uninfected).

Here, we assume that:
1) The total population of the study area never changes by time, and the natural birth rate and mortality rate are not considered.
2) The number of susceptible individuals affected by infectious diseases changes in direct proportion to the number of susceptible and infectious individuals.
3) The growth rate of the number of quarantined and removal individuals is directly proportional to the number of infected individuals.
4) Both the diagnosed without quarantined and the undiagnosed can infect individuals.
5) The quarantined confirmed case can not infect individuals.
6) Tracking close contact with confirmed cases and quarantine some undiagnosed individuals, which assume that per confirmed case can cause the average number of quarantined individual is \( \rho \).

D. Define SUIR Model HyperParameters and Differential Equations

In the modeling of mathematical, which essential to set an initial susceptible population (\( S_0 \)). In this regard, we
assumed that $S_0$ is the population base of the country or city to be estimated. However, this hypothesis has some drawbacks in which the entire population was infected. To solve the challenge of $S_0$ initialization, Heesterbeek et al. [8] offered the $R_0$ HyperParameter, which represents the average number of secondary cases of disease caused by a single infected individual over his or her infectious period. Therefore, We carried out simulation experiments based on the SIR model and applied the pretraining $R_0$ sequence to estimate the number of peak infections (the total number of peak $I$ and $R$), and regarding the number of peak infections as initial $S_0$.

Here, we utilized two approaches to locate the pretraining $R_0$ sequence. The first is based on the [16] approach to estimate the valid reproduction number ($R_0$) by per day. The second assumed that other countries adopted the same control measures as Wuhan, China, to estimate $R_0$ by using the historical incidence rate of Wuhan [8].

Due to the Eq. (1), the relationship among the $R_0$, $\beta$ and $\gamma$ is $R_0 = \frac{\beta}{\gamma}$. (5) Consequently, if $R_0$ and $\gamma$ are specified, merged with the SIR model and $R_0$ to executed in the simulation experiment, assuming that the experiment lasts for $T$ days, the terminal estimated $S_0$ is the sum of $I(T)$ and $R(T)$. $I(T) + R(T) = S_0$. (6)

SUIR model includes six HyperParameters:

$\beta$: The infection rate of contact between diagnosed and susceptible population.

$\sigma$: The infection rate of undiagnosed cases in contact with the susceptible population.

$\rho$: The average quarantine number of close contacts with confirmed cases.

$\varepsilon$: The probability of undiagnosed infection by confirmed.

$\lambda$: The probability of quarantine of confirmed cases.

$\gamma$: The probability of removal of confirmed cases. (cure and death)

Differential Equations of SUIR:

$$\frac{dS}{dt} = -\beta SI - \sigma S \cdot \max(U - \rho IS), 0, (7)$$

$$\frac{dU}{dt} = \beta SI + \sigma S \cdot \max(U - \rho IS), 0 - \varepsilon U, (8)$$

$$\frac{dI}{dt} = (1 - \lambda) \cdot \varepsilon U - \gamma I, (9)$$

$$\frac{dIS}{dt} = \lambda \cdot \varepsilon U - \gamma IS, (10)$$

$$\frac{dR}{dt} = \gamma (I + IS), (11)$$

In this study, an investigation unit represents the transition relationship between susceptible ($S$) and undiagnosed ($U$) for one day, including two categories. One is obtaining the infection from the infected individuals ($I$), which represents the $\beta SI$ in Eq. (7), similar to the traditional SIR model, the other is to obtain the infection from contact with undiagnosed individuals ($U$), with a rate of $\sigma$. Note that we assumed that the quarantine $\rho$ (undiagnosed individuals) could be quarantined by tracking close contact with the confirmed cases; therefore, the number of undiagnosed infections is $\sigma \cdot S \cdot \max(U - \rho IS), 0)$. In each investigation unit, $\varepsilon \cdot U$ (undiagnosed individuals) were diagnosed with a quarantine rate of $\lambda$. Therefore, the total newly diagnosed individuals $((1 - \lambda) \cdot \varepsilon \cdot U)$ was converted into Infected ($I$) individuals, and $\lambda \cdot \varepsilon \cdot U$ was converted into Infected & quarantined ($IS$) individuals, as Eq. (9) and (10). Finally, similar to the SIR model, the transition probability between confirmed and removal individuals (cured or death) is $\gamma$, as Eq. (11).

We defined $S(t)$, $U(t)$, $I(t)$, $IS(t)$, $R(t)$ as the number of susceptible, undiagnosed, infected, infected and quarantined and removal individuals at time $t$, $\Delta t$ represent the unit time, the differential equations are summarized:

$$S(t + \Delta t) = S(t) - \beta S(t)I(t) - \sigma S(t)\max(U(t) - \rho IS(t), 0), (12)$$

$$U(t + \Delta t) = U(t) + \beta S(t)I(t) + \sigma S(t)\max(U(t) - \rho IS(t), 0) - \varepsilon U(t), (13)$$

$$I(t + \Delta t) = I(t) + (1 - \lambda)\varepsilon U(t) - \gamma I(t), (14)$$

$$IS(t + \Delta t) = IS(t) + \lambda\varepsilon U(t) - \gamma IS(t), (15)$$

$$R(t + \Delta t) = R(t) + \gamma (I(t) + IS(t)) (16)$$

The total number of population is $M$. $S(t) + U(t) + I(t) + IS(t) + R(t) = M, (17)$

The cumulative confirmed cases $C(t) = I(t) + IS(t) + R(t), (18)$

The number of treated patients $A(t) = I(t) + IS(t), (19)$

The SUIR model is implemented by an overall flowchart (see Algorithm 1).

**Algorithm 1 : SUIR Model**

**Input:** $R_0(t)$, $(\beta_0, \sigma_0, \rho_0, \varepsilon_0, \lambda_0, \gamma_0)$, cumulative confirmed $C(t)$, removal $R(t)$, $T$

**Output:** $S(t), U(t), I(t), IS(t), R(t)$

1. **Initialization:** $\beta_0, \sigma_0, \rho_0, \varepsilon_0, \lambda_0, \gamma_0$

2. **Pretraining $S_0$:** Apply $R_0(t)$, $\gamma$ on Eq. (1), (2), (3) and (5), obtain $S_0$ from Eq. (6)

3. **Estimation:**

4. Apply $(\beta_0, \sigma_0, \rho_0, \varepsilon_0, \lambda_0, \gamma_0)$ on Eq. (12)-(16), obtain $C(t)$ and $R(t)$ from Eq. (16) and (18)

5. Obtain MSE of $C(t)$ and $\hat{C}(t)$, $\hat{R}(t)$ and $\hat{R}(t)$

6. Solve $(\beta, \sigma, \rho, \varepsilon, \lambda, \gamma)$ by using Nelder-Mead solver to minimize MSE

7. **Simulation:**

8. for $t = 1$ to $T$

9. Apply $(\beta, \sigma, \rho, \varepsilon, \lambda, \gamma)$ on Eq. (12)-(16), update $S(t), U(t), I(t), IS(t)$ and $R(t)$

10. **end for**

This deterministic epidemic model studied the hypothesis of 1, 2, 3, 4, 5 and 6; therefore, there is an incorrect hypothesis in other infectious diseases. But in 2019-nCoV with a high probability of the correct hypothesis.
III. RESULTS

A. Database description

We adopted the National Health Commission (NHC) of China daily epidemic statistics report [20] as the Database for the prediction of experiments in China and summarized in Table 1 (e. g. Wuhan). The data are composed of the cumulative number of infectious, recovered and death cases in China. In the case of overseas, the JHU CSSE Database [21] are summarized in Table 2 (e. g. USA). Since January 22, 2020, the JHU CSSE Database was updated per day and composed of three sections, including the cumulative number of infectious, recovered and death cases. We selected 15 days before the predicted date to fit the model, such as on the trend of the USA epidemic on April 1, which chooses the data of the USA from March 17 to March 31.

| Date    | Cumulative Infectious | Cumulative Recovered | Cumulative Deaths |
|---------|-----------------------|----------------------|------------------|
| 1/27/20 | 1590                  | 47                   | 85               |
| 1/28/20 | 1905                  | 47                   | 104              |
| 1/29/20 | 2261                  | 51                   | 129              |
| 1/30/20 | 2639                  | 72                   | 159              |
| 1/31/20 | 3215                  | 123                  | 192              |
| 2/1/20  | 4109                  | 155                  | 224              |
| 2/2/20  | 5142                  | 166                  | 265              |
| 2/3/20  | 6384                  | 303                  | 303              |
| 2/4/20  | 7828                  | 368                  | 362              |
| 2/5/20  | 10117                 | 431                  | 414              |
| 2/6/20  | 11618                 | 534                  | 478              |
| 2/7/20  | 13603                 | 698                  | 545              |
| 2/8/20  | 14982                 | 877                  | 608              |
| 2/9/20  | 16902                 | 1044                 | 681              |
| 2/10/20 | 18454                 | 1206                 | 748              |

B. Hyperparameter simulations for the SUIR model

The purpose of the Hyperparameter experiment was to adopted two sections of $R_0$ based on the SIR model to obtain the upper bound $S_0$. Simple statistical analysis was used to collect the $R_0$ from [16], we employed the outbreak countries of $R_0$, which demonstrated the relationship between $R_0$ and time. Figure 2 shows an overview of $R_0$ of Wuhan. Figure 3 provides the range of $R_0$ sequences for some outbreak countries. Table III provides the estimation results of $S_0$ obtained from two groups of $R_0$ functioning in different countries.

| $S_0$ | From Wuhan’s $R_0$ | From Local $R_0$ by [15] |
|-------|--------------------|----------------------------|
| Italy | 51,100             | 161,000                    |
| US    | 78,000             | 345,000                    |
| Iran  | 40,000             | 84,000                     |
| UK    | 29,000             | 86,000                     |
| Spain | 71,000             | 180,000                    |
| France| 26,000             | 147,000                    |
| Germany | 35,000        | 130,000                    |

C. Analytic solution of the SUIR model

To obtain the fitted parameter, we shaped the Historical data and Hyperparameter $S_0$ on the SUIR model. The results of fitted parameters are shown in Table IV. Depending on the finding that fitted parameters, we applied ($\beta$, $\sigma$, $\rho$, $\varepsilon$, $\lambda$, $\gamma$) on Eq. (12)-(16), to obtain the ($S$, $U$, $I$, $IS$, $R$) of

Figure 2. The infection dimension of confirmed cases under intervention ($R_0$) in Wuhan
outbreak countries in the future and estimate the cumulative number of confirmed cases and removed cases, which Figure 4 and Figure 5 illustrate the summary statistics for Italy and Germany. As can be seen from Figure 4, we can see that the number of confirmed cases in Italy showed an increasing trend before the middle of April, and then tended to be flat. The number of active cases first increased and then decreased with time, approaching a peak in April, with a total of approximately 84000 cases. As shown in Figure 5, we can see that the number of confirmed cases in Germany also showed an increasing trend before the middle of April, and active cases peaked in mid-April, including approximately 94000 cases, a large proportion of confirmed cases.

### TABLE IV
Fitted parameters of outbreak countries

| Country | $\beta$ | $\sigma$ | $\rho$ | $\epsilon$ | $\lambda$ | $\gamma$ |
|---------|---------|----------|-------|-----------|----------|----------|
| Italy   | 2.86E-05| 2.59E-07 | 4.29  | 0.11      | 0.74     | 3.07E-02 |
| US      | 6.67E-06| 1.38E-06 | 1.32  | 0.75      | 0.84     | 1.68E-03 |
| Iran    | 7.79E-05| 1.17E-06 | 16.25 | 0.06      | 0.92     | 6.95E-02 |
| UK      | 5.71E-06| 1.26E-08 | 17.50 | 0.79      | 0.19     | 2.27E-02 |
| Spain   | 3.32E-06| 1.92E-06 | 10.10 | 0.30      | 0.43     | 4.96E-02 |
| France  | 4.65E-05| 1.37E-06 | 10.00 | 0.29      | 0.95     | 3.56E-02 |
| Germany | 4.43E-05| 1.80E-04 | 10.00 | 0.30      | 0.95     | 2.61E-02 |

### D. Prediction Error of the SUIR model

In this study, we assume the prediction date between $t$ and $T$, define the error of prediction equation is

$$e(t, T) = \frac{|C(t + T) - \hat{C}(t + T)|}{C(t + T)}, \quad (20)$$

where $C(t)$ denotes the cumulative confirmed cases predicted by SUIR model and $\hat{C}(t)$ denotes the cumulative confirmed cases of the JHU CSSE Database. In the experiment, we can obtain the average error of prediction. Table V below compares the prediction results of SIR and SUIR model in outbreak countries; there is a clear trend of the traditional model accuracy that has a negative performance.

### IV. DISCUSSION

Our results suggest that the prediction accuracy of the SUIR model is precise than the traditional SIR model in 2019-nCoV. On the question of initial dimension $S_0$ (susceptible individual) settings, this study discovered that applied $R_0$ sequence [16] on the SIR model to pretraining, which can
TABLE V
PREDICTION ERROR OF SIR AND SUIR MODEL AFTER T DAYS

| Country | Model | 1   | 2   | 3   | 4   | 5   | 6   | 7   |
|---------|-------|-----|-----|-----|-----|-----|-----|-----|
| Italy   | SIR   | 0.94% | 2.07% | 3.13% | 4.12% | 4.88% | 5.15% | 5.02% |
|         | SUIR  | 0.43% | 1.01% | 1.49% | 1.90% | 2.25% | 2.55% | 2.73% |
| US      | SIR   | 2.07% | 2.88% | 3.06% | 3.98% | 4.80% | 5.43% | 6.83% |
|         | SUIR  | 2.02% | 2.64% | 2.69% | 2.59% | 2.78% | 5.06% | 6.62% |
| Iran    | SIR   | 5.00% | 9.61% | 13.56% | 16.88% | 19.72% | 22.02% | 23.90% |
|         | SUIR  | 1.61% | 3.09% | 4.64% | 6.08% | 7.31% | 8.20% | 8.83% |
| UK      | SIR   | 3.28% | 5.66% | 6.12% | 6.31% | 6.90% | 7.06% | 5.95% |
|         | SUIR  | 2.96% | 5.36% | 5.09% | 3.50% | 2.86% | 2.35% | 2.63% |
| Spain   | SIR   | 2.91% | 5.74% | 8.03% | 9.53% | 10.11% | 10.07% | 9.73% |
|         | SUIR  | 1.72% | 2.71% | 3.20% | 3.85% | 4.10% | 4.13% | 4.15% |
| France  | SIR   | 2.26% | 4.38% | 4.38% | 4.74% | 5.34% | 9.26% | 11.34% |
|         | SUIR  | 1.50% | 2.47% | 2.57% | 4.18% | 5.29% | 8.43% | 9.55% |
| Germany | SIR   | 2.56% | 4.51% | 5.62% | 6.13% | 6.34% | 5.90% | 5.08% |
|         | SUIR  | 1.88% | 3.35% | 4.00% | 4.66% | 5.05% | 4.93% | 4.50% |

obtain the estimation of $S_0$ and also contributes a reference for establishing $S_0$. These results in Table 3 highlight $S_0$ estimation results obtained by performing two sections of $R_0$ to different countries. It can be seen from the results in Table 3 that the $S_0$ from Wuhan $R_0$ sequence is smaller than that from local $R_0$ sequence. A possible explanation for these results may be the lack of same control measures as Wuhan, China. Consequently, national control measures will affect the infected individual trend.

The actual epidemic trend since our analyses has present the Hyperparameters has a significant weight on predict. A detailed study by Kermack-McKendrick [6] indicates that the relationship among $\beta$, $\gamma$, and $\sigma$ is $\sigma = \beta / \gamma$. In this regard, $\sigma$ determines the spread of infectious diseases, which $R_0 < 1 / \sigma$ represents the transmission is limited [22]. Our study generally supports [6] and [22] speculations; we believe the fluctuation of $\beta$ and $\gamma$ indicates the epidemic infectivity. Our results in Table IV compares an overview of Hyperparameters in seven countries, Italy, Iran, France, and Germany have higher $\beta$ than other countries, indicating that 2019-nCoV more infectious in these countries. In addition, the most obvious finding to emerge from the analysis is that $\gamma$ of the United States located at a lower level than other countries, indicating that confirmed cases in the United States have a postponed treatment period than in other countries. Another important finding was that Iran has a low level of $\varepsilon$, which suggests there is a higher risk of undiagnosed infections. As a result, Hyperparameters value determines the fitting quality and prediction precision.

Error statistics of the model validates the accuracy of the SUIR model. Applying two models to 7-day prediction in multiple outbreaks countries (Table 5), the most obvious finding to emerge from the analysis is that the SUIR model can minimize the estimation errors. On the first day of prediction, the performance of the two models is exact, but with the increase of the prediction period, the accuracy of the two models began to perform unstably, and the error also increased continuously.

Some limitations of our model are the initialization of the parameters, such as $\beta$ and $\gamma$. Under the improper setting, the model will not be able to fit the historical data well and also cause a high prediction error. Another limitation of our study is that we did not account for the impact of imported cases. However, these problems could be solved if we apply empirical models to trial and error and often to update the data source. Further studies, which take these variables into account, will need to be undertaken.

V. CONCLUSION AND FUTURE WORK

The 2019-nCoV outbreak, meanwhile, studied the traditional infectious disease model, we propose a SUIR model and combine the characteristics of 2019-nCoV epidemic to simulate and predict the future trend of the epidemic. These experiments confirmed that our prediction model could precisely predict the number of infected and recovered individuals in 2019-nCoV under the database of [20] and [21] with a low error rate. The evidence from this study suggests that utilizing $R_0$ [16] to predict the future trend of susceptible individuals, it has a significant effect observed from the model. If global countries can adopt the same management measurements as Wuhan and consider the $U$ state of patients, the 2019-nCoV epidemic will have a high probability of controlled under our deterministic model. The most important limitation lies in the fact that until we complete this study, the 2019-nCoV outbreak in some countries, such as the United States, has not recorded the outbreak stage. A further study could assess the long-term effects of recovery cases on infectiousness. In the future, it will be essential to explore the potential use of complex infectious disease models.
REFERENCES

[1] Duarte R, Furtado I, Sousa L, Carvalho C. The 2019 Novel Coronavirus (2019-nCoV): Novel Virus, Old Challenges Acta Médica Portuguesa. 2020;33.

[2] Coronavirus disease (COVID-19) Pandemic 2020. [Online]. Available at https://www.who.int/emergencies/diseases/novel-coronavirus-2019.

[3] Coronavirus disease 2019 (COVID-19) Situation Report 62 2020. [Online]. Available at https://www.who.int/emergencies/diseases/.

[4] Zhang J, Wang L, Wang J. SIR Model-based Prediction of Infected Population of Coronavirus in Hubei Province 2020.

[5] Bacar N. A Short History of Mathematical Population Dynamics . 2011.

[6] Kermack W, McKendrick A. A Contribution to the Mathematical Theory of Epidemics Proc. Roy. Soc. Edinburgh. 1927;115:700-721.

[7] Beretta E, Takeuchi Y. Global stability of an SIR epidemic model with time delays Journal of Mathematical Biology. 1995;33:250-260.

[8] Cooke K, Driessche P. Analysis of an SEIRS epidemic model with two delays Journal of mathematical biology. 1997;35:240-60.

[9] Huo J, Zhao H. Dynamical analysis of a fractional SIR model with birth and death on heterogeneous complex networks Physica A: Statistical Mechanics and its Applications. 2015:448.

[10] Ottar N, Barbel F, Bryan T. Dynamics of Measles Epidemics: Estimating Scaling of Transmission Rates Using a Time Series SIR Model Ecological Monographs. 2002;72:169-184.

[11] Jiang Z, Wei J. Stability and bifurcation analysis in a delayed SIR model Chaos, Solitons & Fractals. 2008;35:609-619.

[12] Xu R, Ma Z. Global Stability of a SIR Epidemic Model with Nonlinear Incidence Rate and Time Delay Nonlinear Analysis: Real World Applications. 2009;10:3175-3189.

[13] Mccluskey C. Global stability for an SIR epidemic model with delay and nonlinear incidence Nonlinear Analysis-Real World Applications. 2010;11:3106-3109.

[14] Li M, Graef J, Wang L, Karsai J. Global dynamics of a SEIR model with varying total population size Mathematical biosciences. 1999;160:191-213.

[15] Smith H, Wang L, Li M. Global Dynamics of an SEIR Epidemic Model with Vertical Transmission SIAM Journal of Applied Mathematics. 2001;62:58-69.

[16] Wang J, Tang K, Feng K, Lv W. High Temperature and High Humidity Reduce the Transmission of COVID-19 2020.

[17] Bailey N. The Simple Stochastic Epidemic: A Complete Solution in Terms of Known Functions Biometrika. 1963;50:235-240.

[18] Heesterbeek J. A brief history of $R_0$ and a recipe for its calculation. Acta Biotheoretica. 2002;50:189-204.

[19] Pierre-Yves B, Thomas O. R0: Estimation of R0 and Real-Time Reproduction Number from Epidemics 2015.

[20] Outbreak notification 2020. [Online]. Available at https://github.com/CSSEGISandData/COVID-19/.

[21] CSSEGISandData 2020. [Online]. Available at https://github.com/CSSEGISandData/COVID-19/.

[22] Fan Z, Zhang J. A SIR epidemic model with infection coefficient beta(N) Journal of North University of China(Natural Science Edition). 2006:84-86.