

The susceptible-unidentified infected-confirmed (SUC) epidemic model for estimating unidentified infected population for COVID-19

Chaeyoung Lee^a, Yibao Li^b, Junseok Kim^{a,*}

^aDepartment of Mathematics, Korea University, Seoul 02841, Republic of Korea

^bSchool of Mathematics and Statistics, Xi'an Jiaotong University, Xi'an 710049, China

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ABSTRACT

In this article, we propose the Susceptible-Unidentified infected-Confirmed (SUC) epidemic model for estimating the unidentified infected population for coronavirus disease 2019 (COVID-19) in China. The unidentified infected population means the infected but not identified people. They are not yet hospitalized and still can spread the disease to the susceptible. To estimate the unidentified infected population, we find the optimal model parameters which best fit the confirmed case data in the least-squares sense. Here, we use the time series data of the confirmed cases in China reported by World Health Organization. In addition, we perform the practical identifiability analysis of the proposed model using the Monte Carlo simulation. The proposed model is simple but potentially useful in estimating the unidentified infected population to monitor the effectiveness of interventions and to prepare the quantity of protective masks or COVID-19 diagnostic kit to supply, hospital beds, medical staffs, and so on. Therefore, to control the spread of the infectious disease, it is essential to estimate the number of the unidentified infected population. The proposed SUC model can be used as a basic building block mathematical equation for estimating unidentified infected population.

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1. Introduction

The coronavirus disease 2019 (COVID-19) was first identified in Wuhan, China in December 2019 [1]. The numbers of the COVID-19 confirmed cases in China from 21 January to 24 February 2020 are shown in Fig. 1. The data was reported by World Health Organization (WHO) as of 24 February 2020 [2].

Currently, there are many active research about COVID-19: In [3], the authors presented the impact of reduced travel volume to and from China on the transmission dynamics of COVID-19 outside China. Roosa et al. [4] used phenomenological models to generate short-term forecasts of cumulative reported cases in Guangdong and Zhejiang, China. In [5], the authors presented the distribution of incubation periods estimated for travellers from Wuhan with confirmed COVID-19 infection in the early outbreak phase. Hellewell et al. [6] developed a stochastic transmission model to assess the effects of isolation and contact tracing.

In this paper, we propose the Susceptible-Unidentified infected-Confirmed (SUC) epidemic model for estimating the unidentified infected population for COVID-19 in China. In the Susceptible-

Unidentified infected-Confirmed (SUC) epidemic model, the total population N is divided into the susceptible $S(t)$, unidentified infected $U(t)$, and confirmed $C(t)$ individuals at time t :

$S(t)$ = susceptible; individuals who are not infected but are capable of contracting the disease and becoming infective.

$U(t)$ = unidentified infected; individuals who are infected but have not yet been confirmed, and therefore are not isolated.

$C(t)$ = confirmed; individuals who have been infected and confirmed, including all cases of recovery or death (i.e., the removed).

Based on the assumptions above, the equations governing the SUC model are as follows:

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)U(t)}{N}, \quad (1)$$

$$\frac{dU(t)}{dt} = \beta \frac{S(t)U(t)}{N} - \gamma U(t), \quad (2)$$

$$\frac{dC(t)}{dt} = \gamma U(t). \quad (3)$$

Here, N is the total population and thus we assume that $N = S(t) + U(t) + C(t)$ is always satisfied. We disregard changes in population due to birth and death irrelevant to the infectious disease.

* Corresponding author.

E-mail address: cfdkim@korea.ac.kr (J. Kim).

URL: <http://math.korea.ac.kr/cfdkim> (J. Kim)

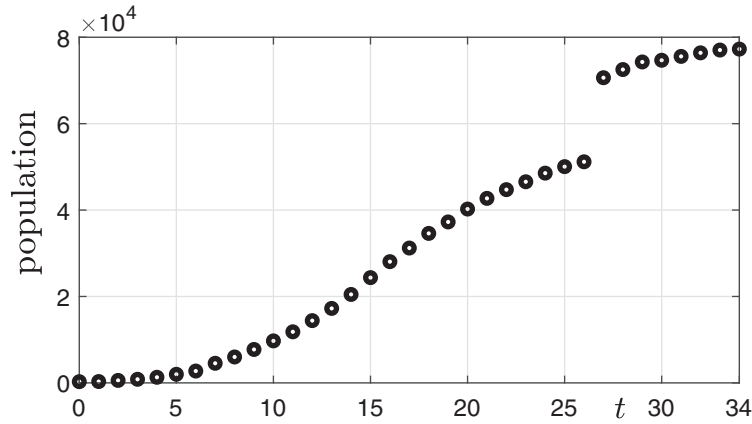


Fig. 1. Epidemic curve of COVID-19 confirmed cases from 21 January to 24 February 2020.

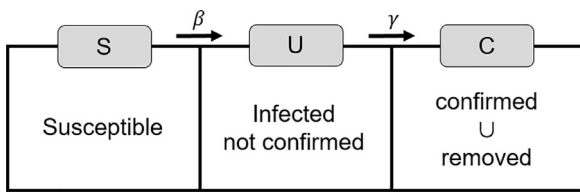


Fig. 2. Flow chart of the SUC model: S is susceptible, U is infected but not confirmed (i.e., unidentified infected), and C is confirmed or removed. Here, the removed indicates the recovered or dead cases.

Therefore, Eq. (3) can be replaced by Eq. (4).

$$C(t) = N - S(t) - U(t). \tag{4}$$

The transmission is expressed by the standard incidence $\beta \frac{SU}{N}$, where β represents the disease transmission rate [7]. We assume the unidentified infected $U(t)$ are not yet hospitalized and still can spread the disease to the susceptible $S(t)$.

The parameter γ is the probability of cases where disease is confirmed among the unidentified infected. We assume that the confirmed $C(t)$ are all cases who have been confirmed to have COVID-19 and recovered or died from the disease. That is, $C(t)$ is the cumulative number. Once confirmed, patients are no longer able to spread the disease because they become isolated completely from the susceptible and the unidentified infected population. Furthermore, in this paper we ignore specific cases, such as infection in medical staff or confirmed patients not isolated, to reduce the complexity of model. Fig. 2 illustrates the transition diagram of the SUC model with three states.

The ordinary differential Eqs. (1)–(3) for the proposed model are identical to the classical epidemic model, the Susceptible-Infected-Recovered (SIR) epidemic model [8] which is widely used to estimate transmission dynamics in emerging epidemics [9]. However, we impose different meanings of the epidemic variables. The susceptible, the unidentified infected, and the confirmed in the SUC model correspond to the susceptible, the infected, and the recovered in the SIR model, respectively. Various epidemic models have been proposed by modifying the SIR model, such as SIRS (Susceptible-Infected-Recovered-Susceptible) [10], SIRD (Susceptible-Infected-Recovered-Dead) [11], SIS (Susceptible-Infected-Susceptible) [12], SEIR (Susceptible-Exposed-Infected-Recovered) [13], SIIR (a modified SIR with a latent period) [14], and SIR/V (Susceptible-Vaccinated-Infected-Recovered) [15] models. Moreover, fractional-order epidemic models as applications of classical models have been studied [16,17]. We intend to consider the epidemic with a

similar framework but new interpretation in a different way. In this paper, we propose a simple model as the first step.

2. Numerical solution algorithm

Let $S_n = S(n\Delta t)$, $U_n = U(n\Delta t)$, and $C_n = C(n\Delta t)$, where Δt is a time step. The governing equations can be solved by discretizing time and applying the explicit Euler method. Then, we have the following equations:

$$S_{n+1} = S_n - \Delta t \beta \frac{S_n U_n}{N}, \quad n = 0, 1, 2, \dots, \tag{5}$$

$$U_{n+1} = U_n + \Delta t \left(\beta \frac{S_n U_n}{N} - \gamma U_n \right), \tag{6}$$

$$C_{n+1} = N - S_{n+1} - U_{n+1}. \tag{7}$$

Here, the unknown parameters are β , γ , U_0 . Once these parameter values are known, then we can solve the discrete system of Eqs. (5)–(7). To find the optimal values of the parameters (β , γ , U_0) which best fit the confirmed case data in the least-squares sense, that is,

$$\min_{\beta, \gamma, U_0} \frac{1}{2} \sum_{i=1}^p (C_{n_i} - \hat{C}_i)^2, \tag{8}$$

where p is the number of the given real data \hat{C}_i ($i = 1, 2, \dots, p$) and C_{n_i} ($i = 1, 2, \dots, p$) are the numerical solutions from Eqs. (5)–(7) at the corresponding times. We use a MATLAB routine, **lsqcurvefit**, which is a nonlinear curve-fitting solver function that uses the trust-region-reflective algorithm in a least-squares sense [18]:

$$[\beta, \gamma, U_0] = \text{lsqcurvefit}('SUCmodel', [\beta^0, \gamma^0, U_0^0], \mathbf{Tdata}, \mathbf{Cdata}, \mathbf{lb}, \mathbf{ub}), \tag{9}$$

where β, γ, U_0 are the optimized parameters, *SUCmodel* is the SUC model which returns the numerical confirmed cases at times **Tdata**, **Cdata** is the confirmed real case data, **lb** and **ub** are the lower and upper bound vectors of the parameters.

3. Computational experiments

In this section, we estimate the number of the unidentified infected population using Eqs. (5)–(7) and **lsqcurvefit** (9). We use the time series data of the confirmed cases listed in Table 1. For all numerical computations, we use the following parameter values: $\Delta t = 0.001$, $\beta^0 = 1$, $\gamma^0 = 1$, $U_0^0 = 0.1C_0$, **lb** = $(10^{-3}, 10^{-3}, 0.01C_0)$, and **ub** = $(10, 10, 5C_0)$. Here, the time unit is one day, which corresponds to 1000 time steps when $\Delta t =$

Table 1
Numbers of the confirmed cases of COVID-19 from 21 January to 24 February 2020 [2].

Situation report	Date	Confirmed cases	Situation report	Date	Confirmed cases
1	21-Jan-2020	278	19	8-Feb-2020	34,598
2	22-Jan-2020	309	20	9-Feb-2020	37,251
3	23-Jan-2020	571	21	10-Feb-2020	40,235
4	24-Jan-2020	830	22	11-Feb-2020	42,708
5	25-Jan-2020	1297	23	12-Feb-2020	44,730
6	26-Jan-2020	1985	24	13-Feb-2020	46,550
7	27-Jan-2020	2741	25	14-Feb-2020	48,548
8	28-Jan-2020	4537	26	15-Feb-2020	50,054
9	29-Jan-2020	5997	27	16-Feb-2020	51,174
10	30-Jan-2020	7736	28	17-Feb-2020	70,635
11	31-Jan-2020	9720	29	18-Feb-2020	72,528
12	1-Feb-2020	11,821	30	19-Feb-2020	74,280
13	2-Feb-2020	14,411	31	20-Feb-2020	74,675
14	3-Feb-2020	17,238	32	21-Feb-2020	75,569
15	4-Feb-2020	20,471	33	22-Feb-2020	76,392
16	5-Feb-2020	24,363	34	23-Feb-2020	77,042
17	6-Feb-2020	28,060	35	24-Feb-2020	77,262
18	7-Feb-2020	31,211			

Table 2
Computed numbers of the unidentified infected patients of COVID-19 on 11 February 2020 and ratio β/γ .

p/N	10^9	10^8	10^7
22	5028 (1.10)	5068 (1.10)	1914 (1.04)
14	3449 (1.04)	3526 (1.04)	1506 (1.02)
7	2422 (0.93)	2438 (0.93)	2436 (0.94)

Table 3
Computed numbers of the unidentified infected patients of COVID-19 on 24 February 2020 and ratio β/γ .

p/N	10^9	10^8	10^7
8	456 (0.61)	423 (0.64)	436 (0.63)

0.001. Note that we perform a practical identifiability analysis of the parameters, β and γ , in Section 4.

Let p be the number of data, **Cdata** and we take the most recent p data in Table 1. Fig. 3 shows the computational results with various N ; and $p = 22, 14$, and 7 . In this test, we consider three different N (i.e., $N = 10^9, 10^8, 10^7$) to use the effective population appropriate to each situation. When investigating actual cases of epidemic spread, we can see that most infections have occurred in certain areas such as Wuhan in China rather than across the whole country, and then spread across the country. Therefore, it is good to choose an effective population size to suit the situation. As we can observe from the results of figures, if we use the recent small number of data, then we have better fitting results to the time series data. Furthermore, we can observe the number of the unidentified infected population decreases as time increases.

Table 2 shows the computed numbers of unidentified infected population of COVID-19 on 11 February 2020 and a ratio β/γ . In a strict sense, the ratio is not equivalent to the basic reproduction number R_0 in the SIR model because our proposed model has a different meaning from the SIR model and we assume that the confirmed cases of infection are isolated completely from the susceptible population. Therefore, we present the ratio as a reference only.

Next, we perform the computational tests with various N and $p = 8$ from 17 February 2020. Fig. 4 shows the computational results on 24 February 2020 with various N and $p = 8$. As shown in Fig. 4, we have the best fitting data of the confirmed cases. Table 3 shows the computed numbers of unidentified infected population of COVID-19 on 24 February 2020 and the ratio β/γ .

4. Practical identifiability analysis

We perform the practical identifiability analysis of our proposed model using the Monte Carlo simulation (MCS) [19,20]. We use the same data and parameter set as in Fig. 4. First, we solve the SUC model numerically with the obtained parameters β and γ ; and obtain the vector C_i with $\Delta t = 0.001$ for $i = 0, 1, \dots, 7000$. Second, we generate M parameter sets, (β_j, γ_j) for $j = 1, \dots, M$. We take $M = 1000$. Here, (β_j, γ_j) are the optimized parameters with which the SUC model best fits with randomly perturbed confirmed data $P_{i,j}$ from C_i , where $P_{i,j} = C_i + C_i \epsilon_{i,j}$, $\mathbb{E}(\epsilon_{i,j}) = 0$, and $\text{Var}(\epsilon_{i,j}) = \sigma_0^2$ for each j . σ_0 is the standard deviation. Third, we compute the average relative estimation errors (AREs):

$$ARE(\beta) = \frac{1}{M} \sum_{j=1}^M \frac{|\beta - \beta_j|}{\beta} \times 100 \%,$$

$$ARE(\gamma) = \frac{1}{M} \sum_{j=1}^M \frac{|\gamma - \gamma_j|}{\gamma} \times 100 \%. \tag{10}$$

Let us consider that a parameter is very sensitive to the noise. In [20], the parameter is not practically identifiable if ARE is higher than the measurement error σ_0 . In this case, even with a moderate and reasonable level of measurement error, it may result in a seriously large ARE. Table 4 lists AREs for the parameters β and γ with respect to various noise levels σ_0 . As expected, increasing σ_0 increases the AREs. Both the parameters β and γ are practically identifiable because the AREs are smaller than the measurement error σ_0 . Therefore, the proposed model is practically identifiable, which implies the model parameters can be estimated from real data.

5. Discussion

We proposed a new approach for modeling an epidemic disease, COVID-19, to estimate the unidentified infected case U . The proposed model is in a framework similar to the standard SIR model. However, our model suggests a different interpretation of a worldwide epidemic. The main purpose of the proposed model is to predict the number of the unidentified infected population who are infected but have not yet been confirmed.

The SUC model is potentially useful for determining the effectiveness of interventions. We can find out if various policy/strategy work well, and monitor their strengths and weakness by analyzing the changes of U after taking some actions. Furthermore, the model is helpful for predicting the extent of infection spread, i.e., U can

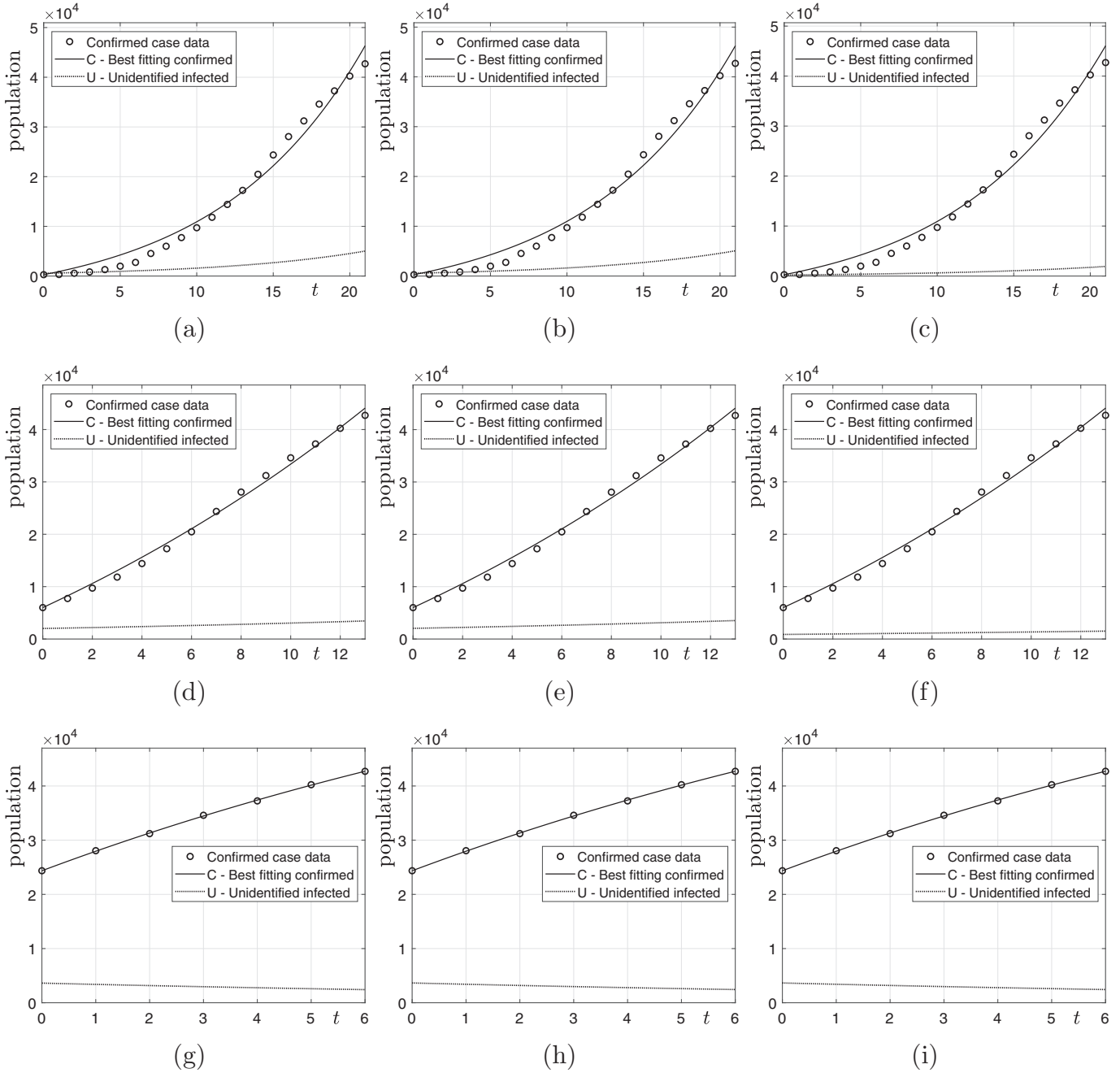


Fig. 3. Computational results: (a), (b), and (c) are results with $N = 10^9, 10^8, 10^7$ and $p = 22$; (d), (e), and (f) are results with $N = 10^9, 10^8, 10^7$ and $p = 14$; (g), (h), and (i) are results with $N = 10^9, 10^8, 10^7$ and $p = 7$.

Table 4
Average relative estimation errors for parameters β and γ .

N	10 ⁹		10 ⁸		10 ⁷	
	σ_0 (%)	ARE(β) (%)	ARE(β) (%)	ARE(γ) (%)	ARE(β) (%)	ARE(γ) (%)
0	0.00	0.00	0.00	0.00	0.00	0.00
1	1.87	1.26	0.87	0.57	0.48	0.37
5	3.98	2.93	2.54	1.82	1.54	1.36
10	6.02	4.64	4.15	3.25	2.82	2.59
20	10.03	7.87	7.93	5.95	5.42	4.67
30	13.65	11.23	10.55	9.80	7.29	7.91

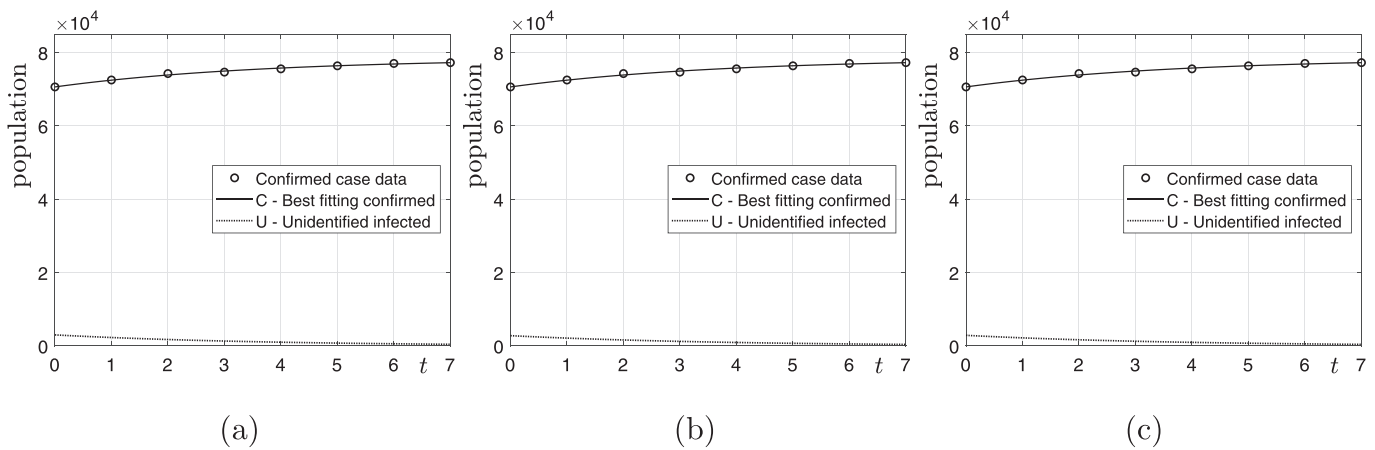


Fig. 4. (a), (b), and (c) are results with $p = 8$ and $N = 10^9$, 10^8 , and 10^7 , respectively, from 17 February 2020.

be used as a criterion. Thus, we can prepare the proper quantity of protective masks or COVID-19 diagnostic kit to supply, hospital beds, medical staffs, and so on. It is significantly important to prevent the spread of infectious diseases and the incalculable damage caused by the epidemics.

However, the proposed model is as simple as possible under many constraints, assuming the ideal situation. In this paper, we reduced the complexity and focused on a basic building block. Thus, we excluded several realistic elements, for example, interventions, a latent period of virus, changes in population due to birth and death, infection in medical staff or confirmed patients not isolated, etc. In future works, we will complement various conditions for specific and realistic situations not covered in this paper to improve the model.

The accurate estimation of the unidentified infected using the proposed model depends on the reliable and accurate confirmed data. We used the number of the confirmed cases and deaths reported by WHO. There may be differences in how data is aggregated for each country or region. In fact, the criterion for classifying the confirmed cases in China has been changed twice, and it has led to sharp increase in the number of confirmed cases on 17 February 2020. Nevertheless, the proposed model can be modified by applying various situations for each system and culture in diverse countries. We only used the data on China, however, if the model is supplemented, it can be applied to many different countries with a variety of spread patterns.

6. Conclusion

The proposed SUC epidemic model for computing the unidentified infected for COVID-19 in China is very simple and is robust in computation. The model only uses the numbers of the total population and the available time series confirmed cases. The computational results from the model can be useful in controlling of the disease because we can estimate the size of the unidentified infected population. We performed the practical identifiability analysis of the proposed model using MCS. Finally, we clarified the importance of the proposed model and added its limitations. In the Appendix, we provide the source program code so that the interested readers can use and modify it for their own needs. In future works, we will improve the SUC model with more specific conditions such as a latent period, changes in population due to birth

and death, infection in medical staff or confirmed patients not isolated. We will also develop a novel and proper index corresponding to the basic reproduction number used to investigate infectious diseases and compare to other diseases.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

CRediT authorship contribution statement

Chaeyoung Lee: Methodology, Software, Validation, Formal analysis, Investigation, Data curation, Writing - original draft, Writing - review & editing, Visualization, Funding acquisition. **Yibao Li:** Validation, Investigation, Writing - original draft, Writing - review & editing, Funding acquisition. **Junseok Kim:** Conceptualization, Methodology, Software, Validation, Formal analysis, Writing - original draft, Writing - review & editing, Supervision, Funding acquisition.

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Appendix A

The following MATLAB codes are available from the corresponding author's webpage:

<http://elie.korea.ac.kr/cfdkim/codes/>

The following code is a function and should be saved with the file name 'SUCmodel.m' and placed in the same folder where the main code is.

```

function f = SUCmodel(Parameter, Tdata)
global N C0;
b = Parameter(1);
g = Parameter(2);
U(1) = Parameter(3);
C(1) = C0;
S(1) = N-C(1)-U(1);
Nt = 1000*Tdata(end);
dt = 0.001;
for i = 1:Nt
    S(i+1) = S(i) - dt*b*S(i)*U(i)/N;
    U(i+1) = U(i) + dt*(b*S(i)*U(i)/N - g*U(i));
end
C = N-S-U;
t = linspace(0,Tdata(end),Nt+1);
f = interp1(t,C,Tdata);

```

The following code is the main program.

```

clear; format long; global N C0 ts;
p = 8; ts = [1:35]; given = ts(end);
Tdata = ts(given+1-p:given); Tdata = Tdata-Tdata(1);
Cs = [278 309 571 830 1297 1985 2741 4537 5997 7736 9720 {11,821} 14411 {17,238} 20471 {\ldots}
{24,363} 28060 {31,211} 34598 {37,251} 40235 {42,708} 44730 {46,550} 48548 {50,054} 51174 {\ldots}
{70,635} 72528 {74,280} 74675 {75,569} 76392 {77,042} 77262];
Cdata = Cs(given+1-p:given); p = Tdata(end);
N = 1.0e+8; C(1) = Cdata(1); C0 = C(1); b0 = 1.0; g0 = 1.0; Us = 0.1*C0;
param = lsqcurvefit(@SUCmodel,[b0 g0 Us],Tdata,Cdata,{\ldots}
[1.0e-3 1.0e-3 0.01*C0],[10 10 5*C0]);
b = param(1); g = param(2); U(1) = param(3); S(1) = N-U(1)-C(1);
Nt = 1000*p; dt = 0.001;
for i = 1:Nt
    S(i+1) = S(i) - dt*b*S(i)*U(i)/N;
    U(i+1) = U(i) + dt*(b*S(i)*U(i)/N - g*U(i));
end
C = N-S-U;
figure(1); clf; grid on; hold on
t=linspace(0,p,Nt+1);
plot(Tdata,Cdata,'ko','linewidth',2);
plot(t,C,'k','linewidth',1.5); plot(t,U,'k','linewidth',2);
legend('Confirmed_case_data','C--Best_fitting_confirmed',{\ldots}
'U--Unidentified_infected','Location','best')
axis([t(1) t(end) 0 1.1*max(U(end),C(end))]); xlabel('t'); ylabel('population')

```

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