A Modified SAIR Model for the Spread of COVID-19 in China

Yijun Guo
School of Pharmaceutical Sciences, Sun Yat-Sen University, Guangzhou, 510006, China

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Abstract: The study aims to modify the SIR model with consideration of asymptomatic patients for the spread of COVID-19 in China. The data is obtained from the National Health Commission of the PRC. Data fitting based on Chinese epidemic data is conducted to find the value of parameters. Besides, sensitivity analysis is applied on parameters, and the new modified model is compared with model having a similar structure in the previous study. For further investigation, the basic reproduction number, R_0, turning point and ratio between asymptomatic and total infected ones are calculated. The fitting and sensitivity analysis reveals that loss of immunity, ratio between infection rate of asymptomatic ones and infected ones will not significantly influence the SAIR model. The analysis results also show that structure of previous model with related infection rates does not work well on chosen data. On the contrary, transformation rate from asymptomatic ones to infected patients plays a critical role in the epidemic. mentioned above. Further evaluation shows that it can be used as a reference for the arrangement of testing. The model can be used to predict the general evolution of the disease spread. The increase of the transformation rate can alleviate the spread of disease. Transformation rate can be interpreted as the frequency of testing, which further confirms the necessity of these methods and provides some application values. The model is plausible but more analysis is still needed to evaluate the different conditions to apply.

1 INTRODUCTION

COVID-19, a respiratory disease, has caused the death of 4.29 million people, and approximately 202 million positive cases have been detected from Dec 30th 2019 till Aug 10th 2021(*Coronavirus disease (COVID-19) pandemic*, 2021). Vaccination is considered to be an effective method to suppress the spread of COVID-19. However, the biosecurity of vaccination and duration of immunity still need time to prove (Huang, 2021; Vashishtha & Kumar, 2021). What's more, the mutation rate of SARS-CoV-2 is fast and diversified, which can hardly be caught up by the speed of vaccination development. The mutation of highly pathogenic strain "Delta" to "Delta-plus", or "AY.1" detected in June 2021 in India brings more challenges (Banerjee et al., 2021). Until now, we can still assume that stable immunity against COVID-19 has not been totally built among people.

Asymptomatic patients with COVID-19 will unconsciously spread disease to their contacts since they may not receive diagnosis because they do not show symptoms (Kronbichler et al., 2020). The asymptomatic can be divided into two groups, one will recover without the symptoms, and the other will show the symptoms and become the normally assumed "infected people" in epidemiology concepts. Multiple detection and tracking methods can be applied to screen out asymptomatic population, which will promote the performance of isolation, treatment and other strategies to control the influence of this group (Chaimayo et al., 2020; Rivett et al., 2020).

The Susceptible-Infected-Removed (SIR) model is commonly used in the epidemiological studies and prediction for outbreak of certain disease (Lounis & Bagal, 2020). Traditional SIR model divides people into three groups: the susceptible (S), the infected (I), and the removed (R). However, the design of traditional model cannot display the true infected situation well. Patients who recovered from the disease can be easily infected again (Abou-Ismail, 2020). Here, we consider the condition that part of people recovered from disease will not get stable immunity. We also take asymptomatic patient into account, since they may have different infected and recovery rates as the infected ones. In this study, we

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evaluate the newly built model and parameters based on the simulation of R. Besides, by data fitting and sensitivity analysis, we investigate the role of these parameters in the model. According to the analysis of parameters, we further evaluate the strategies that can be applied to control the disease.

2 SAIR MODEL

2.1 Model Equations

As mentioned above, infected individuals can be divided into two parts, the infected ones and the asymptomatic ones. In the SAIR model, the four groups we concern are S (t) for susceptible, I (t) for infected, A (t) for asymptomatic and R (t) for recovered. Figure 1 shows the interrelationships of these parts.

The model set assumptions as follows: 1) demographical changes for the asymptomatic, the susceptible and the recovered are ignored; 2) only death rate of the infected will be considered here; 3) part of asymptomatic patients will transform into infected ones; 4) infected ones and asymptomatic ones have different infection rate and recovery rate; 5) the total population is denoted by N (t), and contains four groups, S (t), I (t), A (t) and R (t). Change of four fractions can be described by the following differential equations.

$$\frac{dS}{dt} = -\frac{(\beta I+\beta_1 A)S}{N} + m\gamma I + \gamma_1 A \quad (1)$$

$$\frac{dA}{dt} = \frac{(1-q)(\beta I+\beta_1 A)S}{N} - (\gamma_1 + \kappa)\, A \quad (2)$$

$$\frac{dI}{dt} = \frac{q(\beta I+\beta_1 A)S}{N} - (\gamma + \mu)I + \kappa A \quad (3)$$

$$\frac{dR}{dt} = \gamma I(1-m) + \mu I \quad (4)$$

$$N = S + I + A + R = 1 \quad (5)$$

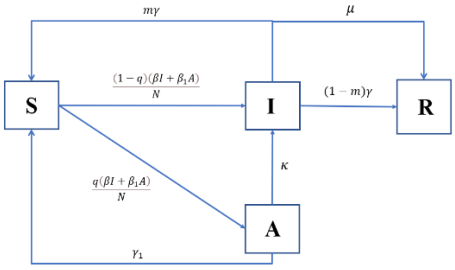


Figure 1: Flow chart of the SAIR model.

Parameters above in this model are positive and can be interpreted as follows:

- β is the infection rate of infected individuals;
- β_1 is the infection rate of asymptomatic individuals;
- γ is the recovered rate of infected individuals;
- γ_1 is the recovery rate of asymptomatic ones;
- μ is the death rate of infected ones;
- κ is the possibility for asymptomatic patients to become infected ones at a certain time, which means they will show the symptoms or be regarded as infected by certain criteria;
- q is the possibility for susceptible people who contact with asymptomatic ones and infected ones to become infected ones, while 1-q means the possibility to become asymptomatic ones;
- m means the possibility for recovered asymptomatic people to become susceptible again. They are assumed to have no stable immunity.

2.2 Analysis of Mathematical Model

2.2.1 Basic Reproduction Number

The basic reproduction number, R_0 of the SAIR model was calculated using the next generation matrix methods (Diekmann et al., 2010). To calculate the basic reproductive number, the approximation of S (t) could be N when $t \approx 0$. Based on Eq. (1)-(5), Eq. (2) and Eq. (3) could be expressed as:

$$\begin{cases} \frac{dA}{dt} = (1-q)(\beta I + \beta_1 A) - (\gamma_1 + \kappa)A \\ \frac{dI}{dt} = q(\beta I + \beta_1 A) - (\mu + \gamma)\, I + \kappa A \end{cases} \quad (6)$$

From Eq. (6) we can get the matrix

$$X = \begin{pmatrix} A(t) \\ I(t) \end{pmatrix} = \begin{pmatrix} (1-q)(\beta I+\beta_1 A) \\ q(\beta I+\beta_1 A) \end{pmatrix} + \begin{pmatrix} (\gamma_1+\kappa)A \\ (\mu+\gamma)\, I-\kappa A \end{pmatrix} = F_{1,2}(A,I) + V_{1,2}(A,I) \quad (7)$$

$$F = Jacobian(F_{1,2}(A,I)) = \begin{pmatrix} (1-q)\beta_1 & (1-q)\beta \\ q\beta_1 & q\beta \end{pmatrix} \quad (8)$$

$$V = Jacobian(V_{1,2}(A,I)) = \begin{pmatrix} \gamma_1+\kappa & 0 \\ -\kappa & \mu+\gamma \end{pmatrix} \quad (9)$$

R_0 can be calculated as the eigenvalues of FV^{-1}:

$$R_0 = \frac{(1-q)\,\beta_1}{\gamma_1+\kappa} + \frac{\beta(\kappa+\gamma_1 q)}{(\gamma_1+\kappa)(\mu+\gamma)} \quad (10)$$

R_0 is normally used to evaluate whether the outbreak of disease will happen. When $R_0 \leq 1$, the

system is supposed to have disease-free equilibrium and the number of infected people will decrease. On the contrary, endemic equilibrium will exist when $R_0 > 1$. An increase of μ and γ leads to decrease of R_0, which leads to the elimination of disease. In the fitting part, we will discuss influence of value of κ to R_0. Parameter m seems to have little influence on basic reproduction number.

2.2.2 Simulation of SAIR Model

To find numerical solutions of the model, we set the following initial values for parameters:
$N(0) = 1, S(0) = N(0) - I(0),$
$I(0) = 0.0005, A(0) = 0,$
$\beta = 0.3, \beta_1 = 0.5, \gamma = 1/7, \gamma_1 = 1/21,$
$\mu = 0.002, m = 0.6, q = 0.2, \kappa = 1/14$

By introducing the normalization condition, where N is set to be 1, the effect of the total population on the modeling outcome can be eliminated to some extent. The time evolution of four fractions is displayed in Figure 2.

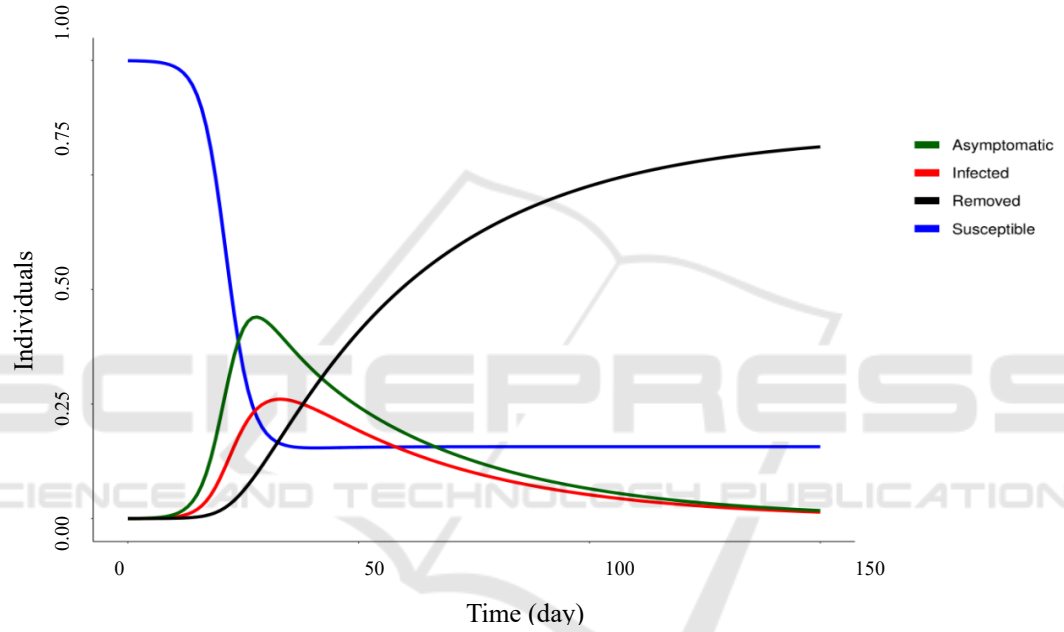


Figure 2: Numerical solutions for fractions of susceptible, asymptomatic, infected, and recovered in the SAIR model. Parameter values: β =0.3, β_1 = 0.5, γ =1/7, γ_1 =1/21, μ = 0.002, m =0.6, q = 0.2, κ = 1/14. Initial values for fractions: $N(0)$ = 1, $S(0) = N(0) - I(0)$, $I(0)$ = 0.0005, $A(0)$ = 0.

As for the set of initial values of parameters, we initially assume asymptomatic ones will have stronger infection ability than infected ones because infected ones are more probable to be isolated. People with a certain knowledge of the disease will also keep distance from symptomatic ones. Recovery rate represents reciprocal of time needed for patients to recover. Here we set γ and γ_1 as 1/7 and 1/21 respectively according to the previous research (Neves & Guerrero, 2020). Some of the asymptomatic people will get normal unconsciously without showing symptoms in this model. The other part of the asymptomatic population will become infected ones. Transformation rate without inference can be assumed as length of incubation period. Since most countries set the quarantine for 14 days, we can primarily set κ as 1/14 (Gaeta, 2020). In that case, the transformation rate, κ, is primarily set to be 1/14 days^{-1}. And the death rate is set according to the analysis of death cases in real data, which will be introduced in the data fitting part. Since the number of asymptomatic behind the confirmed cases is usually larger than confirmed number, q is set to be lower than 0.5 to simulate that condition.

2.2.3 Conditions for Elimination of Disease

The total infected ones can be represented as I (t) +A (t), and disease starts to eliminate when:

$$\frac{d(A+I)}{dt} < 0 \quad (11)$$

The number of asymptomatic patients is much larger than infected ones and they can transform into infected ones according to the model. The most important is that A (t) has a stronger infection ability compared with I (t) based on assumptions of this model. For the reasons above, we assume I (t) / A (t) ≈ 0, and we use A (t) to substitute whole infected people. We can get:

$$S(t) < \frac{(\gamma_1+\kappa)A}{(1-q)(\beta I+\beta_1 A)} \quad (12)$$

Combined with Eq. (2) and Eq. (11), Eq. (12) can be transformed into:

$$S(t) < \frac{\gamma_1+\kappa}{(1-q)(\frac{\beta I}{A}+\beta_1)} \approx \frac{\gamma_1+\kappa}{\beta_1(1-q)} \quad (13)$$

We can see that when asymptomatic patients play a critical role during the epidemic of the disease, the elimination of total infected ones will start when S (t) reaches $\frac{\gamma_1}{\beta_1}$. Recovery rate and infection rate of asymptomatic patients decide the peak of disease. However, one thing that should be paid attention to is that conclusion above can only be achieved when A(t) plays main role in the system, so the value of q should be small.

2.2.4 Comparison between Modified SAIR Model and SAIR Model in Previous Study

In the SAIR model sourced from previous study (Neves & Guerrero, 2020), an SAIR model was built:

$$\frac{dS}{dt} = -\beta_0 S(I+\mu A) \quad (14)$$

$$\frac{dA}{dt} = \beta_0(1-\xi)S(I+\mu A) - \gamma_\alpha A \quad (15)$$

$$\frac{dI}{dt} = \beta_0 \xi S(I+\mu A) - \gamma_s I \quad (16)$$

$$\frac{dR_s'}{dt} = \gamma_s I \quad (17)$$

$$\frac{dR_\alpha'}{dt} = \gamma_\alpha A \quad (18)$$

$$\boldsymbol{N = S + I + A + R_s' + R_\alpha'} \quad (19)$$

We can call this model P, and the new model in this paper is model M. In model P, γ_α and γ_s denotes recovery rates of asymptomatic ones and infected ones. Infection rate of infected patients and asymptomatic patients are represented by β_0 and $\mu\beta_0$. Table 1 shows a simple comparison of the two models.

Table 1: Comparison of two SAIR models.

Items	Model M	Model P
Variables	4	5
Basic reproduction number	$\frac{(1-q)\beta_1}{\gamma_1+\kappa} + \frac{\beta(\kappa+\gamma_1 q)}{(\gamma_1+\kappa)(\mu+\gamma)}$	$\beta_0[\frac{\xi}{\gamma_s} + \frac{\mu(1-\xi)}{\gamma_\alpha}]$
Death rate	μ	None
Immunity duration	Unstable	Stable
Infection rates	A (t) : β_1, I (t) : β	A (t) : $\mu\beta_0$, I (t) : β_0
Relations between two infection rates	Unrelated	Related
S (t) for elimination of disease	$\frac{\gamma_1+\kappa}{\beta_1(1-q)}$	$\frac{\gamma_\alpha}{\beta_0(1-\xi)\mu}$
Transformation rate from A (t) to I (t)	κ	None

From the comparison we can see main differences between the two models. Model P does not consider death rate (μ in model M), transformation rate (κ) or unstable immunity (m). As for infection rates, β and β_1 in Model M are not related as model P.

3 FITTING THE EPIDEMIC DATA OF COVID-19 ON SAIR MODEL

3.1 Fitting the Epidemic Data in China

Data used for fitting is from National Health Commission of the PRC (*Official report of COVID-19*, 2021). Present confirmed cases, death cases, recovered cases and the number of people under observation are reported every day. Observation cases in China include people who show slight symptoms and people who are tracked to have contact with infected ones. Figure 3 shows evolution of four kinds of data from 21st Jan, 2020 to 10th Apr, 2020. We choose the initial stage of the COVID-19 in China because isolation strategy worked well later, which significantly influenced the spread of disease. Timeframe from 21st Jan to 10th Apr includes just single peak of confirmed cases, which is also compatible with assumption of model M.

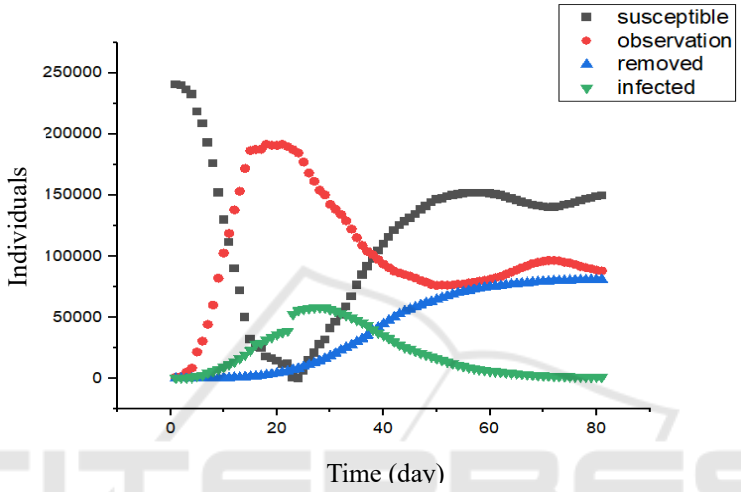


Figure 3: Epidemic data in China from 21st Jan, 2020 to 10th Apr, 2020 by National Health Commission of the PRC. *N* is set to be 241835.

We can see from Figure 3 that both removed and infected cases finally reach a plateau. Infected cases have a single peak during the timeframe. However, the number of cases under medical observation has a small fluctuation after the peak. This group of population may be influenced by a newly discovered case or some policies.

For the total size of population, N, we cannot choose population of the full country as N (Ahmetolan et al., 2020), because epidemic of SARS-CoV-2 in China is highly heterogeneous. The max sum of confirmed cases (55748), cumulative death cases (1380), cumulative recovery cases (6732) and present observation cases (177984) appeared on 13th Feb 2020, which can be used to substitute N at initial stages. Asymptomatic ones are hard to be detected and reported. We can consider the worst condition that all of the people who show slight symptoms or have contact with the infected ones could be asymptomatic. Here, we assume number of observation cases is approximate to asymptomatic ones. *N*' denotes the population at initial stage, which is 241835. Confirmed cases reported by government can be treated as infected ones in this model. Death ones can be precisely estimated by death cases reported. Here, we can divide *R* into two parts, one is for the death (R_d), and the other is for the recovered ones (R_a). So Eq. (4) could be transformed as follows:

$$\frac{dR_d}{dt} = \mu I \tag{20}$$

$$\frac{dR_a}{dt} = (1-m)\gamma I \tag{21}$$

To calculate μ, we use R to apply regression diagnosis on reported daily infected cases and daily death cases to find if linear regression can be used on true data. Figure 4 shows diagnosis results regarding to normality, linearity, homoscedasticity and simple observation points. We can see from the result that it number of death cases is linear with confirmed cases, which reflect the relationship in Eq. (20). So here, we could use true data to calculate μ. μ is calculated to be 0.002 by R.

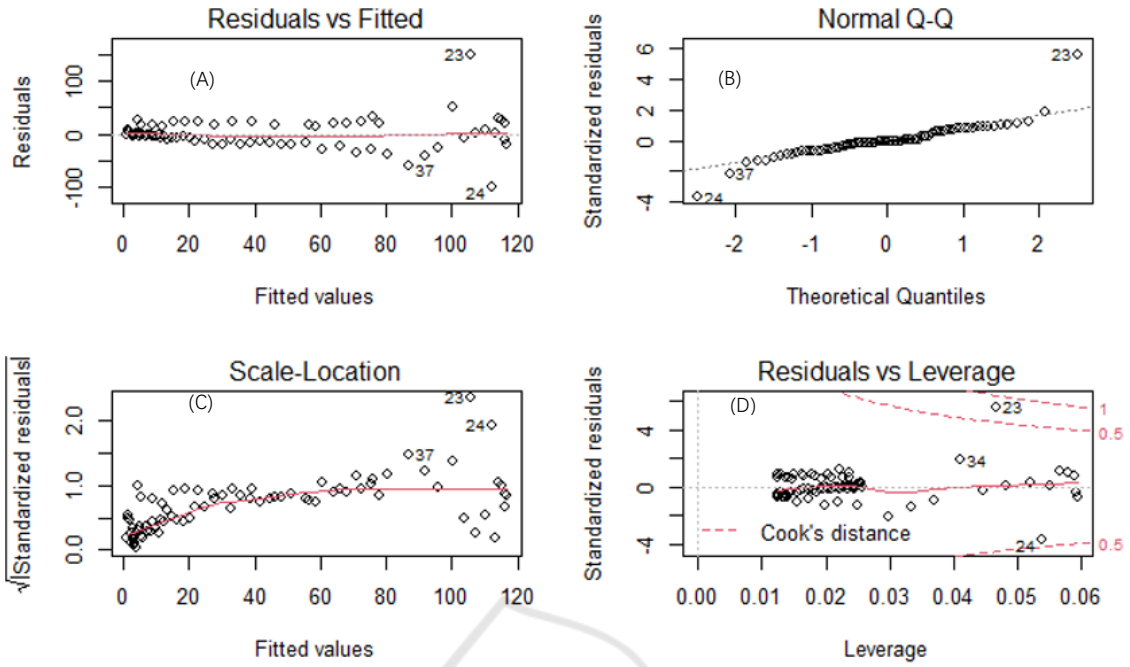


Figure 4: Diagnosis of linear regression of daily infected cases and daily death cases. (A) Plot of residuals vs fitted. (B) Normal Q-Q plot. (C) Scale-Location plot. (D) Plot of residuals vs leverage.

We use confirmed cases to estimate these parameters here because death cases and asymptomatic cases were proved to be proportional to infected cases (Ahmetolan et al., 2020; Grunnill, 2018). The cost function between predicted data and true data can be described as follows (Ianni & Rossi, 2020).

$$J^2{}_I(\hat{\theta}) = \sum_i \left(I(t_i;\hat{\theta}) - N_I(t_i)\right)^2 \quad (22)$$

$$J^2{}_A(\hat{\theta}) = \sum_i \left(A(t_i;\hat{\theta}) - N_A(t_i)\right)^2 \quad (23)$$

$$J^2{}_D(\hat{\theta}) = \sum_i \left(D(t_i;\hat{\theta}) - N_{R_d}(t_i)\right)^2 \quad (24)$$

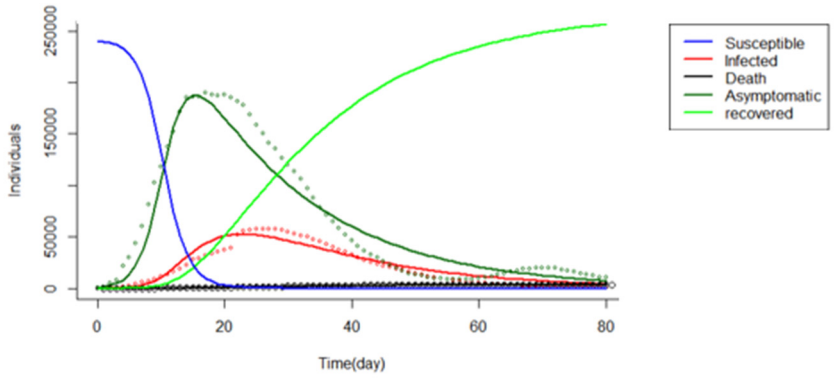
$N_{I,A,R_d}(t_i)$ represents true data cases in the time frame till t_i. $\hat{\theta} = \{\beta, \beta_1, \gamma, \gamma_1, m, \mu, \kappa, q, N, I(0), A(0), R_d(0)\}$. The value of parameters can be estimated based on the least cost. Initial values of parameters are set in Figure 2. We set initial values according to epidemic data at the start of time frame:

$$N(0) = 92388, S(0) = N(0) - I(0), I(0) = 291, A(0) = 922$$

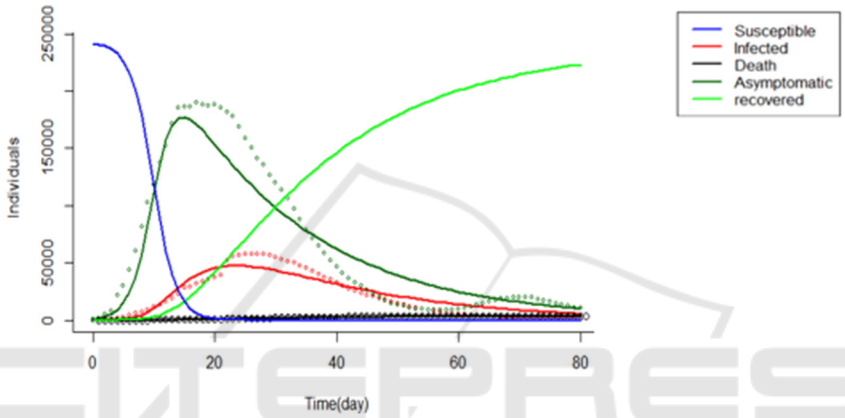
The fitting of the data is conducted by FME package in R.

Eq. (22-24) are used to fit the data, the result is as follows:

(A)



(B)



(C)

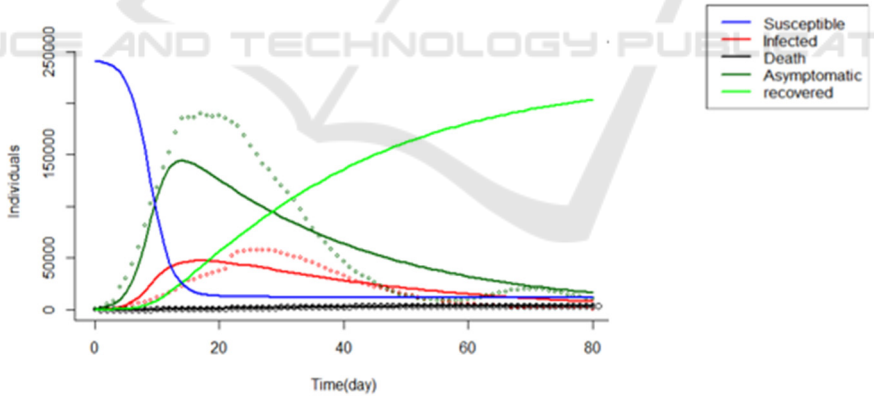


Figure 5: Fitting of I (infected), A (asymptomatic) and R_d (death) on Chinese data from 21st Jan, 2020 to 10th Apr, 2020. (A) Fitting without related infection rate. (B) Fitting with related infection rate. (C) Fitting with several selected parameters.

We can see from Figure 5 (A) that the model fits data well at the initial stage but not very well around the peak. The model can depict the general changing trend of five parts. By investigating the parameters, we find that the fitting result is not compatible with our assumptions. In our assumptions of model, infection rate of infected ones should be lower than asymptomatic ones. So here, we relate β with β_1 by n ($\beta = n\beta_1$, $0< n <1$) like model P, so that we could guarantee β_1 is always larger than β. n is initially set to be 0.6. In this way, we could also find whether the relationship between infection rates matters in this model. The fitting result is showed in Figure 5 (B) and Table 2. There is no significant change between results. From the fitting results, we can conclude that ratio between β and β_1 does not play a critical role in the fitting of Chinese data.

Table 2: Comparison of parameters with and without fixed parameters.

Parameters	Value		
	Original parameter	Related infection rate	Selection of parameters
β	0.999	/	0.999
γ	0.124	0.125	0.119
β_1	0.497	0.543	0.564
γ_1	$1.40*10^{-7}$	$8.93*10^{-8}$	$4.76*10^{-2}$ (fixed)
κ	$4.55*10^{-2}$	$4.57*10^{-2}$	$4.36*10^{-2}$
q	$4.78*10^{-7}$	$3.31*10^{-7}$	0.200 (fixed)
m	$1.32*10^{-6}$	$8.71*10^{-7}$	0.600 (fixed)
μ	$2.12*10^{-3}$	$2.12*10^{-3}$	$2.12*10^{-3}$
n	/	0.999	/

3.2 Sensitivity Analysis of Parameters

Sensitivity analysis is conducted on parameters in the first column in Table 2 ($\beta \neq n\beta_1$) to show the influence of parameters (Table 3). m, γ_1 and q seem to have little influence on this dataset, which confirmed the parameter calculation results in Table 2. We choose parameters except m, γ_1 and q as parameters to fit; the results are in Figure 5 (C) and Table 2. Interestingly, we find that the fitting result is not as well as the first two sets of parameters. From the original plot, we can conclude that the source of data lead to that result. Since data used to describe asymptomatic is the number of people under medical observation, so there is a time lag between growth of A (t) and I (t). m, γ_1 and q might work here to guarantee the time lag. If the model fitting is conducted without m, γ_1 or q, growth of A (t) will be synchronized with growth of I (t) as Figure 5 (C) shows.

Sensitivity also shows that κ has a great impact on model and almost remain unchanged when we change the design of model as above. κ represents rate of asymptomatic ones to become infected ones. The value of κ is about 0.0457, which means that time need for asymptomatic ones to become infected ones is about 22 days (1 / 0.0457 day-1).

Table 3: Sensitivity analysis of parameters.

Parameter	Item					
	value	L1	L2	Mean	Min	Max
β	0.999	0.120	0.178	0.0450	-0.0850	0.553
γ	0.124	0.555	0.749	-0.547	-1.49	0.0168
β_1	0.497	0.528	0.779	0.183	-0.388	2.55
γ_1	$2.33*10^{-7}$	$3.12*10^{-7}$	$4.53*10^{-7}$	$-2.66*10^{-7}$	$-1.31*10^{-6}$	$1.32*10^{-7}$
κ	$4.55*10^{-2}$	0.872	1.15	-0.317	-3.18	1.01
q	$8.84*10^{-7}$	$1.61*10^{-6}$	$2.73*10^{-6}$	$6.07*10^{-7}$	$-1.06*10^{-6}$	$9.92*10^{-6}$
μ	$2.12*10^{-3}$	0.331	0.567	0.320	-0.0254	0.999
m	$2.34*10^{-6}$	$2.10*10^{-6}$	$3.22*10^{-6}$	$2.10*10^{-6}$	0.000	$9.06*10^{-5}$

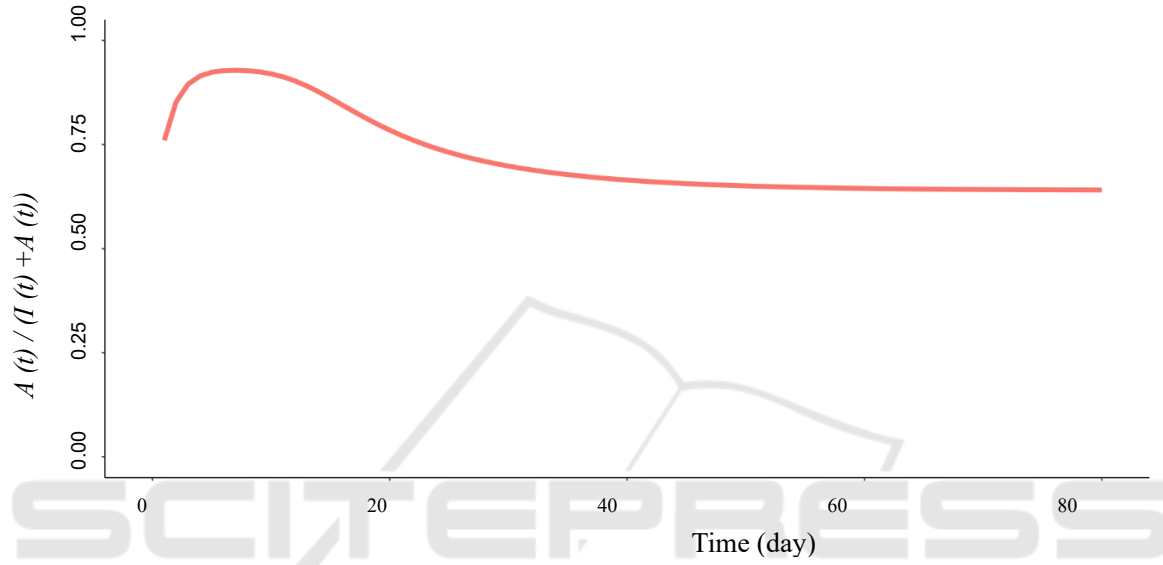
3.3 Epidemic Items and Strategies to Alleviate COVID-19 based on *K*

Several items regarding epidemic evolution are calculated with the original set of parameters. The results are displayed in Table 4. R_0 is 18.8 ($R_0 > 1$), which indicates that the outbreak of disease is still potential without inference. R_0 also considers the existence of asymptomatic patients at the end of time frame. Though the number of infected ones has been eliminated, asymptomatic patients may still bring fluctuations. S (t) / N can work as evidence of the turning point of disease. Value of S (t) / N indicates that the turning point of disease is approximately on the 20th day. Figure 5 further confirmed the prediction of turning point. A (t) / (I (t) +A (t)) (Figure 6 (A)) indicates that ratio between asymptomatic ones and total infected ones will finally reach the plateau (0.641), which could be used to predict fractions and number of asymptomatic ones.

Table 4: Several epidemic items calculated by model.

Item	Value
R_0	18.8
$S(t)/N$	0.0915
$A(t)/(I(t)+A(t))$	0.641

(A)



(B)

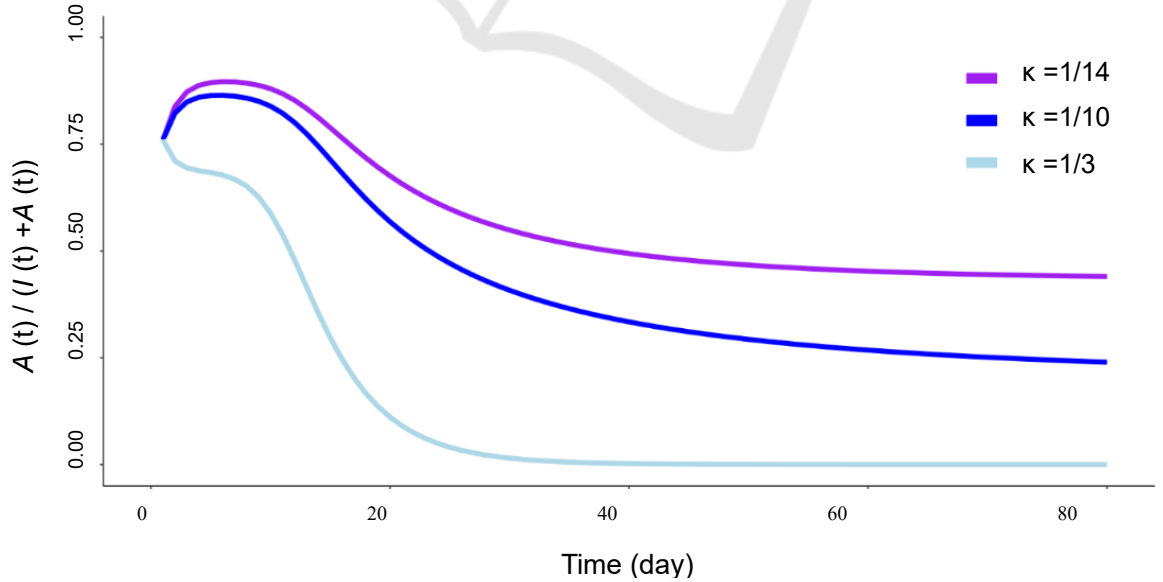


Figure 6: Ratio of $A(t)/(I(t)+A(t))$. (A) $A(t)/(I(t)+A(t))$ calculated by original parameters in Table 2. (B) $A(t)/(I(t)+A(t))$ under different values of κ (1/14, 1/10,1/3).

Since the role of κ is confirmed by sensitivity analysis, we further evaluate how R_0, S (t) and A (t) / (I (t) +A (t)) can be influenced by κ. Here, changes of A (t) / (I (t) +A (t)) and R_0 under different values of κ are shown in Figure 6 (B) and Figure 7. The results show that plateau proportion of asymptomatic will decrease. Furthermore, R_0 become smaller if we change the value of κ from 0 to 1 based on this set of parameters. From Eq. (13) we can know that S (t) will increase with the increase of κ.

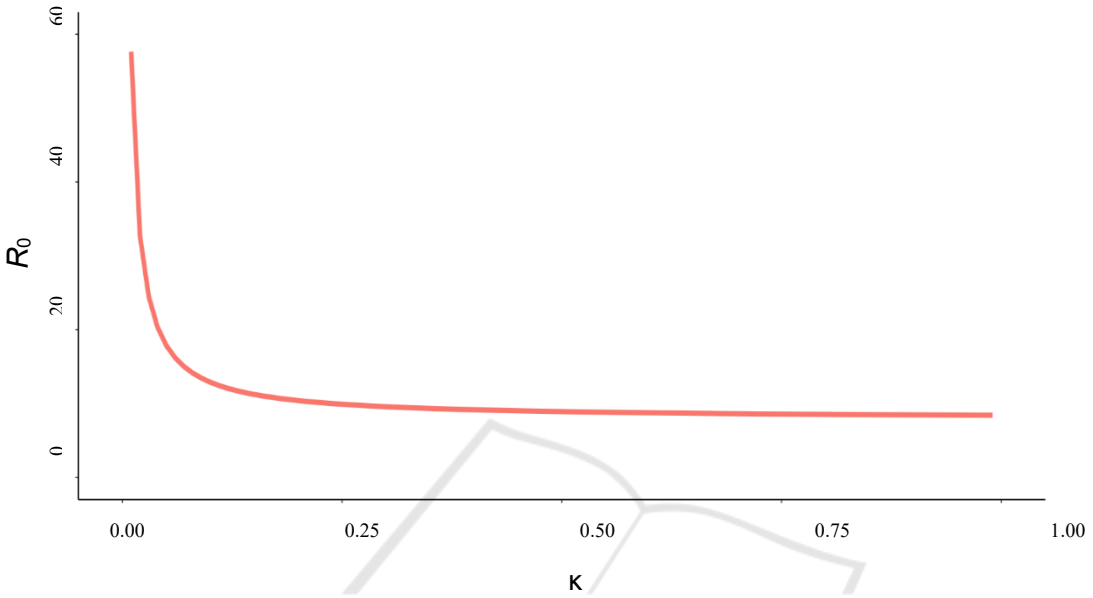


Figure 7: R_0 calculated by original parameters under different values of κ ($0 < \kappa < 1$)

To sum up, the burden of asymptomatic patients and the spread of disease can be alleviated by regulating of κ. Several methods can be applied based on interpretation of κ such as nucleic acid amplification testing (NAT) like oropharyngeal (OP) (Rivett et al., 2020), tracking or isolation. If we assume κ as the frequency of NAT, we can get more information for reference from κ. We can see in Figure 7 that the decrease of R_0 gradually gets slower after κ is smaller than certain value. The value in this system is approximate 0.25. Figure 6 (B) also confirms that when κ gets close to 1/3, there will not be an initial increase of A (t) / (I (t) +A (t)), and the ratio will quickly get down. From the above results, we can infer that the proper testing frequency can be set as once per three days or four days in the spread condition of China. If there is a lack of source for frequent testing, evaluations regarding κ can also be taken as a reference for testing arrangement.

4 CONCLUSION

For the consideration of asymptomatic patients, we build new SAIR model to better fit the real condition of the disease. Asymptomatic patients will keep infecting the susceptible because they show no syndrome and will not be detected, isolated and treated. So here, the model is modified to find the influence of this group. And previous study about model with a similar structure is used for comparison in this study (Neves & Guerrero, 2020).

Our model adds the assumption that the infected ability of asymptomatic patients will not be related to the infected ability for infected groups. We also evaluate the role of transformation rate from the asymptomatic to the infected. And immunity will not be built on all people who recovered. By comparison with previous model, we also find that it is too haste to just relate two infection rates by a simple coefficient ($\beta = n\beta_1$) because of choice of data representing asymptomatic population. Data evolution from hospital regarding people under medical observation may have a time lag of change on infected people. So, if we choose medical observation data as asymptomatic ones, two parameters cannot be simply related when fitting. From the fitting results and sensitivity analysis we can conclude that parameters regarding part immunity dose not significant the fitting results.

Transformation rate plays a critical role in the evolution of disease. Here, we assume κ can be interpreted as frequency of NAT. We find that several epidemic items can be calculated to display influence of κ on testing arrangement.

The model used here is a simple design of SAIR model. Focusing on the influence of asymptomatic ones, it does not take into account of multiple factors.

In other studies, spread in different communities, countries and between different groups of people, for example, the elder and teenagers are evaluated (Cooper et al., 2020; Harris, 2020; Purkayastha et al., 2021). Some models also considered the removed or isolated ones which will make the total population heterogeneous (Maheshwari & Albert, 2020). In the more sophisticated design, recovered and infected groups could be divided into more groups to improve the applicability of model (Tomochi & Kono, 2021). In that case, the model still has a large potential to develop and attain higher application value.

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