The Model of COVID-19 Pandemic

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***Abstract*—To Investigate the pandemic model of COVID-19 based on traditional SIR model and formulate an ideal Time Lagging-SEIR model of COVID-19, author starts from giving basic SEIR model, and gradually refines it with taking consider more unique factors which contained by COVID-19. After giving the refined COVID-19 model function, author states that there are several parameters cannot be derived currently, thus the model function needed to be simplified. Several necessary parameters are given by using data collected in WuHan and citing from research papers from others, and liner regression is used to find rate of death and recovery which are always changing during the whole spreading process. In the end of this paper, author gives a function group of COVID-19 model which have all necessary parameters given in the paper.**

Keywords—SEIR model, time-lagging, COVID-19

I. Introduction

COVID-19 is currently most important issue almost relates with every humans since its extremely high rate of prevalence and comparatively high potential to kill people. Up to now, the total cases of being confirmed is approaching 400 Billion, and the cases of death has been over 30 Million. 'To flat the curve', advocated by government, and it seems we can derive this curve by applying mathematics skills. Thus I decided to take a try to find functions of the curve and to model it to see when exactly could we flat the curve. Author try to first complete the pandemic model of COVID-19, and then using data reported from WuHan providence to calculate those parameters of the partial differential function, and then to ensure the model's reliability. This model, if reliable, could help people to use to find when the curve would be flatten to thus plan early.

II. Literature Review

Susceptible Infected Recovered Model, also SIR model, was firstly stated in Kermack and McKendrick works which laid foundation to the following study on Dynamic Model of Infectious Diseases. The formula of SIR model is written as function (1).

$$\begin{cases} S'(t) = -\alpha S(t)I(t) \\ I'(t) = \alpha S(t)I(t) - \beta I(t) \\ R'(t) = \beta I(t) \end{cases} \quad (1)$$

In this group of functions, S means susceptible people who could be infected by disease, I means people who has already be infected and R indicate people who has already recovered from the disease; and S + I + I = Constant. dS/dt is the change of S in quantity over time, and same to other two functions. Also, α is the rate of being infected, and β is the rate of recovering. SIR model illustrate the most basic way of virus spreading process, but it needs to be improve specifically to handle various viruses' different features.

The visual representation of the dynamic process of SIR model could be seen in Fig. 1.

Fig.1. The dynamic process of SIR model

To take the SIER model for instance, the Susceptible Infected Exposed Recovered Model induce a new node E to the SIR model according to the feature of infectious diseases. E is those who have been infected but are not yet infectious.

$$\begin{cases} S'(t) = -\alpha S(t)I(t) \\ E'(t) = \alpha S(t)I(t) - \varepsilon E(t) \\ I'(t) = \varepsilon E(t) - \beta I(t) \\ R'(t) = \beta I(t) \end{cases} \quad (2)$$

The dynamic process of SEIR model is shown by Fig. 2.

Fig. 2. The dynamic process of SEIR model

In the paper: Stability Analysis of a Class of Delay SIR Model with Non linear Incidence Rate[7]. It mentions a time-delay factor which could be taken into consideration while producing the model. Exposed people needs time to transfer to Infected people, and thus people who has been in E node for time τ shall transfer to Infected people, namely people who are in E node at time (t - τ) shall transfer to I node. This is the SEIR model with considering time-delaying factor:

$$\begin{cases} S'(t) = -\alpha S(t)I(t) \\ E'(t) = \alpha S(t)I(t) - E(t-\tau) \\ I'(t) = E(t-\tau) - \beta I(t) \\ R'(t) = \beta I(t) \end{cases} \quad (3)$$

In the paper: Analysis of an SEIR Epidemic Model with Vaccination and Re-infection[7]. It claims that for some disease, people in the R node may not hold antibody for ever, which means they may be infected again after recovering. The dynamic process of this Infectious diseases with super-infection could be seen from Fig. 3.

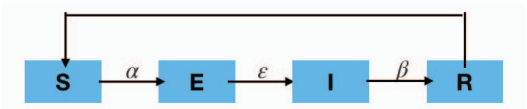

Fig. 3. The dynamic process of SEIR model with Re-infection

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The function group of diseases with superinfection is written as function (4).

$$\begin{cases} S'(t) = -\alpha S(t)I(t) + I(t-\mu) \\ E'(t) = \alpha S(t)I(t) - \varepsilon E(t) \\ I'(t) = \varepsilon E(t) - \beta I(t) \\ R'(t) = \beta I(t) - I(t-\mu) \end{cases} \quad (4)$$

After a period of time μ, people in the R node will lose its antibody to the disease, and they would transfer to S node which may be infected again.

SEIR model, people in E node sometimes will transfer directly to R node, which means those people could self-recover. The dynamic process of self-recovered SEIR model could be seen from Fig. 4.

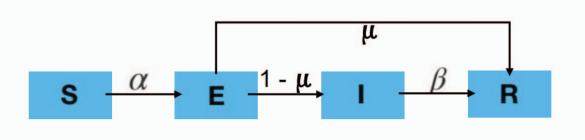

Fig. 4. The dynamic process of SEIR model with self-recovery

The function group of SEIR mode which has selfrecovery, the rate of self recovery equals to μ. The rate for people in E node to transfer to I node equals to (1 - μ). The group function is given as function (5).

$$\begin{cases} S'(t) = -\alpha S(t)I(t) \\ E'(t) = \alpha S(t)I(t) - E(t-\tau) \\ I'(t) = (1-\mu)E(t-\tau) - \beta I(t) \\ R'(t) = \beta I(t) + \mu E(t-\tau) \end{cases} \quad (5)$$

In the E node of infectious diseases, the symptoms which could increase the infectivity of diseases will not be exposed, it means that the infectivity in E node will lower than that of I node. Thus there will be two different infectivity in E and I nodes, so the group function is given as function (6).

$$\begin{aligned} S'(t) &= -\lambda_1 S(t)E(t) - \lambda_2 S(t)I(t) \\ E'(t) &= \lambda_1 S(t)E(t) + \lambda_2 S(t)I(t) \\ &\quad -\lambda_1 S(t-\tau)E(t-\tau) - \lambda_2 S(t-\tau)I(t-\tau) \\ I'(t) &= \left(\lambda_1 S(t-\tau)E(t-\tau) + \lambda_2 S(t-\tau)I(t-\tau)\right) - rI(t) \\ R'(t) &= rI(t) + \left(\lambda_1 S(t-\tau)E(t-\tau) + \lambda_2 S(t-\tau)I(t-\tau)\right) \end{aligned} \quad (6)$$

The dynamic process of diseases with double infectivity is given as Fig. 5.

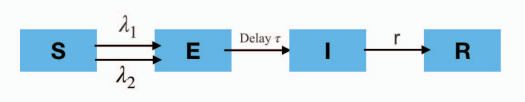

Fig. 5. The dynamic process of SEIR model with double infectivity

$\lambda 1$ and $\lambda 2$ are two difference infectivity, $\lambda 1 < \lambda 2$. When people in S node contact with people in E node, the infectivity will be $\lambda 1$; when people in S node contact with people in I node, the infectivity will be $\lambda 2$.

III. Methodology

In order to produce an ideally perfect model, all features of a specific infectious disease must be taken into consideration. COVID-19 is an infectious diseases which has E node, and also could cause death. According to the medical analysis to COVID-19, people who are in E node also could be infectious to others, but the infectivity is weaker than people in I node, and they could self-recover during E node, directly transfer to R node. Also, the time-lagging factor should be added to the function. The dynamic process of COVID-19's SEIR model could be seen in Fig. 6.

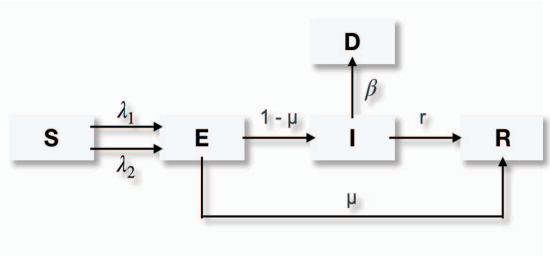

Fig. 6. The dynamic process of ideal SEIR model of COVID-19

According to those features of COVID-19, we can construct the function group one by one. And the first is the function (7) in S node:

$$S'(t) = -\lambda_1 S(t)E(t) - \lambda_2 S(t)I(t) \quad (7)$$

$\lambda 1$ is the infectivity when Exposed contacts with susceptible, and $\lambda 2$ is infectivity when Infected contacts with susceptible, and $\lambda 1 < \lambda 2$.

The function transfer in E node is function (8):

$$\begin{aligned} E'(t) &= S(t)(\lambda_1 E(t) + \lambda_2 I(t)) \\ &\quad -(1-\mu)\begin{pmatrix} \lambda_1 S(t-\tau)E(t-\tau) \\ -\lambda_2 S(t-\tau)I(t-\tau) \end{pmatrix} \end{aligned} \quad (8)$$

The rate of change in time t of E node equals to the decreased amount of susceptible people in time t plus the increased amount of Exposed people in time t - τ. And also, there is possibility of μ for Exposed people to self-recover, and thus there is a possibility (1 - μ) to transfer to Infected people. $(1-\mu)(\lambda 1 S(t-\tau)E(t-\tau) - \lambda 2 S(t-\tau)I(t-\tau))$ is the increased cases in R node in time t.

In I node, infected people could transfer to D node and R node is function (9):

$$I'(t) = (1-\mu)\begin{pmatrix} \lambda_1 S(t-\tau)E(t-\tau) \\ +\lambda_2 S(t-\tau)I(t-\tau) \end{pmatrix} - \beta I(t) - rI(t) \quad (9)$$

β is the rate of death, and r is the rate of recovering. $\beta I(t) + rI(t)$ is the amount of infected people transfer to R node and D node respectively.

Thus we can conclude the function group of ideal COVID-19 model:

$$
\begin{aligned}
S'(t) &= -\lambda_1 S(t)E(t) - \lambda_2 S(t)I(t) \\
E'(t) &= \lambda_1 S(t)E(t) + \lambda_2 S(t)I(t) - S(t-\tau)(\lambda_1 E(t-\tau) \\
&\quad +\lambda_2 I(t-\tau)) \\
I'(t) &= (1-\mu)\begin{pmatrix}\lambda_1 S(t-\tau)E(t-\tau) \\ +\lambda_2 S(t-\tau)I(t-\tau)\end{pmatrix} - I(t)(\beta + r) \quad (10) \\
D'(t) &= \beta I(t) \\
R'(t) &= rI(t) + \mu\begin{pmatrix}\lambda_1 S(t-\tau)E(t-\tau) \\ +\lambda_2 S(t-\tau)I(t-\tau)\end{pmatrix}
\end{aligned}
$$

IV. RESULT

COVID-19 is a new found infectious disease, and it has not yet been recognized fully. Thus Author cannot collect all necessary parameters to the ideal pandemic model as time-lagging and infectivity of Exposed people cannot be Fig.d out by statistic method. Author needs to reshape the function group to make it can be modeled with currently available parameter.

Based on data from WuHan during January 20 to March 30 about daily death, confirmed and recovered number, we can apply liner regression on those data to find. The way to calculate Daily Death Rate follows this function (11)[5]:

$$\text{DailyDeathRate} = \frac{\text{DailyDeathCases}}{\text{DailyConfirmedCases}} \quad (11)$$

And the Daily Recovered Rates follows:

$$\text{DailyRecoveredRate} = \frac{\text{DailyRecoveredCases}}{\text{DailyConfirmedCases}} \quad (12)$$

By applying Liner Regression to all the daily death rates and daily recovered rate, Author derives the relationship between rates and dates. $y=-0.0002701x+0.01324$ describes the relation between death rates and dates, and the death rate is gradually decreasing. And for the recovered rate, $y=0.002059x-0.01760$ describes the relation, and the recovered rate was gradually increasing. The *R squares* of both data sets' liner regressions are over *0.85* which means it can be trustworthy. This kind of trend illustrates the positive effect of government intervention as the awareness had been raised and people started to take care, the medical cares were fully assigned. This effect could be referred to any other counties, the daily death rate and recovered rate would go in the almost same way with local government's interventions.

Thus Author can presume that r and β are two always changing variables, and death rate is downward slope, recovered rate is upward slope according to the Fig. 7.

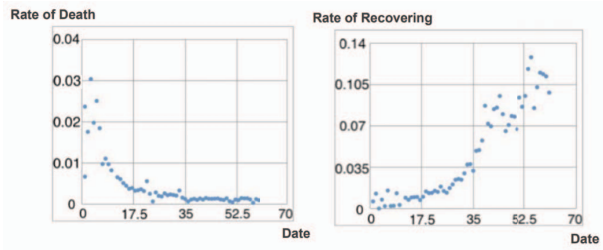

Fig. 7. Liner regression of daily death rate and recovery rate in Wu Han

The $\lambda 1$ and $\lambda 2$ needs to be Fig.d out by sophisticated biology experiment, thus we could simply consider the only infectivity parameter as $\lambda 1$. need to be derived from MCMC method, and we could jump from sophisticated processes to calculate the parameter, use the infectivity from paper: Estimation of the Transmission Risk of the 2019-nCoV and Its Implication for Public Health Interventions[6]. The Author of this paper calculate infectivity by multiplying Contact rate, Probability of transmission per contact and infective ability, which are respectively *q, c,*. The result of multiplying in quantity is $4.10*10^{-9}(1*2*2.05*10^{-9})$, and thus infectivity equals to $4.10*10^{-9}$

About the time-lagging factor τ, it could be derived from paper Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus–Infected Pneumonia. *Fig. 2* illustrates the frequency of time taken for transferring from infection to symptom, namely from E node to I node, those data comes first 425 confirmed cases of COVID-19 in WuHan. According to this graph, most exposed people would transfer to symptom in 7 days, and the average time-delay is 5.2 days.

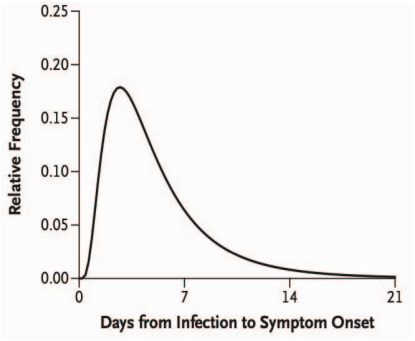

Fig.8. The estimated incubation period distribution

The rest of those parameters: rate of self recovery and the two differences infectivity of people in E node and I node cannot be given here because current investigation has not solved it out. So the process of COVID-19 spreading which could be determined by current parameters could be considered as Fig. 8. People in S node will transfer to E node with infectivity λ, and people in time (t - τ) of E node will transfer to I node. In I node, people could transfer to D node and R node, and β + r = 1.

The parameter table is given as Table I.

TABLE I. AVAILABLE PARAMETERS

Parameter	τ	β	r	λ
Estimated Value or Function	5.2	$y=-0.0002701x+0.01324$	$y=0.002059x-0.0176$	4.1×10^{-9}
Definition	Time Delay $Time$	Rate Of Death	Rate Of Recovery	Infectivity

The visual representation of process of virus spreading is given as Fig. 9.

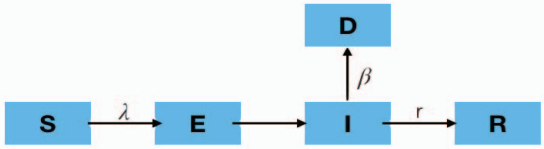

Fig. 9. Dynamic process of COVID-19 which could be modeled with available parameters

V. Conclusion

With available parameters given, the pandemic function group could be used to model the general trend of the pandemic. The reshaped Time-lagging-SEIR model based on those available parameters could be given as:

$$\begin{cases} S'(t) = -\lambda S(t)E(t) - \lambda S(t)I(t) \\ E'(t) = \lambda S(t)E(t) + \lambda S(t)I(t) - \lambda(S(t-\tau)E(t-\tau) \\ \quad +S(t-\tau)I(t-\tau)) \\ I'(t) = \left(\lambda S(t-\tau)E(t-\tau) + \lambda S(t-\tau)I(t-\tau)\right) \\ \quad -\beta I(t) - rI(t) \\ D'(t) = \beta I(t) \\ R'(t) = rI(t) + \lambda(S(t-\tau)E(t-\tau) \\ \quad +S(t-\tau)I(t-\tau)) \end{cases} \tag{13}$$

About the improvement on this model, the self-recovery could also be taken into consideration, and also the double infectivity while people in S node contacting with people in E node and I node. With more investigation, those parameters could also be derived. There are several other factors could be taken into consideration of COVID-19's pandemic model, for example, another time-lagging while people in S node transfer to E node. And to make the model more reliable, government's interaction, for example, to ask people to wear mask, to start to take lockdown and to prompt citizens to wash hands, should also be considered as ways to lower the infectivity.

The current model could only give a basic modeling of the trend of COVID-19 pandemic under universal phenomenon. Apparently, a more reliable COVID-19 dynamic model, available to conduct real data simulations, needs more investigations and researches to be built.

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