

Future Development of COVID-19

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Abstract

Due to the outbreak of the COVID-19 epidemic in 2020, people are very worried about the situation of the epidemic. Being able to model the number of cases over time is crucial. This model is used to predict numbers of people who may get diseases in the future. We construct a model with some unknown parameters and decide those parameters by making the mean square error of the predicted value with actual data. The epidemic model is generalized SEIR model and it helps us to match with reality. The data we use are from database built by Hopkins University. The result shows that disease will finally disappear. We can see that the virus increase at a very fast speed at first but begin to decrease from the curve. It is because that more people to take actions for protecting themselves. This result shows the virus can be defeated if we put effort to stop spreading them.

Keywords

COVID-19 future development; SEIR Model; Parameters.

1. INTRODUCTION

Now as the COVID-19 pandemic continues going on. Many people tries various ways to predict the future condition of this disease. And many of them are choosing statistical ways like time series or applying mathematical modeling of infectious disease to make the prediction. We choose to solve this problem by using the mathematical models to fit the data to determine the parameters first and then simulate the model to make the prediction.

In this passage, we use dynamic systems to construct a model with some unknown parameters and decide those parameters by making the mean square error of the predicted value with the actual data least. This is a traditional deterministic way using the initial guess of undetermined parameters and the data we want to fit to solve for those optimal choices of undetermined parameters that makes the MSE least. And we use a function in MATLAB given by Cheynet E. [1].

The epidemic model we choose is actually a "generalized SEIR model", which was made by Peng et al. (2020) [2] in the analysis of the SARS-CoV-2 outbreak in China. This model is a system of linear ordinary differential equations, and it is actually a modification of our traditional SEIR model. In a traditional SEIR model there are various parameters describing many effects during the outbreak of a transparent disease, like transparent rate, and death rate. And most importantly, in the traditional SEIR model, those parameters are all treated like constant, and independent of time. But in the generalized model, Peng modify the SEIR model's parameters and change the recover rate and death rate to variables that are time dependent. And this modification helps to match the reality better, since as people get more familiar with the disease

compared with when the begging of the disease's outbreak the cure rate and death rate should also change.

2. SEIR MODEL OVERVIEW

The classical SEIR model has four categories, which are susceptible(S), exposed(E), infective(I) and recovered(R) people.

$$\frac{dS(t)}{dt} = -\beta * I(t) * \frac{S(t)}{N}$$

$$\frac{dE(t)}{dt} = \beta * I(t) * \frac{S(t)}{N} - \gamma * E(t)$$

$$\frac{dI(t)}{dt} = \gamma * E(t) - (\lambda + k) * I(t)$$

$$\frac{dR(t)}{dt} = (\lambda + k) * I(t)$$

The susceptible(s) represents number of people who may get infected (has not get infected yet). At the beginning, since no one get infected and S will be the whole population. The exposed(E) represents the number of people who have been infected but who have not yet shown symptoms and belong to the undetected population. The infective (I) means people who have been infected and found. At the end, the recovered (R) means people who have recovered. In classic SEIR model, R also includes number of people who already dead. SO we can get this following equation that shown below from known information:

$$S(t)+E(t)+I(t)+R(t)=N$$

The classic SEIR controled by several parameters as β, γ, λ and κ .

β is the infection rate. It is the number of people who get infected everyday. It also equals to the probability that the average number of people is exposed to everyday.

γ is the inverse of the average latent time and represents the number of days between the incubation period and the onset of symptoms. In the equation above, it transfers people from the E category to the I category.

λ and κ are the recovery rate from the disease and the death rate. They are counted together in a single parameter in the classical SEIR model. $1/\lambda$ is the average recovery time.

By considering the complexity of the disease, we used a generalized SEIR model following the recent publication by Peng et al.(2020) It shows as following:

$$\frac{dS}{dt} = -\beta(t)I * \frac{S}{N} - \alpha S$$

$$\frac{dP}{dt} = \alpha S(t)$$

$$\frac{dE}{dt} = \beta(t)I * \frac{S}{N} - \gamma E$$

$$\frac{dI}{dt} = \gamma E - \delta I$$

$$\frac{dQ}{dt} = \delta I - (\lambda(t) + k(t))Q$$

$$\frac{dR}{dt} = \lambda(t)Q$$

$$\frac{dD}{dt} = \kappa(t)Q$$

The generalized SEIR model has three changes on the categories based on that. First, protected people is added. S multiplied by α , which is protection rate, passed from susceptible category to protected category. Protection rate is determined by lockdown policies and improvements on health behaviour. The second added category is quarantined people. Infected people multiplied by δ is passed to quarantined category, where δ is the inverse of average time required to quarantine a person with symptoms. Since infected people who are not detected yet cannot be quarantined, quarantined category also reflects the number of detected infective people. Third, the generalized model separates recovered category in the classical model to recovered and dead categories, linked to quarantined category through parameters λ and κ , the cure rate and the mortality rate. As the disease spreads, more effective therapies should be developed, so λ should be constantly increasing and κ should be decreasing. Theoretically, the cure rate will converge toward a constant value and the mortality will approach zero as time goes.

$$\lambda(t) = \lambda^0 [1 - \exp(-\lambda_1 t)] \quad \kappa(t) = \kappa_0 \exp(-\kappa_1 t)$$

There are some changes in parameters, too. The parameter λ and κ are changed into time dependent factors. κ_0 is the final asymptotic value of the cure rate, determined by the health system's ability and health of citizens in a country. λ_1 reflects how fast a country implement policies.

$$\lambda(t) = dR / (dt \cdot Q)$$

κ_0 is the initial value of mortality rate, related to the health system's ability and health of citizens in a country. λ_1 is a factor that the larger it is, the faster the mortality rate decreases. Infection rate beta is now time-dependent and is proportional to the contact rate b .

The generalized SEIR-model scheme is described in the figure 1 below.

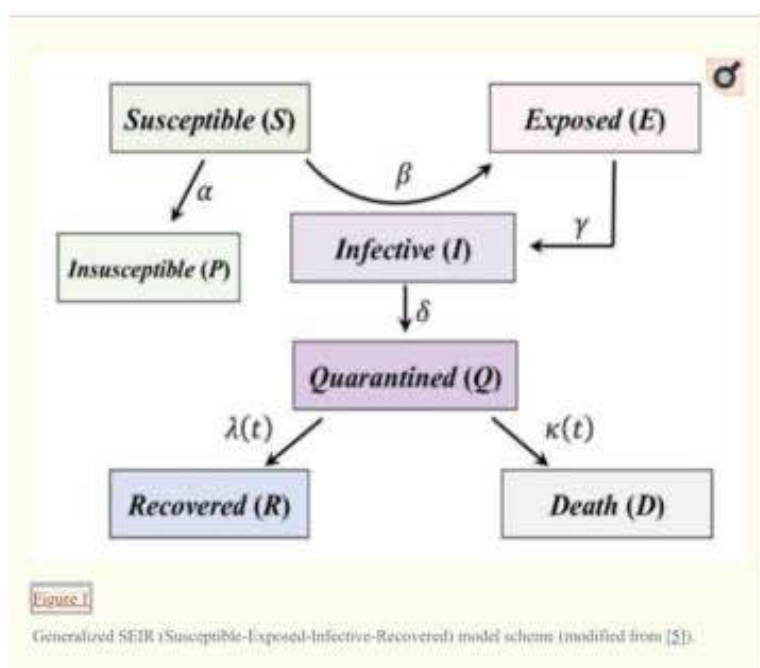


Figure 1. Generalized SEIR model scheme

The main outputs of the model are the following data series: S, the target time-histories of the susceptible cases, E, the target time-histories of the exposed cases, I, the target time-histories of the infective cases, Q, the target time-histories of the quarantined cases, R, the target time-histories of the recovered cases, D, the target time-histories of the death cases, P, the target time-histories of the insusceptible cases.

3. RESULT

Data base

First of all, all the data that we are using to match and prediction are provided by John Hopkins university [3], and this data is continuing updating at least daily.

And then we can run the model in MATLAB using deterministic method. Below is a chart of the initial guess that has references in order to make sure we do get a non-trivial solution other than trapped in some local minimum value of MSE.

Initial value table:

Table 1. Constant parameter

Parameter	Value	Reference
α	0.06	Peng et al. (2020)[1] value used for wuhan
β	0.69	Dandekar et al. (2020)[4]
Latent time in days	5	By WHO wuhan COVID- 19 report 2019 [5]
δ	0.1	Peng et al. (2020)

Peng's team study the case of Wuhan and other provinces of China during the beginning period 20, January to 9 February. And he gives the estimation of α and δ . Thus this should provide a good initial guess for α which is the rate of persons become insusceptible due to government's policy of quarantine and δ the rate of infected people get quarantined. What's more important is that he also used this kind of deterministic way minimizing the mean square error least, so the parameter he got in the end can be used as guidance without modification. As for Dandekar, he used a way far different from the traditional deterministic ways. However he gave the estimation of COVID-19's transmission speed in U.S., which is surely far different from other places like China and Italy, since the population density and policies and many other effects. So we just choose this as a guidance of initial guess about the transmission rate. And the latent time of COVID-19 is given by WHO's report about Wuhan. It shows that the most people feel obvious symptoms in like 5 to 6 days, so we just choose 5 as the initial guess.

Table 2. Result

parameters	value
α	0.124
β	0.7256
γ	0.2321
δ	0.0053
$\lambda_0 \quad \lambda_1 \quad \lambda_3$	0.0079 0.3219 17.8103
$\kappa_0 \quad \kappa_1 \quad \kappa_2$	0.0009 0.0133 0.1256
NRMSE	0.0154

Now that we have got the parameters out, we are going to simulate our dynamic model using Runge-Kutta methods to compare with the actual data.

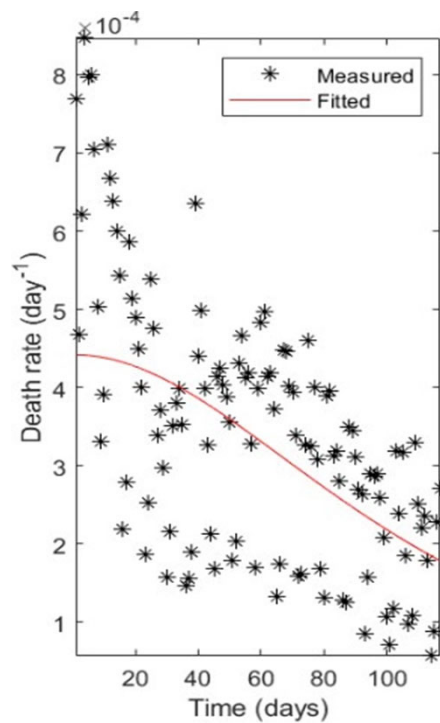


Figure 2. Projection result of death rates

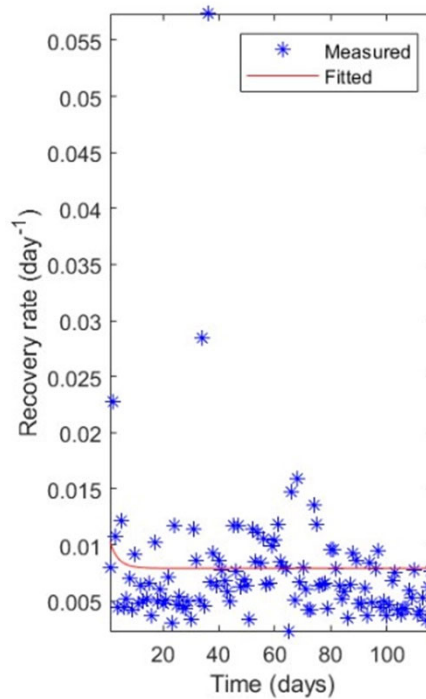


Figure 3. Projection of recovery rates

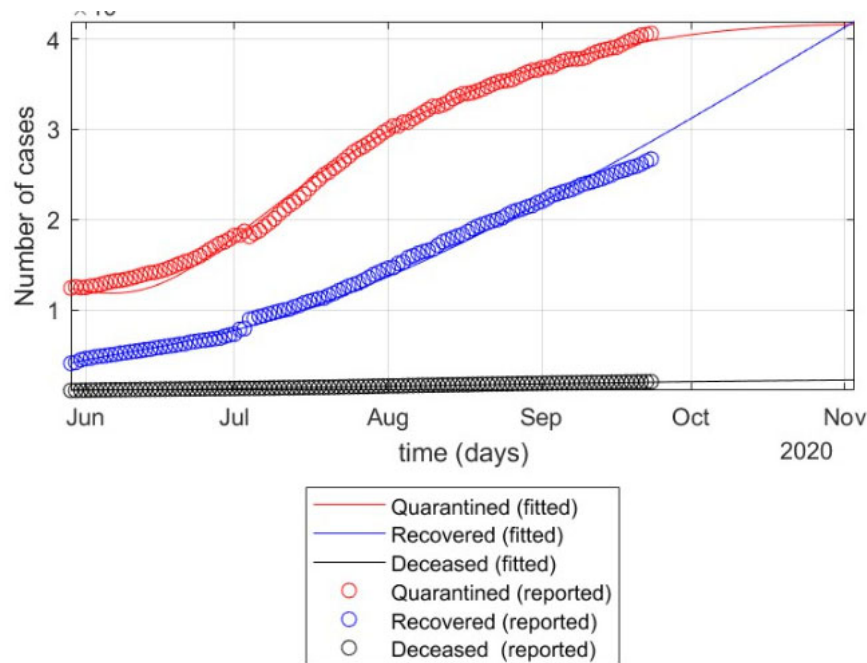


Figure 4. Projection result of total numbers of cases

And we also do the calculation of normalized root mean square error (NRMSE) to know how well this model fits the data. In table 2, 0.0154 NRMSE shows that this model fits really well for the given data.

And from the result we can see that actually, the recover rate is relatively stable. The result of deterministic way that the recover rate is not a constant may be effected by those unexpected high recovered rates on some days. These abnormal recovery rate is likely due to the delay report of the person who recovered from the disease. So to get a better result, may be it is reasonable to sift out those significantly high recovered rate data.

4. CONCLUSION

We do the projection for the US covid 19 outbreak using a deterministic way. The data are from the database built by Hopkins University. The model to simulate is the generalized SEIR model given by Peng's [1] team, which takes the quarantined people into consideration. The result shows a hopeful future, that the disease will finally disappear. And if there is vaccine to this virus, the condition will be better. From the curve, it is apparently that the virus increase at a very fast speed at first but begin to decrease after sometime. It is because that people become more and more aware of taking various action to protect themselves, like social distancing and wearing masks. This trend can implicitly show that social distancing are indeed doing their job and the virus can be defeated if we all try to stop spreading them.

REFERENCES

- [1] Cheynet E. Generalized SEIR Epidemic Model (Fitting and Computation) ; website url: <https://it.mathworks.com/matlabcentral/fileexchange/74545-generalized-seir-epidemic-model-fitting-and-computation>
- [2] Peng L, Yang W., Zhang D., Zhuge C., Hong L. Epidemic analysis of COVID-19 in China by dynamical modeling. MedRxiv Epidemiol. 2020 doi: 10.1101/2020.02.16.20023465. <https://arxiv.org/abs/2002.06563>

- [3] COVID-19 Data Repository by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University. url:[https://github.com/ CSSEGISandData/COVID-19](https://github.com/CSSEGISandData/COVID-19)
- [4] Dandekar R., Barbastathis G. Neural Network aided quarantine control model estimation of global COVID-19 spread. url:<https://arxiv.org/abs/2004.02752>
- [5] Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19) url:[https://www.who.int/docs/default-source/coronaviruse/ who-china-joint-mission-on-covid-19-final-report](https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report)