COMP90005: A mathematical model of COVID-19 and policy impact

Saransh Srivastava - 1031073*[1], Yuansan Liu - 1037351†[2], and Zuo Huang - 1040978‡[3]

[1] *Master of Data Science, University of Melbourne*
[2] *Master of Computer Science, University of Melbourne*
[3] *Master of Data Science, University of Melbourne*

Dated: July 21, 2020

1 Introduction

Almost all living beings present today in the world have never experienced a pandemic before. The coronavirus (SARS-CoV-2) has brought nations into standstill and forced people to stay indoors and observe distancing. Almost all nations at some point have observed some kind of restrictions to avoid the spread of the virus. Since its first known cases originating from the vet market of Wuhan in the Hubai province of The Republic of China in December 2019, the global scientific community have actively researched and has given us some answers. We know much more about the virus and how to detect it and how to wipe it clean using sanitizers. As the situation in China is improving and most of the people effected by it are recovering, scientist all around the world are working together to find its vaccine.

With this in mind, governments in different part of the world are implementing their own form of social restrictions in order to 'flatten the curve' while vaccine development is underway.

In this report, we present a novel method of modelling the population of a country and provide our analysis on the cumulative infection and death in the country, based on the reported death numbers.

In section 3 we will discuss our problem statement and formalise the optimization problem. In section 4 we will describe our methodology and analyse the convergence of the function. Next we will present our experimental analysis in section 5 and finally our conclusion in section 6.

*Electronic address: saranshs@student.unimelb.edu.au
†Electronic address: yuansanl@student.unimelb.edu.au
‡Electronic address: zuhuang@student.unimelb.edu.au

2 Related Works

Mathematical models of infectious diseases were first introduced by John Graunt as early as the 17th century Graunt (1939). The 1920's saw the rise of compartmental models for a closed population having fixed number of people. The Reed-Frost Abbey (1952) and KermackâĂŞMcKendrick epidemic model Kermack und McKendrick (1932) Kermack und McKendrick (1991) Kermack und McKendrick (1933) gained significant importance, both describing the relationship among susceptible, infectious and recovered people. Many hybrid models were then created based on this basic SIR model and our mdoel is also inspired from this.

As recently as 2020, there has been a surge of research papers trying to predict the trend COVID-19 is going to take. In CRISP Herbrich u. a. (2020) model, which is based on the SEIR mdoel uses a probabilistic graphical mdoel to predict infection spread. They go on to develop a Monte Carlo EM algorithm to infer contact-channel infection spread. In EpiLM Vineetha Warriyar K u. a. (2020), also based on SIR compartmental framework, provides tools for simulation and inference for discrete-time indivisual-level models. The inference is set in a Bayesian framework and is carried out via Metropolis-Hastings Markov chain Monte Carlo (MCMC).

Others Lorch u. a. (2020) design a more fine-grained spatiotemporal predictions of the course of the disease in the population. They make use of the data obtained through the contact tracing technologies and use real data for prediction.

3 Problem Formulation

3.1 Model formulation

3.1.1 SEIR model

In Aron und Schwartz (1984), the author proposed a epidemic model where the total population is divided into four parts, S(susceptible, those able to contract the disease), E(exposed, those who have been infected but are not yet infectious), I(infected, those capable of transmitting the disease), R(removed, those who have become immune, dead or recovered).

Comparing to SIR model, the SEIR model adds an exposed group to represent people in latent period. this is helpful for researching the specific virus which has a latent period, in other words, people might not be infectious or symptomatic in first few days after they caught the virus. As is already known, coronavirus has at most 14 days latent period, which makes an SEIR based model more suitable for our task.

3.1.2 A two-group-SEIDR model

Greenhalgh u. a. (2001) derived a two-group-SEIR model to study the effects of condom usage

on preventing the HIV spread, which is similar to the current COVID-19 situation where there are two groups of people during the pandemic, one of them follow the suggestion to take precautions, while another group just behave as normal. To reflect such situation more accurately, we also divided the population into two groups.

Now, suppose there are two groups of people, first group take actions to protect themselves from the disease, such as wearing masks or keeping social distance, meanwhile, another group take no actions. Let the $\alpha_1, (0 < \alpha_1 \leqslant 1)$ denote the probability of actions did not affect the spreading, by which, $\alpha_1 = 1$ means the actions have no effect to prevent the virus. To study the trajectory of the death number, we extracted death number from the removed population. And we have the spreading model:

$$S_1(t+1) = S_1(t) + p_1 p_s(\lambda - \mu) - \frac{\beta c \alpha_1 S_1(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} + M_{21}S_2(t) - M_{12}S_1(t) \quad (1)$$

$$S_2(t+1) = S_2(t) + (1-p_1)p_s(\lambda - \mu) - \frac{\beta c S_2(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} + M_{12}S_1(t) - M_{21}S_2(t) \quad (2)$$

$$E_1(t+1) = E_1(t) + p_1(1-p_s)(\lambda - \mu) + \frac{\beta c \alpha_1 S_1(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} + N_{21}E_2(t) - (N_{12} + \sigma)E_1(t) \quad (3)$$

$$E_2(t+1) = E_2(t) + (1-p_1)(1-p_s)(\lambda - \mu) + \frac{\beta c S_2(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} + N_{12}E_1(t) - (N_{21} + \sigma)E_2(t) \quad (4)$$

$$I(t+1) = I(t) + \sigma(E_1(t) + E_2(t)) - (\gamma + \alpha)I(t) \quad (5)$$

$$D(t+1) = D(t) + \alpha I(t) \quad (6)$$

$$R(t+1) = R(t) + \gamma I(t) \quad (7)$$

$$N(t) = \sum_{i=1}^{2} S_i(t) + E_i(t) + I(t) + D(t) + R(t)$$

Where:
S_i : number of susceptible people in group i.
E_i : number of exposed people, who are asymptomatic but infectious, in group i.
I : number of infected people.
D : number of death population.
R : number of recovery population.
p_1 : Rate of people in group 1.
p_s : Rate of people is normal.
α_1: Probability of protections not preventing virus.
λ : Population inflow.
μ : Population outflow.
β : Average risk per infected contact.
c : Average contacts per person per day. Related to the policy like lock down and quarantine.

σ : Incubation rate, at which infected people develops symptoms.
M_{ij} : Per capita rate of migration of susceptible people from group i to j.
N_{ij} : Per capita rate of migration of infected ones from group i to j.
$\mathscr{d}$: Death rate per day.
$\mathscr{r}$: Recovery rate per day.

Figure 1 shows the structure of the model which might hopefully help with understanding the model.

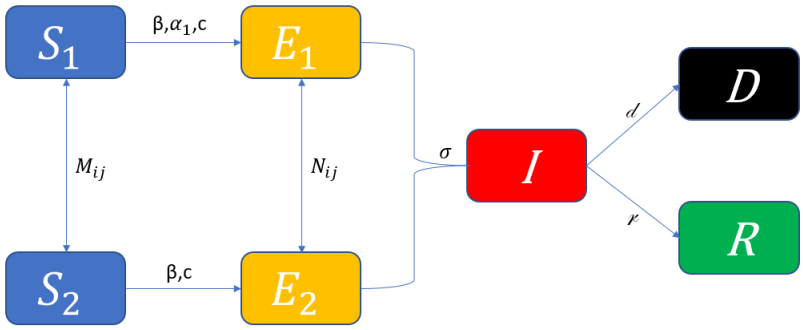

Figure 1: The flowchart of model

In this model, the parameters $c, \lambda, \mu, M_{ij}, N_{ij}$ are all related to the government policy. To be specifically, lock down the country can decrease the amount of c, λ and μ, while forcing citizen taking precautions can increase M_{21}, N_{21} which means more people getting into the group 1. By change these parameters, we can study the way policy affect the virus spreading.

3.1.3 A special two-group-SEIDR

To simplify the model and make the fitting job more feasible, we assume people only migrate from unsafe group to safety one, but not in reverse direction, thus $M_{12} = N12 = 0$. Now our model becomes:

$$S_1(t+1) = S_1(t) + p_1 p_s(\lambda - \mu) - \frac{\beta c \alpha_1 S_1(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} + M_{21} S_2(t) \quad (8)$$

$$S_2(t+1) = S_2(t) + (1-p_1)p_s(\lambda - \mu) - \frac{\beta c S_2(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} - M_{21} S_2(t) \quad (9)$$

$$E_1(t+1) = E_1(t) + p_1(1-p_s)(\lambda-\mu) + \frac{\beta c \alpha_1 S_1(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} + N_{21} E_2(t) - \sigma E_1(t) \quad (10)$$

$$E_2(t+1) = E_2(t) + (1-p_1)(1-p_s)(\lambda-\mu) + \frac{\beta c S_2(t)(\alpha_1(E_1(t) + I(t)) + E_2(t))}{N(t)} - (N_{21}+\sigma) E_2(t) \quad (11)$$

$$I(t+1) = I(t) + \sigma(E_1(t) + E_2(t)) - (\mathscr{r} + \mathscr{d}) I(t) \quad (12)$$

$$D(t+1) = D(t) + \mathscr{d} I(t) \quad (13)$$

$$R(t+1) = R(t) + \gamma I(t) \tag{14}$$

$$N(t) = \sum_{i=1}^{2} S_i(t) + E_i(t) + I(t) + D(t) + R(t)$$

3.2 Optimization Problem

To study the behaviour of the death number, we need to fit the model on the death curve, hence our optimization problem is to minimize the mean squared error(MSE) between predicted death number and the real death number. We define an MSE function $J(\theta)$ as following formula:

$$J(\theta) = \frac{1}{T} \sum_{t=1}^{T} (\mathscr{D}_t - D_t(\theta))^2$$

where θ is the parameter vector, considering our model, $\theta = \langle p_1, p_s, \beta, c, \alpha_1, \sigma, M_{21}, N_{21}, \mathscr{d}, \gamma \rangle$. T is the number of data used for training(in this project it represents days), $D_t(\theta)$ is cumulative death number that predicted by model, $\mathscr{D}_t$ is the real cumulative death number. And our goal is to find the minimum of $J(\theta)$.

Notice that from (13) we can get the recursion of the cumulative death number in model:

$$\begin{aligned} D(t) &= D(t-1) + \mathscr{d} I(t-1) \\ D(t-1) &= D(t-2) + \mathscr{d} I(t-2) \\ &\vdots \\ D(1) &= D(0) + \mathscr{d} I(0) \\ D(0) &= 0 \end{aligned}$$

adding together, we get $D(t) = \mathscr{d} \sum_{i=0}^{t-1} I(i)$.

Thus the optimization problem is find the parameters' values to solve the minimization under the constrains as table 1 shows:

$$\min_{\theta \in \mathbb{R}^{10}} J(\theta) = \frac{1}{T} \sum_{t=1}^{T} (\mathscr{D}_t - D_t(\theta))^2 = \mathbb{E}[(\mathscr{D}_t - \mathscr{d} \sum_{i=0}^{t-1} I(i))^2]$$

4 Methodology and Convergence Analysis

In this section, we will first introduce the python packages which we have used to program our methodology and latter describe our convergence analysis.

4.1 Non linear least-square minimization and curve fitting

Non-linear least square minimization is a form of least square optimization using parameter refinement by successive iteration. Python provides a package *lmfit* to build complex fitting models using deterministic non-linear least-squares and applying these to real data. There are two important aspect of this package which were helpful for our analysis and we discuss them in this subsection.

4.1.1 Model function

The model function takes an objective function (SEIDR model) and an array of fitting variables and calculates an array of values that are to be minimized in the least square sense. Internally the minimization is performed using the LevenbergâĂŞMarquardt algorithm (LMA) Levenberg (1944) first published in 1944. The LMA is the most commonly used algorithm for non-linear curve fitting and depends upon a reduction of residuals to linear form by first order Taylor approximation. It finds only local minima and requires us to provide an initial starting parameter value as close as possible to the actual value and with a certain bound to reflect real-world scenario.

For our model consider a set of N data points, (x_1, y_1), (x_2, y_2), (x_3, y_3), ..., (x_N, y_N) and a curve model function defined as y=f(x, θ) where θ represents the parameters, y is dependent on with $\theta = (\theta_1, \theta_2, \theta_3 ..., \theta_M)$, and M $\leqslant$ N. We wish to reduce the sum of squares defined as follows:

$$S = \sum_{i=1}^{N} r_i^2 \tag{15}$$

where *r* represents residuals defined as follows:

$$r_i = y_i - f(x_i, \theta) \tag{16}$$

for i = 1,2,....,N

In a non-linear setting, the derivates of $\frac{dr_i}{d\theta_j}$ are functions of both x and θ. Based on the initial value set of the parameters, a local minima is found using successive approximations. In each iteration step, the parameter vector θ is replaced by a new estimate $\theta + \delta$. The δ is determined by the following equation:

$$f(x_i, \theta + \delta) \approx f(x_i, \theta) + J_i.\delta \tag{17}$$

where J represents the Jacobian matrix defined as follows:

$$J_i = \frac{df(x_i, \theta)}{d\theta} \tag{18}$$

The LMA algorithm uses our minimization function as described in the previous section.

4.1.2 Parameter function

As mentioned above, another important aspect of this implementation is the parameter tuning and the initial values associated with it. A Parameter is an object that can be varied in a fit, or one of the controlling variable in a model. It replaces the plain floating point number and allows bounds and other statistical properties associated with a parameter estimation. It is important to note here that because the model has multiple local minimas, it is crucial to specify initial values of the parameters for the algorithm to converge appropriately. Based on the geo-political scenarios of our case study of US and UK we bounded our parameters as described in table 1

4.1.3 Randomness in recorded data

It is important to address the selection of country and death data in our problem. Multiple key factors influenced our decision while problem formulation. 1) The recorded data for most countries include a)number of reported infected people, b) number of reported dead people, c) number of reported recovered people from COVID-19. We decided to fit our model on number of reported dead people because out of the three, that is the most reliable data. This is because we know by now that not everyone who is infected is symptomatic and not everyone reports their symptoms. 2) In order to create our model as real as possible, we decided to choose countries where number of tests per thousand people is highest (as of June 28, 2020). USA and UK are among the top such countries Max Roser und Hasell (2020). Keeping these randomness in mind, we believe that the stochasticity in data can be approximated by our deterministic model. Next, we present our convergence analysis.

Parameters	US	UK
β: Average risk per infected contact	[2.5, 3.5]	[0, 5]
c: Average contacts per person per day	[0.1, 0.5]	[0, 2]
σ: Incubation rate	[0, 0.4]	[0, 0.4]
M_{10}: Migration rate of Suspected from group 1 to 0	[0.2, 0.8]	[0.2, 1]
N_{10}: Migration rate of Infected from group 1 to 0	[0.4, 0.95]	[0.4, 1]
$\mathscr{d}$: Death rate per day	[0, 0.002]	[0, 0.002]
$\mathscr{r}$: Recovery rate per day	[0.0001, 0.05]	[0.0001, 0.05]
α: Probability of protections not preventing virus	[0, 0.3]	[0, 0.3]
p_1: Rate of people in group 1	[0.3, 0.9]	[0.3, 0.9]
p_s: Rate of people is normal(not infected)	[0.5, 0.9]	[0.5, 0.9]

Table 1: Parameter Constrains of Models

4.2 Convergence Analysis

In this project, we used a python package *lmfit* to find the parameters of the model, but in this part, we will show the feasibility of stochastic approximation for this project. Let's begin with defining the target field $G(\theta)$:

$$G(\theta) = -\nabla_\theta J(\theta).$$

Next, we will show that the optimization problem is well posed and target field is coercive. Firstly, the number of data is more than one which which assure the solution will be finite. Secondly, consecutive observations of the data are i.i.d, and have finite variance. This implies that there is a unique point θ^* with $\|\theta\| < \infty$ that minimize $J(\theta)$. Since the target field is coercive, following the result of Example 2.9 in textbook, we know that ODE:

$$\frac{dx}{dt} = -\nabla J(x(t)) \tag{19}$$

has bounded trajectory.

Noting that:

$$\frac{\partial}{\partial \mathscr{d}} J(\theta) = \mathbb{E}\big[2\big(\mathscr{D}_t - \mathscr{d}\sum I_{t-1}\big)\big(\sum I_{t-1} + \mathscr{d}\sum \nabla_{\mathscr{d}} I_{t-1}\big)\big]$$
$$\frac{\partial}{\partial \theta^{(i)}} J(\theta) = \mathbb{E}\big[2\big(\mathscr{D}_t - \mathscr{d}\sum I_{t-1}\big)\big(\mathscr{d}\sum \nabla_{\theta^{(i)}} I_{t-1}\big)\big]$$

where $\sum I_{t-1}$ is simplified version of $\sum_{i=0}^{t-1} I_i$ and $\theta^{(i)} \in \langle p_1, p_s, \beta, c, \alpha_1, \sigma, M_{21}, N_{21}, \gamma\rangle$ the parameters other than $\mathscr{d}$.

Now let's consider the stochastic approximation:

$$\theta_{n+1,1} = \theta_{n,1} + \epsilon_n\big(\mathscr{D}_t - \mathscr{d}\sum I_{t-1}\big)\big(\sum I_{t-1} + \mathscr{d}\sum \nabla_{\mathscr{d}} I_{t-1}\big)$$
$$\theta_{n+1,i(\neq 1)} = \theta_{n,i} + \epsilon_n\big(\mathscr{D}_t - \mathscr{d}\sum I_{t-1}\big)\big(\mathscr{d}\sum \nabla_{\theta^{(i)}} I_{t-1}\big)$$

from Example 4.1 we can conclude that choosing $\epsilon_n = \mathcal{O}(n^{-1})$ and applying either truncation or variance control argument to the original problem can meet the assumptions of Theorem 4.1 so that the algorithm converge to the solution of ODE (19).

5 Experimental results

We fitted our models to the data from Actionsuser u. a. (2020)'s COVID19 dataset which source is maintained by CSSE of John Hopkin University to get the best parameters and then project the number of death, recovery and infected of UK and US in the next 250 days.

5.1 UK model

Figure 2 shows that the UK model suggests that the number of death will reach to about 47000 in the next 250 days. Figure 3 shows the number of infected in UK will reach to about 690000 in

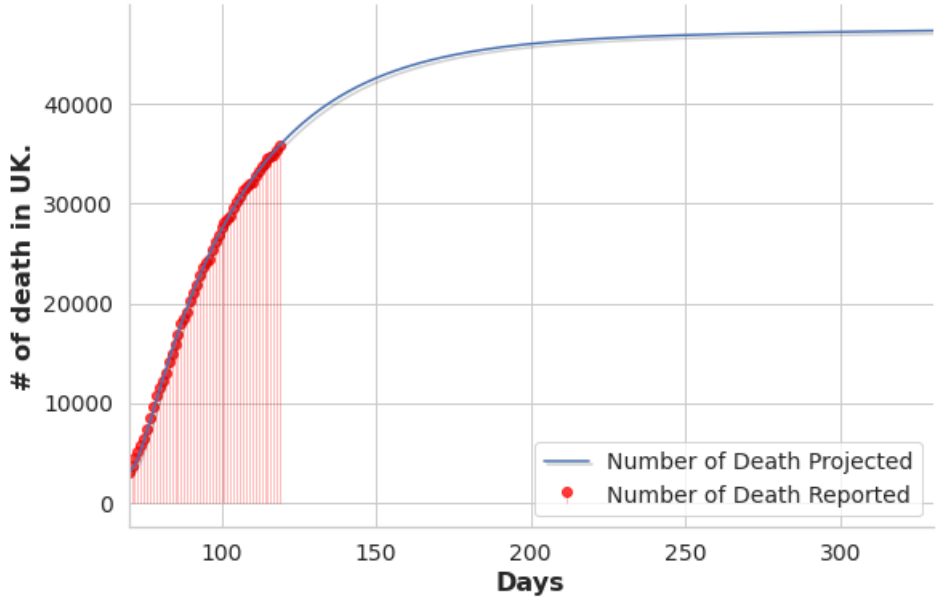

Figure 2: Red dots are reported number of death used to fit the model, from 2020-04-01 to 2020-05-20

the next 250 days. One can observe that the number of infected people are significantly larger than reported data. We believe that the over-estimation is reasonable because, as discussed earlier, we know that not everyone reports an infection and not everyone is symptomatic. Some people are not even aware of the infection and go on to pass it in the community. Day (2020) and Hu u. a. (2020).

Although the reported number of infections keep on increasing untilÂă2020-06-22, the model shows that the pandemic in UK have already passed the worst phase because the projected number of infection has already converged.

However, the projected number of death will need about 2 months to converge, and the model suggest at least 60,000 infected case in UK in 2020-06-22. This implies that UK still needs a long time before it can get out of the pandemic.

Figure 4 shows the validation result of UK model, one can find the projected numbers are very close to the reported number. Figure 5 shows the residuals of UK model are bounded between -200 and 300, one can find that theÂăresiduals of projections areÂăbounded between -100 and 200 in the last 10 days of validation period, so we believe that the model is valid for at least next 30 days after fitting.

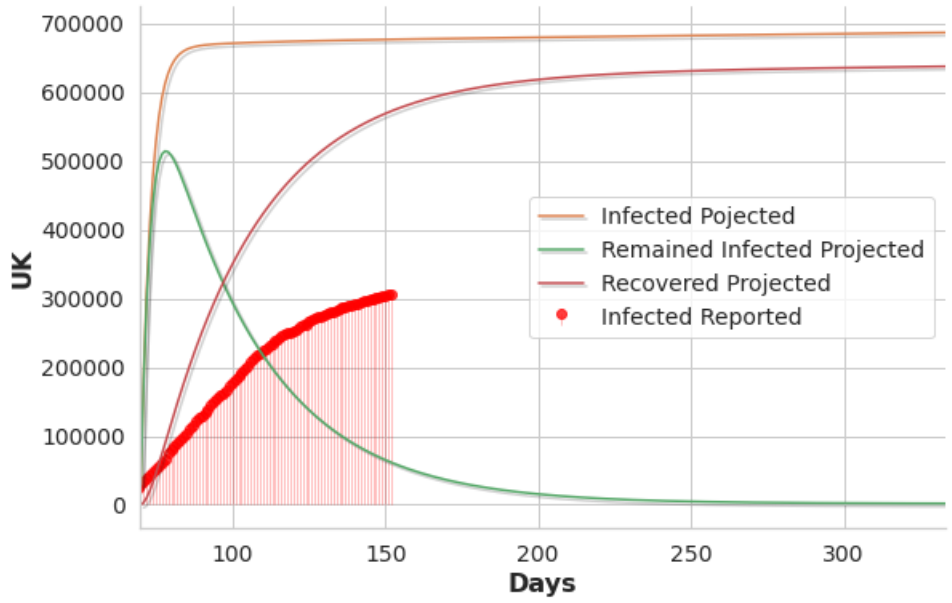

Figure 3: Pojection of UK model, red dots are reported number of Infected, up to 2020-06-22

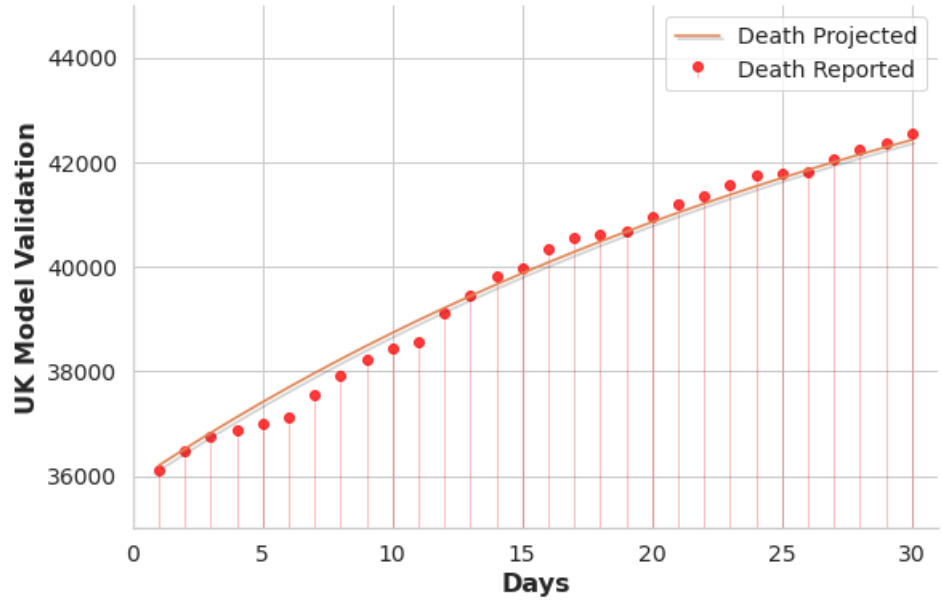

Figure 4: Validation of the projection of UK model in 30 days (from 2020-05-20 to 2020-06-19)

5.2 US model

US model suggests that the number of death will reach to about 138000 in the next 250 days in figure 6. Figure 7 shows the number of infected will reach to 4,800,000 in the same period. One can find that number of infected is larger than report data significantly as we found in the UK model.

For validation, figure 8 shows the projected number of death is very close to the reported number in the first 25 days. One can notice that US model starts to under-estimate Âăfrom 2020-06-01. We hypothesize that the changes in the situation or the parameters caused this under-estimation.

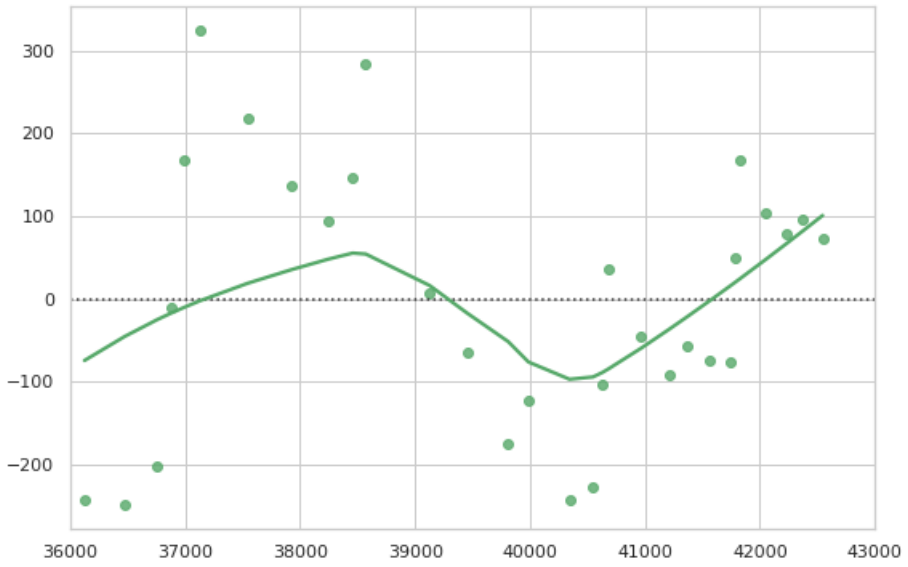

Figure 5: Residual of projection of UK model in 30 days (from 2020-05-20 to 2020-06-19)

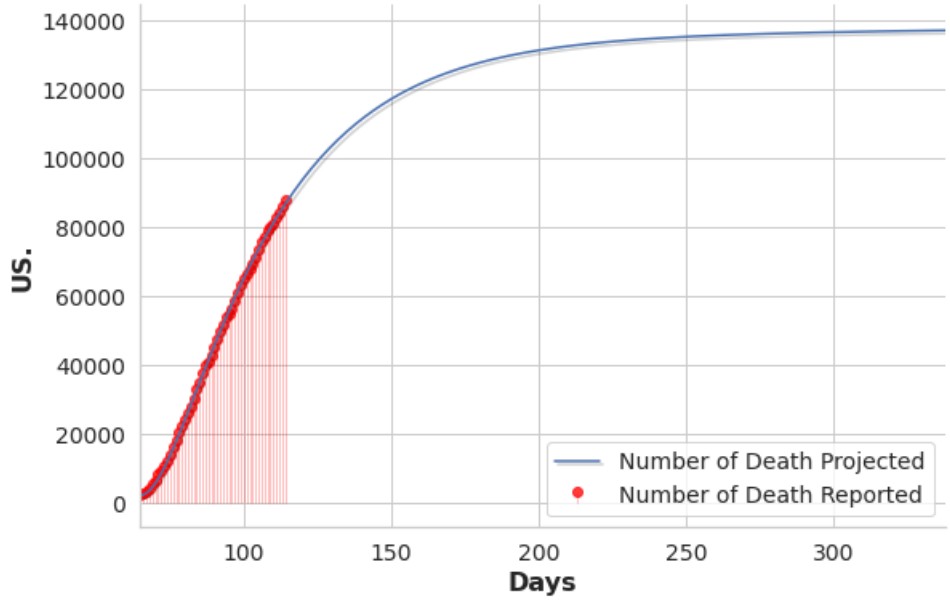

Figure 6: Red dots present reported number of death used to fit the model, from 2020-03-27 to 2020-05-15

In June 2020, the country-wide protests caused by the death of a US Black citizen under police custody escalated very rapidly. We believe that the protest led to people not following virus preventing policies and this led to increase community infection. Figure 9 shows that the reported number of infection increased significantly from 2020-06-12 to 2020-06-22.

Figure 10 shows the residuals of US model is bounded between -400 and 600, although there is a under-estimation.

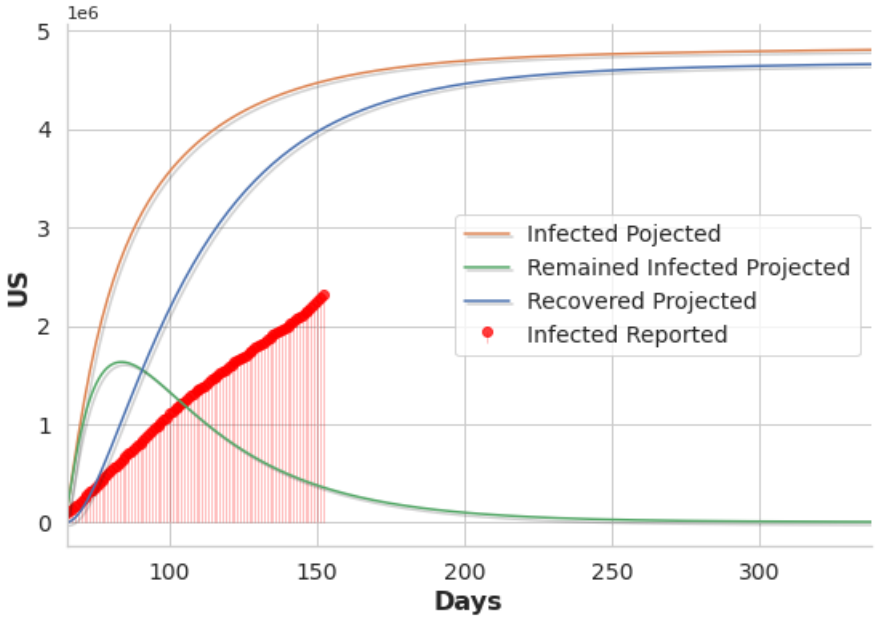

Figure 7: Red dots present the reported number of Infected, up to 2020-06-22

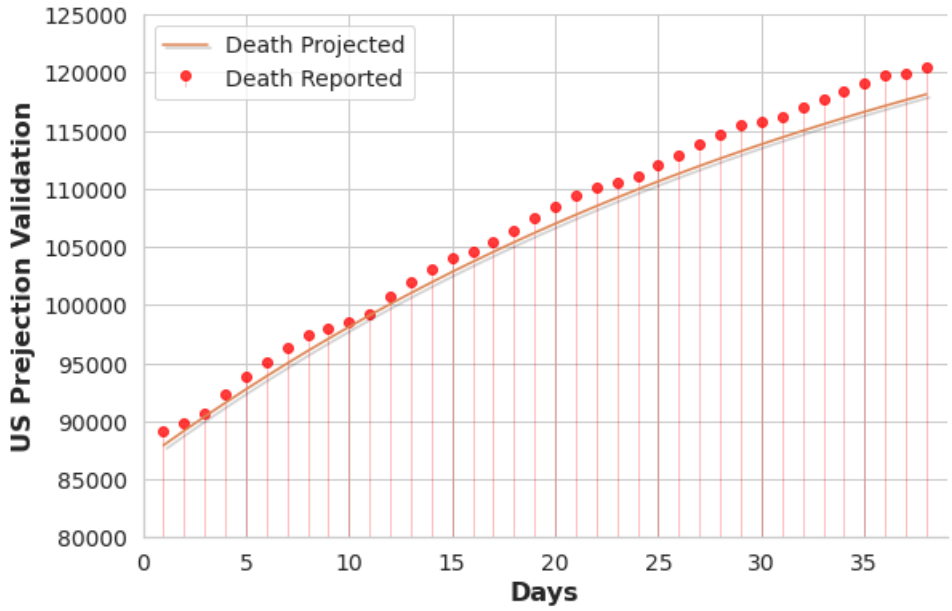

Figure 8: Validation of the projection of US model for 38 days,up to 2020-06-22

5.3 Parameters Analysis

The parameters in table 2 show a certain level of independence and dependency to US and UK model. The parameter β(average risk per infected contact) of US and UK model is similar, one can argue that it shows a weak dependence to the model. While parameters such as c,α,M_{10},N_{10}, $\mathscr{d}$,$\mathscr{r}$ have strong dependencies to the model.
We notice that the parameter σ, which is incubation rate of the COVID19, show a strong dependence to the countries. We suspect that there are two factors lead to this contradiction, the first

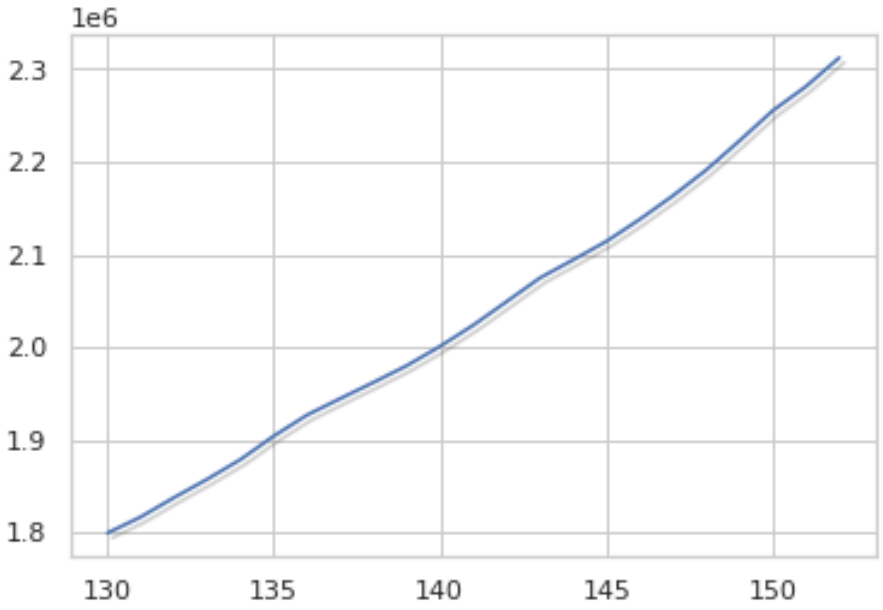

Figure 9: the number of Infected report in Jun 2020

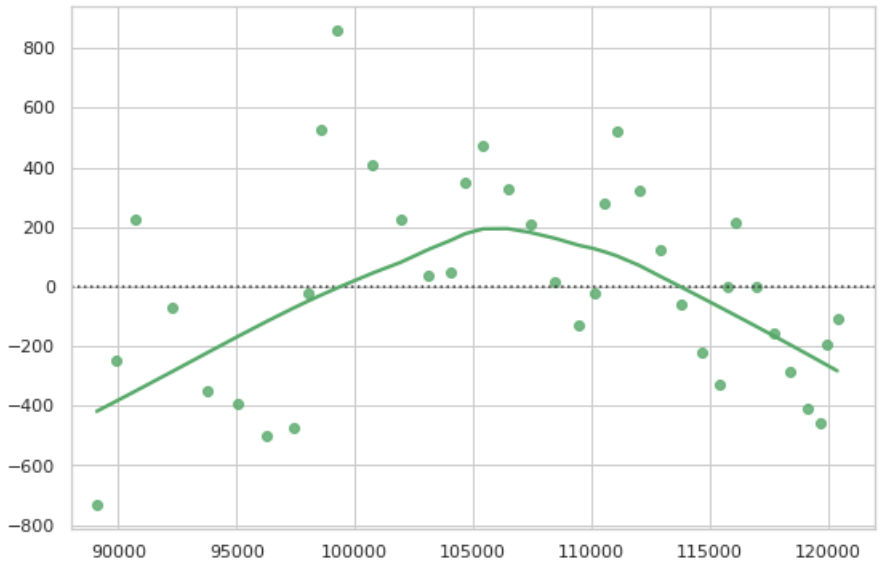

Figure 10: Residuals of the projection of US model for 38 days, up to 2020-06-22

one is the multi-local minima problem of this multi-parameters model; the second reason is that σ could also be affected by the structure of the population of a country.

Parameters	US	UK
β: Average risk per infected contact	2.6891	2.3357
c: Average contacts per person per day	0.2282	0.1188
σ: Incubation rate	0.0860	0.3346
M_{10}: Migration rate of Suspected from group 1 to 0	0.5000	0.2084
N_{10}: Migration rate of Infected from group 1 to 0	0.8601	0.4961
d: Death rate per day	0.001335	0.001999
r : Recovery rate per day	0.04616	0.02882
α: Probability of protections not preventing virus	0.1361	0.03471
p_1: Rate of people in group 1	0.3852	0.5547
p_s: Rate of people is normal(not infected)	0.6430	0.8999

Table 2: Final parameters of Models

5.4 Parameters Adjustment for US model

The previous section shows that the US model started to underestimate the number of death in June 2020. To prove our hypothesis of the impact of the protest, we adjusted the c parameter to test the impact on the projected number of deaths and infection. Figure 11 shows that when we set c to 0.5, the trend of projected number of death fits the trend of the reported numbers best. This is better than $c = 0.4$ and $c = 0.6$. Therefore we believe the increase in contact rate caused the reported number of deaths to increase faster than the estimation by our US model.

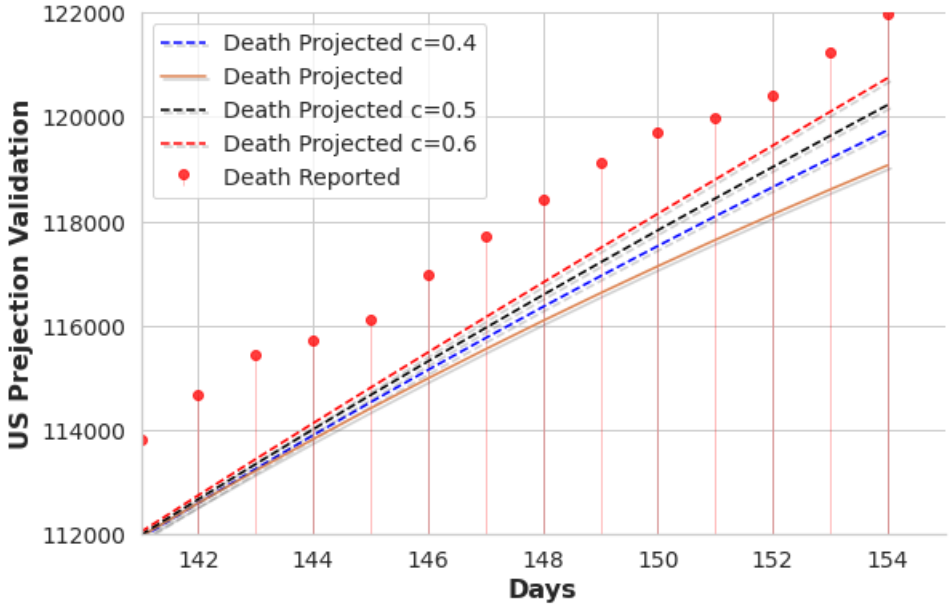

Figure 11: Validation of model with adjusted parameter by using data from 2020-06-11 to 2020-06-24, red line present the projection before adjustment

Figure 12 and Figure 13 shows that the change of parameter c has a significant impact on the number of death and infection. Although we can not conclude that the increase of contact rate

was caused by the protest activities, it raises our concern of the situation in US. One can observe that if we set $c = 0.5$, the projectedÂănumber of deaths andÂăinfectionsÂăwill reach to 187,000 and 6,650,000 respectively; if we set $c = 0.6$, the projected number of deaths andÂăinfection will reach to 258,000 and 9,200,000 respectively, in the next 250 days. It also implies that the pandemic situation in US will become worse and worse in the following 250 days, since the projected numbers by the model will not converge in this period as shown in figure 12.

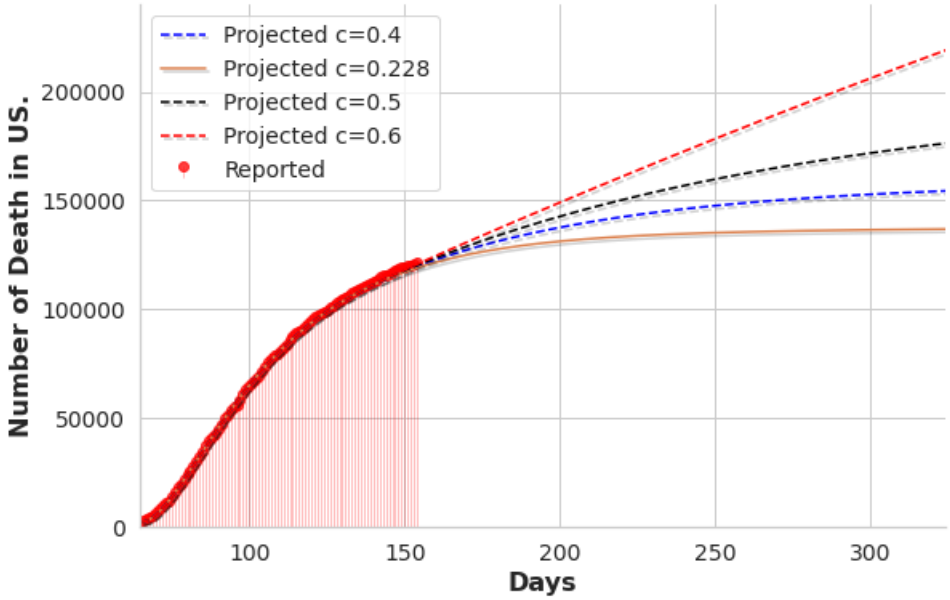

Figure 12: Projection of number of death by the adjusted parameter(from 2020-06-01), red line present the projection before adjustment

6 Conclusion

The project proposed a dynamic system to study the trend of the COVID-19 pandemic, the system consists of seven differential equations with several parameters, we use Theorem 4.1 from textbook to prove that the parameters of the SEIDR model will converge to the ODE (19), and using the package *lmfit* to fit the curve.

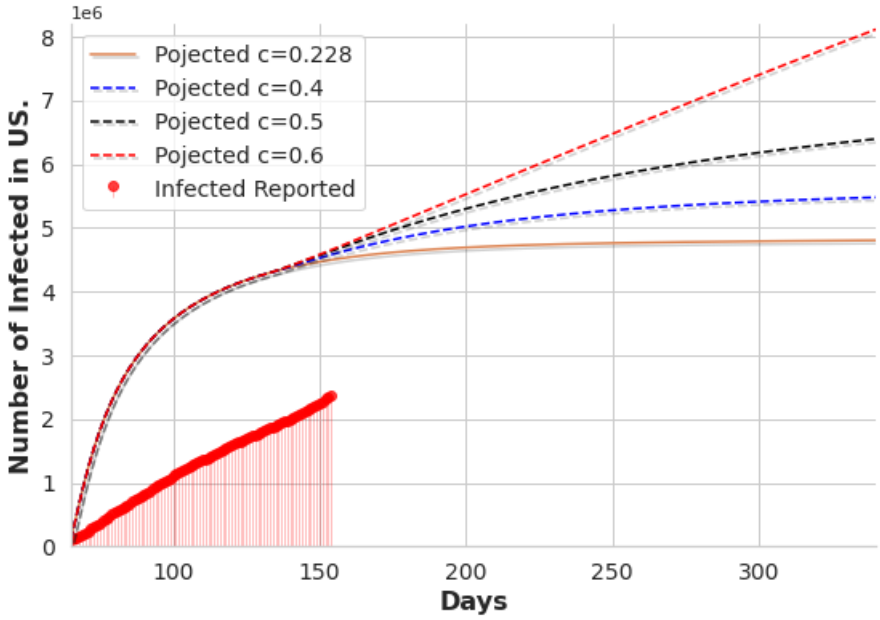

Figure 13: Projection of number of infected by the adjusted parameter(from 2020-06-01), red line present the projection before adjustment

The models suffer a multi-local minima problem although both models can fit the data well and have a good accuracy of projection in validation. If we change the initial values of parameters or the range of parameter in table 1, the models tend to reach different local minimas. In some scenarios the fitted parameters predicts untraceable projections as well. To deal with this problem, we fine-tuned the initial value and range of the parameter manually in order to get reasonable parameter value reflecting real world scenario. In future, We will like to develop a systematic fine-tuning mechanism to increase robustness of the system.

The models did not consider the actual impact of the migration of the population. Instead of using the statistics of international migration, we assumed a constant increase in the population of a country per day. We wish to use the real world population migration data in future.
We also would like to fit Brazilian data to SEIDR model, however it is very difficult to do that right now because the reported number of Brazil is in the stage of exponential increase, which always make the projection converge to the herd immunity level. We will do that when reported number becomes more stable.

For future research, we wish to adjust the model by adding stochasticity, removing the population bound to make it closer to reality and other possible ways. A deeper research related to the latency of data arrival needs to be done with respect to the divergence of the projection and the real infection number.

7 Code

We implemented the models and conduct data analysis in Colab of Google, please click the following links to access them:

US Model

UK Model

References

[Abbey 1952] ABBEY, Helen: An examination of the Reed-Frost theory of epidemics. In: *Human biology* 24 (1952), Nr. 3, S. 201

[Actionsuser u. a. 2020] ACTIONSUSER, Zelima u. a.: *Datasets/COVID-19*, 2020. – URL https://github.com/datasets/covid-19

[Aron und Schwartz 1984] ARON, J.L. ; SCHWARTZ, I.B.: Seasonality and period-doubling bifurcations in an epidemic model. In: *J. Theor. Biol. 110:665-679* (1984)

[Day 2020] DAY, Michael: *Covid-19: four fifths of cases are asymptomatic, China figures indicate*. 2020

[Graunt 1939] GRAUNT, John: *Natural and political observations made upon the bills of mortality*. The Johns Hopkins Press, 1939 (2)

[Greenhalgh u. a. 2001] GREENHALGH, D. ; DOYLE, M. ; LEWIS, F.: A mathematical model of AIDS and condom use. In: *IMA J. Math. Appl. Med. Biol.* (2001), S. 225–262

[Herbrich u. a. 2020] HERBRICH, Ralf ; RASTOGI, Rajeev ; VOLLGRAF, Roland: CRISP: A Probabilistic Model for Individual-Level COVID-19 Infection Risk Estimation Based on Contact Data. In: *arXiv preprint arXiv:2006.04942* (2020)

[Hu u. a. 2020] HU, Zhiliang ; SONG, Ci ; XU, Chuanjun ; JIN, Guangfu ; CHEN, Yaling ; XU, Xin ; MA, Hongxia ; CHEN, Wei ; LIN, Yuan ; ZHENG, Yishan u. a.: Clinical characteristics of 24 asymptomatic infections with COVID-19 screened among close contacts in Nanjing, China. In: *Science China Life Sciences* 63 (2020), Nr. 5, S. 706–711

[Kermack und McKendrick 1991] KERMACK, William O. ; MCKENDRICK, Anderson G.: Contributions to the mathematical theory of epidemicsâĂŤI. In: *Bulletin of mathematical biology* 53 (1991), Nr. 1-2, S. 33–55

[Kermack und McKendrick 1932] KERMACK, William O. ; MCKENDRICK, Anderson G.: Contributions to the mathematical theory of epidemics. II.âĂŤThe problem of endemicity. In: *Proceedings of the Royal Society of London. Series A, containing papers of a mathematical and physical character* 138 (1932), Nr. 834, S. 55–83

[Kermack und McKendrick 1933] KERMACK, William O. ; MCKENDRICK, Anderson G.: Contributions to the mathematical theory of epidemics. III.âĂŤFurther studies of the problem of endemicity. In: *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character* 141 (1933), Nr. 843, S. 94–122

[Levenberg 1944] LEVENBERG, Kenneth: A method for the solution of certain non-linear problems in least squares. In: *Quarterly of applied mathematics* 2 (1944), Nr. 2, S. 164–168

[Lorch u. a. 2020] LORCH, Lars ; TROULEAU, William ; TSIRTSIS, Stratis ; SZANTO, Aron ; SCHÖLKOPF, Bernhard ; GOMEZ-RODRIGUEZ, Manuel: A spatiotemporal epidemic model to quantify the effects of contact tracing, testing, and containment. In: *arXiv preprint arXiv:2004.07641* (2020)

[Max Roser und Hasell 2020] MAX ROSER, Esteban Ortiz-Ospina ; HASELL, Joe: Coronavirus Pandemic (COVID-19). In: *Our World in Data* (2020). – https://ourworldindata.org/coronavirus

[Vineetha Warriyar K u. a. 2020] VINEETHA WARRIYAR K, V ; ALMUTIRY, Waleed ; DEARDON, Rob: Individual-level modelling of infectious disease data: Epiilm. In: *arXiv* (2020), S. arXiv–2003