Amath 383 term paper: Modelling on COVID 19

Not for W credits

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Abstract

At the beginning, this report demonstrates the methods applied for modelling the novel COVID 19. By visualizing the transmission network models, we are going to predict on the infections and outbreak periods in Seattle, and explore on how effective measures against epidemics are.

1 Introduction

As the World Health Organization has reported, COVID 19 is a novel corona virus that causes severe pneumonia, with death rate of approximately 2%. As a student in the field of applied maths, I feel motivated to model and predict on the future infections to raise the public's awareness since the novel virus is an enemy for all mankind.

Effective actions towards COVID 19 have been taken by Chinese public and government, such as mask wearing and collective self-isolation starting from the early stage till now. However, people in United States don't seem to realize the severity of this epidemic. Instead of discriminating on those wearing masks, people should be aware of that taking these actions above can reduce transmission ability of the virus and thus significantly decrease number of infections.

2 Theoretical Background, Modelling

2.1 The SI Model without vital dynamics

To start modelling, let's introduce the simplest model for epidemic, the SI model without vital dynamics, which is defined as:

$$\begin{aligned} \frac{dI}{dt} &= \frac{r\beta IS}{N} \\ \frac{dS}{dt} &= -\frac{r\beta IS}{N} \end{aligned} \tag{1}$$

, where r represents the number of people an infected person closely contacts every day and β denotes the probability for one susceptible to get infected. Thus, multiplying β and r gives us the efficiency of epidemic spreading. We also have N as the total population which stays constant under this circumstance and I, S represents the infected and susceptible group respectively.

Let's assume a closed society of a total 10000 population is suffering from an epidemic, with corresponding parameters r to be 10, β to be 2%, and $I(0)$ to be 10, that is, 10 people are infected at t_0. It would then generate a plot as follow:

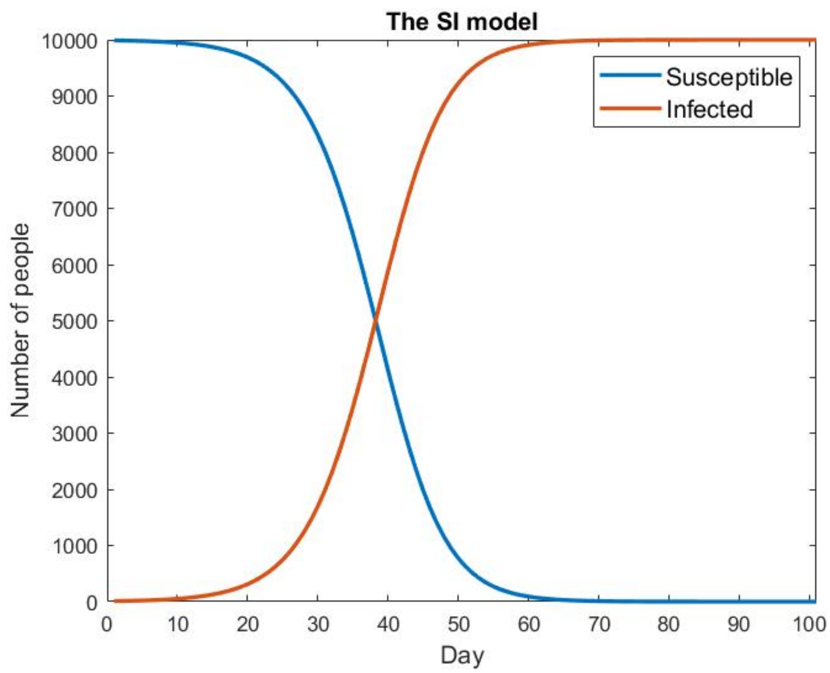

Figure 1: The SI model

We can see an exponential growth of infected would start from day 20 due to r of 10 and even it's just 2% rate to get infected, almost all of this society are infected on day 60.

2.2 The SIR model without vital dynamics

By introducing the recovered group R to the above SI model, we then have the SIR model being defined as:

$$
\begin{aligned}
\frac{dI}{dt} &= \frac{r\beta IS}{N} - \gamma I \\
\frac{dS}{dt} &= -\frac{r\beta IS}{N} \\
\frac{dR}{dt} &= \gamma I
\end{aligned}
\tag{2}
$$

with all parameters defined the same as those in the SI model and the additional γ shows the natural rate for recovery (death included) rate. In this case, if a person is recovered, then he/she is no longer at risk of getting infected again.

We choose a γ of 0.02 and we are still going to use the same data for plotting. The plot is shown as follow:

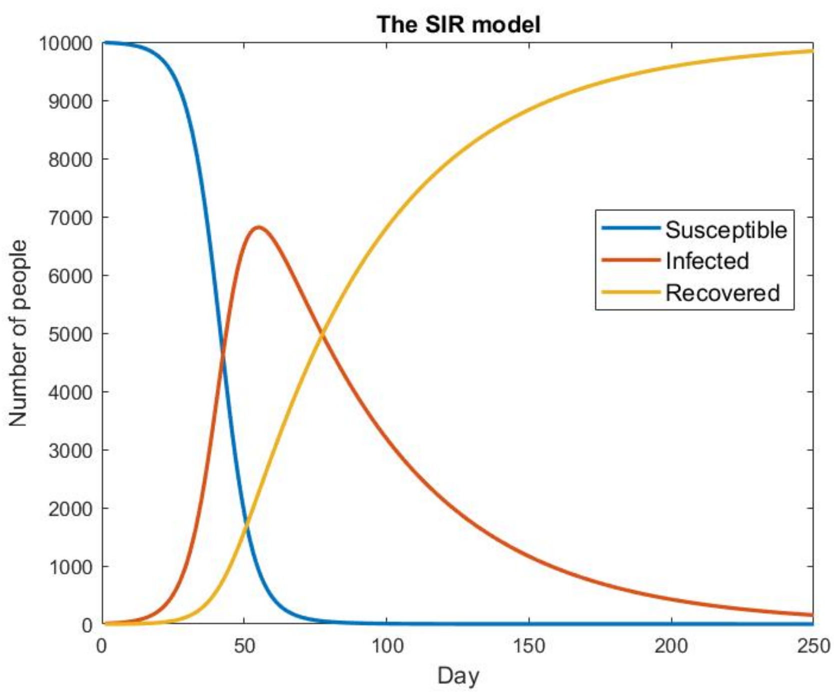

Figure 2: The SIR model

This plot looks quite similar to the epidemic in real life. We can see that initially around day 25, the infected group starts to exponentially grow in numerical and then an outbreak takes place around day 60. After that, as people receive treatment and recover (or died), more and more people have antibodies and thus, the virus is under control and gradually less will be infected.

The basic reproduction number R_0 tells us, during when all individuals are susceptible to infection, the number of susceptibles being infected directly generated by one case of infection. Finding R_0 is necessary as it could tell the severity of an epidemic and inform us what actions need to be taken. R_0 is not a biological constant and it's sensitive to the behaviours of infected group [1].

Essentially, R_0 could tell us if an epidemic can spread among population and what the proportion of the population should be immunized to eradicate the disease. If it's larger than 1, we know that the epidemic can be transferred among people, but not if it's less than 1. The proportion of population that should be immunized to prevent further spreading should be larger than $1 - 1/R_0$. Generally, the larger R_0 is, the harder to control the epidemic [1].

If we are using SIR model, we can then predict R_0 by substituting $S = N$ into $\frac{dI}{dt}$, as initially we may assume almost all of the population are susceptibles, we then have:

$$R_0 = \frac{r\beta}{\gamma} \tag{3}$$

, from which we can clearly see that R_0 is directly proportional to the number of people in contact by infected and the probability of infections. Thus, wearing masks and self-isolating are proved to be effective measures to get the virus under control [1].

Taking the real-life parameter into consideration helps us to generate a model, that can be used to predict virus transmissibility and the outbreak period of an epidemic.

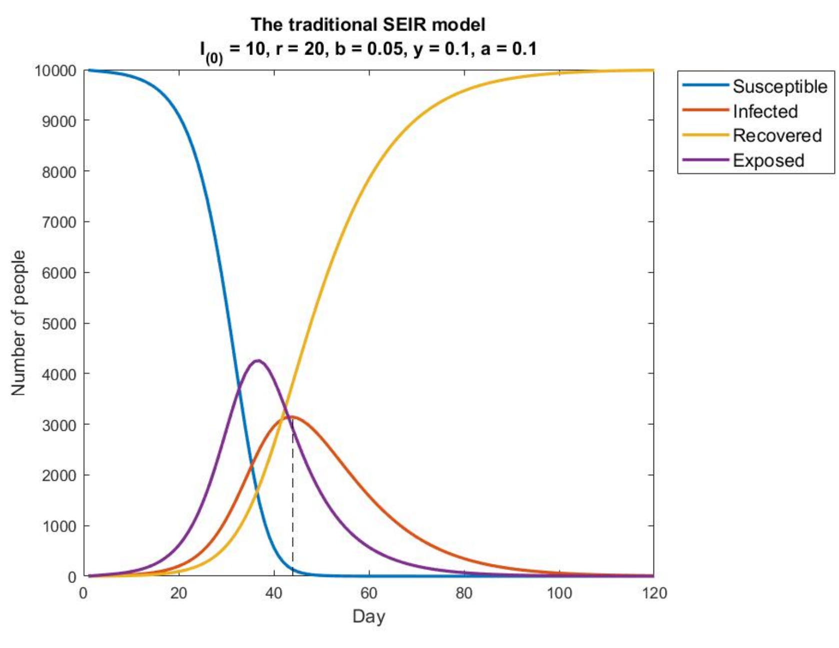

Figure 3: The conventional SEIR model

2.3 The conventional SEIR model without vital dynamics

As we know, most epidemics have an incubation period, and so do COVID 19. So it's necessary to introduce the Exposed group E into the SIR model. Due to the low mortality rate, we may not have to take vital dynamics into account in order to generate a good model.

I'll first introduce the conventional SEIR model, which is defined as:

$$
\begin{aligned}
\frac{dE}{dt} &= \frac{r\beta IS}{N} - \alpha E \\
\frac{dS}{dt} &= -\frac{r\beta IS}{N} \\
\frac{dI}{dt} &= \alpha E - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned}
\tag{4}
$$

, where α denotes the probability of an exposed to be infected. Mathematically, α is the same as the reciprocal of the incubation duration.

Different parameters are set to clearly show the relations between each group in **Figure 3** above, in which we can see that the outbreak occurs around day 45, and approximately 1/3 of the whole population will be infected.

We may also estimate R_0 by referring to the Exposed group in the early stage. With corresponding parameters, we could predict initial R_0 to be 3.5, and then stays between 3.2 and 3.3 till day 20.

2.4 A more realistic SEIR model without vital dynamics

In additional to the conventional model, COVID 19 is also proven to be infectious during the incubation period by Chinese scientific community. We may interpret it as, there's also a probability β_2 such that a susceptible can be infected and transferred to the Exposed group due to one case of latency. This ODE system is then defined as:

$$
\begin{aligned}
\frac{dE}{dt} &= \frac{r\beta IS}{N} + \frac{r\beta_2 ES}{N} - \alpha E \\
\frac{dS}{dt} &= -\frac{r\beta IS}{N} - \frac{r\beta_2 ES}{N} \\
\frac{dI}{dt} &= \alpha E - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned}
\tag{5}
$$

Choosing β_2 as 0.03 and other parameters the same as in **Figure 3**, we can generate a plot of a new SEIR model as shown in **Figure 4**. We may soon catch that the outbreak would take place about 20 days in advance. Besides, the virus

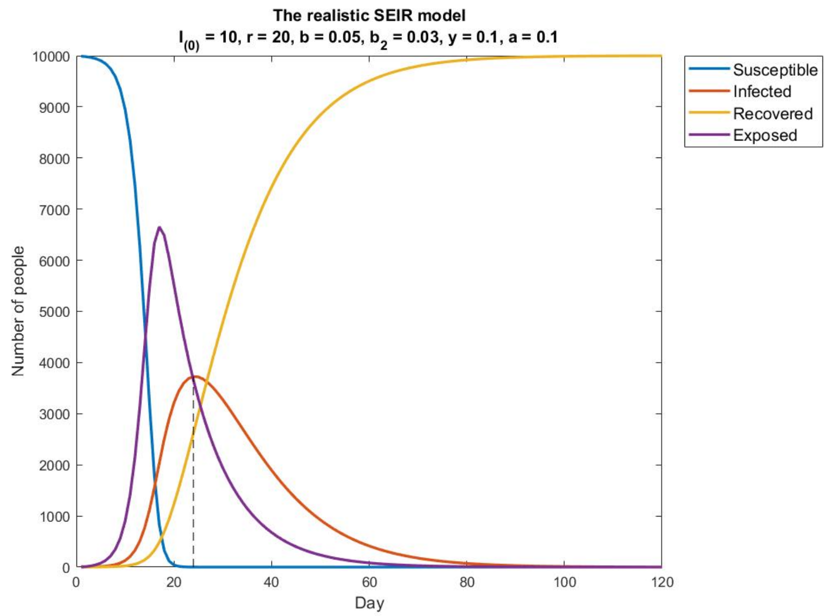

Figure 4: The realistic SEIR model

would stay latent in over 6500 people and more than 3500 would be infected due to the infectivity during incubation. In this case, the prediction on R_0 is about 7.5 for the first 10 days. We've received a result two times larger than that using conventional model and thus make it significantly harder to control epidemic from spreading, all that because of another 3% infection rate during incubation.

3 Implementation, development, and interpretation

3.1 Modelling what's going on in Seattle

Substituting appropriate parameters into the SEIR model gives prediction for real-life scenarios. The incubation period of COVID 19 is about 14 days, thus, α should be $\frac{1}{14}$. Since United States is currently in the early stage of epidemic and data are not sufficient for predictions, public data from mainland China are used as reference. First, I refer to the number of confirmed cases of corona virus in China initially (from Jan, 25th to Feb, 6th) [2] and data of HuBei province are removed to stay unbiased. These can give us good estimations of β and β_2, probabilities of infections in early stage. Assuming that one would only closely contact 10 people a day on average (since people would intentionally avoid contacting others, this number r should be relatively small). An underdetermined system:

$$[rI, rE] \begin{bmatrix} \beta \\ \beta_2 \end{bmatrix} = \frac{dE}{dt} + \alpha E \tag{6}$$

can be formulated from data of each of the 13 days and I then call command **pinv** to get a non-trivial solution. A vector of β and β_2 can then be generated and taking average would give us β of 0.004 and β_2 of 0.013.

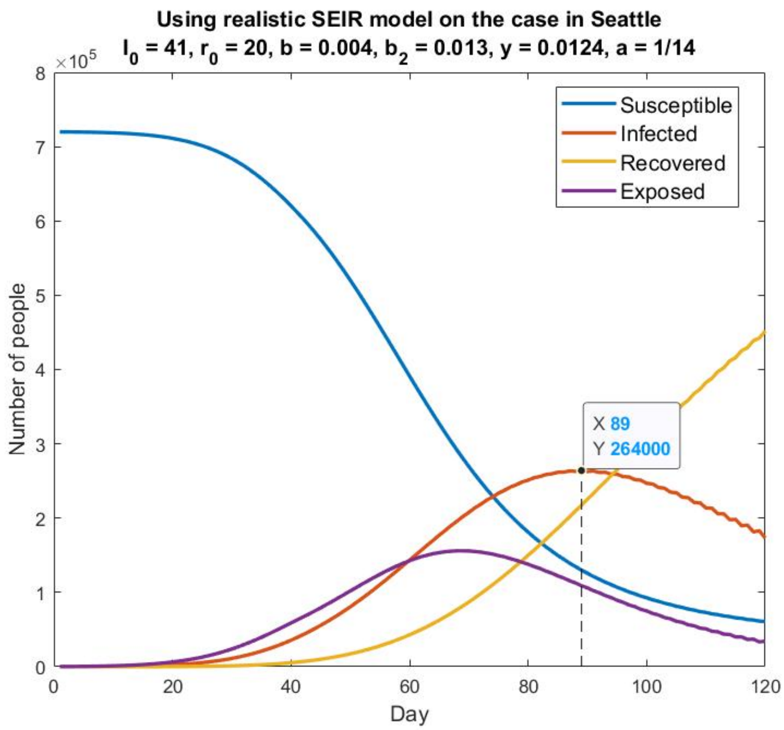

Figure 5: Modelling of COVID 19 in Seattle ($r_0 = 20$, $r_\infty = 10$, 100% effective)

To derive a good estimation of recovery rate γ, I look for the data of recovered and dead from Jan, 27th to Feb, 6th [2] and add them up, which would give me a vector:

$$R = [19, 30, 42, 64, 87, 123, 191, 247, 383, 534, 741] \tag{7}$$

Taking the number of infected in the same period and substituting them into $\frac{dR}{dt} = \gamma I$ would give us a vector of γ:

$$\gamma = [0.0064, 0.0070, 0.0072, 0.0076, 0.0112, 0.0117, 0.0159, 0.0207, 0.0234] \tag{8}$$

Midpoint method is applied here to generate an accurate growth rate of recovered group, as the rate grows much faster in February than in January. I then average it up and derive a γ of 0.0124. In my models, I add 0.0002 to it every single day to simulate the development of therapies or drugs, or maybe a worse case in which the death rate rises. This also makes γ adds to the current recovery rate in China, which is $\frac{1707+27}{80859} = 0.021$.

Let t_0 be March, 4th, when 41 cases are confirmed by Public Health Department in Seattle [3], a city of approximately 720,000 population. As news also reported that 27 cases were confirmed on March, 3rd, we can set $\frac{dI}{dt}$ at time t_0 to be 14 and can then easily find E_0, which is 203. Since US public haven't realize how severe the epidemic is, let's set our r to be 20, which means that a person would closely contact 20 people a day on average. As the epidemic goes on, the public may somehow be aware of it and let r be reduced by 1/4 person a day till r becomes 10. Public Health Seattle also reported at least 10 deaths and 1 recovery have been confirmed, so I set $R_{(0)}$ to be 11. Using β and β_2 determined above, I apply the midpoint method for iterations as well for more accurate predictions and the result is shown in **Figure 5** above.

As shown, if one doesn't take it seriously (I.e. with an initial r of 20), and no actions being taken to get COVID 19 controlled, we would expect an exponential growth of infected and exposed starting from day 20. One and a half month after then, virus would stay latent among at maximum 156,000 people. 1000, 10,000, 100,000 infected will be hit on day 15, 30, and 54, which are March, 18th, Apr, 2nd, and Apr. 26th respectively. We can also predict for an outbreak, with at most 264,000 people being infected, on day 89 from March, 4th. However, this graph only shows an ideal case that seldom has done to control the epidemic and thus may not accurately predict the late stage.

We can also look into the basic reproduction number R_0. For the first month, it gradually decreases from 3.7 to 2.3 and stays the same until the outbreak. Since in this case, R_0 is much larger than 1, we know that it can spread among population relative quickly and thus, the public should definitely take actions as soon as possible.

3.2 What if we take actions timely?

Instead of wandering around that helps to spread out the virus, if we choose to self-isolate and mind our own business, that would significantly reduce the parameter r. Suppose one is just contacting the family, roommates, or a few friends, choosing r of 10 is a good assumption here. Besides, if most of the public choose to wear masks that helps to cut off transmission and could possibly reduce β and β_2 by at least 20%. The recovery rate γ is also added by 0.002 each day until it reaches 0.04. The simulation of this case on one-year scale is shown in **Figure 6** below.

At first, we would expect a steady state of only slight increase in both infected and exposed groups for about 75 days. As it goes on, not only are we going to expect the outbreak being postponed to day 157, but also about 110,000 less will be infected. As the outbreak being delayed, therapies and drugs are

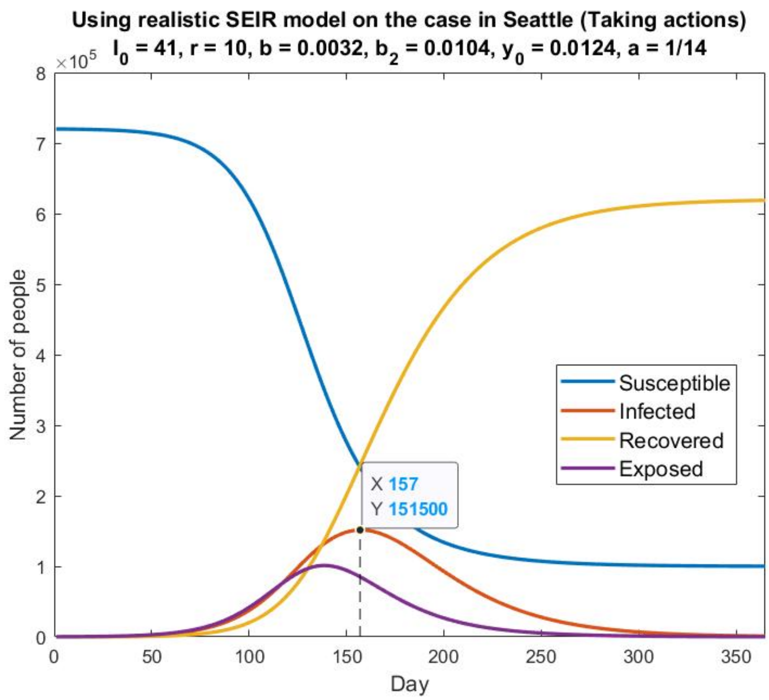

Figure 6: Modelling of COVID 19 in Seattle (r = 10, 80% effective, $\gamma_\infty = 0.04$)

much more likely to be developed, that may further increase the recovery rate γ beyond 4% over time and dynamically slows down the growth of infected, so that we may even eradicate the epidemic before the outbreak takes place. Then I check the basic reproduction number is this case, which is initially 1.5 and grows so slowly that it stays under 2.0 for the first 134 days. Adding up the first 120 R_0 values and take the mean, I get 1.83. Since we would also expect the ratio of susceptible over whole population to be gradually smaller, R_0 would simultaneously diminish according to this ratio. Thus, we would expect it to be less than the average 1.83, due to the limitation of only well predicting the early stage. Even though epidemic is still not easy to be controlled, we would expect a much better situation.

If the delayed outbreak results in developed drugs that would accelerate the growth of γ, let's say γ_∞ now is 0.1 and it grows 3 times or 5 times faster after 2 months. The resulting models are shown respectively in the left and the right of **Figure 7**. In both cases we would expect significantly less population being infected during the outbreak period.

What if somehow, the public has a premonition or they are extremely self-disciplined, so they simply just decide to contact 5 people a day and also wear masks in time that makes transmission only 80% effective? Using exactly the

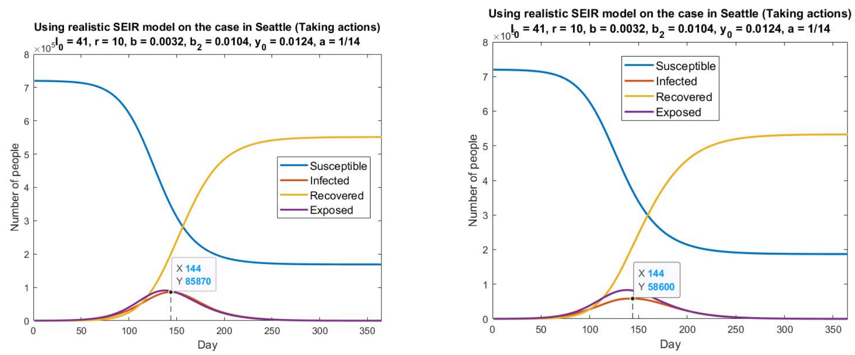

Figure 7: Modelling of COVID 19 in Seattle (r = 10, 80% effective, γ_∞(left) = 0.06, γ_∞(right) = 0.1)

same parameters above yields the result in **Figure 8**, that after two years, the outbreak takes place with a maximum infection of 5668, which would seem insignificant comparing to a common influenza in United States. On the scale of

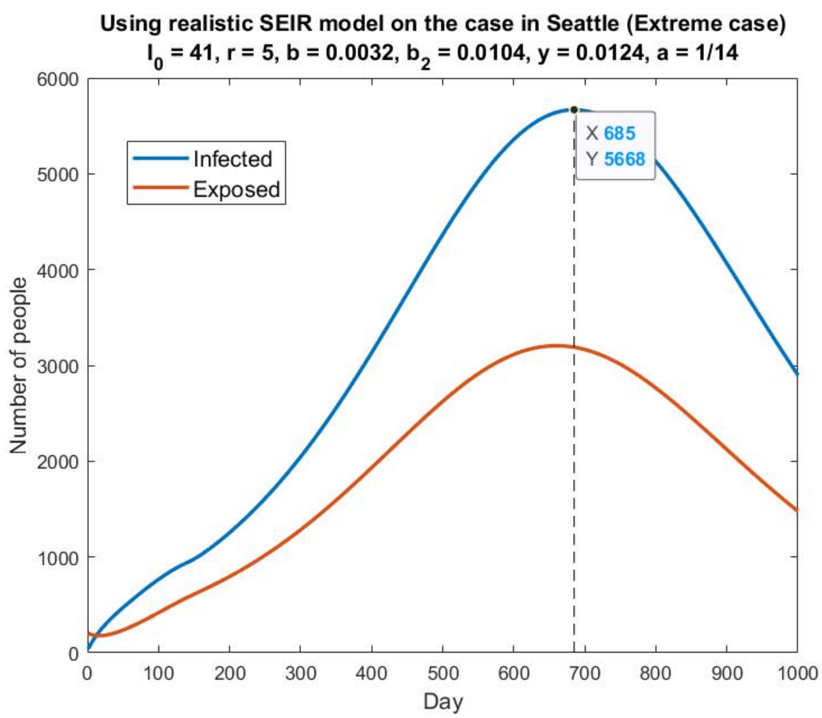

Figure 8: Modelling of COVID 19 in Seattle (r = 5, 80% effective, γ_∞ = 0.04)

whole population, 5668 is quite trivial to 720,000, even if not taking successfully developed medicines into account. During the whole time span of 1000 days, R_0 is at max 1.15, and stays less than 1 for the first 16 days, which makes eradication of epidemic possible ahead of time.

4 Conclusion

To sum up, we would generally expect significantly less infected and latency cases even though we only reduce r from 20 to 10 (collective self-isolation) and transmission ability by 20% (wearing masks), which is due to the interacting ODE system of realistic SEIR system. If we would like to get COVID 19 controlled in Seattle, we better start now. There are also several limitations to this study. First, the models are constructed without vital dynamics, that means noticeable changes in birth or death rate would yield a completely different model. Second, from what I've learned of, COVID 19 would not cause reinfection so a SEIR model is applied. However, if some mutation happens to the virus that makes reinfection possible, we would have to use a SEIRS model instead that there's also a chance to make the recovered susceptible again. Third, as it's stated throughout the report, these models are only able to well predict the early stage due to the dynamically changing real-life environment.

References

[1] Wikipedia: Basic reproduction number.
https://en.wikipedia.org/wiki/Basic_reproduction_number 2020.

[2] National Health Commission of the People's Republic of China: Update of the new corona virus pneumonia from Jan, 25th to Feb, 6th.
http://www.nhc.gov.cn/ 2020.

[3] Public Health - Seattle and King County: Local health officials announce new recommendations to reduce risk of spread of COVID-19.
https://www.kingcounty.gov/depts/health/news/2020/March/4-covid-recommendations.aspx 2020.

5 Appendix

```
%%
% SI model
N = 10000;
I(1) = 10;
S(1) = N - I(1);
r = 10;
b = 0.02;
t = 1 : 101;
for i = 1 : 100
    I(i + 1) = S(i) * I(i) * r * b / N + I(i);
    S(i + 1) = -S(i) * I(i) * r * b / N + S(i);
end

plot(t, S, t, I, 'linewidth', 2)
xlabel('Day', 'FontSize', 12)
ylabel('Number of people', 'FontSize', 12)
title('The SI model', 'FontSize', 12)
legend('Susceptible', 'Infected', 'FontSize', 12)
xlim([0 101])

%%
% SIR model
N = 10000;
I(1) = 10;
S(1) = N - I(1);
R(1) = 0;
r = 10;
b = 0.02;
y = 0.02;
t = 1 : 251;
for i = 1 : 250
    I(i + 1) = S(i) * I(i) * r * b / N + I(i) - y * I(i);
    S(i + 1) = -S(i) * I(i) * r * b / N + S(i);
    R(i + 1) = R(i) + y * I(i);
end

plot(t, S, t, I, t, R, 'linewidth', 2)
xlabel('Day', 'FontSize', 12)
ylabel('Number of people', 'FontSize', 12)
title('The SIR model', 'FontSize', 12)
legend('Susceptible', 'Infected', 'Recovered', 'FontSize'
    , 12, 'Location', 'Best')
xlim([0 250])
```

```
%%
% Conventional SEIR model
N = 10000;
I(1) = 10;
S(1) = N - I(1);
R(1) = 0;
E(1) = 10;
r = 20;
b = 0.05;
y = 0.1;
a = 0.1;
t = 1 : 121;
R0 = [];

for i = 1 : 120
    I(i + 1) = I(i) + a * E(i) - y * I(i);
    S(i + 1) = - S(i) * I(i) * r * b / N + S(i);
    R(i + 1) = R(i) + y * I(i);
    E(i + 1) = E(i) - a * E(i) + S(i) * I(i) * r * b / N;
    R0(i) = r * b * I(i) / (a * E(i));
end
R0 = R0(4 : 14);
plot(t, S, t, I, t, R, t, E, 'linewidth', 2)
xlabel('Day', 'FontSize', 12)
ylabel('Number of people', 'FontSize', 12)
title({'The traditional SEIR model', 'I_{(0)} = 10, r = 20, b = 0.05, y = 0.1, a = 0.1'}, 'FontSize', 12)
[val, ind] = max(I);
hold on
plot([ind, ind], [0, val], '--k')
legend('Susceptible', 'Infected', 'Recovered', 'Exposed', 'FontSize', 12, 'Location', 'Bestoutside')

xlim([0 120])

%%
% Real-life SEIR model
N = 10000;
I(1) = 10;
S(1) = N - I(1);
R(1) = 0;
E(1) = 10;
r = 20;
b = 0.05;
b2 = 0.03;
```

```
y = 0.1;
a = 0.1;
t = 1 : 121;
for i = 1 : 120
    I(i + 1) = I(i) + a * E(i) - y * I(i);
    S(i + 1) = - S(i) * I(i) * r * b / N - S(i) * E(i) * r * b2 / N + S(i);
    R(i + 1) = R(i) + y * I(i);
    E(i + 1) = E(i) - a * E(i) + S(i) * I(i) * r * b / N + S(i) * E(i) * r * b2 / N ;
    R0(i) = (r * b * I(i) + r * b2 * E(i)) / (a * E(i));
end
R0 = R0(4 : 14);

plot(t, S, t, I, t, R, t, E, 'linewidth', 2)
xlabel('Day', 'FontSize', 12)
ylabel('Number of people', 'FontSize', 12)
title({'The realistic SEIR model', 'I_{(0)} = 10, r = 20, b = 0.05, b_2 = 0.03, y = 0.1, a = 0.1'}, 'FontSize', 12)
[val, ind] = max(I);
hold on
plot([ind, ind], [0, val], '--k')
legend('Susceptible', 'Infected', 'Recovered', 'Exposed', 'FontSize', 12, 'Location', 'Bestoutside')

xlim([0 120])

%%
% estimating parameters
clear all; close all; clc;
I(1) = 923;
I(2) = 1321;
I(3) = 1801;
I(4) = 2420;
I(5) = 3125;
I(6) = 3886;
I(7) = 4638;
I(8) = 5306;
I(9) = 6028;
I(10) = 6916;
I(11) = 7646;
I(12) = 8353;
I(13) = 9049;

a = 1/14;
```

```
y = 0.04;
r = 10;

E(1) = (I(2) - I(1) + y * I(1)) / a;
for i = 2 : 12
    E(i) = (((I(i + 1) - I(i - 1)) / 2) + y * I(i)) / a;
end
E(13) = (I(13) - I(12) + y * I(13)) / a;

dE(1) = E(2) - E(1);
for i = 2 : 12
    dE(i) = (E(i + 1) - E(i - 1)) / 2;
end
dE(13) = E(13) - E(12);

for i = 1 : 13
    dE(i) = dE(i) + a * E(i);
end

for i = 1 : 13
    A = [r * I(i), r * E(i)];
    beta(:, i) = pinv(A) * dE(i);
end
beta = mean(beta, 2);

beta2 = beta(2);
beta = beta(1);

R = [13, 23, 34, 55, 77, 113, 180, 236, 372, 520, 723];
D = [6, 7, 8, 9, 10, 10, 11, 11, 11, 14, 18];
R = R + D;
I = I(3:end);
y = [];
for i = 1 : 9
    y(i) = (R(i + 2) - R(i)) / (2 * I(i));
end



%%
% Modelling on COVID 19 in Seattle
clear all; close all; clc;
N = 720000;
y = 0.0124;
a = 1/14;
I(1) = 41;
```

```
E(1) = (14 + I(1) * y) / a;
S(1) = N - I(1);
R(1) = 11;
beta = 0.004;
beta2 = 0.013;
r = 20;
t = 1 : 120;

I(2) = I(1) + a * E(1) - y * I(1);
S(2) = - S(1) * I(1) * r * beta / N - S(1) * E(1) * r * beta2 / N + S(1);
R(2) = R(1) + y * I(1);
E(2) = E(1) - a * E(1) + S(1) * I(1) * r * beta / N + S(1) * E(1) * r * beta2 / N ;


for i = 2 : 119
    I(i + 1) = I(i - 1) + 2 * (a * E(i) - y * I(i));
    S(i + 1) = 2 * (- S(i) * I(i) * r * beta / N - S(i) * E(i) * r * beta2 / N) + S(i - 1);
    R(i + 1) = R(i - 1) + 2 * y * I(i);
    E(i + 1) = E(i - 1) - 2 * (a * E(i) - S(i) * I(i) * r * beta / N - S(i) * E(i) * r * beta2 / N);
    if r > 10
        r = r - 1/4;
    end
    R0(i) = (r * beta * I(i) + r * beta2 * E(i)) / (a * E(i));
    y = y + 0.0002;
end
R0 = R0(2 : 119);
plot(t, S, t, I, t, R, t, E, 'linewidth', 2)
xlabel('Day', 'FontSize', 12)
ylabel('Number of people', 'FontSize', 12)
title({'Using realistic SEIR model on the case in Seattle', 'I_0 = 41, r_0 = 20, b = 0.004, b_2 = 0.013, y = 0.0124, a = 1/14'}, 'FontSize', 12)
hold on
[val1, ind1] = max(I);
plot([ind1, ind1], [0, val1], '--k')
legend('Susceptible', 'Infected', 'Recovered', 'Exposed', 'FontSize', 12, 'Location', 'Best')
xlim([0, 120])
[val2, ind2] = max(E);
```

```
%%
% Take actions
clear all; close all; clc;
N = 720000;
y = 0.0124;
a = 1/14;
I(1) = 41;
E(1) = (14 + I(1) * y) / a;
S(1) = N - I(1);
R(1) = 11;
beta = 0.004 * 0.8;
beta2 = 0.013 * 0.8;
r = 10;
t = 1 : 365;


for i = 1 : 364
    I(i + 1) = I(i) + a * E(i) - y * I(i);
    S(i + 1) = - S(i) * I(i) * r * beta / N - S(i) * E(i) * r * beta2 / N + S(i);
    R(i + 1) = R(i) + y * I(i);
    E(i + 1) = E(i) - a * E(i) + S(i) * I(i) * r * beta / N + S(i) * E(i) * r * beta2 / N ;
    R0(i) = (r * beta * I(i) + r * beta2 * E(i)) / (a * E(i));

    if y < 0.1 & i < 60
        y = y + 0.0002;
    elseif y < 0.1 & i >= 60
        y = y + 0.001;
    end
end
R0 = R0(1:120);


plot(t, S, t, I, t, R, t, E, 'linewidth', 2)
xlabel('Day', 'FontSize', 12)
ylabel('Number of people', 'FontSize', 12)
title({'Using realistic SEIR model on the case in Seattle (Taking actions)', 'I_0 = 41, r = 10, b = 0.0032, b_2 = 0.0104, y_0 = 0.0124, a = 1/14'}, 'FontSize', 12)
hold on
[val1, ind1] = max(I);
plot([ind1, ind1], [0, val1], '--k')
legend('Susceptible', 'Infected', 'Recovered', 'Exposed', 'FontSize', 12, 'Location', 'Best')
```

```
xlim([0, 365])
[val2, ind2] = max(E);



%%
% A more extreme case
clear all; close all; clc;
N = 720000;
y = 0.0124;
a = 1/14;
I(1) = 41;
E(1) = (14 + I(1) * y) / a;
S(1) = N - I(1);
R(1) = 11;
beta = 0.004 * 0.8;
beta2 = 0.013 * 0.8;
r = 5;
t = 1 : 1001;

for i = 1 : 1000
    I(i + 1) = I(i) + a * E(i) - y * I(i);
    S(i + 1) = - S(i) * I(i) * r * beta / N - S(i) * E(i) * r * beta2 / N + S(i);
    R(i + 1) = R(i) + y * I(i);
    E(i + 1) = E(i) - a * E(i) + S(i) * I(i) * r * beta / N + S(i) * E(i) * r * beta2 / N;

    R0(i) = (r * beta * I(i) + r * beta2 * E(i)) / (a * E(i));
    if y < 0.04
        y = y + 0.0002;
    end

end

plot(t, I, t, E, 'linewidth', 2)
xlabel('Day', 'FontSize', 12)
ylabel('Number of people', 'FontSize', 12)
title({'Using realistic SEIR model on the case in Seattle (Extreme case)', 'I_0 = 41, r = 5, b = 0.0032, b_2 = 0.0104, y = 0.0124, a = 1/14'}, 'FontSize', 12)
hold on
[val1, ind1] = max(I);
plot([ind1, ind1], [0, val1], '--k')
legend('Infected', 'Exposed', 'FontSize', 12, 'Location',
```

```
        'Best')
xlim([0, 1000])
[val2, ind2] = max(E);
```