Influenza Epidemics

Wenhan Gao

State University of New York at

Stony Brook December 2020

Introduction

     An epidemic is defined as a period of time with an incidence of occurrence that is significantly above the "expected" or "average" outbreak of a disease. In the epidemic model, individuals are assigned to different subgroups according to their disease status. The model consists of three compartments labeled susceptible (S), infective or contagious (I), and removed (R). Susceptible individuals are those who could become infected. Infective individuals are infected and can ass the disease to others. Removed individuals are not susceptible nor infective, and thus they do not play a direct role in disease progression. In this report, we will delve the SIR model in relation to influenza, and implement a mathematical model in MATLAB that simulate the spread of a strain of influenza.

(a) Modeling an Epidemic

     The passage of a given strain of influenza may be reasonably modeled as an SIR disease, with individuals becoming infected once, and then gaining immunity. An SIR disease is modeled by:

$$S \xrightarrow{\beta SI} I \xrightarrow{\gamma I} R :$$

$$\frac{d\hat{S}}{dt} = -\beta N \hat{I} \hat{S}$$
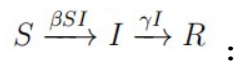
$$\frac{d\hat{I}}{dt} = (\beta N \hat{S} - \gamma)\hat{I}$$

$$\frac{d\hat{R}}{dt} = \gamma \hat{I}$$

$\hat{S} = \dfrac{S}{N}, \hat{I} = \dfrac{I}{N}, \hat{R} = \dfrac{R}{N}$, where S is number of susceptible individuals, I is number of infective individuals, R is number of removed(recovered) individuals.

     Let the recovery rate γ to be 5% per individual per day, and the infection rate β to be 5×10^{-7}. The unit of β is **per individual²**, and this **is reasonable** because β describes the likelihood that a single infective individual would pass the disease to an arbitrary susceptible. Suppose we have one million, 10^6, susceptibles, the likelihood for each infective to pass the disease to an arbitrary susceptible in one day is $5 \times 10^{-7} \times 10^6 = 0.5$, which is pretty reasonable.

     Next, we will Use MATLAB to implement this model with an initial population of one million, and 10 of which are infected over the course of a year, 365 days. Forward Euler method will be used to approximate differential equations with a time step of 0.01 day. MATLAB codes are attached at the end of this report as **Appendix A.**

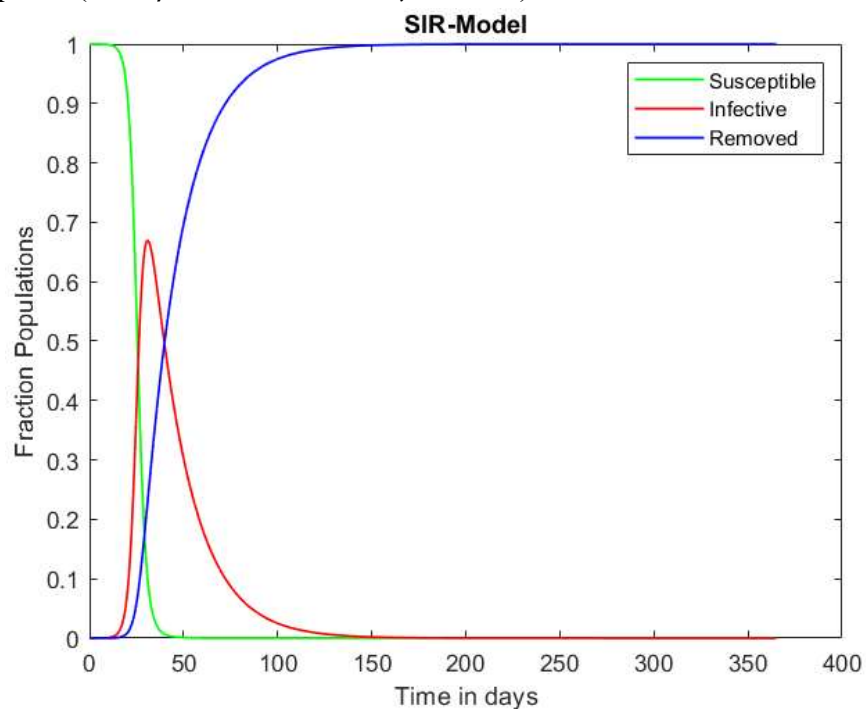Resulting plots: (with $\beta = 5 \times 10^{-7}$ and $\gamma = 0.05$)
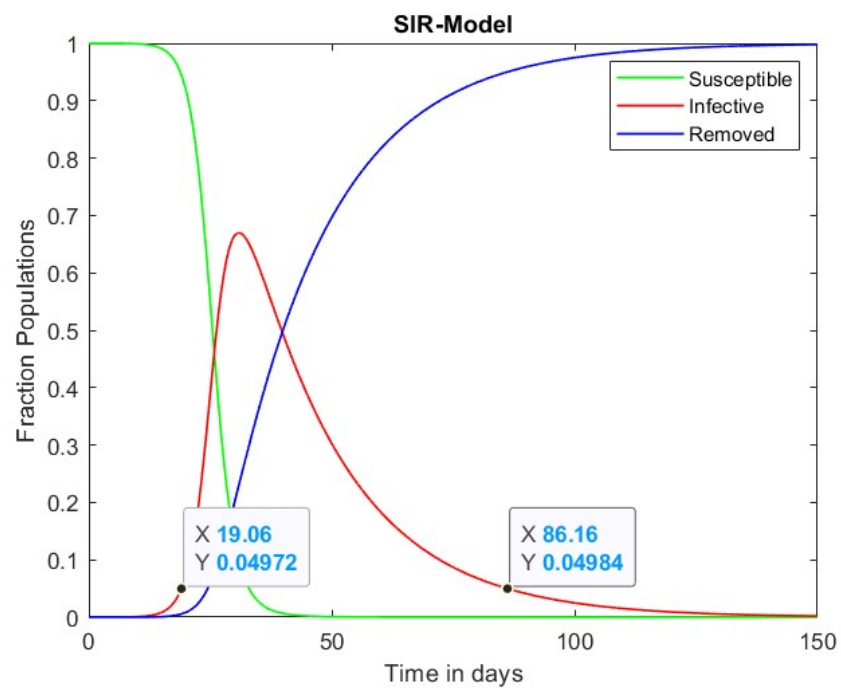

Figure 1: Time domain

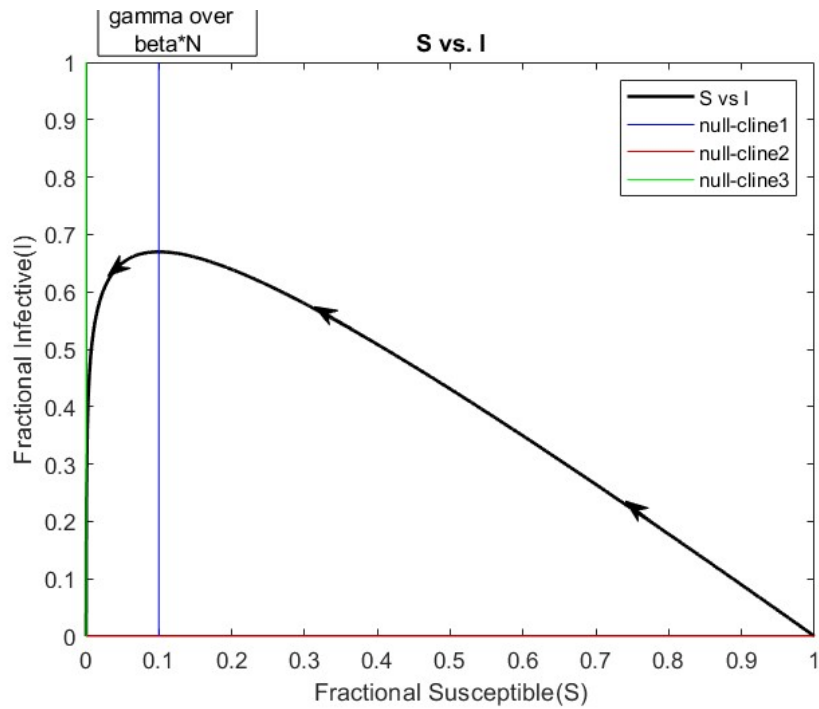**Figure 1a: Re-scale Fig.1 to observe**

Figure 2: S vs. I

From above plots, we can observe the dynamics of the resulting epidemics. Initially, there is only a small amount of infectives, the infection increases slowly, also the rate of increase grows as infection increases. At the same time, the susceptible population is decreasing, and eventually the system will reach a point where $\beta N \hat{S} = \gamma$, which is a null cline for $\hat{I}$. At this point, the infected population will begin to decline. Overall, the infective population increases first, and then starts to decrease at the null-cline, while susceptible population is monotonically decreasing and removed population is monotonically increasing. Also, from Fig. 2, we can see that **the epidemic approximately starts at the 19th day and ends at the 86th day, lasting approximately 67 days(here take 0.05 as the threshold, if more than 0.05 of the total population are infected, we consider the epidemic is happening).** As in Fig.1, the removed(R) fractional population converges to 1 eventually; it basically means that **everyone has been infected**, in other words, one million people have been infected, **no one avoided the disease** . Therefore, with a mortality rate of 5%, $1000000 \times 0.05 = 50000$, **50 thousand people would die**.

Next, let's increase the infection rate β by 10 fold to 5e-6, results are:
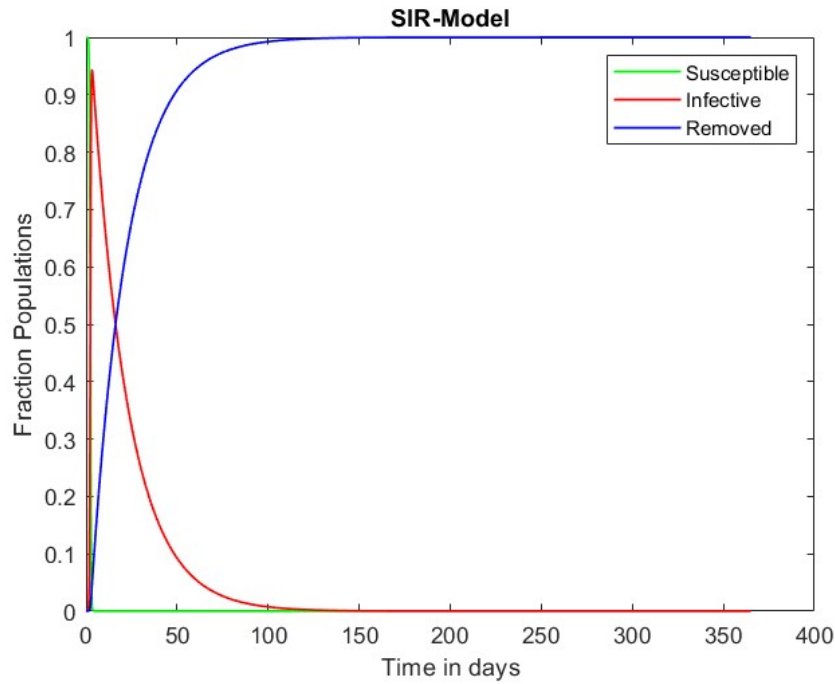
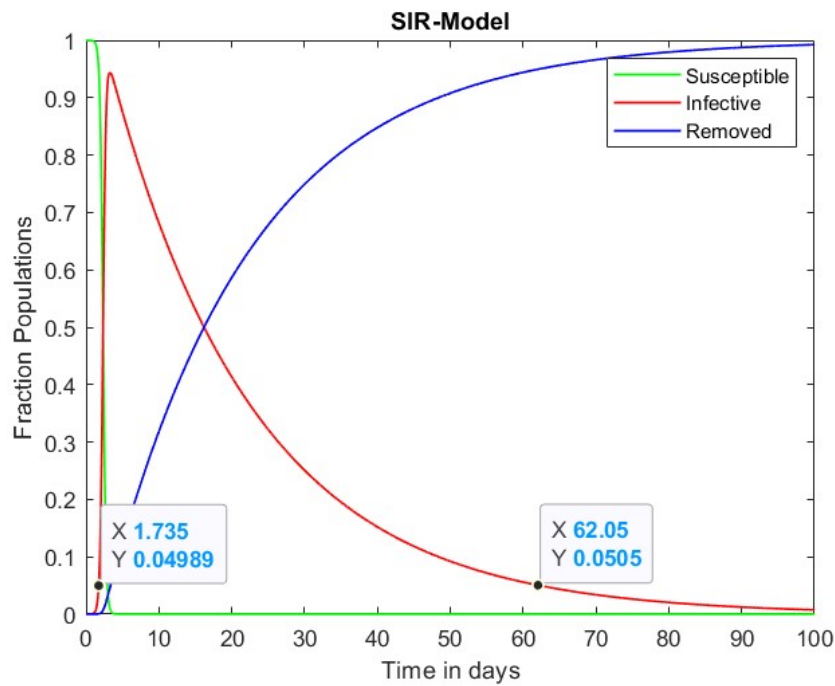**Figure 3: Increasing beta by 10-fold**

Figure 4: Zoom in Fig 3 to observe

Overall, the dynamics behaves similarly to that of Fig.1, an increase followed by a decrease. The main difference is that the infective population grows more rapidly and reaches the peak earlier(around day 4 compared to day 40). In this case, **the epidemic starts from the second day and ends at the 62th day, lasting 60 days.**

Next, let's also increase the recovery rate γ by 10-fold to 0.5, results are:
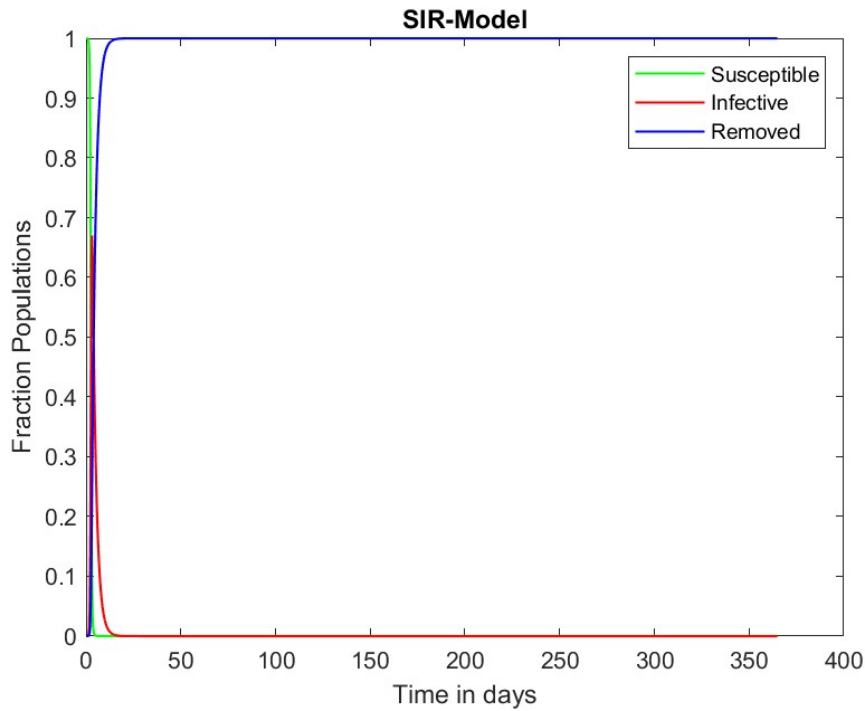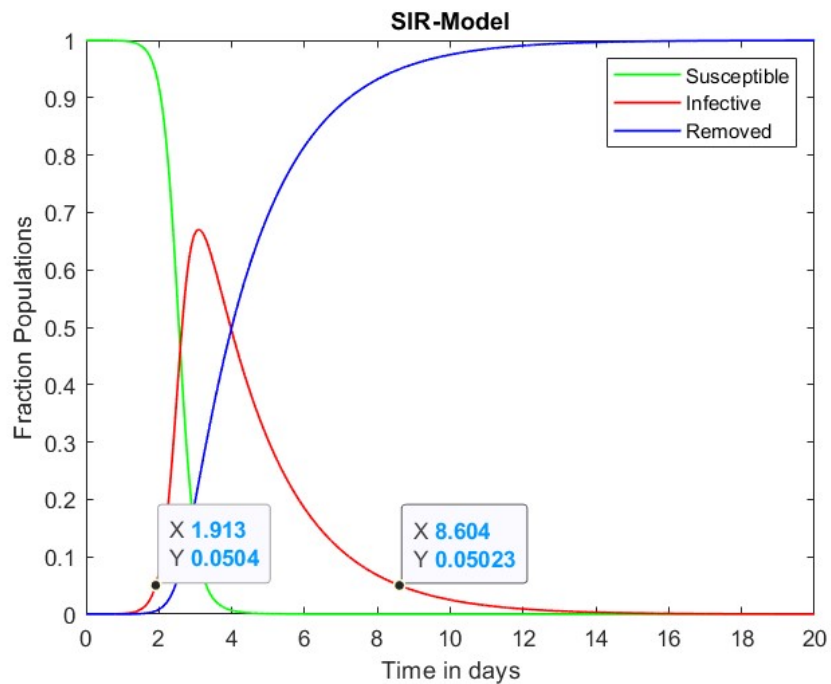

Figure 5: Increasing gamma also by 10-fold

Figure 6: Zoom in Fig 5 to observe

Again, the overall dynamics behaves similarly to that of previous results, an increase followed by a decrease, and this time, the increase is even more rapidly than that of Fig. 3, and the decrease happens even much earlier. In this case, **the epidemic starts from the second day and ends at the 9th day, lasting 7 days.**

This change in behavior can be **interpreted biologically**. When we only increase the infection rate, people get infected more quickly; however, if the recovery rate is still the same, the epidemic will not end much earlier. On the other hand, if we increase both the infection and recovery rate, not only people get infected more quickly but also recover more quickly; therefore, the epidemic will end sooner.

Next, let's decrease β by a factor of 10 (with respect to the original values) keeping γ unchanged, results are:
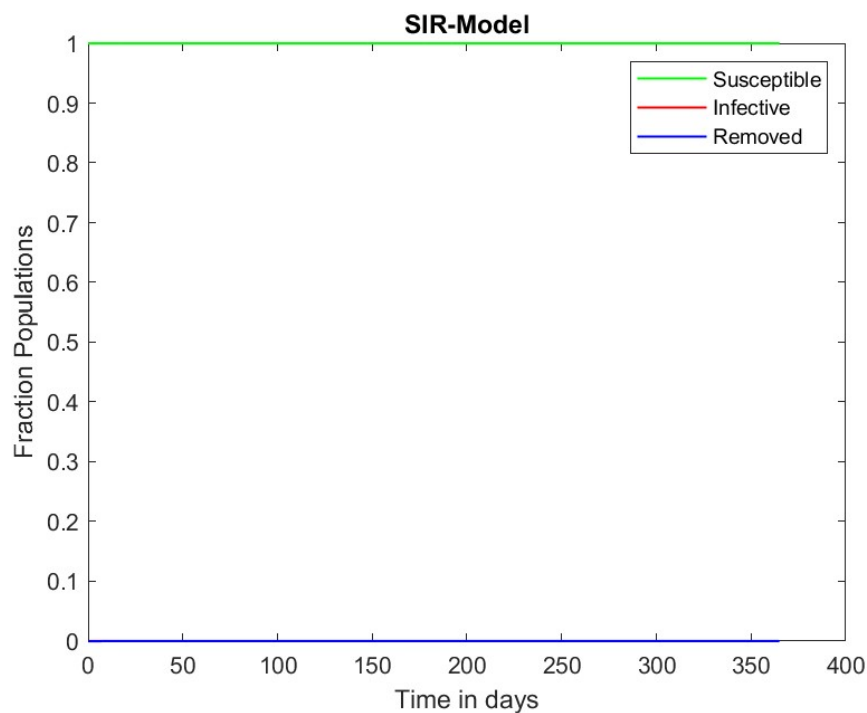

Figure 7: Decrease beta by 1/10

Notice that the infective is invisible in this scale, so we want to change the y-scale to observe the behaviour of I and R.
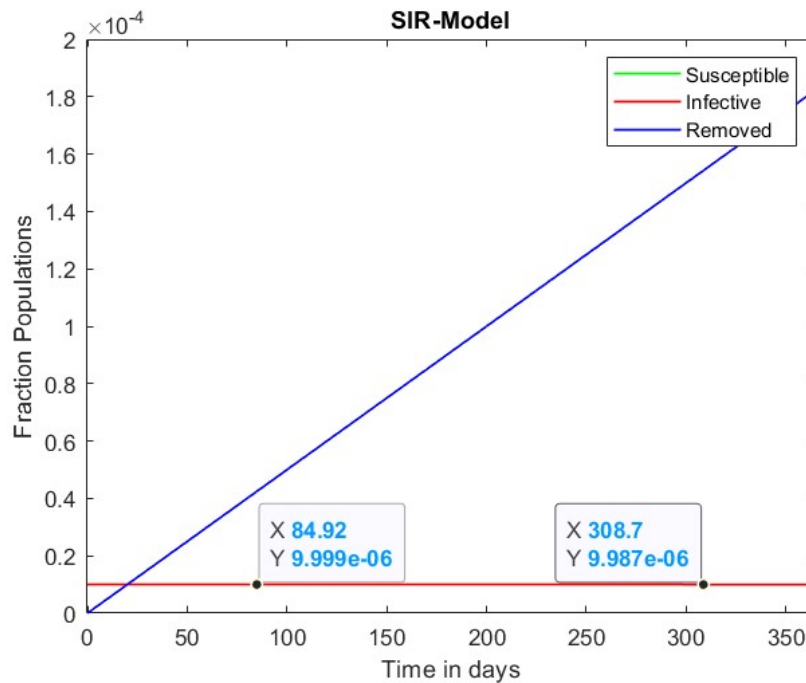
Figure 8: Change Fig.7 scale

As we can see in Figure 8, the **infective population is declining** very slowly, and **this is different from previous results** where infective population is increasing.

By a simple MATLAB command, we can see that, at the end of a year, around 192 individuals have been infected, around 10 individuals are infected, and around 182 individuals have recovered.

```
N-S(end)*N
```
```
ans = 192.3637
```
```
I(end)*N
```
```
ans = 9.9815
```
```
R(end)*N
```
```
ans = 182.3821
```

Next increase γ by a factor of 10 (returning β to the original value), results are:
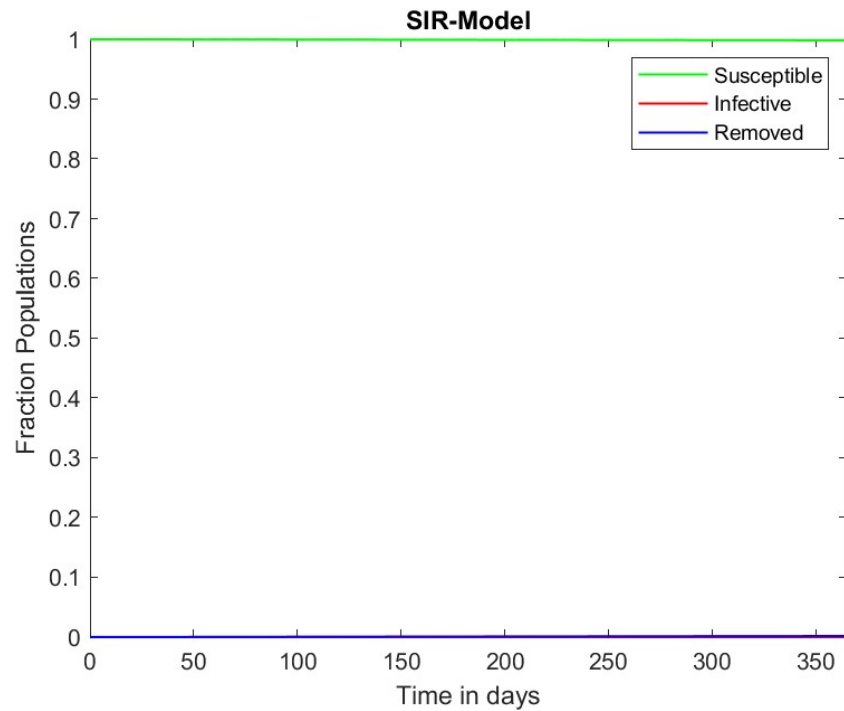

Figure 9: Increase gamma by 10-fold

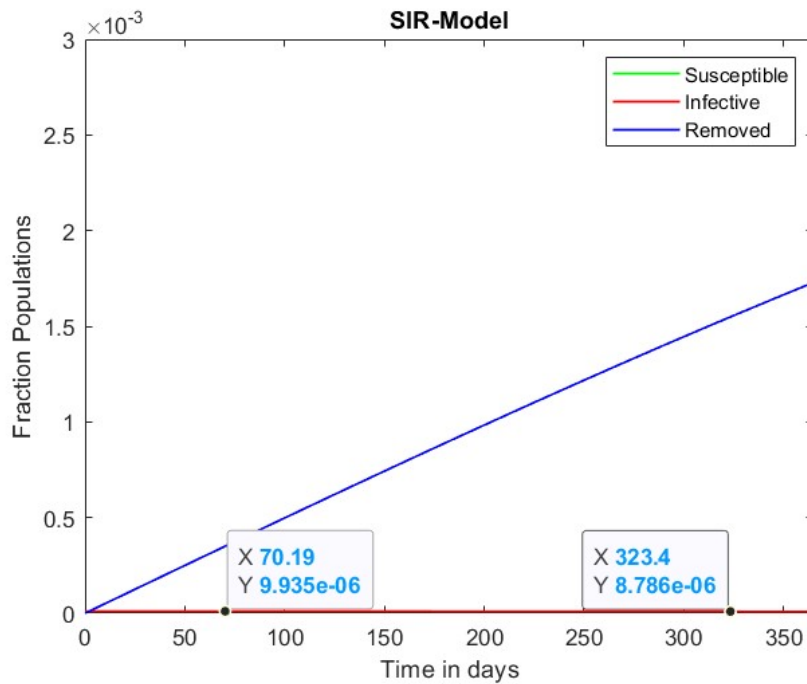Again, we want to re-scale the y-axis to observe.

Figure 10: Change Fig.9 scale

The system behaves similarly as that of Fig.7, the infective population is decreasing slowly. This time, at the end of a year, around 1737 individuals have been

infected, around 8 to 9(8.49) individuals are infected, and around 1729 individuals have recovered.

From above results, an increase in the infection rate will result in faster growth(sharper curve) in infective population, and more people will be infected at the same time. An increase in the recovery rate γ will shorten the duration of epidemic, and when $\gamma > \beta N\hat{S}$, the infective population will not grow, but steadily decrease. An decrease in the infection rate β can also flatten the curve, and when $\beta < \dfrac{N\hat{S}}{\gamma}$, the infective population will steadily decrease. Therefore, in simple public health, **to prevent the spread of disease, we need to both increase the recovery rate and decrease the infection rate.** Increasing the recovery rate can reduce the number of current infective individuals so that they can no longer pass the disease to someone else. Decreasing the infection rate will lower the likelihood of an infective individual spreading the disease. With increased recovery rate and decreased infection rate, the maximum number of infected patients at the same time(lower peak) will be smaller, so that we can avoid the shortage of healthcare workers and PPEs during the pandemic, and also less total infected individuals over the long run.

(b) Understanding the Effects of Quarantine and Vaccination

One mechanism of reducing the spread of an epidemic is to quarantine infected individuals. This involves identifying those who are infected, and removing them from the general public until they have recovered.

We can alter the SIR model in (a) to add this feature by introducing new parameters. In the following implementation, we will use the original recovery and infection rate, that is γ to be 5% , the infection rate β to be 5×10^{-7}. Also, we need to consider the total deaths with a mortality rate of 5%. Notice that this mortality rate is not time-based; it is infection-based. To include that, we create a new death compartment that absorbs 5% of the removed(R) population. In other words, instead of thinking of recovery rate 5%, we treat it as "removal" rate to include both recovery and death, and with a mortality rate of 5%, we move 5% of the removed population to death compartment, and 95% still remains as recovered.

I. With Quarantine

We will introduce a new parameter q per individual per day, the percentage of infective individuals under quarantine, to indicate the effectiveness of the quarantine response. Quarantined infective individuals will no longer play a role in the progression of the epidemic, thus will be moved to the removed(R) population.

$$\frac{d\hat{S}}{dt} = -\beta N \hat{I} \hat{S}$$
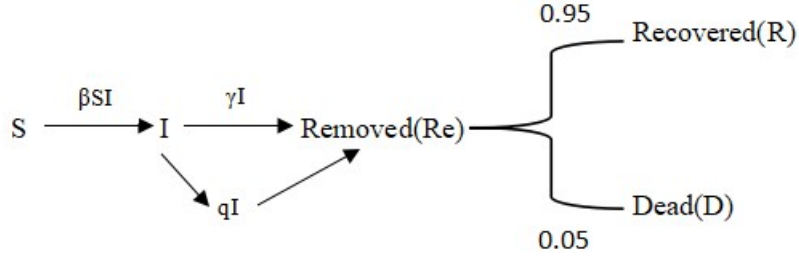
$$\frac{d\hat{I}}{dt} = (\beta N \hat{S} - \gamma - q)\hat{I}$$

$$\frac{d\,\hat{Re}}{dt} = \gamma\hat{I} + q\hat{I} = (\gamma + q)\hat{I}$$

$$\hat{R} = 0.95\hat{Re}$$

$$\hat{D} = 0.95\hat{Re}$$

Let's implement this model in MATLAB(Appendix B). Without quarantine, the result is:
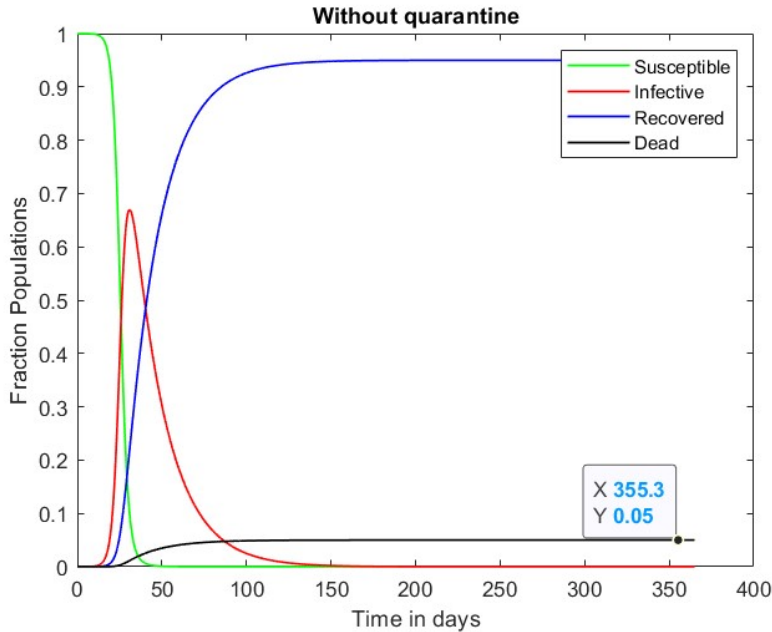

Figure 11: Without Quarantine

In above result, we have the same result as in part (a) Fig.1 since we set the quarantine rate to be 0(without quarantine). We can observe that no one has avoided the epidemic, and 5% of the population died.

Next, let's implement this with different quarantine rate q = 0.1, 0.3, and 0.45:
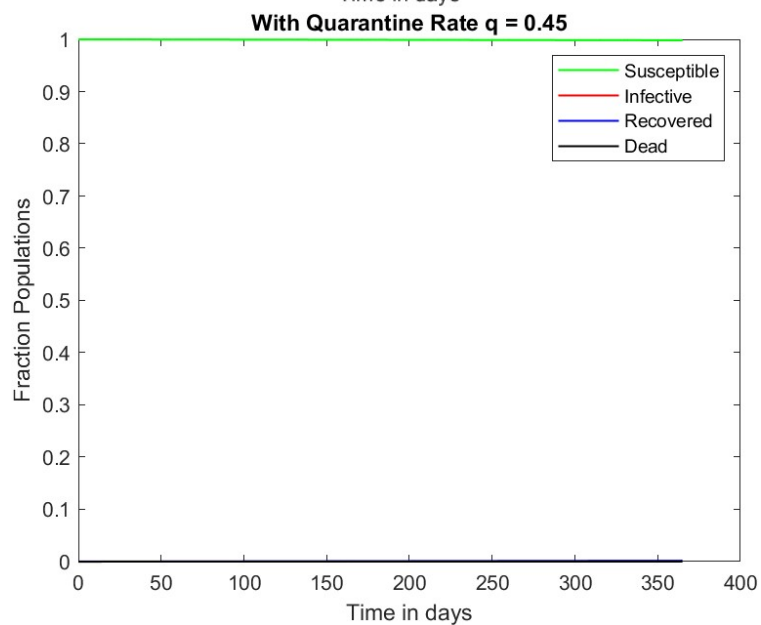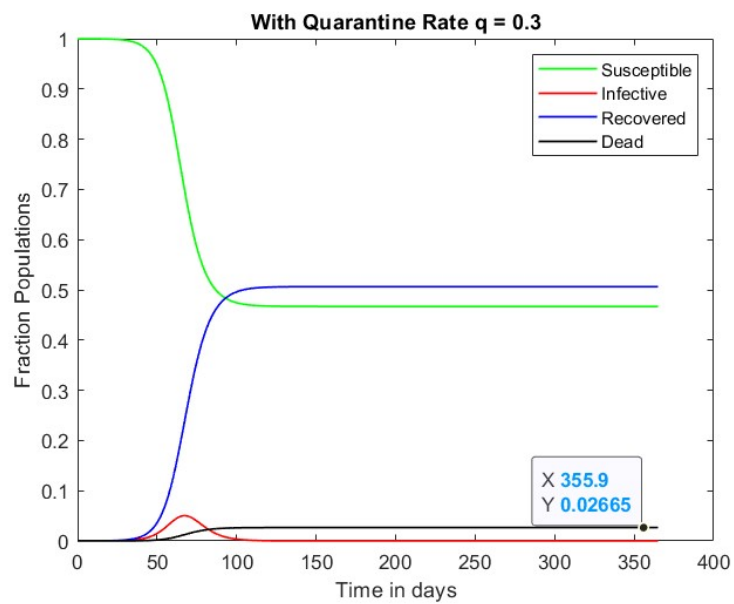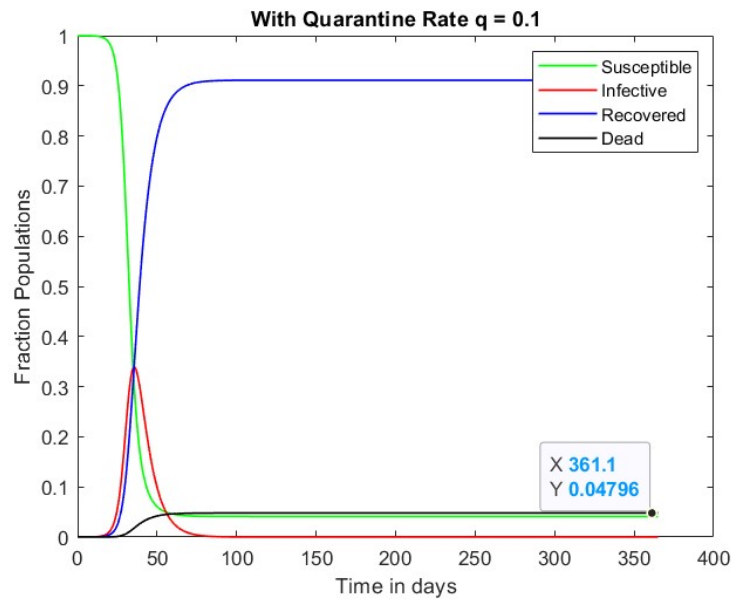
Figure 12-14: With Different Quarantine Rate

There is clearly a difference in the way an epidemic develop with quarantining. We can see that once we introduced quarantine to this model, the total infections decreased and the peak in infective population was lowered. As we increase the quarantine rate q, total infection decreases more, and the peak lowers more. And when q reaches the threshold 0.45(which is the null-cline for I), the infective population will not grow anymore.

Since we have a fixed constant mortality rate, total deaths will be linear with total infections as total deaths = mortality rate * total infections.
The total infections can be calculated by:

First, from above differential equations, we have:
$\hat{R}e$ denotes fractional removed population, including both recovered and dead).

$$\frac{d\hat{S}}{d\hat{R}e} = \frac{-\beta N \hat{I} \hat{S}}{(\gamma+q)\hat{I}} = \frac{-\beta N \hat{S}}{\gamma+q}$$

This is simply a linear function of S, which we know have exponential solution:

$$\hat{S}(\hat{R}e) = \hat{S}_0 e^{\beta N \hat{R}e/(\gamma+q)}$$

Let X represent the fractional total infections, we know that at the end of the epidemic, R = X and S = 1 - X since I = 0. Therefore, we have:

$$1 - X = \hat{S}_0 e^{\beta N X /(\gamma+q)}$$

Manipulate algebraically, we have the expression for q:

$$q = \frac{-XN\beta}{\ln(1-X)} - \gamma$$

Since the total infections and total deaths are linear, to reduce total deaths to a fraction, we just reduce total infections to the same fraction.

To reduce total deaths by 50%, q should be:

```
X = 0.5;
q = (-b*N*X)/(log(1-X)) - g

q =
0.310673760222241
```

This means that the quarantine should be effective to a level where 31% of the current infective population should be quarantined everyday to reduce the total deaths by 50%.

Implement this quarantine rate q = 0.310673760222241, to check if the above formula of calculating q with known death reduce rate is correct:
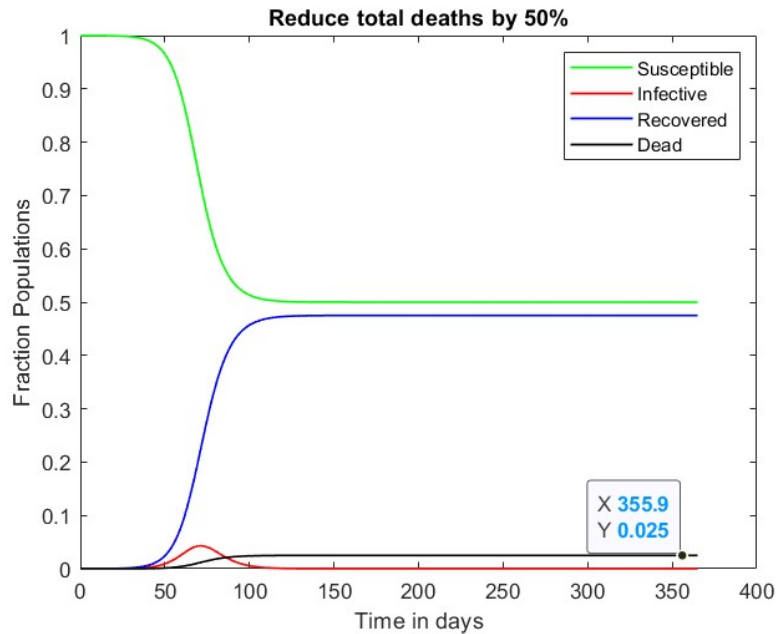
Figure 15: Reduce death by 50% with quarantine

In above plot, we can see that with such quarantine rate, the totals death indeed reduce by 50%, from 5% of the total population to 2.5%.

By similar code, to reduce total deaths by 90%, q = 0.4246(rounded), and to reduce total deaths by 99%, q = 4475. **This solution is totally feasible**. Sending 44% of all current infective population to quarantine is physically possible. However, this might be somewhat difficult if the disease can spread by persons who are asymptomatic(just like COVID-19), since it will be hard to test and identify asymptomatic infective individuals first.

II. **With Vaccination**

Another approach to control the spread of epidemics is to vaccinate. We consider an initial vaccinated population R0, and without loss of generality, we assume the vaccine works, and thus all of them are immune to the disease.
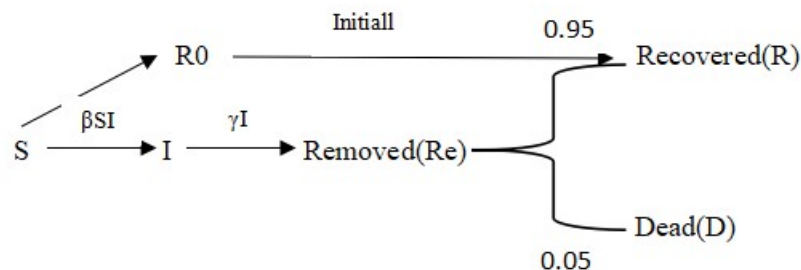
$$\frac{d\hat{S}}{dt} = -\beta N \hat{I} \hat{S}$$

$$\frac{d\hat{I}}{dt} = (\beta N \hat{S} - \gamma)\hat{I}$$

$$\frac{d\hat{R}e}{dt} = \gamma \hat{I}$$

$$\hat{R} = 0.95\hat{R}e$$

$$\hat{D} = 0.95\hat{R}e$$

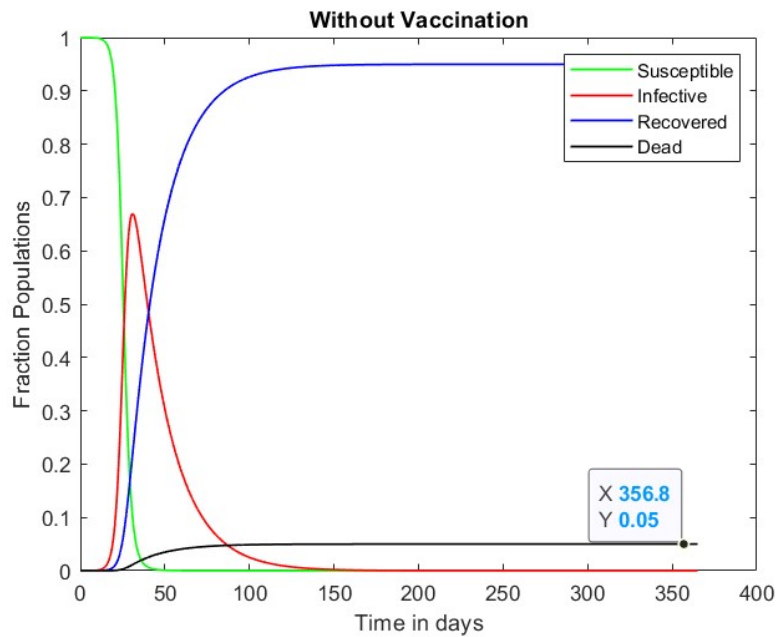Now, use MATLAB(Appendix C) to implement this model without vaccination:

Figure 16: Without Vaccination

Again we have the same result as in part(a) since the original vaccinated population R0 = 0, 5% of the population will die at the end.
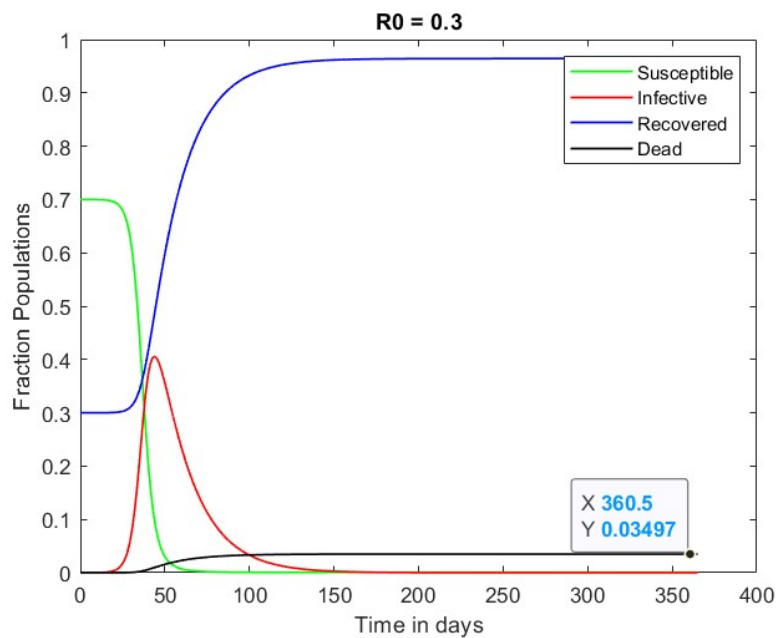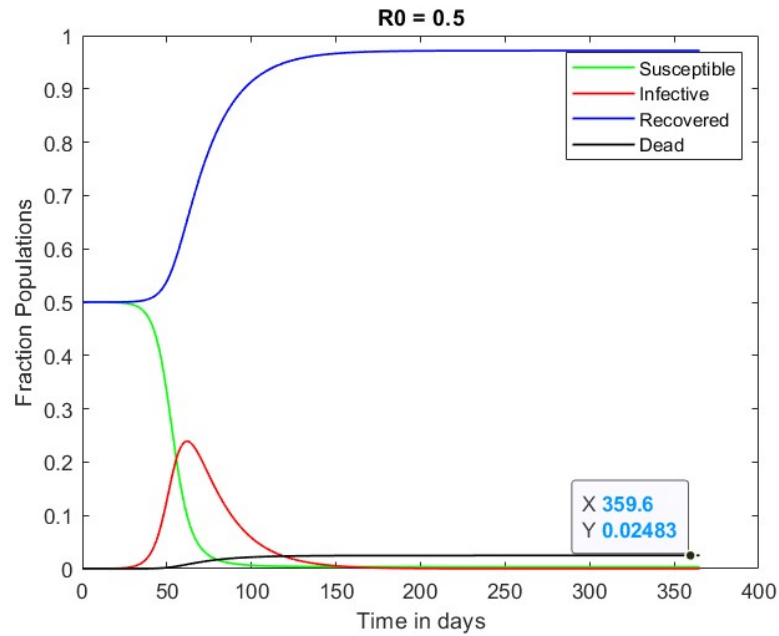Now, try different values of R0, results:

Figure 17: R0 = 0.3

Figure 17: R0 = 0.5
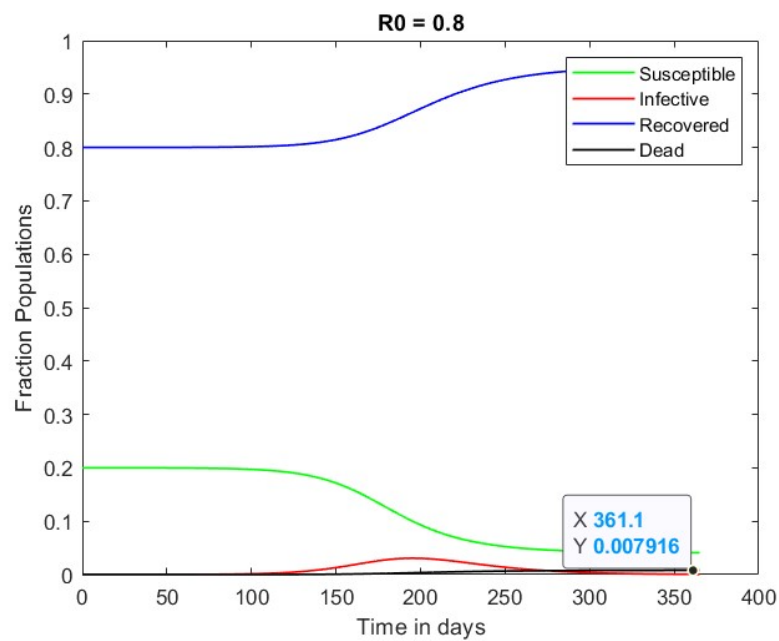
Figure 17: R0 = 0.8

From above results, we can see that the infective population has decreased as we introduced initial vaccinated population. Also, the infection peak has lower as we increase R0. When R0 = 0.5, the total deaths reduced by 50% from 5% to around 2.5%, and after some trials with different R0 values in MATLAB, we get that when R0 = 0.835, the total deaths will be reduced by around 90% and when R0 = 0.867, the total

This **solution may and may not be feasible** depends on the disease. For

example, we vaccinate people before flu arrives, and the flu shot was based on the flu virus strain from the other hemisphere(the Southern Hemisphere). However, this vaccinate is not guaranteed to work. We may be able to vaccinate everyone, but the vaccinate just does not work as expected, so we end up with so many individuals who are vaccinated, but are not immune to the disease, and hence the adjusted vaccinated fractional population will not reach 0.862, or even 0.5. Also, many cases, we don't even have a vaccine before the epidemic starts, for example, we are not going to have COVID-19 vaccine available for the public until early 2021.

Appendix A: Modeling an Epidemic

```matlab
S = zeros(365000,1);
I = zeros(365000,1);
R = zeros(365000,1);
N = 1e6;
S(1) = 999990/N; % fractional population
I(1) = 10/N;
R(1) = 0;
b = 5e-7;
g = 0.05;
delt = 0.001; % time step
t = 0:delt:365;
% apply forward euler
for n = 1:365000
    dSdt = -b*N*I(n)*S(n);
    dIdt = (b*N*S(n)-g)*I(n);
    dRdt = g*I(n);
    S(n + 1) = S(n) + dSdt * delt;
    I(n + 1) = I(n) + dIdt * delt;
    R(n + 1) = R(n) + dRdt * delt;
end
plot(t,S,'g','LineWidth',1.0);
hold on
plot(t,I,'r','LineWidth',1.0);
plot(t,R,'b','LineWidth',1.0);
ylabel('Fraction Populations');
```

```matlab
xlabel('Time in days');
title('SIR-Model');
legend('Susceptible','Infective','Removed');
hold off
% plot S vs I
plot(S,I, 'k','LineWidth',1.5);
ylabel('Fractional Infective(I)');
xlabel('Fractional Susceptible(S)');
title('S vs. I');
axis([0 1 0 1]);
hold on;
plot([g/(b*N) g/(b*N)],[0 1], 'b') % gamma over beta*N
plot([0 1],[0 0], 'r') % x axis
plot([0 0],[0 1], 'g') % y axis
legend('S vs I','null-cline1','null-cline2','null-cline3');
hold off;
```

Appendix B: With Quarantine

```matlab
S = zeros(365000,1);
I = zeros(365000,1);
R = zeros(365000,1);
D = zeros(365000,1);
N = 1e6;
S(1) = 999990/N; % fractional population
I(1) = 10/N;
R(1) = 0;
D(1) = 0;
b = 5e-7;
g = 0.05;
m = 0.05;
q= 0.310673760222241
```

```
q = 0.3107
```

```matlab
delt = 0.001; % time step
t = 0:delt:365;
% apply forward euler
for n = 1:365000
    dSdt = -b*N*I(n)*S(n);
    dIdt = (b*N*S(n)-g-q)*I(n);
    dRdt = (g+q)*I(n);
    S(n + 1) = S(n) + dSdt * delt;
    I(n + 1) = I(n) + dIdt * delt;
    R(n + 1) = R(n) + dRdt * delt * (1-m);
    D(n + 1) = m*R(n+1)/(1-m);
end
plot(t,S,'g','LineWidth',1.0);
hold on
plot(t,I,'r','LineWidth',1.0);
plot(t,R,'b','LineWidth',1.0);
plot(t,D,'k','LineWidth',1.0);
```

```matlab
ylabel('Fraction Populations');
xlabel('Time in days');
title('With Quarantine Rate q = 0.45');
legend('Susceptible','Infective','Recovered', 'Dead' );
hold off
```

Appendix C: With Vaccination

```matlab
S = zeros(365000,1);
I = zeros(365000,1);
R = zeros(365000,1);
D = zeros(365000,1);
N = 1e6;
% fractional population
R0 = 0.867;
I(1) = 10/N;
R(1) = R0;
D(1) = 0;
S(1) = 1-R(1)-I(1);
b = 5e-7;
g = 0.05;
m = 0.05;
delt = 0.001; % time step
t = 0:delt:365;
% apply forward euler
for n = 1:365000
    dSdt = -b*N*I(n)*S(n);
    dIdt = (b*N*S(n)-g)*I(n);
    dRdt = (g)*I(n);
    S(n + 1) = S(n) + dSdt * delt;
    I(n + 1) = I(n) + dIdt * delt;
    R(n + 1) = R(n) + dRdt * delt * (1-m);
    D(n + 1) = m*(R(n+1)-R0)/(1-m);
end
plot(t,S,'g','LineWidth',1.0);
hold on
plot(t,I,'r','LineWidth',1.0);
plot(t,R,'b','LineWidth',1.0);
plot(t,D,'k','LineWidth',1.0);
ylabel('Fraction Populations');
xlabel('Time in days');
title('R0 = 0.8');
legend('Susceptible','Infective','Recovered', 'Dead' );
hold off
```