Patryk Kwoczak

(a)

Original parameters: $\beta = 0.05, \gamma = 5 * 10^{-7}, N_{total} = 1{,}000{,}000.$

Following the S-I-R model, we will use the rules of change with the following differential equations (in particular, the fractional variation represented by the hat):

$$\frac{d\hat{S}}{dt} = -\beta N_{total} \hat{I}\hat{S}$$

$$\frac{d\hat{I}}{dt} = \beta * N_{total} * \hat{I}\hat{S} - \gamma * \hat{I}$$

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

To preserve the units of $\frac{dS}{dt}$ as individual/day, we get that

$$\text{unit}(\beta \text{IS}) = \frac{\text{ind}}{\text{day}}$$

$$\text{unit}(\beta) * \text{ind}^2 = \frac{\text{ind}}{\text{day}}$$

$$\text{unit}(\beta) = \frac{1}{\text{ind} * \text{day}}$$

In other words, the units of beta are per individual per day.

The number seems reasonable, as it states that there is a (1/20) proportionality coefficient for individuals going from susceptible to infected, relative to the populations of the two groups. If there was a 5% mortality rate, then 5% of the total which were infected would not have survived, in this case, since the final percent of recovered was 100%, then the number of individuals recovered was 1,00,000, and the number who would not have survived would be $0.05 * 1{,}000{,}000 = 50{,}000$. Every number an individual, with a life that was cut short, and a family that would grieve. Below in figure 1, one can see the evolution of the (fractional) Infected population and the Susceptible with time, as well as the dynamics in Susceptible-Infected space (including the two fixed points of the system, at (1,0) and $(\frac{\gamma}{\beta N}, 1 - \frac{\gamma}{\beta N})$). As can be seen, the epidemic begins around the 20th day and ends around the 80th. If β were to be scaled up by a factor of ten, then as we can see in figure 2, the epidemic begins and ends

significantly earlier, starting at about the second day until 70th , at about 2 days, there is nobody left susceptible. Furthermore, when gamma is scaled up by the same factor of ten, then the dynamics are displayed in figure 3; we can see that the dynamics are proportional to those in figure 1, except hastened. Thus the data represents the same biologically: case B shows the virus spreads to everyone because of the pure increase in growth, while in C it gets neutralized by the equal increase to gamma.

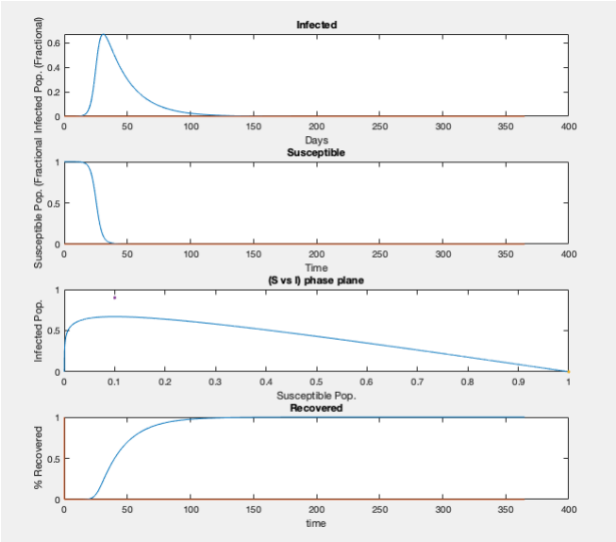

Figure 1 (A)

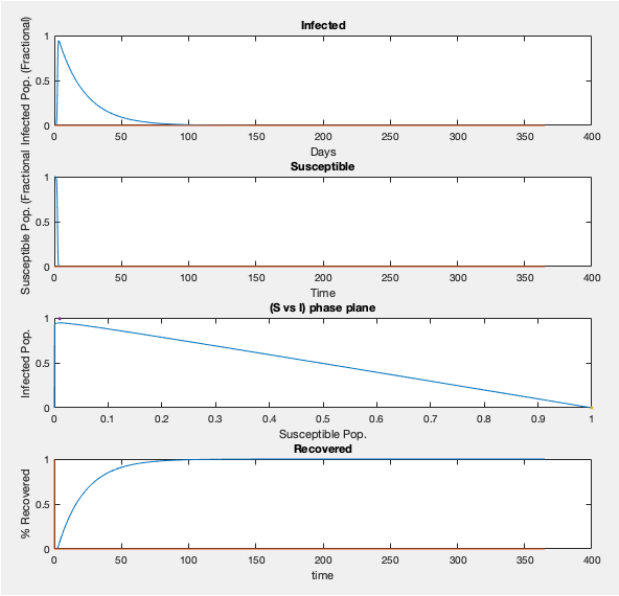

Figure 2 (B)

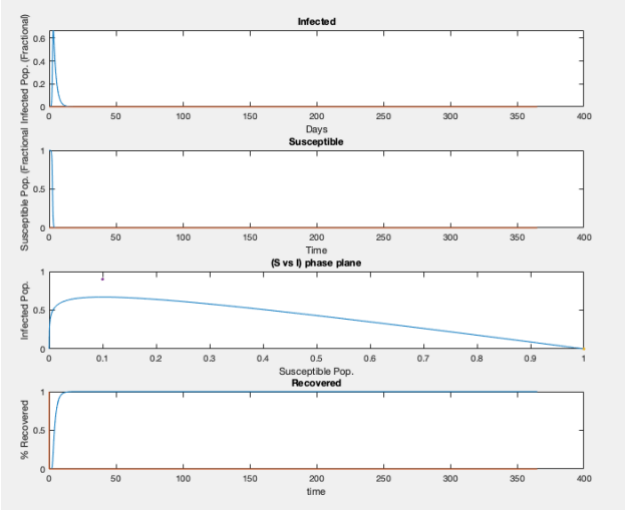

Figure 3. (C)

One can see in figure 4, case D, that when beta is lowered w.r.t. the original value, keeping gamma as was, then the infection rate decreases more than it increases, resulting in fewer individuals being infected with time, and in fact at the end of the year, there are 10 people recovered and zero infected, meaning the original ten who got sick recovered. In the final case, E, we can see that raising the recovery rate by the same magnitude, while keeping the original rate of birth, will lead to the infectious population decreasing, and those people recovering slowly.

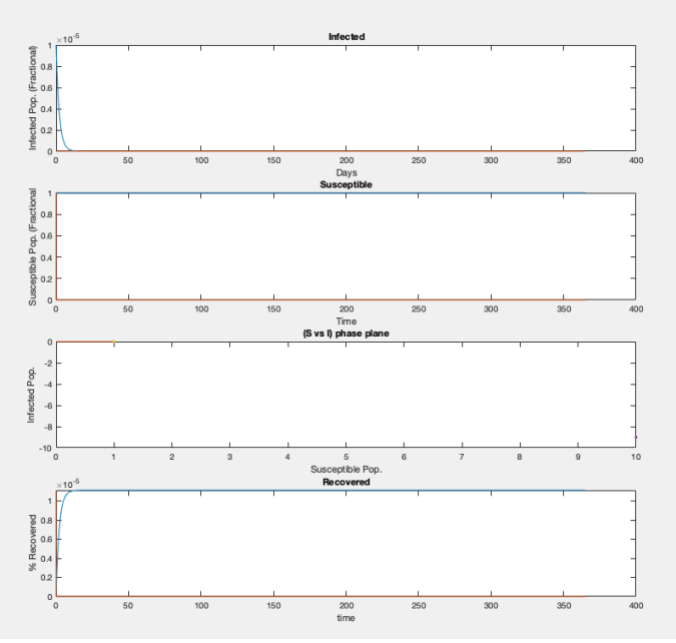

Figure 4 (D)

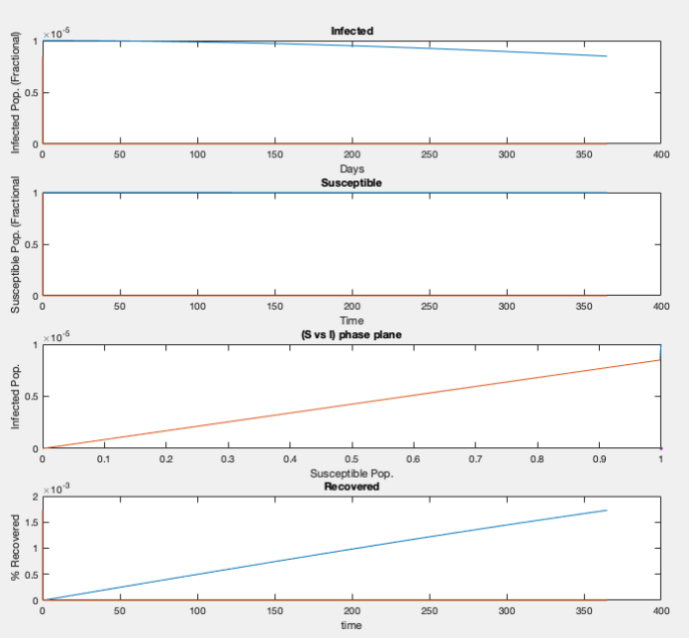

Figure 5 (E)

Hence both the measure of decreasing the rate of transmissibility and finding a way to increase the rate of recovery will lead to fewer cases and having the events happen over a longer period of time (which would allow hospitals to not be overwhelmed), this can be achieved through vaccinating against virus, as well as taking preventative measures of safety, like keeping distance and wearing a mask.

(B)

One can see in figure 6 below the effect of quarantine, even when the rate of going into quarantine isn't particularly high, in fact, to decrease the number of people who die as a result of the virus in half, all we need is a quarantine constant $\delta = 0.311$, where we use a new S-I-(Q)-R model following the following system of differential equations, Q being a new category of individuals who are infected and go into quarantine (of course, implemented using the fractional variation):

$$\frac{dS}{dt} = -\beta SI$$

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

$$\frac{dQ}{dt} = \delta I - \gamma Q$$

$$\frac{dR}{dt} = \gamma I + \gamma Q$$

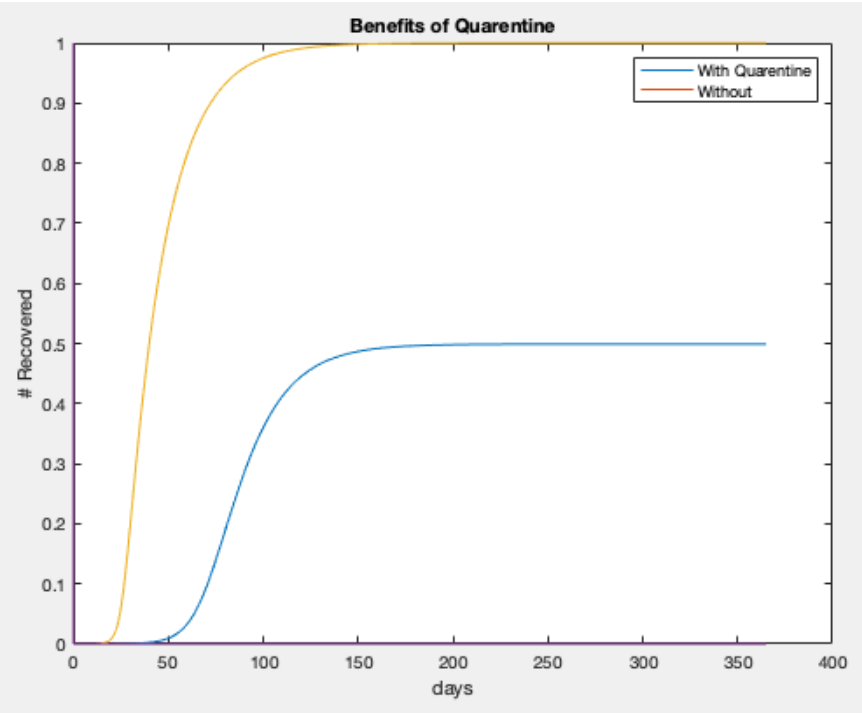

Figure 6.

The other constants are the originally discussed values. We can see that the number of individuals recovered has converged onto ½, while the number without quarantine had grown to include 100% of the given population. Hence, if given the same rate of mortality for two populations, then the population following such a quarantine would have the level of deaths halved. This is simply because even though those already infected, including those in quarantine, will still have the same chance of death, they won't additionally be exposing others to this chance. All that's needed to reduce deaths by 90% is a quarantine rate of 0.423, the outcome in figure 7. To reduce by 99%, only .441 (Figure 8).; these are absolutely all very realistic and practical values.

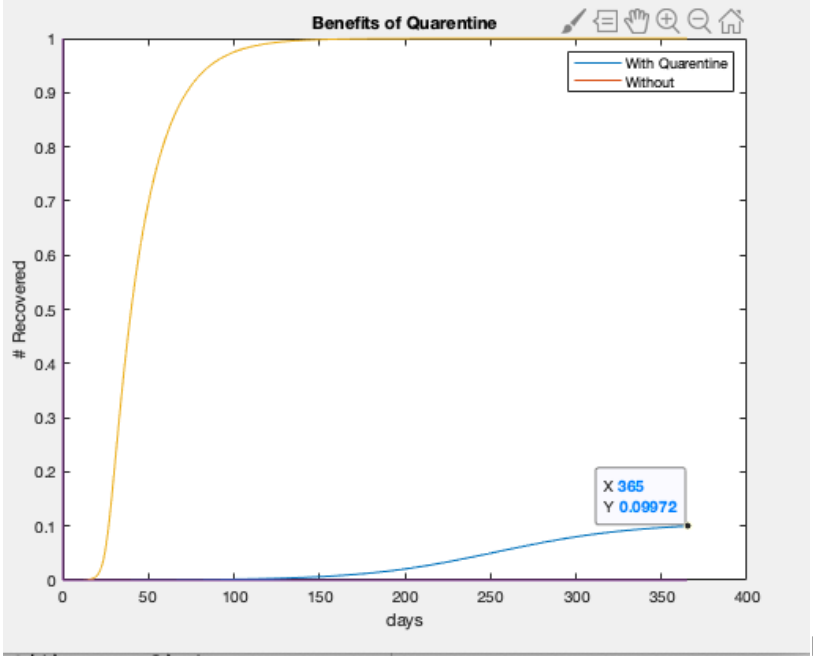

Figure 7.

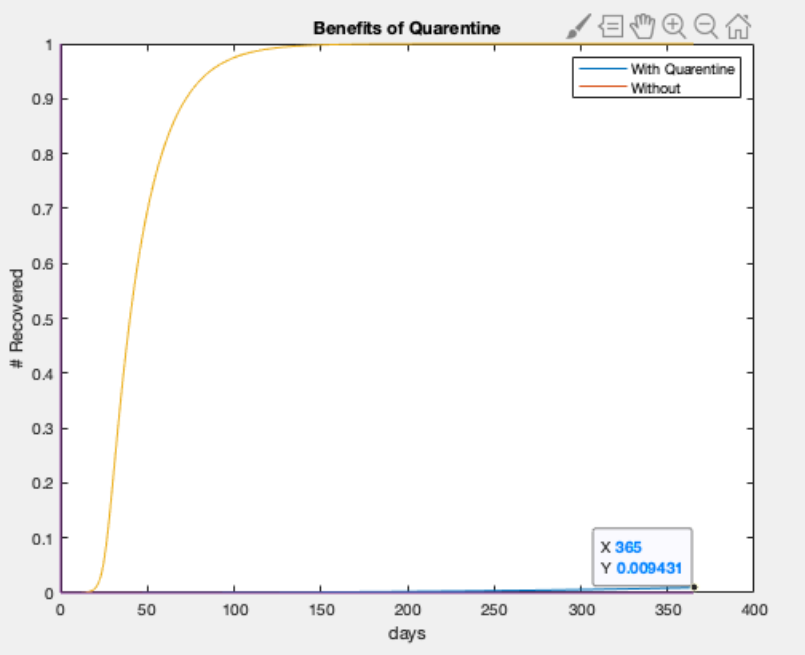

Figure 8.

(C):

The SIS model is the most simple form of infectious model, such as a population of susceptible individuals who become infected, and heal, but are once more susceptible to the infection again. An example would be to the common cold. The SIR model is another simple one: infected

individuals go on to recover and are safe from getting the infection once more, such as in cases of chicken-pox. SEIR takes this model one step further, taking into account exposed individuals and secluding them from the rest of the population: this can happen for numerous reasons, one such being an example of the Covid-19 pandemic: we remove exposed individuals from the population to remove the risk of them infecting others, thus trying to limit spread through containment.

Given the difference equations for an SIS model, as we had seen in class,

$$S_{i+1} = S_i - \alpha\xi S_i \frac{I_i}{N} + \gamma I$$

$$I_{i+1} = I_i + \alpha\xi \frac{I_i}{N} - \gamma I$$

We can see how to go from one form of the equations (Difference and Differential) to the other, as when we implement Euler's method, we are discretizing the differential equation into an equation of differences; in particular, the difference between the current value and the jump to the next value. Analytically, this means that $N_{i+1} = N_i + \int_{t_i}^{t_{i+1}} \left(\frac{dN}{dt}\right) dt$, which, as stated above, can be converted into a map if we can substitute in known parameters into the integrand. As $\frac{dS}{dt} = -\frac{dI}{dt} = -\beta IS + \gamma I$, then applying Euler's method to the incremental integrand (for finite but small dt), we can get new parameters that absorb the step-size and therefore produce the desired difference equations as above. In the same way that we integrated the differential equation to get a difference equation, we can produce a finite-difference discretized differentiation process to obtain a differential equation out of the difference, through the fact that integration and differentiation are inverse operations.

Code:

```
close all; clear; clc %take out the trash
format short;

%constants
```

```
gamma = 0.05;
beta = 5*10^(-7);

N_total = 1000000; %total population 1 million
I_0 = 10; %initial infected pop. is 10
S_0 = N_total - I_0; %total susceptible is total - infected

maxT = 365; %total time is 365 days
dT = 0.001; %time increment is (0.001) of a day
t=0:dT:maxT;%1 year with 0.001 per day step-size
numIter=size(t,2);

%convert to fractional populations
Ifr_0 = I_0 / N_total;
Sfr_0 = S_0 / N_total;

Ifr = zeros(size(t,2),2);
Sfr = zeros(size(t,2),2);
Rfr = zeros(size(t,2),2);
Ifr(1) = Ifr_0;
Sfr(1) = Sfr_0;
Rfr(1) = 0;


for i=1:numIter
 Ifr(i+1) = Ifr(i) + dIdt(beta,gamma,Ifr(i), Sfr(i),N_total)*dT;
 Sfr(i+1) = Sfr(i) + dSdt(beta,Ifr(i), Sfr(i),N_total)*dT;
 Rfr(i+1) = Rfr(i) + dRdt(gamma,Ifr(i))*dT;
end
fixed1S = 1;
fixed1I = 0;

fixed2S = gamma / (beta*N_total);
fixed2I = 1 - fixed2S;



% subplot(4,1,1); %display all four plots adjacent (if instead
% %                 %they were overlapped then the one with greatest
%                 %magnitude would have overwhelmed the rest)
% plot(t,Ifr,'-');
% xlabel('Days');
% ylabel('Infected Pop. (Fractional)');
% title('Infected')
%
% subplot(4,1,2);
% plot(t,Sfr,'-');
% xlabel('Time');
% ylabel('Susceptible Pop. (Fractional');
% title('Susceptible')
%
```

```
% subplot(4,1,3);
% plot(Sfr,Ifr,'-');
% hold on
% plot(fixed1S, fixed1I,'.')
% plot(fixed2S, fixed2I,'.')
% hold off
% xlabel('Susceptible Pop.');
% ylabel('Infected Pop.');
% title('(S vs I) phase plane')
%
% subplot(4,1,4);
% plot(t,Rfr);
% xlabel('time')
% ylabel('% Recovered')
% title('Recovered')
% %
% disp(Ifr(numIter)*1000000)
%remember to multiply by N_total so that we don't accidentally get 1/N^2 when
%multiplying two fractional populations.

%redo with added quarentine measure delta
%gamma = .05;
%beta = 5*10^(-7);
delta = 0.441;
Ifr2 = zeros(size(t,2),2);
Sfr2 = zeros(size(t,2),2);
Rfr2 = zeros(size(t,2),2);
Qfr2 = zeros(size(t,2),2);
Ifr2(1) = Ifr_0;
Sfr2(1) = Sfr_0;
Rfr2(1) = 0;
Qfr2(1) = 0;



for i=1:numIter
 Ifr2(i+1) = Ifr2(i) + dIdt2(beta,gamma,delta,Ifr2(i), Sfr2(i),N_total)*dT;
 Sfr2(i+1) = Sfr2(i) + dSdt(beta,Ifr2(i), Sfr2(i),N_total)*dT;
 Qfr2(i+1) = Qfr2(i) + dQdt2(gamma,delta, Ifr2(i), Qfr2(i))*dT;
 Rfr2(i+1) = Rfr2(i) + dRdt2(gamma,Ifr2(i),Qfr2(i))*dT;

end

plot(t,Rfr2,'-');
hold on;
plot(t,Rfr,'-');
legend('With Quarentine','Without')
title("Benefits of Quarentine")
ylabel("# Recovered")
xlabel("days")
% plot(t,Qfr2,'-');
```

```
hold off;

function der = dSdt(beta, I_val, S_val,N_total)
    der = -1*beta*I_val*S_val*N_total;
end

function der = dIdt(beta,gamma, I_val, S_val,N_total)
    der = beta*I_val*S_val*N_total - gamma*I_val;
end


function der = dRdt(gamma, I_val)
    der = gamma*I_val;
end
% 2 meaning quarantine case
function der = dIdt2(beta,gamma,delta, I_val, S_val,N_total)
    der =  beta*I_val*S_val*N_total - gamma*I_val - delta*I_val;
end


function der = dQdt2(gamma, delta, I_val,Q_val)
    der = delta*I_val - gamma*Q_val;
end

function der = dRdt2(gamma, I_val, Q_val)
    der = gamma*I_val + gamma*Q_val;
end
```