Assignment 1 — Simple Epidemic Models (ODEs)

2019862s

Monday 29th February, 2016

Question 1. *Consider the modified SIR model:*

$$\frac{ds}{dT} = \mu n - \beta si - \mu s \tag{1}$$

$$\frac{di}{dT} = \beta si - \gamma i + \sigma \beta ir - \mu i \tag{2}$$

$$\frac{dr}{dT} = \gamma i - \sigma \beta ir - \mu r, \tag{3}$$

where β, γ, $\mu > 0$ *are constants and* $0 \leq \sigma \leq 1$.

Solution 1 (a). In general, the model assumes a well-mixed population, which can be divided into the following three major classes:

- Susceptibles $s(T)$ – the individuals, who can become infected;
- Infectives $i(T)$, – those, who are infected and can transmit the disease to others;
- Removed $r(T)$ – individuals, who are isolated, recovered, immune, or simply dead.

Consider Equation 1, which describes the rate of change of the susceptible class.

$$\frac{ds}{dT} = \underbrace{\mu n}_{\text{number of individuals born}} - \underbrace{\beta si}_{\substack{\text{susceptibles become infected due to} \\ \text{interaction with infectives at rate } \beta}} - \underbrace{\mu s}_{\text{susceptibles die out at rate } \mu},$$

where n is the total number of individuals; μ denotes both the birth and death rate, as they are equal in this model; β is the rate at which a proportion of the susceptibles move to the infectives class due to interaction between the two classes.
Now consider Equation 2, describing the rate of change of the infectives.

$$\frac{di}{dT} = \underbrace{\beta si}_{\substack{\text{the number of infectives} \\ \text{increases due to interaction} \\ \text{with susceptibles at rate } \beta}} - \underbrace{\gamma i}_{\substack{\text{infectives move to} \\ \text{recovered class at rate } \gamma}} + \underbrace{\sigma \beta ir}_{\substack{\text{a proportion } \sigma \text{ of} \\ \text{the recovered becomes} \\ \text{infected again due to} \\ \text{interaction with} \\ \text{the infectives at rate } \beta}} - \underbrace{\mu i}_{\substack{\text{death rate of} \\ \text{the infective class}}},$$

where $0 \leq \sigma \leq 1$ denotes proportion — that is, a proportion of the recovered become infected again at rate β; β is the rate at which the infectives increase due to interaction between the susceptibles and the infected; γ is the recovery rate — the rate at which infectives become recovered; and μ denotes, as in the previous equation, the death rate of this class.
Finally, consider Equation 3, which describes the rate of change of the removed class.

$$\frac{dr}{dT} = \underbrace{\gamma i}_{\substack{\text{recovered population} \\ \text{increases since some of the} \\ \text{infected recover}}} - \underbrace{\sigma\beta ir}_{\substack{\text{a proportion } \sigma \text{ of the recovered} \\ \text{become infected due to} \\ \text{interaction with the infectives}}} - \underbrace{\mu r}_{\substack{\text{death rate of the} \\ \text{recovered}}},$$

where γ, σ, β, and μ are as explained above, but the positive signs denote an increase in the recovered class for the respective terms; μ is simply the death rate of the recovered.
Now add Equations 1, 2, and 3 to obtain

$$\frac{ds}{dT} + \frac{di}{dT} + \frac{dr}{dT} = \mu n - \cancel{\beta si} - \mu s + \cancel{\beta si} - \cancel{\gamma i} + \cancel{\sigma\beta ir} - \mu i + \cancel{\gamma i} - \cancel{\sigma\beta ir} - \mu r$$

$$\therefore \frac{d}{dT}\Big(s(t) + i(t) + r(t)\Big) = \mu(n(t) - s(t) - i(t) - r(t)),$$

but s(t) + i(t) + r(t) = N(t), hence,

$$\frac{d}{dT}\Big(s(t) + i(t) + r(t)\Big) = \mu(N(t) - n(t)).$$

Now integrate and impose the initial condition $N(0) = n$ to obtain

$$\begin{aligned} \mu\left(n - n(0)\right) = 0 \quad \therefore \quad n(0) = n \implies \frac{d}{dT}\Big(s(t) + i(t) + r(t)\Big) = 0 \\ \therefore \quad s(t) + i(t) + r(t) = \text{constant} = n, \quad \forall T \geq 0. \end{aligned}$$

Therefore, as n is the total size of the population, we can consider only two independent variables, as the third can be represented as the remainder of the difference between the total and the two independent classes. That is, $r(t)$ can be expressed as $r(t) = n - s(t) - i(t)$, so it is sufficient to consider Equations 1 and 2, and later derive $r(t)$. Thus, the following system of 2 ODEs listed in Equations 4 will be analyzed further.

$$\begin{aligned} \frac{ds}{dT} &= \mu n - \beta si - \mu s, \\ \frac{di}{dT} &= \beta si - \gamma i + \sigma\beta i\big(n - (s + i)\big) - \mu i. \end{aligned} \tag{4}$$

□

Solution 1 (b). Consider the provided substitutions, namely,

$$\begin{aligned} s = Sn \implies ds = n dS, \\ i = In \implies di = n dI, \\ T = \frac{t}{(\mu + \gamma)} \implies \frac{1}{dT} = (\mu + \gamma)\frac{1}{dt}, \end{aligned}$$

where S, I, and t denote the scaled susceptibles, infectives, and time respectively. Using these, Equation 1 is non-dimensionalized as follows:

$$(\mu+\gamma)\cancel{n}\frac{dS}{dt} = \mu\cancel{n} - \beta SIn\cancel{^2} - \mu S\cancel{n},$$

$$\frac{dS}{dt} = \frac{\mu}{\mu+\gamma} - \frac{\beta n}{\mu+\gamma}SI - \frac{\mu}{\mu+\gamma}S,$$

$$\therefore \quad \boxed{\frac{dS}{dt} = e - R_0 SI - eS}, \tag{5}$$

where $R_0 = \dfrac{\beta n}{\mu+\gamma}$, $e = \dfrac{\mu}{\mu+\gamma}$. Similarly, Equation 2 becomes

$$(\mu+\gamma)\cancel{n}\frac{dI}{dt} = \beta SIn\cancel{^2} - \gamma\cancel{n}I + \sigma\beta I\cancel{n}\big(n - (Sn + In)\big) - \mu I\cancel{n},$$

$$\frac{dI}{dt} = \frac{\beta n}{(\mu+\gamma)}SI - \frac{\gamma}{\mu+\gamma}I + \sigma\frac{\beta n}{\mu+\gamma}I(1-S-I) - \frac{\mu}{\mu+\gamma},$$

$$\frac{dI}{dt} = \frac{\beta n}{\mu+\gamma}SI - \frac{\cancel{\mu+\gamma}}{\cancel{\mu+\gamma}}I + \sigma\frac{\beta n}{\mu+\gamma}I(1-S-I),$$

$$\therefore \quad \boxed{\frac{dI}{dt} = R_0 SI - I + \sigma R_0 I(1-S-I)}, \tag{6}$$

where $R_0 = \dfrac{\beta n}{\mu+\gamma}$. Note that R_0 is directly proportional to βn, which is the rate at which infectives are created as a proportion of the total population n, and $(\mu+\gamma)$ is the average lifetime of being infected. Thus, R_0 is the basic reproduction number of the infection, that is — the number of new infections from one infected individual in a fully susceptible population. □

Solution 1(c). The following function file contains the non-dimensionalized Equations (5) and (6).

Listing 1: Function file for the simple SIR Model.

```
%% Lab 1 ID: 2019862s
%% Question 1c

function dy = sirModel(t, y)

% This function file contains the non-dimensionalized
% equations for the Simple SIR Model, Eqn. (5) and (6),
% with parameter values e=0.0012, R_{0}=3.5, \sigma=0.25.

% Define the parameter values
ro=3.5;
e = 0.0012;
sigma = 0.25;
dy=zeros(2, 1);
% Set up labels for the variables
S=y(1);
I=y(2);
% Define the equations for the ODEs
dy(1) = e - ro*S*I - e*S;
dy(2) = ro*S*I - I + sigma*ro*I*(1-S-I);
end
```

The following script file calls the `ode45` solver and accesses the equation file `sirModel.m`.

Listing 2: Main script used to run the `sirModel` function.

```
%% Lab 1 ID: 2019862s
%% Question 1c
% ODE45 is used to solve the system of ODEs
% in sirModel.m with initial conditions S(0)=0.99, I(0)=0.01,
% and parameters e = 0.0012, Ro = 3.5, sigma = 0.25.
% The plot produced shows the number of susceptibles, S(t),
% and the number of infected, I(t).

figure
[T, Y] = ode45(@sirModel,  [0:0.01:50], [0.99, 0.01]);
disp([T,Y]);
plot(T,Y(:,1),'k')
hold on
plot(T,Y(:,2),'k--')
xlabel('Time')
ylabel('Population dynamics')
legend('S(t), susceptibles', 'I(t), infected')
```

Figure 1 below shows the resulting plot from running `sirModel.m`. The dashed curve represents the population dynamics of the class of infectives and the non-dashed — the dynamics of the susceptibles. The parameters are $e = 0.0012$, $R_0 = 3.5$, $\sigma = 0.25$. The initial conditions are $I(0) = 0.01$, $S(0) = 0.99$ and the plot is generated for $0 \leq t \leq 50$. Call this the base case.

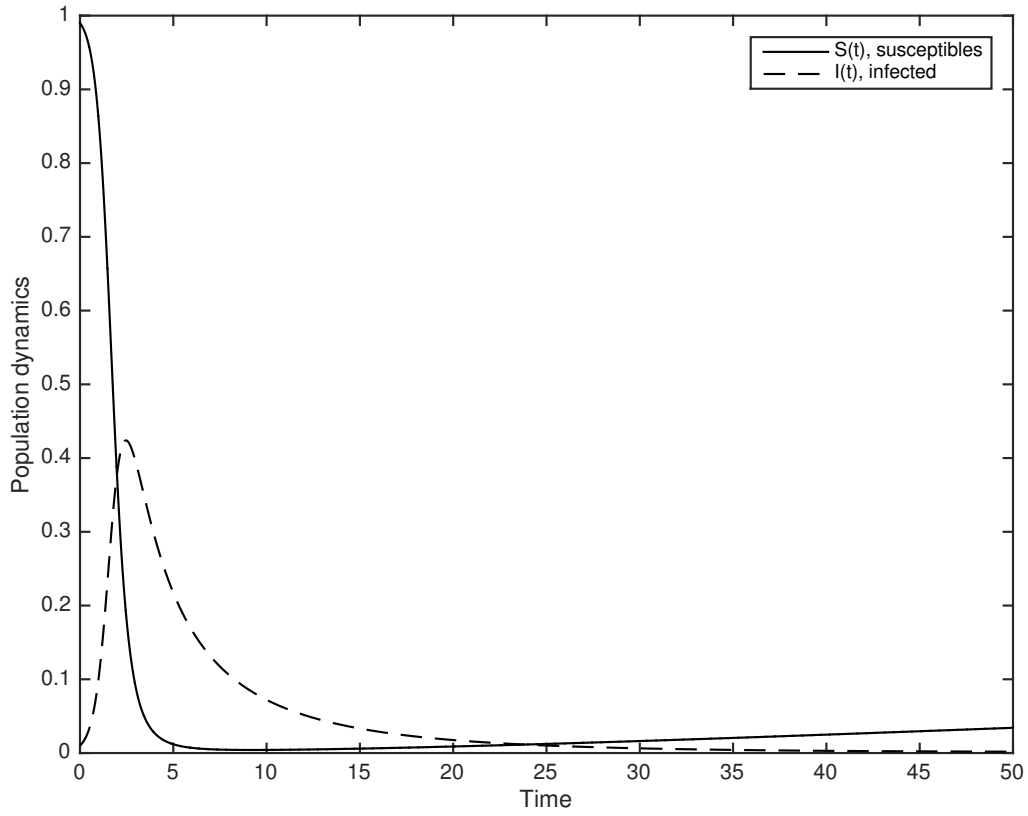
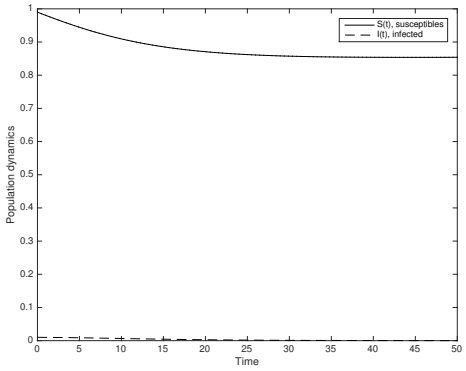


Figure 1: Plot of $I(t)$ and $S(t)$ vs. t for $t \in [0, 50]$ and $e = 0.0012$, $R_0 = 3.5$, $\sigma = 0.25$.

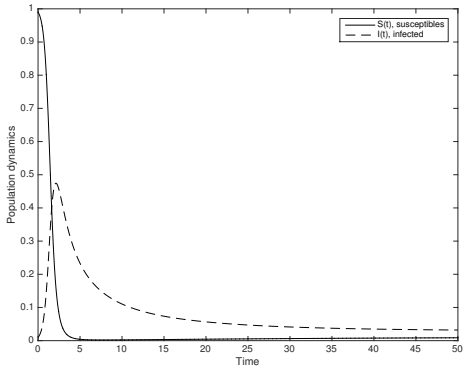
Let us now analyze the produced plot. When $t = 0$ only 1% of the population is infected, as stated in the initial conditions. Then, the susceptible class of the population experiences a rapid drop, and by $t \approx 4$ almost all of the susceptibles have moved to the infectives class. We can also see that the infectives rapidly increase (the graph does so with approximately the same speed, in fact), for the same values of t. Observe that the infection has a peak at $t \approx 3$. As expected, during the peak of the infection technically all of the population is infected. The infection then starts to decrease slowly up to when $t \approx 30$ and then eventually dies out. The susceptible population begins to recover at $t \approx 15$ and will then stabilize for some $t > 50$. In summary, with the given initial conditions of only 1% of the population being infected and with the basic reproduction number of $R_0 = 3.5$, there is an infection peak at $t \approx 4$ and the majority of the population becomes infected by $t = 5$. Then eventually the infection dies out and the number of susceptibles stabilizes.

Next, we vary the value of the basic reproduction number of the disease R_0 in order to

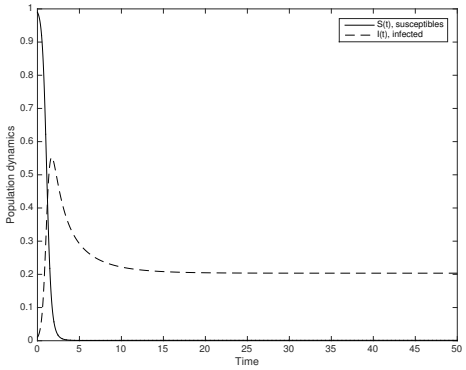
examine its effect on the two classes.



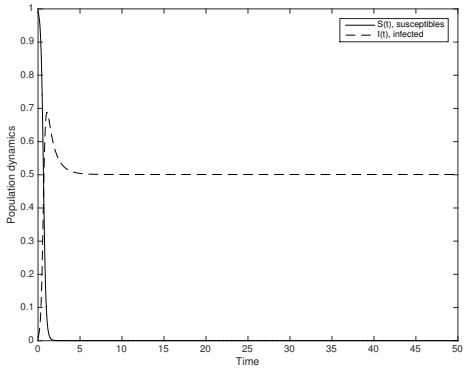
(a) Plot of $I(t)$ and $S(t)$ vs. t when $R_0 = 1$.



(b) Plot of $I(t)$ and $S(t)$ vs. t when $R_0 = 4$.



(c) Plot of $I(t)$ and $S(t)$ vs. t when $R_0 = 5$.



(d) Plot of $I(t)$ and $S(t)$ vs. t when $R_0 = 8$.

Figure 2: Four plots of $I(t)$ vs. t with varying values of the reproduction number R_0.

In Figure 2a the value of R_0 is set to 1. With the given initial conditions and $R_0 = 1$, a tiny proportion of the population gets infected and the infection eventually dies out. As we can see from the graph, the susceptibles slowly decrease and stabilize at being $\approx 85\%$ of the total population. Thus, with such a low reproduction number, the infection is unable to effectively spread among the population and dies out very rapidly.
In Figure 2b, $R_0 = 4$. There is a peak of the infection just as in the base case $R_0 = 3.5$, but the number of infectives decreases more slowly. Further, the infection doesn't die out completely before t reaches 50. As far as the susceptibles, there is only a slighter improvement, visible for $t > 35$. Hence, even a slighter increase in the reproduction number causes the infection to persist.
We set $R_0 = 5$ in Figure 2c. This yields an infection peak just like in the base case, but the infection clearly persists for $t > 10$. Furthermore, the susceptibles die out completely for $t > 3$. Therefore, we can conclude that the infection definitely stabilizes for values of $R_0 > 3.5$. In Figure 2d, $R_0 = 8$. The peak of infection occurs earlier compared to the base case. Agan, the infection persists and the susceptibles die out, which indeed confirms that when $R_0 > 3.5$, the infection is stable.
In summary, if the reproduction number of the infection R_0 is very small, or in general

$R_0 < 3.5$, the infection reproduces quite slowly, does not manage to infect a large proportion of the susceptibles, the peak occurs later and is smaller in magnitude, and eventually the disease dies out. However, if $R_0 > 3.5$, the infection spreads rapidly, stabilizes, i.e. persists, the peak occurs earlier and is greater in magnitude, and causes the susceptible class of the population to die out. We can think of the reproduction number as the number of individuals getting the infection from interacting with an already infected individual. So in general, if one infected individual transmits the disease to less than 3.5 other individuals, not all of the population will become infected. If, however, one infected individual transmits the disease to more than 3.5 other individuals, then the infection will persist and cause the susceptibles to die out. □

Solution 1 (d). Consider the S-nullcline, that is

$$\frac{dS}{dt} = 0 \quad \therefore \quad e - R_0SI - eS = 0 \quad \therefore \quad S(R_0I + e) = e$$
$$\therefore \quad S = \frac{e}{R_0I + e}. \tag{7}$$

Substituting the expression for S from Equation in the equation of the I-nullcline yields

$$\frac{dI}{dt} = \frac{R_0Ie}{R_0I + e} - I + \sigma R_0 I\left(1 - \frac{e}{R_0I + e} - e\right)$$

$$\frac{dI}{dt} = \frac{R_0Ie}{R_0I + e} - I + \sigma R_0 I\left(\frac{R_0I + \cancel{e} - \cancel{e} - R_oI^2 - Ie}{R_0I + e}\right)$$

$$\frac{dI}{dt} = \frac{R_0Ie - R_0I^2 - Ie + \sigma R_0 I\big(R_0I - R_0I^2 - Ie\big)}{R_0I + e}$$

$$\frac{dI}{dt} = I\left(\frac{R_0e - R_0I - e + \sigma R_0^2 I - \sigma R_0^2 I^2 - \sigma R_0 Ie}{R_0I + e}\right). \tag{8}$$

Now, since $I \neq 0$, consider the expression in the brackets, that is,

$$I\Big(R_0e - R_0I - e + \sigma R_0\big(R_0I - R_0I^2 - Ie\big)\Big) = 0$$
$$I\Big(-\sigma R_0^2I^2 + I\big(\sigma R_0^2 - \sigma R_0e - R_0\big) + \big(R_0 - 1\big)e\Big) = 0.$$

Again, as $I \neq 0$, consider the following quadratic equation for I

$$\Big(-\sigma R_0^2I^2 + I\big(\sigma R_0^2 - \sigma R_0e - R_0\big) + \big(R_0 - 1\big)e\Big) = 0. \tag{9}$$

The discriminant of Equation 9 is

$$D = e^2R_0^2\left(\left(\frac{\sigma R_0 - 1}{e} - \sigma\right)^2 + 4\sigma\left(\frac{R_0 - 1}{e}\right)\right). \tag{10}$$

Using the expression for the discriminant D from Equation 10 to derive the roots of the quadratic yields

$$I_{1,2} = \frac{R_0\left(1+\sigma e-\sigma R_0\right) \pm \sqrt{D}}{-2\sigma R_0^2},$$

where $I_{1,2}$ denotes the two roots of the quadratic equation I_1 and I_2. However, note that we are only interested in the positive root as it does not make sense to have a negative amount of individuals. Thus, the root, say I^*, is

$$I^* = \frac{R_0\left(1+\sigma e-\sigma R_0\right) + \sqrt{D}}{-2\sigma R_0^2}$$

$$I^* = \frac{R_0\left(1+\sigma e-\sigma R_0\right) + eR_0\sqrt{\left(\frac{\sigma R_0-1}{e}\right)^2 + \frac{4\sigma(R_0-1)}{e}}}{-2\sigma R_0^2}$$

$$I^* = \frac{e\cancel{R_0}}{-2\sigma R_0^{\cancel{2}}}\left[-\sqrt{\left(\frac{1-\sigma R_0}{e}+\sigma\right)^2 + \frac{4\sigma(R_0-1)}{e}} + \left(\frac{1-R_0\sigma}{e}+\sigma\right)\right]$$

$$\boxed{I^* = \frac{e}{2\sigma R_0}\left[\sqrt{\left(\frac{1-\sigma R_0}{e}+\sigma\right)^2 + \frac{4\sigma(R_0-1)}{e}} - \left(\frac{1-R_0\sigma}{e}+\sigma\right)\right]}. \tag{11}$$

Thus, the number of infectives in the unique steady state, for $I \neq 0$ is given by Equation 11 as required. □

Solution 1(e). In order to determine the stability of the unique endemic state, we need to consider the Jacobian matrix J of the system. Recall the non-dimensionalized expressions for S and I that is, Equations 5 and 6 respectively.

$$\frac{dS}{dt} = e - R_0SI - eS,$$

$$\frac{dI}{dt} = R_0SI - I + \sigma R_0 I(1-S-I).$$

Let us now examine their nullclines. When $\dot{S}=0$ and $\dot{I}=0$, we have

$$e - R_0SI - eS = 0$$

$$\underbrace{I}_{I\neq 0}\left(\underbrace{R_0S - 1 + \sigma R_0\left(1-S-I\right)}_{g(S,I)}\right) = 0.$$

Since we are interested in the stability of the system, we need to find simultaneous solutions for the two equations. Define the expression in the brackets by the function $g = g(S, I)$ and note that $I \neq 0$ implies that $g(S, I) = 0$. Next consider the Jacobian matrix J with entries the partial derivatives of the two equations.

$$J = \begin{bmatrix} -R_0 I - e & -R_0 S \\ R_0 I - \sigma R_0 I & \underbrace{g(S,I)}_{g(S,I)=0} - \sigma R_0 I \end{bmatrix}$$

$$\therefore \quad J = \begin{bmatrix} -R_0 I - e & -R_0 S \\ R_0 I - \sigma R_0 I & -\sigma R_0 I \end{bmatrix}.$$

Now evaluate the determinant and the trace of the matrix J. In order to prove that the steady state is stable, we require that $\det J > 0$ and $\operatorname{tr} J < 0$, where $\det J$ and $\operatorname{tr} J$ are the determinant and the trace of the Jacobian matrix respectively. Thus,

$$\begin{aligned} \det J &= (R_0 I + e)(\sigma R_0 I) + R_0 S(R_0 I - \sigma R_0 I) \\ &= \underbrace{\sigma R_0 I^2}_{>0} + \underbrace{e\sigma R_0 I}_{>0} + R_0^2 I S \underbrace{(1-\sigma)}_{\geq 0} \end{aligned}$$

$$\therefore \quad \det J > 0.$$

Similarly,

$$\begin{aligned} \operatorname{tr} J &= -R_0 I - e - \sigma R_0 I \\ &= -(R_0 I + e + \sigma R_0 I) \\ &= -\left(R_0 I \underbrace{(1+\sigma)}_{>0} + \underbrace{e}_{>0} \right) \end{aligned}$$

$$\therefore \quad \operatorname{tr} J < 0.$$

Thus, the steady state is stable, as required. □

Solution 1 (f). The following MATLAB script is used to plot the steady state value of I given in Equation 11 versus R_0 for $1 \leq R_0 \leq 6$, where $\sigma = 0.25$ and $e = 0.0012$.

Listing 3: Script used to plot I versus R_0.

```
%% Lab 1 ID: 2019862s

% This produces a plot of I versus Ro, where
% Ro=[1,6], e=0.0012, sigma = 0.25, and I is given
% by the expression defined in Question 1d.

% Define the parameter values
ro=linspace(1,6);
e = 0.0012;
sigma = 0.25;

% The expression for I(t) as derived in Question 1d
i=e*(2*ro.*sigma).^(-1).*((((1-ro.*sigma)./e+sigma).^2.+...
    +4*(ro-1).*sigma./e).^(1/2)-...
    ((1-ro.*sigma).*e^(-1)+sigma));

% Plot the resulting graph
figure
plot(ro,i,'k')
xlabel('The reproduction number Ro')
ylabel('Infected population I')
```

Figure 3 shows the resulting plot.

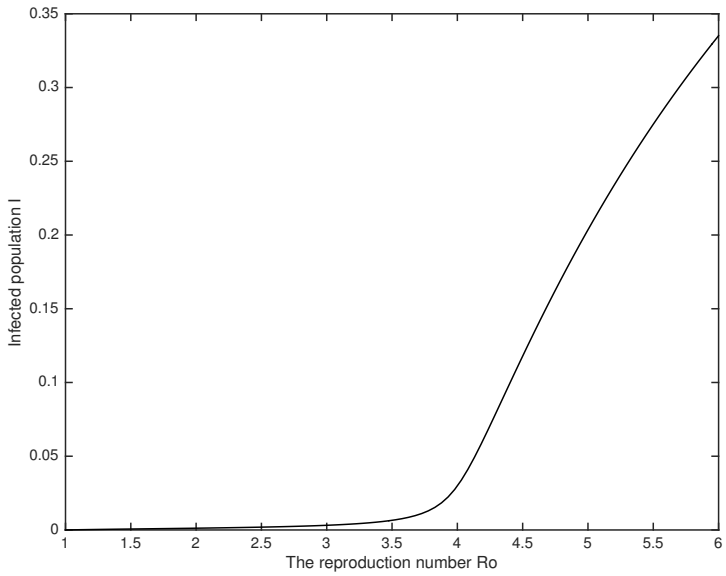


Figure 3: Plot of $I(t)$ vs. R_0 for $1 \leq R_0 \leq 6$.

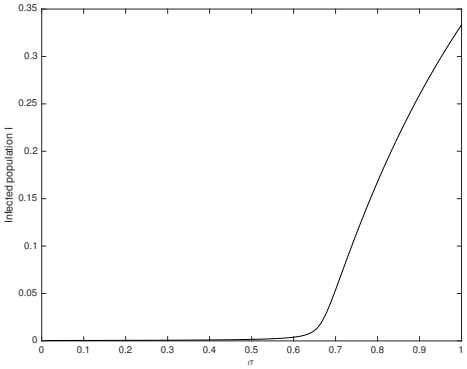
Indeed, Figure 3 confirms our findings from Question 1 part (c). For values of $R_0 < 3.5$, the infected population is approximately zero. When $R_0 > 3.5$, the number of infected individuals increases rapidly. This means that in order for the infection to persist (stabilize) and to cause the susceptibles to die out, we require that one infected individual transmits the disease to more than 3.5 other non-infective individuals. □

Solution 1 (g). We know that $\sigma \in [0, 1]$ shows the proportion of the recovered population, which may return back to the infectives at a rate β. In this part of the question, we examine the effect of partial immunity, i.e. the part of the population, which cannot become infected again. The following MATLAB script is used to plot the steady state value of I given in Equation 11 versus σ, where σ is varied between $0 \leq \sigma \leq 1$.

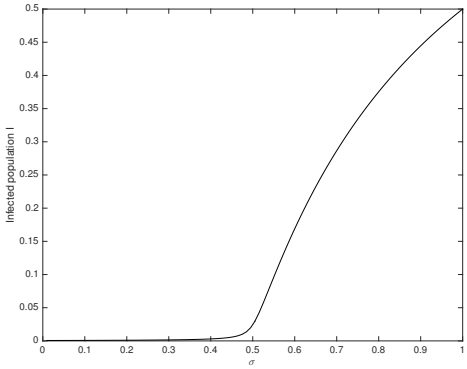
Listing 4: Script used to plot I versus σ.

```
%% Lab 1 ID: 2019862s
%% Question 1g

% This produces a plot of I versus sigma, where
% sigma=[0,1], e=0.0012, Ro=3.5, and I is given
% by the expression defined in Question 1d. Observe
% that if sigma>0.3, the infection increases rapidly,
% that is, if more than 1/3 of the population is
% infected, the infection is stable.

e = 0.0012;
hold on
for i=0:9
    ro=1.5+i*0.5;
    I=e*(2*ro.*sigma).^(-1).*((((1-ro.*sigma)./e+sigma).^2.+...
    +4*(ro-1).*sigma./e).^(1/2)-((1-ro.*sigma).*e^(-1)+sigma));
figure
plot(sigma,I,'k')
xlabel('\sigma')
ylabel('Infected population I')
disp(ro);
disp(sigma);
end
```

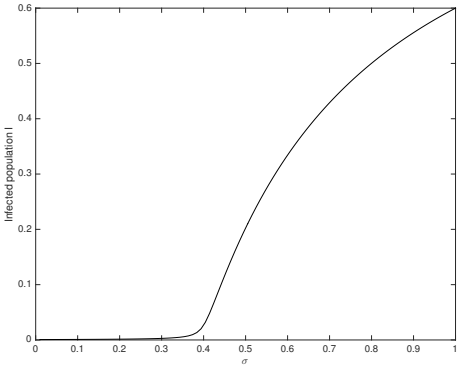
Figure 5 shows the resulting plots.



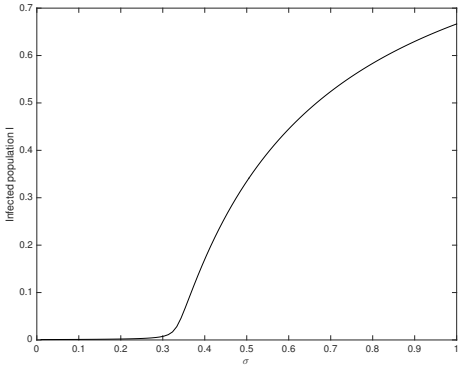
Plot of $I(t)$ vs. σ when $R_0 = 1.5$.



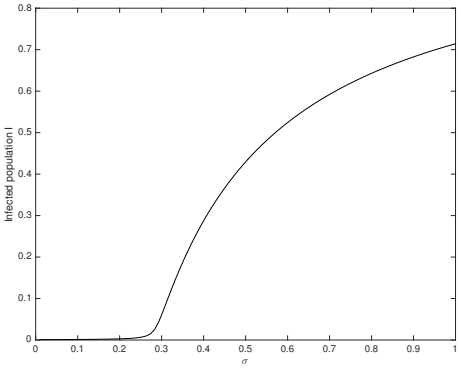
Plot of $I(t)$ vs. σ when $R_0 = 2$.



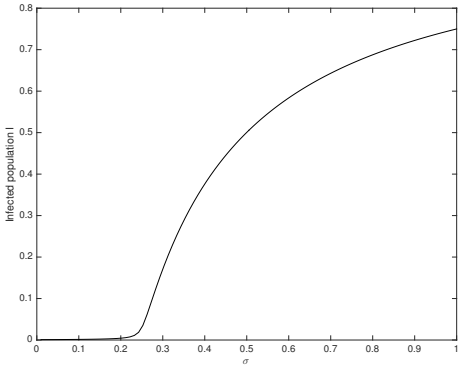
Plot of $I(t)$ vs. σ when $R_0 = 2.5$.



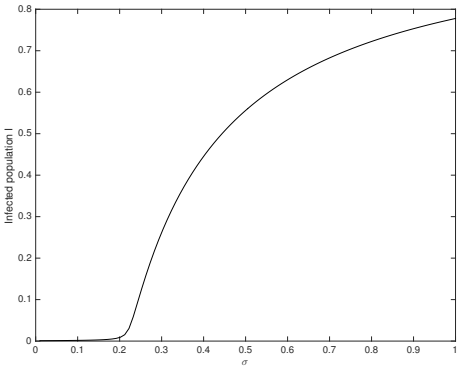
Plot of $I(t)$ vs. σ when $R_0 = 3$.



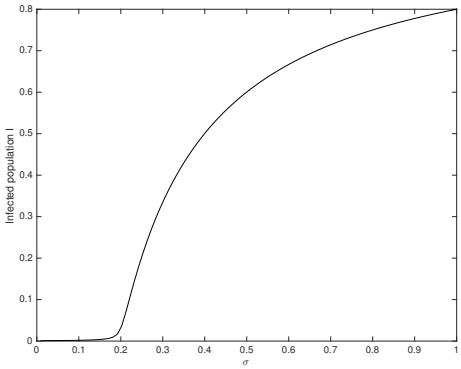
Plot of $I(t)$ vs. σ when $R_0 = 3.5$.



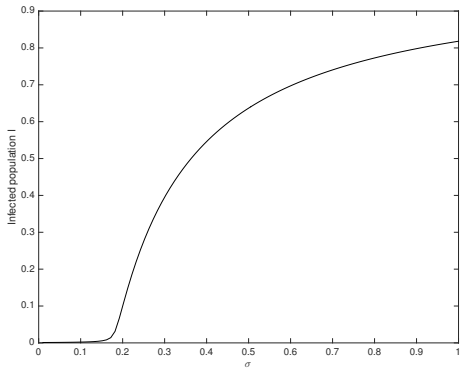
Plot of $I(t)$ vs. σ when $R_0 = 4$.



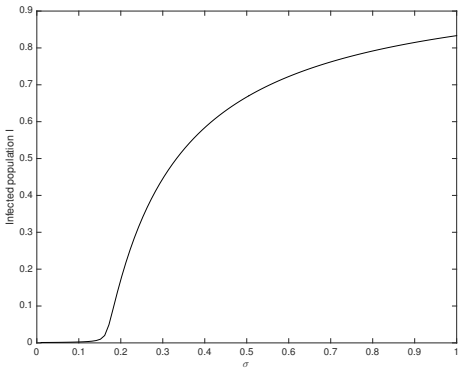
Plot of $I(t)$ vs. σ when $R_0 = 4.5$.



Plot of $I(t)$ vs. σ when $R_0 = 5$.



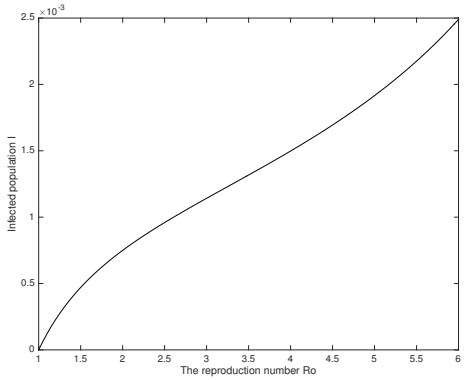
Plot of $I(t)$ vs. σ when $R_0 = 5.5$.



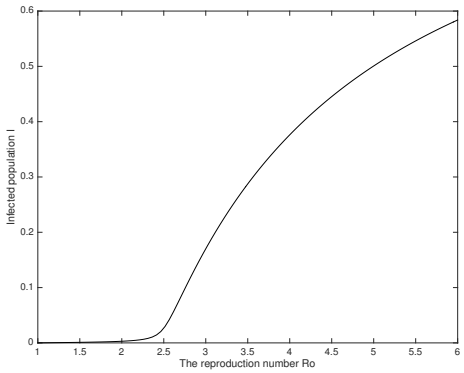
Plot of $I(t)$ vs. σ when $R_0 = 6$.

Figure 5: Ten plots of $I(t)$ vs. σ with varying values of the reproduction number R_0.

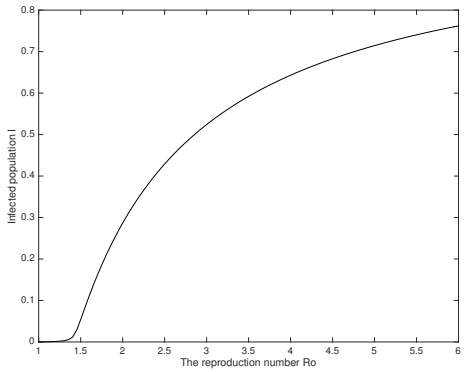
The ten graphs are produced by running the MATLAB script with a `for` loop, which is iterated for values of R_0, starting at 1.5 and increasing with a step of 0.5. In the first four graphs, when $R_0 \leq 3$ we can see that the infection spreads somewhat slowly. In general, for values of the reproduction number such that $R_0 < 3.5$, we require a large proportion of the recovered to get re-infected for the infection to persist. Now, if $R_0 \geq 3.5$, the infection increases quite rapidly, stabilizes much faster, and persists. So in conclusion, the larger proportion of population that gets re-infected, the faster the disease spreads. Also, an increase in σ results in a decrease in partial immunity. Thus, partial immunity does not change the dynamics of the infected as it does not prevent the recovered from getting re-infected. Alternatively, we can plot $I(t)$ vs. $R_0 \in [1, 6]$ and use several concrete values of σ.



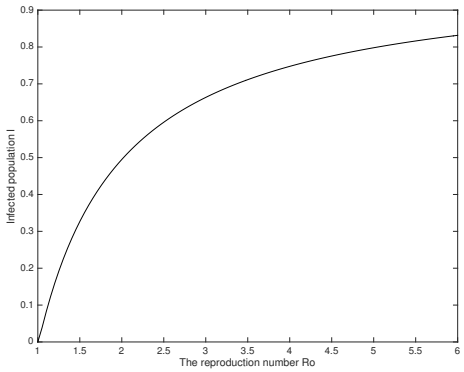
(a) Plot of $I(t)$ vs. R_0 when $\sigma = 0.10$.



(b) Plot of $I(t)$ vs. R_0 when $\sigma = 0.40$.



(c) Plot of $I(t)$ vs. R_0 when $\sigma = 0.70$.



(d) Plot of $I(t)$ vs. R_0 when $\sigma = 0.99$.

Figure 6: Four plots of $I(t)$ vs. t with varying values of the reproduction number R_0.

The subplots in Figure 6 also demonstrate the direct proportionality between the dynamics of the infectives and the proportion σ. Observe that when $\sigma = 0.10$, the basic reproduction number of the infection should be very high in order for the infection to spread and persist. When $\sigma = 0.40$, the infection only starts spreading for values of $R_0 > 2.5$. If $\sigma = 0.70$, then the infection spreads rapidly and the reproduction number needs to be as small as $R_0 = 1.5$. Further, when approximately 99% of the population becomes re-infected, the disease spreads immediately and persists. So we can regard the physical meaning of partial immunity as the difference between the total population and the proportion, which gets re-infected. In terms of the parameters, this is $(1 - \sigma)$. So, when $\sigma \approx 0$, a large proportion of the population is partially immune, thus, does not get re-infected and eventually the infection dies out. When $\sigma \approx 1$, almost all of the individuals get re-infected, which cause the disease to persist and the susceptibles to die out. □

Solution 1 (h). In this part of the question we introduce a parameter v, which denotes the vaccinated fraction of the total population. The system of ODEs is transformed as follows:

$$\frac{dS}{dt} = e(1-v) - R_0 SI - es,$$
$$\frac{dI}{dt} = R_0 SI - I + \sigma R_0 I(1-S-I).$$

We modify our MATLAB code, in order to incorporate the parameter v in the function. The following script solves the system of equations.

Listing 5: Script used to solve the new system.

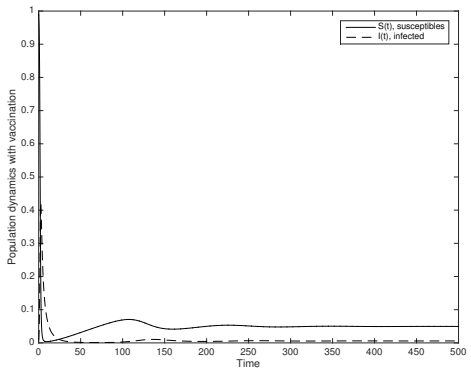
```
%% Lab 1 ID: 2019862s
% Question 1h

function dy = sirModelVac(t,y)

%% This function takes in the current time and
%% variable values and outputs the corresponding
%% time derivatives for the SIR Model with vaccination

% Define the parameter values
e = 0.0012;
ro = 3.5;
sigma = 0.25;
dy=zeros(2, 1);
v=0.5;

% Set up labels for the variables
S=y(1);
I=y(2);

% Define the equations for the ODEs
    dy(1) = (1-v)*e - ro*S*I - e*S;
    dy(2) = ro*S*I- I + sigma*ro*I*(1-S-I);
```

Furthermore, the following modified main script is used to call the ODE solver.

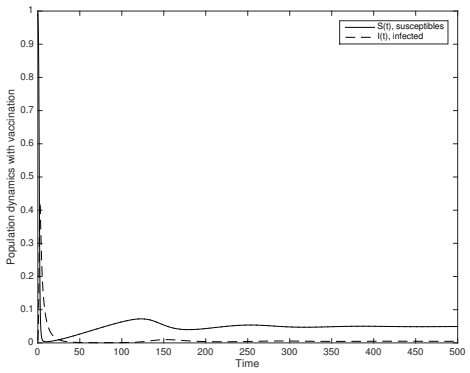
Listing 6: Script used to run `sirModelVac.m`.

```
%% Lab 1 ID: 2019862s
% Question 1h
%
% ODE45 is used to solve the system of ODEs
% with vaccination. The initial conditions are
% e = 0.0012, Ro = 3.5, sigma = 0.25.
% The plot produced shows the number of
% susceptibles, S(t), and the number of
% infected, I(t).

[T, Y] = ode45(@sirModelVac, [0:0.01:500], [0.99, 0.01]);
%disp([T,Y]);
plot(T,Y(:,1),'k')
hold on
plot(T,Y(:,2),'k--')
xlabel('Time')
ylabel('Population dynamics with vaccination')
legend('S(t), susceptibles', 'I(t), infected')
```

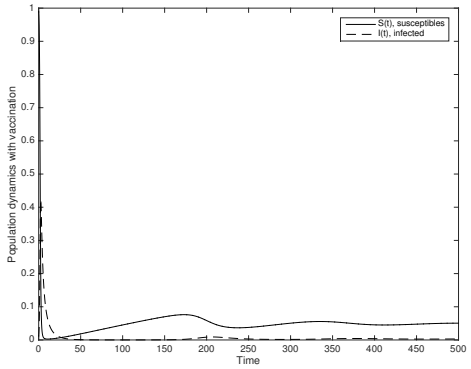
Now, we use several values of the vaccination parameter to examine its effect on the population dynamics.



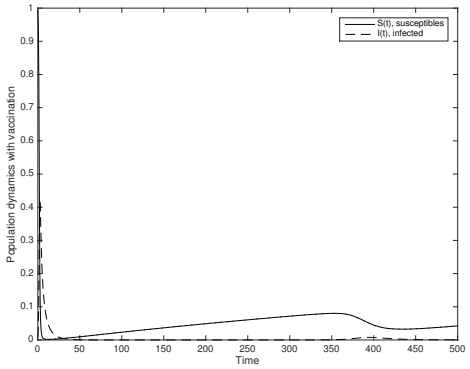
(a) Plot of $I(t), S(t)$ vs. t when $v = 0.10$.



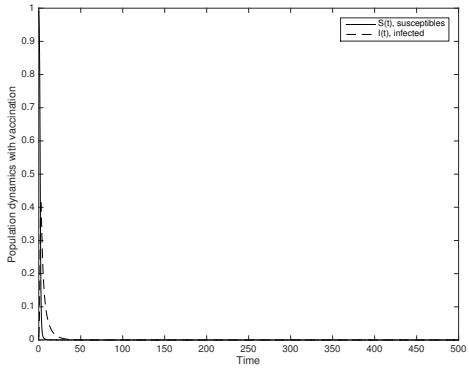
(b) Plot of $I(t), S(t)$, vs. t when $v = 0.25$.



(c) Plot of $I(t), S(t)$ vs. t when $v = 0.50$.



(d) Plot of $I(t), S(t)$ vs. t when $v = 0.75$.

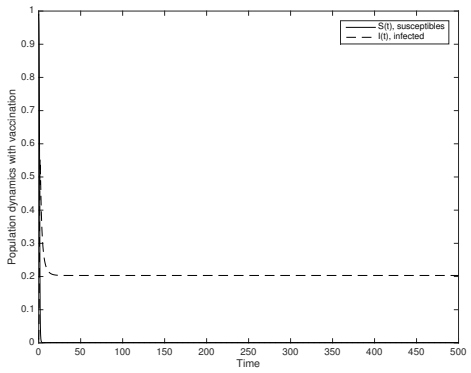


(e) Plot of $I(t), S(t)$ vs. t when $v = 1.00$.

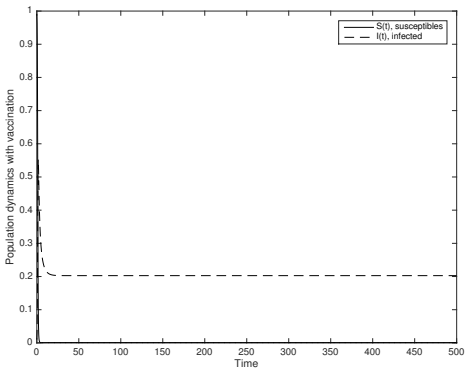
Figure 7: Five plots of $I(t)$ and $S(t)$ vs. t with varying values of the vaccination proportion v and $R_0 = 3.5$.

Now observe the subplots of Figure 7. In Figure 7a observe that there is a peak in the infection, very close to $t \approx 0$. However, we see that the susceptible class manages to recover up to $t \approx 100$, then exhibits a very small disturbance, and finally for $t > 200$, the susceptibles recover and remain constant. The infective class on the other hand, exhibits an increase solely during the peak, and then dies out rapidly. Thus we have to note that the vaccination has a very small effect on the susceptibles, but nonetheless, helps them

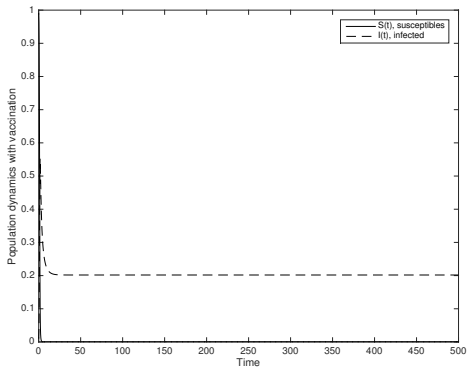
recover. The scenario in Figure 7b is similar. We can think of the effect of the vaccination as a small wave, within the susceptible class. So in this case, when $v = 0.25$, the wave occurs slightly later than the previous case. But eventually the infection dies out and the susceptibles stabilize. The same logic can be applied to both situations, plotted in Figure 7c, where the wave of stabilization in the susceptibles occurs at $t \approx 200$ and Figure 7d, where the population stablizes at $t \approx 300$. However, observe that when $v = 1$, as in Figure 7e, both the infectives and the susceptibles die out. So in general, the larger the value of v, the more time the susceptibles need to recover. Now consider the same values of v, but for a different reproduction number $R_0 = 5$.



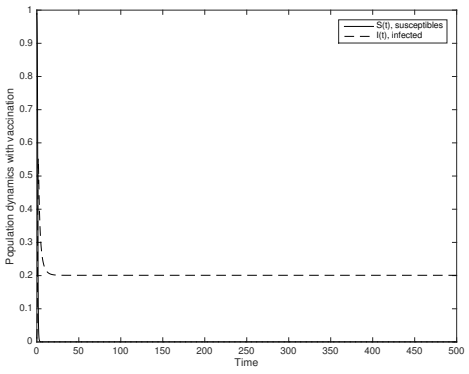
(a) Plot of $I(t)$ vs. t when $v = 0.10$.



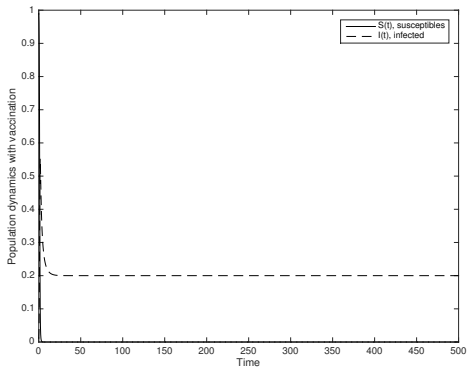
(b) Plot of $I(t)$ vs. t when $v = 0.25$.



(c) Plot of $I(t)$ vs. t when $v = 0.50$.



(d) Plot of $I(t)$ vs. t when $v = 0.75$.



(e) Plot of $I(t)$ vs. t when $v = 1.00$.

Figure 8: Five plots of $I(t)$ and $S(t)$ vs. t with varying values of the vaccination proportion v and $R_0 = 5$.

Observe the subplots of Figure 8. In all subplots, the infection peaks at a very early time $t \approx 0$. This is a result of the high reproduction number R_0. In fact, this holds for any reproduction number, larger than the critical value of $R_0 = 3.5$. In such cases, the infection is uncontrollable, and the partial vaccination is unhelpful and has no net effect on the dynamics of the population. Thus, we have to consider more factors, which may help us stop the infection or at least control it. □

Question 2. *We modify the model to include a new lass V, which is the proportion of the population that are vaccinated and free from the disease and I_v is the proportion that are vaccinated, but become infected with the disease. The non-dimensional model is given by*

$$\begin{aligned}
\frac{dS}{dt} &= (1-v)e - R_0 S(I+I_v) - eS \\
\frac{dI}{dt} &= R_0 S(I+I_v) - I + \sigma R_0 (I+I_v)R \\
\frac{dR}{dt} &= -\sigma R_0 (I+I_v)R + (1-e)I - eR \\
\frac{dV}{dt} &= ve + (1-e)I_v - \sigma_v R_0 (I+I_v)V - eV \\
\frac{dI_v}{dt} &= \sigma_v R_0 V(I+I_v) - I_v,
\end{aligned}$$

with parameters $e = 0.0012$, $R_0 = 3.5$, $\sigma = 0.25$, $v = 0.9$, $\sigma_v = 0.2$ and initial conditions $S(0) = 0.99$, $I(0) = 0.01$, and $V(0) = R(0) = I_v(0) = 0$.

Solution 2 (a). The following MATLAB function is used to solve the system of ODEs with vaccination and partial immunity.

Listing 7: Script used to solve the new system.

```
%% Lab 1 ID: 2019862s
% Question 2a

function dy = sirModelVacImmunity(t, y)

%% This function takes in the current time and
%% variable values and outputs the corresponding
%% time derivatives for SIR Model with vaccination
%% which produces partial immunity

% Define the parameter values
e = 0.0012;
ro = 5;
sigma = 0.25;
v = 0;
sigmaV = 0.2;

dy=zeros(5, 1);

% Set up labels for the variables
S=y(1);
I=y(2);
R=y(3);
V=y(4);
IV=y(5);

% Define the equations for the ODEs
dy(1) = e-v*e - ro*S*(I+IV)- e*S;
dy(2) = ro*S*(I+IV)- I + sigma*ro*R*(I+IV);
dy(3) = -sigma*ro*R*(I+IV)+(1-e)*I-e*R;
dy(4) = v*e+(1-e)*IV-sigmaV*ro*V*(I+IV)-e*V;
dy(5) = sigmaV*ro*V*(I+IV)-IV;

end
```

Then, we run the script `mainFile2a2.m` in order to plot the dynamics of the infected class.

Listing 8: Script used to plot only the infected class.

```
%% Lab 1 ID: 2019862s
%% Question 2 a

% ODE45 is used to solve the system of ODEs
% with vaccination and partial immunity.
% The initial conditions are
% e = 0.0012, Ro = 3.5, sigma = 0.25, v = 0.9,
% sigmaV = 0.2, s(0)=0.99, i(0)=0.01.
% The plot produced shows the number of
% susceptibles, S(t), and the number of
% infected, I(t).

[T, Y] = ode45(@sirModelVacImmunity, [0:0.01:500], ...
    [0.99, 0.01, 0, 0, 0]);
% disp([T,Y]);
hold on
plot(T,Y(:,2),'k--')
xlabel('Time')
ylabel('I(t), infected')
legend('I(t), infected')
```

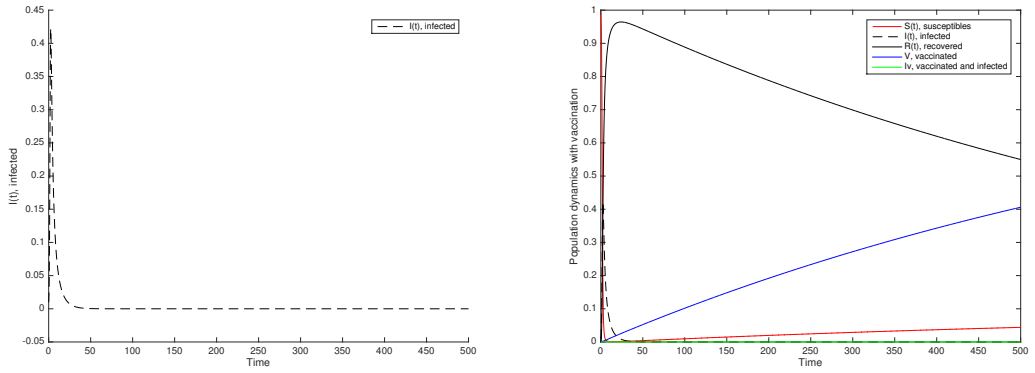
Furthermore, we run the script `mainFile2a.m` to plot the dynamics of the total population.

Listing 9: Script used to plot the solution of the system for all classes.

```
%% Lab 1 ID: 2019862s
%% Question 2 a

% ODE45 is used to solve the system of ODEs
% with vaccination and partial immunity.
% The initial conditions are
% e = 0.0012, Ro = 3.5, sigma = 0.25, v = 0.9,
% sigmaV = 0.2, s(0)=0.99, i(0)=0.01.
% The plot produced shows the number of
% susceptibles, S(t), and the number of
% infected, I(t).

[T, Y] = ode45(@sirModelVacImmunity, 0:0.01:500, ...
    [0.99, 0.01, 0, 0, 0]);
% disp([T,Y]);
plot(T,Y(:,1),'red')
hold on
plot(T,Y(:,2),'k--')
plot(T,Y(:,3),'k')
```

```
plot(T,Y(:,4),'blue')
plot(T,Y(:,5),'green')
xlabel('Time')
ylabel('Population dynamics with vaccination')
legend('S(t), susceptibles', 'I(t), infected'...
    ,'R(t), recovered', 'V, vaccinated' ...
    ,'Iv, vaccinated and infected')
```

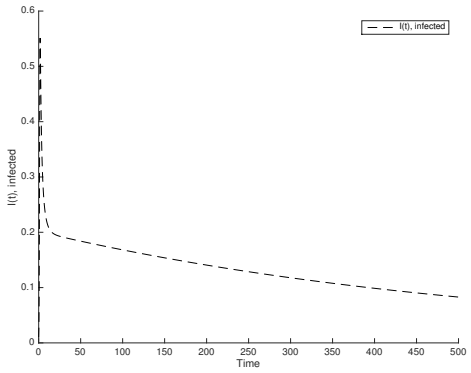
The following graph shows the dynamics of the infectives class for $t \in [0, 500]$ and $R_0 = 3.5$.



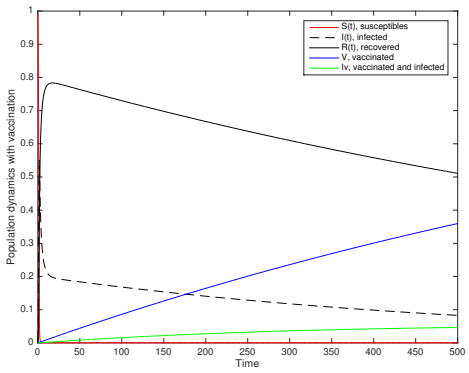
(a) Plot of $I(t)$ vs. t when $R_0 = 3.5$. (b) Plot of all classes vs. t when $R_0 = 3.5$.

Figure 9: Two plots of $I(t)$ vs. t and total population vs t with $v = 0.9$, $\sigma = 0.25$, and $\sigma_v = 0.2$ and $R_0 = 3.5$.

Figure 9a shows that the peak of the infection occurs very early and then the disease starts decreasing. However, the infection vanishes at $t \approx 20$ and dies out. The plot in Figure 9b shows the total population dynamics. Observe that the vaccinated class increases and the susceptibles start stabilizing. In general, the reproduction number has a critical threshold value $R_0 = 3.5$, meaning that for lower values, the infection is not able to spread thoroughly, and for larger values, it infects larger proportion of the population and the disease persists. So when $R_0 = 3.5$, vaccination is not helpful and there is no need to invest in creating and applying vaccines to individuals. Now let us increase the reproduction number to $R_0 = 5$.



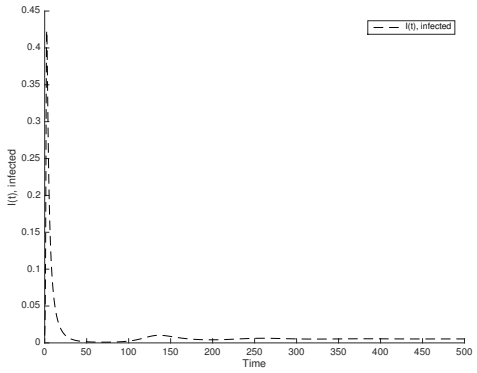
(a) Plot of $I(t)$ vs. t when $R_0 = 5$.



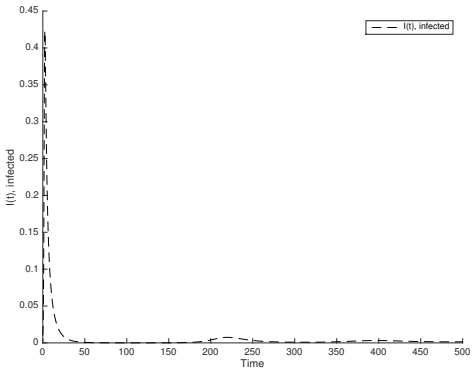
(b) Plot of all classes vs. t when $R_0 = 5$.

Figure 10: Two plots of $I(t)$ vs. t and total population vs t with $v = 0.9$, $\sigma = 0.25$, and $\sigma_v = 0.2$ and $R_0 = 3.5$.

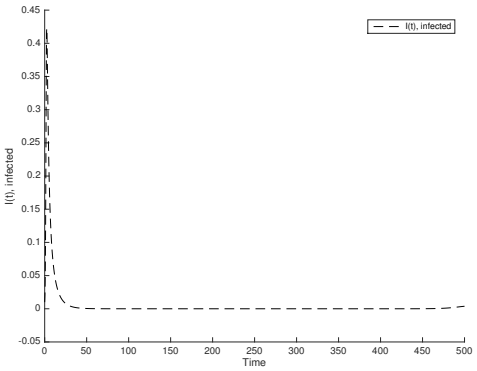
Figure 10a shows that the infection peaks initially, and then starts slowly decreasing. So for $t \in [0, 500]$, we see that the disease slowly dies out, despite its reproduction number being larger than the critical value 3.5. Figure 10b shows the rapid increase in the vaccinated class. So when $v = 0.9$, that is, approximately 90% of the population is vaccinated, the disease is controlled. Hence, we can conclude that for larger values of the reproduction number, i.e. greater than the threshold $R_0 > 3.5$, vaccination is helpful as it eventually causes the disease to die out. We now vary the proportion of the population that is vaccinated, in other words, we change the values of v.



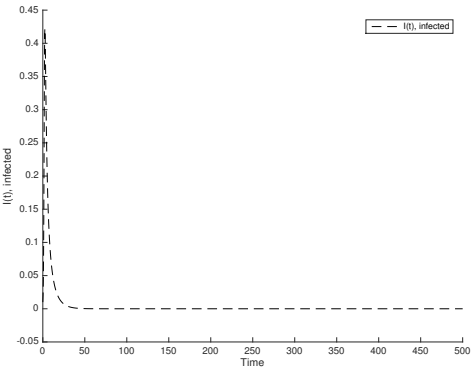
(a) Plot of $I(t)$ vs. t when $v = 0.10$.



(b) Plot of $I(t)$, $S(t)$ vs. t when $v = 0.50$.



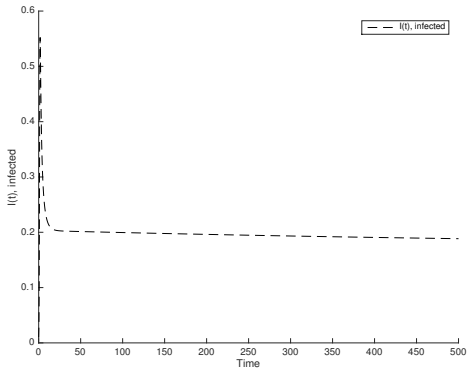
(c) Plot of $I(t)$, $S(t)$ vs. t when $v = 0.75$.



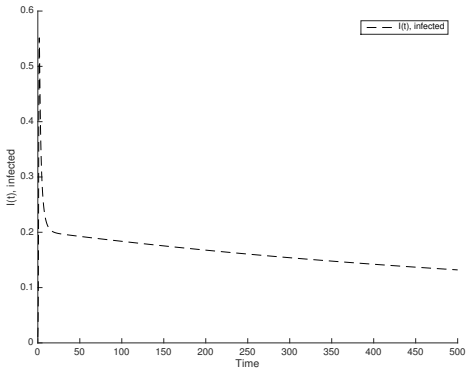
(d) Plot of $I(t)$, $S(t)$ vs. t when $v = 1.00$.

Figure 11: Five plots of $I(t)$ vs. t with varying values of the vaccination proportion v and $R_0 = 3.5$.

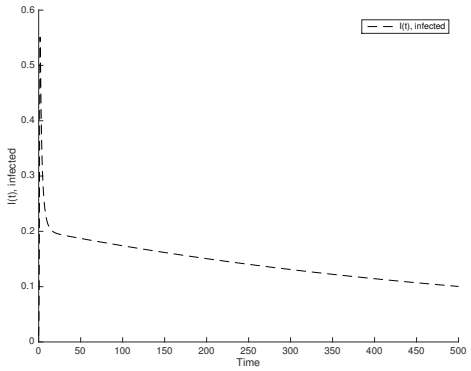
Figure 12 confirms our findings that in general, vaccination is not quite helpful for $R_0 = 3.5$, regardless of the proportion of the population, which is vaccinated. Next we change the value of R_0 to 5 and again we vary v.



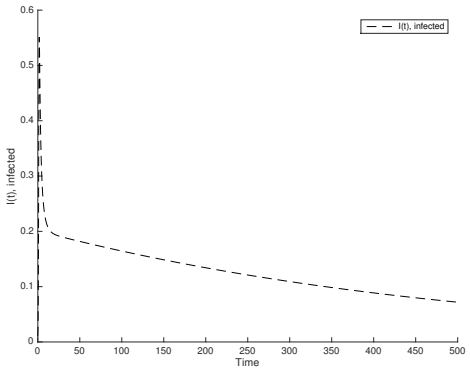
(a) Plot of $I(t)$ vs. t when $v = 0.10$.



(b) Plot of $I(t)$, $S(t)$ vs. t when $v = 0.50$.



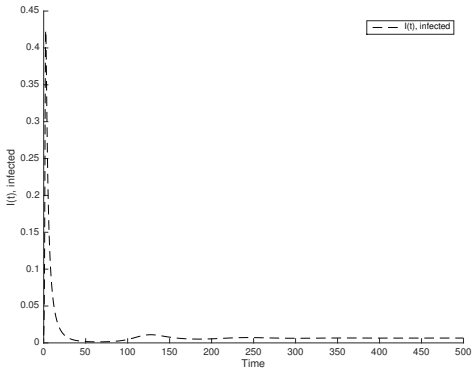
(c) Plot of $I(t)$, $S(t)$ vs. t when $v = 0.75$.



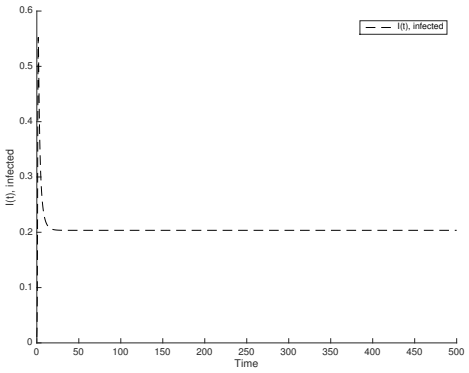
(d) Plot of $I(t)$, $S(t)$ vs. t when $v = 1.00$.

Figure 12: Five plots of $I(t)$ vs. t with varying values of the vaccination proportion v and $R_0 = 5$.

Again, the plots in Figure 12 confirm our findings from before. The larger the proportion of the population that gets vaccinated, the sooner the disease dies out. So for high reproduction numbers, vaccination is quite helpful and controls the disease.
Finally, we plot the dynamics of the infection for both $R_0 = 3.5$ and $R_0 = 5$ and set $v = 0$.



(a) Plot of $I(t)$ vs. t when $R_0 = 3.5$.



(b) Plot of $I(t)$ vs. t when $R_0 = 5$.

Figure 13: Two plots of $I(t)$ vs. t with $v = 0$.

As shown in Figure 13, when there is no vaccination at all and $R_0 = 3.5$, only a very small proportion of the population gets re-infected after the peak, $\approx 3\%$ of the population at $t \approx 125$. On the other hand, the lack of vaccination when $R_0 = 5$ allows the disease to persist, as $\approx 20\%$ of the population remain infected or get re-infected. Therefore, for values of R_0 greater than the threshold 3.5, vaccination is helpful and controls the disease.

In conclusion, as vaccination is very costly, it is important to consider many factors before making a decision. When the diseases spread out very rapidly and they have high reproduction numbers and mortality rates, it is sensible to apply vaccination.

□