

Modeling Disease Epidemics with Markov Chains

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1 Introduction

Markov Chains are statistical models that are useful for modeling random processes. Specifically, Markov Chains are used to describe sequences of events that are independent from one another—in other words, they are useful for situations where the occurrence of a past event has no impact on the chance that future events will occur. Additionally, Markov Chains provide insight into what happens to these events as time goes to infinity. The applications of Markov Chains range extensively, from modeling exchange rates of currencies to understanding population growth. **In this project, we will use Markov Chains to model the spread of disease through a small population.** We begin with a simple model, using four possible states— *Susceptible (S)*, *Exposed (E)*, *Infected (I)*, and *Recovered(R)*— and then extend it further.

2 Background

Markov Chains, as described above, are mathematical descriptions used to describe how a multi-state system advances from one (independent) state to another according to probabilistic rules. Markov Chains can be written as *transition matrices* in which each column of the matrix represents the current states

and each row represents the possible states we could transition to. The stationary probability distribution

3 Calculations

3.1 SEIR Model

We model the spread of disease using a model with four states: Susceptible (S), Exposed (E), Infected (I), and Recovered (R) and refer to this model as an SEIR Model. The graphical representation of the Markov Chain and its corresponding transition matrix are shown below.

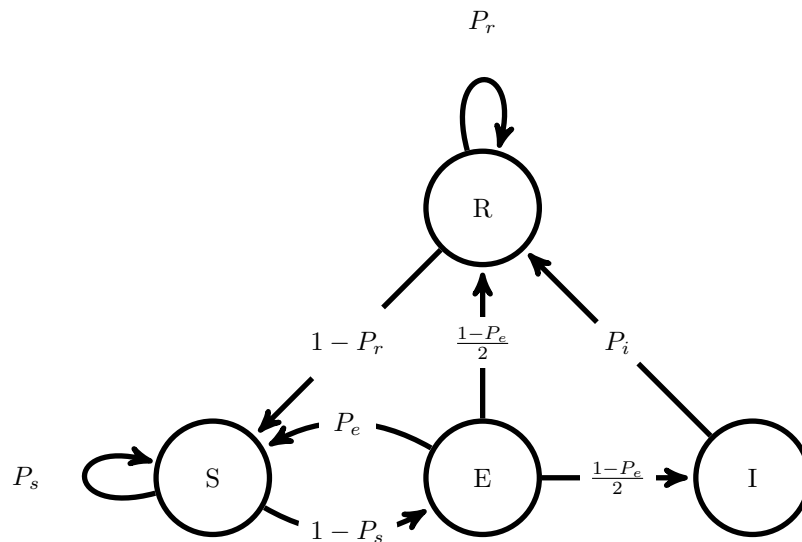


Figure 1: Graphical Representation of Markov Chain for SEIR Model

$$\begin{array}{c}
S \\
E \\
I \\
R
\end{array}
\begin{array}{c}
S \\
E \\
I \\
R
\end{array}
\begin{pmatrix}
P_s & 1 - P_s & 0 & 0 \\
P_e & 0 & \frac{1 - P_e}{2} & \frac{1 - P_e}{2} \\
0 & 0 & 0 & P_i \\
1 - P_r & 0 & 0 & P_r
\end{pmatrix}$$

Figure 2: Markov Transition matrix for SEIR Model

Probability Values: $P_s = 0.7, P_e = 0.4, P_i = 1, P_r = 0.8$

$$P = \begin{bmatrix} 0.7 & 0.3 & 0 & 0 \\ 0.4 & 0 & 0.3 & 0.3 \\ 0 & 0 & 0 & 1 \\ 0.2 & 0 & 0 & 0.8 \end{bmatrix} \tag{1}$$

Transition Matrix 1: SEIR Model with using probability value

The probability that an exposed individual will be in each state after one day of exposure is shown below.

$$\begin{aligned}
\text{Initial state}(X_0) &= \begin{bmatrix} 0 & 1 & 0 & 0 \end{bmatrix} \\
X_0 * P &= \begin{bmatrix} 0.4 & 0 & 0.3 & 0.3 \end{bmatrix}
\end{aligned}$$

The probability that a susceptible individual will be in each state after 5 days of exposure is shown below.

$$\begin{aligned}
\text{Initial state}(X_0) &= \begin{bmatrix} 1 & 0 & 0 & 0 \end{bmatrix} \\
\text{Five days of exposure} &= X_0 * P^5 = \begin{bmatrix} 0.46501 & 0.14655 & 0.04761 & 0.34083 \end{bmatrix}
\end{aligned}$$

The probability that an individual will be in state R after 5 days is $0.34083 = 34.01\%$.

3.2 Stationary Probability Distributions

In this section, we analyze the stationary probability distribution of our model. We begin by finding the stationary states for two different initial conditions by running the Markov Chain until the probability of being in every state approaches a limit. We note that changes associated with the initial state vectors do not affect the stationary distributions. Then, we demonstrate that the stationary distribution is unique and can be computed from only the transition matrix if the structure of the transition matrix is known.

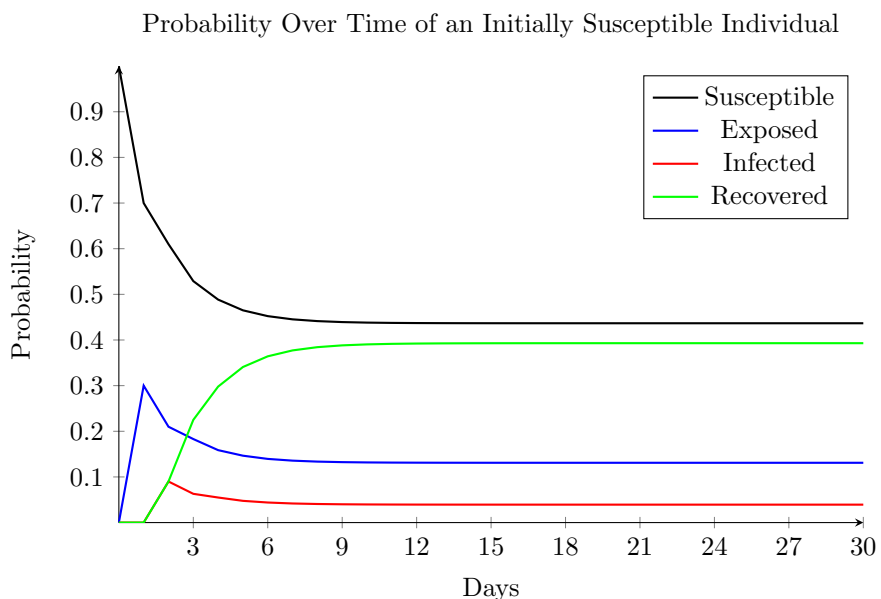


Figure 3: The probability of being in each state for an individual who is 100% susceptible to the disease

Because it appears that the probability of being in each state has remained stable and constant for over 2/3 of our sampling time, we can assume that we know the stationary distribution of this case to within a reasonable error.

The stationary distribution for an individual who is 100% susceptible to the disease is reported below.

Susceptible	Exposed	Infected	Recovered
0.4367	0.1310	0.0393	0.3930

Probability Over Time of an Individual with an 85% Chance of Exposure

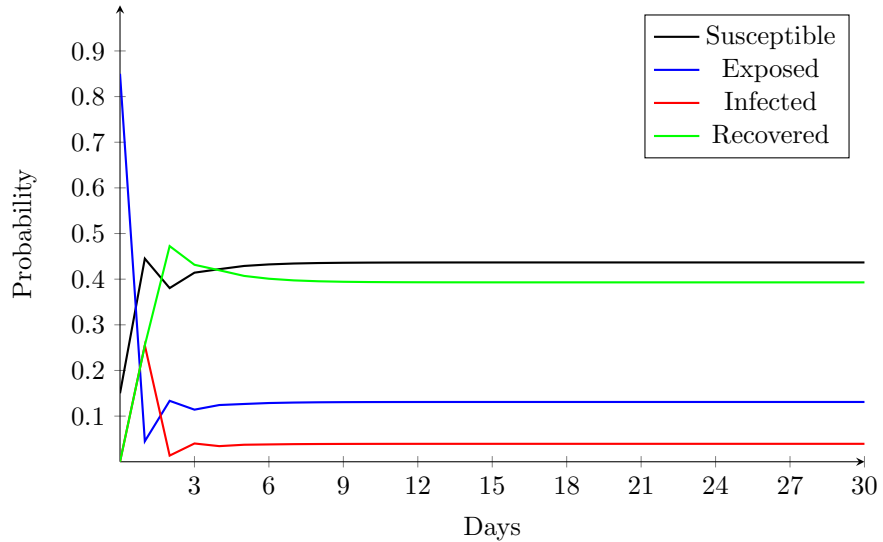


Figure 4: The probability of being in each state for an individual who has an 85% chance of exposure (and 15% susceptibility) to the disease

The stationary distribution for an individual with an 85% chance of exposure and 15% susceptibility is reported below.

Susceptible	Exposed	Infected	Recovered
0.4367	0.1310	0.0393	0.3930

If we compare the values of the probabilities in figures 2 and 3, the major differences are accounted for in the first 10 iterations. A plot of these differences is shown below.

Absolute Difference for First 10 Days

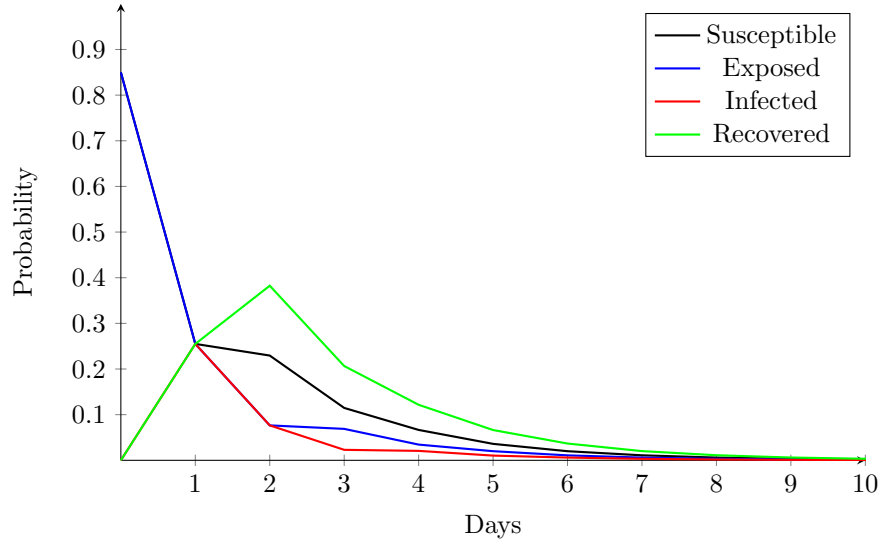


Figure 5: The absolute difference between the probabilities for an individual who is 100% susceptible and an individual who is 85% chance of exposure.

The differences in the initial state vectors can be accounted for by the fact that being exposed greatly increases the chance of an individual contracting the disease and becoming infected. For an individual who is 100% susceptible but has no chance of becoming exposed to the disease, they may remain susceptible (but not become exposed or infected) for a long period of time. In other words, it is a more stable state, because the likelihood of a change in state is lower, particularly in the first 3 days. This is evident in the relatively smooth curves in the probability curves in Figure 3. However, an 85% chance of exposure to the disease causes the probabilities of the other states to spike in the first three days, meaning that a change in state is likely during these days, and then rapidly stabilize. After 10 days, the probability of being in each state stabilizes to the same value. The differences in the initial state vectors do not influence the reported stationary distributions.

Using an initial state vector x_0 and a transition matrix for a Markov Chain \mathbb{P} whose structure is known, we compute the stationary distribution of the Markov Chain without iterating.

Relevant equations:

Definition of eigenvector, where A is a square matrix and λ is a scalar.

$$A\vec{u} = \lambda\vec{u} \quad (2)$$

If \mathbb{P} is an n -dimensional transition matrix with n distinct eigenvalues, it has n distinct eigenvectors. We can express x_0 as a linear combination of the eigenvectors of \mathbb{P} .

$$\vec{x}_0 = c_1\vec{v}_1 + c_2\vec{v}_2 + \dots + c_n\vec{v}_n \quad (3)$$

Using the linear combination found above and the definition of an eigenvector (Equation 2), we can express the N -step state vector \vec{x}_N of the Markov Chain in terms of the transition matrix's eigenvalues and eigenvectors.

$$\begin{aligned} \vec{x}_N &= \mathbb{P}^N(c_1\vec{v}_1 + c_2\vec{v}_2 + \dots + c_n\vec{v}_n) \\ &= c_1\mathbb{P}^N\vec{v}_1 + c_2\mathbb{P}^N\vec{v}_2 + \dots + c_n\mathbb{P}^N\vec{v}_n \end{aligned} \quad (4)$$

Since we know that

$$\mathbb{P}\vec{u} = \lambda\vec{u} \quad (5)$$

from Equation 2, we conclude that $\mathbb{P} = \lambda$. Equation 4 becomes the following:

$$\vec{x}_N = c_1\lambda_1^N\vec{v}_1 + c_2\lambda_2^N\vec{v}_2 + \dots + c_n\lambda_n^N\vec{v}_n \quad (6)$$

If the stationary distribution is unique, the magnitudes of the eigenvalues can be ordered

$$|\lambda_1| > |\lambda_2| \geq \dots \geq |\lambda_n| \quad (7)$$

The largest eigenvalue of the matrix is always

$$\lambda_1 = 1 \tag{8}$$

Since we know all eigenvalues except for λ_1 will be strictly less than 1, and by Equation 8, all terms except the first will go to zero.

$$\lim_{N \rightarrow \infty} c_1 \lambda_1^N v_1 + c_2 \lambda_2^N v_2 + \dots + c_n \lambda_n^N v_n = c_1 \lambda_1^N v_1 = c_1 v_1 \tag{9}$$

Eigenvalues for Transition Matrix:

$$\lambda_1 = 1 > \lambda_2 = 0.5496 \geq \lambda_3 = 0.1579 \geq \lambda_4 = -0.2075 \tag{10}$$

Eigenvectors for Transition Matrix:

$$v_1 = \begin{bmatrix} 0.7239 \\ 0.2172 \\ 0.0652 \\ 0.6515 \end{bmatrix}, v_2 = \begin{bmatrix} -0.4571 \\ -0.2495 \\ -0.1362 \\ 0.8428 \end{bmatrix}, v_3 = \begin{bmatrix} -0.1291 \\ -0.2452 \\ -0.4660 \\ 0.8403 \end{bmatrix}, v_4 = \begin{bmatrix} -0.3136 \\ 0.4534 \\ -0.6557 \\ 0.5158 \end{bmatrix}$$

Since v_1 corresponds to the first eigenvalue λ_1 , we get the stationary distribution by normalizing the vector and we determine that $c_1 = 1/(\text{sum elements of } v_1) \approx 1/1.6578$.

Stationary Distribution:

Susceptible	Exposed	Infected	Recovered
0.4367	0.1310	0.0393	0.3930

The absolute error in the computed stationary distribution at each iteration step is

$$(Abs.Error)_n = |\vec{X}_\infty - \vec{x}_n| \quad (11)$$

We again perform 31 steps of the SEIR Markov chain and plot the semilog-y of the absolute error against the iteration graph below.

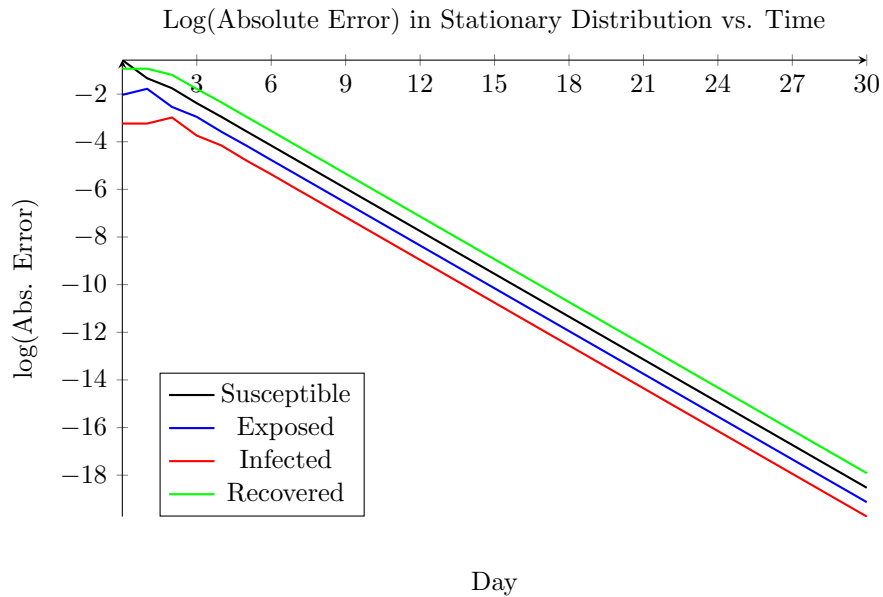


Figure 6: The plot of the $\log(\text{absolute error})$ against iteration step. Note that the result of the graph is linear.

Since the plot is linear on the semi-log y-axis, we conclude that the Markov Chain converges exponentially toward the stationary distribution.

3.3 Further Extending the Model

We now add a fifth state called the Immune (Im) state to extend our model. The new graphical representation of the Markov Chain for the SEIR-Im model is shown below, along with its corresponding probability matrix.

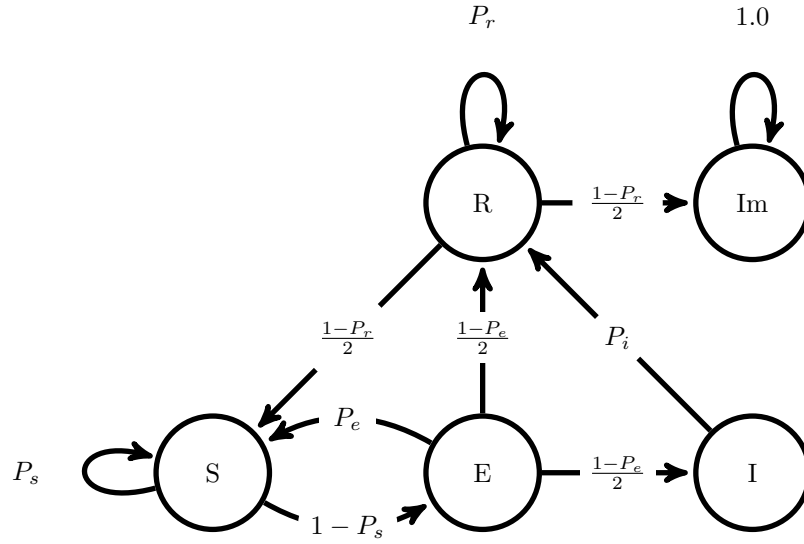


Figure 7: Graphical Representation of Markov Chain for SEIR-Im Model

$$\begin{array}{c}
 S \\
 E \\
 I \\
 R \\
 Im
 \end{array}
 \begin{pmatrix}
 S & E & I & R & Im \\
 P_s & 1 - P_s & 0 & 0 & 0 \\
 P_e & 0 & \frac{1 - P_e}{2} & \frac{1 - P_e}{2} & 0 \\
 0 & 0 & 0 & P_i & 0 \\
 \frac{1 - P_r}{2} & 0 & 0 & P_r & \frac{1 - P_r}{2} \\
 0 & 0 & 0 & 0 & 1.0
 \end{pmatrix}$$

Figure 8: Markov Transition matrix for SEIR-Im Model

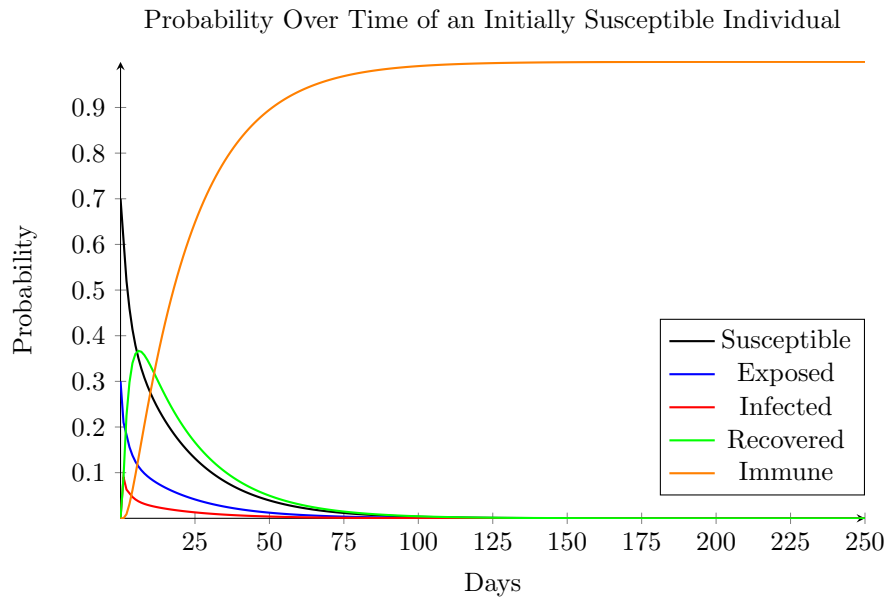


Figure 9: A plot of the probability of being in each state for individual who is 100% susceptible over the course of 250 days

Stationary distribution:

Susceptible	Exposed	Infected	Recovered	Immune
0	0	0	0	1

The stationary distribution for the SEIR-Im model is different from the SEIR model because the transition matrices are different. As a result the eigenvector we use to calculate the stationary distribution will be different, and therefore the stationary distribution will change.

If the only way to develop immunity to the disease is through vaccination, our Markov Chain will change. We represent this new Markov Chain using the

transition matrix below.

$$P = \begin{bmatrix} 0.7 & 0.3 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0.5 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0.2 & 0 & 0 & 0.8 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.25 & 0.75 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \quad (12)$$

Transition Matrix 2: SEIR-VIm Model with using probability value

The eigenvalues of the new transition matrix were computed and are shown below.

$$\lambda_1 = -0.1714 + 0.0000i$$

$$\lambda_2 = 0.3357 + 0.2497i$$

$$\lambda_3 = 0.3357 - 0.2497i$$

$$\lambda_4 = 1.0000 + 0.0000i$$

$$\lambda_5 = 1.0000 + 0.0000i$$

$$\lambda_6 = 0.2500 + 0.0000i$$

The multiplicity of the eigenvalue $\lambda = 1$ is 2. This implies that the stationary distribution is not unique. The structural feature(s) of the transition matrix that might account for this are the 4x4 matrix in the top left corner within the transition matrix and the 2x2 matrix in the bottom right corner. These two matrices represent the SEIR and VIm parts of the probability distribution, respectively. There are two columns of zeros on the right representing the VIm states, which means there is no way to get from the SEIR states to either of the VIm states. The bottom two rows of zeros can be interpreted the same way; there is no way to get from the VIm states to the SEIR states. Thus, there must be multiple stationary distributions.

The graph below shows the probability of being in each state at a given iteration for an individual who is susceptible to the disease with probability 1.

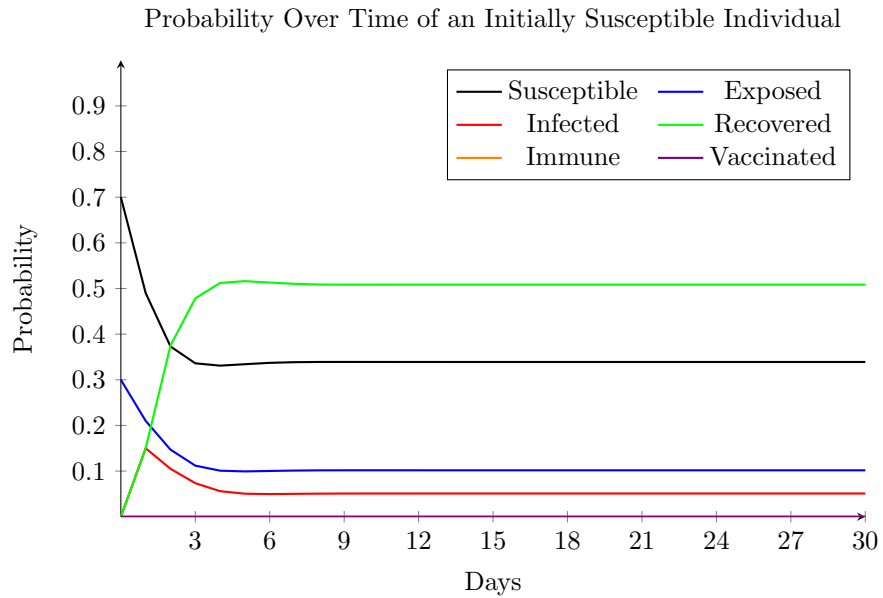


Figure 10: Plot of the probability of being in each state for an individual who is initially 100% susceptible over the course of 30 days using the SEIR-VIm model

Stationary Distribution:

Susceptible	Exposed	Infected	Recovered	Immune	Vaccinated
0.3390	0.1017	0.0508	0.5085	0	0

The graph below shows the probability of being in each state at a given iteration for an individual with a 33% chance of susceptibility and a 67% chance he or she was vaccinated.

Probability Over Time of an Individual with a 67% of Vaccination

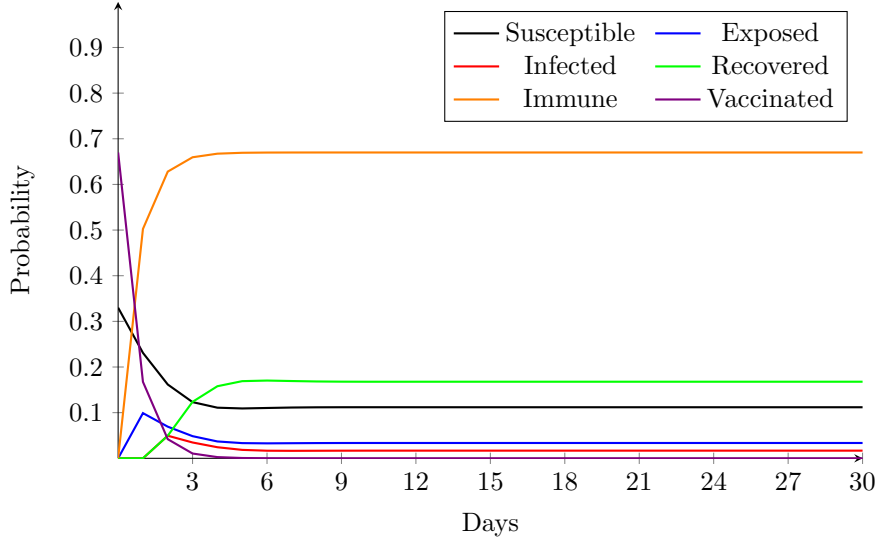


Figure 11: The plot of the probability of being in each state for an individual who is initially 33% susceptible and has a 67% chance of being vaccinated, over the course of 30 days using the SEIR-VIm model

Stationary Distribution:

Susceptible	Exposed	Infected	Recovered	Immune	Vaccinated
0.119	0.0336	0.0168	0.1678	0.67	0

Based on the results above, the stationary distribution depends on the ratio of individuals that begin in the SEIR states or in the VIm states. In the stationary distribution for an individual who is 100% susceptible, the stationary distribution has no individuals that end up in the Immune or Vaccinated states. In the stationary distribution for an individual who is 33% susceptible to disease and has a 67% chance of being vaccinated, the chance of ending up in the SEIR states is 33% times the probabilities of those in the SEIR states for the stationary distribution of 100% susceptibility—the ratios align. Additionally, all 67% of individuals who get vaccinated end up Immune; this is the exact probability of the chance of vaccination. There is no crossover between the SEIR popula-

tion and the VIm population, because there is no path between the two. This is predicted by the same structural feature of the transition matrix as described on page 12.

4 Conclusion

Ultimately, we conclude that all vaccinated individuals have a 100% immunity rate to the disease. Getting vaccinated is better for society than not getting vaccinated due to the model showing there is no feasible way to translate from SEIR states to a state of immunity.

Appendix

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```
clear all;  
close all;
```

SEIR



```
P = [.7,.3,0,0;  
     .4,0,.3,.3;  
     0,0,0,1;  
     .2,0,0,.8];
```

```
%Initially Exposed
```

```
XE = [0,1,0,0];  
OneDay = XE*P;
```

```
disp(OneDay);
```

```
%Initially Exposed
```

```
XS = [1,0,0,0];  
FiveDays = XS*P^5;
```

```
disp(FiveDays);
```

```
0.4000      0      0.3000      0.3000  
0.4650      0.1465      0.0476      0.3408
```

Stationary Probability Distrubutions



```
%Creating a 31 iterated matrix for susceptible  
S_iteration = zeros(31,4);
```

```
for i=1:31  
    val = XS*P^(i-1);  
    S_iteration(i,1:4) = val/sum(val);  
end
```

```

end

csvwrite("3[1a].csv",S_iteration);

%Graphing Probabilities
figure(1)

hold on

plot(1:31,S_iteration(1:31,1))
plot(1:31,S_iteration(1:31,2))
plot(1:31,S_iteration(1:31,3))
plot(1:31,S_iteration(1:31,4))

legend("Susceptible","Exposed","Infected","Recovered")

xlabel("Days")
ylabel("Probability")
title("Susceptible Persons Probabilty Over Time")

hold off

%Creating a 31 interated matrix for susceptible and exposed
SE_iteration = zeros(31,4);

for i=1:31
    val = [.15,.85,0,0]*P^(i-1);
    SE_iteration(i,1:4) = val/sum(val);
end

csvwrite("3[2a].csv",SE_iteration);

%Graphing Probabilities
figure(2)

hold on

plot(1:31,SE_iteration(1:31,1))
plot(1:31,SE_iteration(1:31,2))
plot(1:31,SE_iteration(1:31,3))
plot(1:31,SE_iteration(1:31,4))

legend("Susceptible","Exposed","Infected","Recovered")

xlabel("Days")
ylabel("Probability")
title("Exposed and Susceptible Persons Probabilty Over Time")

hold off

```

```

figure(3)

hold on

plot(1:11,abs(SE_iteration(1:11,1)-S_iteration(1:11,1)))
plot(1:11,abs(SE_iteration(1:11,2)-S_iteration(1:11,2)))
plot(1:11,abs(SE_iteration(1:11,3)-S_iteration(1:11,3)))
plot(1:11,abs(SE_iteration(1:11,4)-S_iteration(1:11,4)))

legend("Susceptible","Exposed","Infected","Recovered")

xlabel("Days")
ylabel("Diference in Probability")
title("Differance Over Time")

hold off

%finding staeady state solutions
loc = find(eig(P')==max(eig(P')));
[V,D] = eig(P');
M = V(:,loc)';M = M./sum(M);
disp("Staedy State Solution")
disp(M)

csvwrite("3[3].csv",abs(SE_iteration-S_iteration));

% 3.1 4d/////////

error = zeros(31,4);
for i=1:31
    N = XS*P^(i-1)./sum(XS*P^(i-1));
    error(i,1:4) = log(abs(N-M));
end

figure(8)
hold on

plot(1:31,error(1:31,1))
plot(1:31,error(1:31,2))
plot(1:31,error(1:31,3))
plot(1:31,error(1:31,4))

legend("Susceptible","Exposed","Infected","Recovered")

xlabel("Days")
ylabel("Probability")
title("3.1 4d")

hold off

csvwrite("3[4d].csv",error);

```

```

%SEIR-Im model

PIm = [.7,.3,0,0,0;
       .4,0,.3,.3,0;
       0,0,0,1,0;
       .1,0,0,.8,.1;
       0,0,0,0,1];

%Creating a 31 iterated matrix for susceptible
SEIR_IM_iteration = zeros(250,5);

for i=1:251
    val = [1,0,0,0,0]*PIm^(i-1);
    SEIR_IM_iteration(i,1:5) = val/sum(val);
end

%Graphing Probabilities
figure(4)

hold on

plot(1:251,SEIR_IM_iteration(1:251,1))
plot(1:251,SEIR_IM_iteration(1:251,2))
plot(1:251,SEIR_IM_iteration(1:251,3))
plot(1:251,SEIR_IM_iteration(1:251,4))
plot(1:251,SEIR_IM_iteration(1:251,5))

legend("Susceptible","Exposed","Infected","Recovered","Immune")

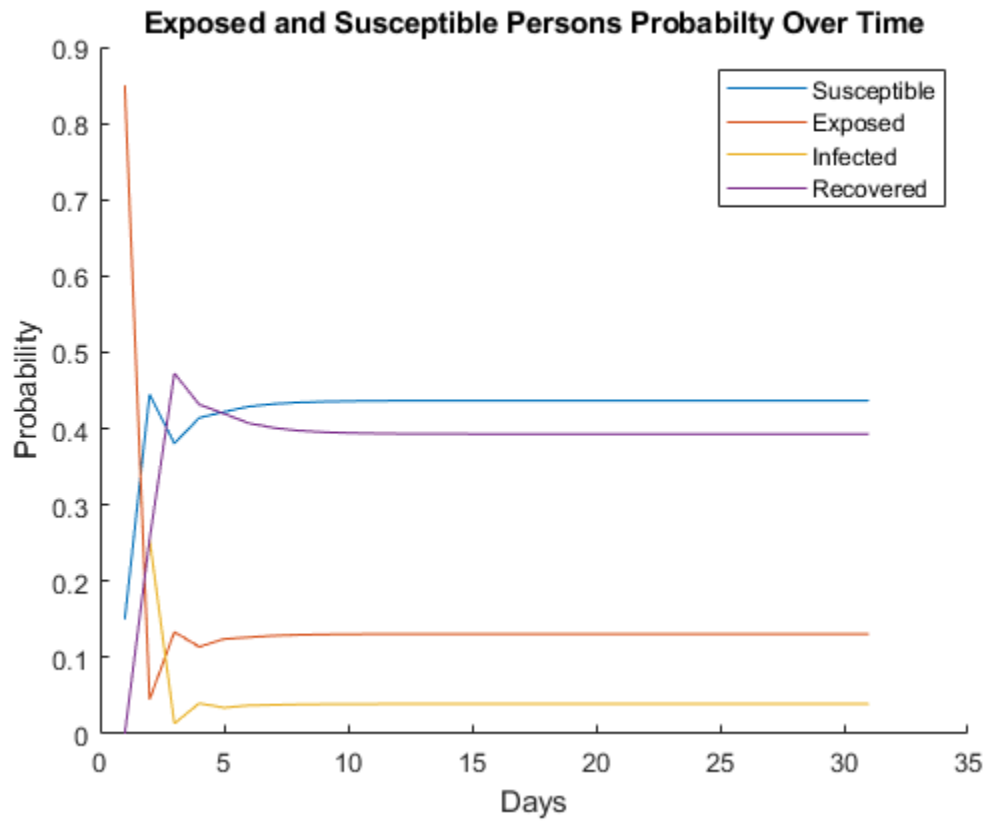
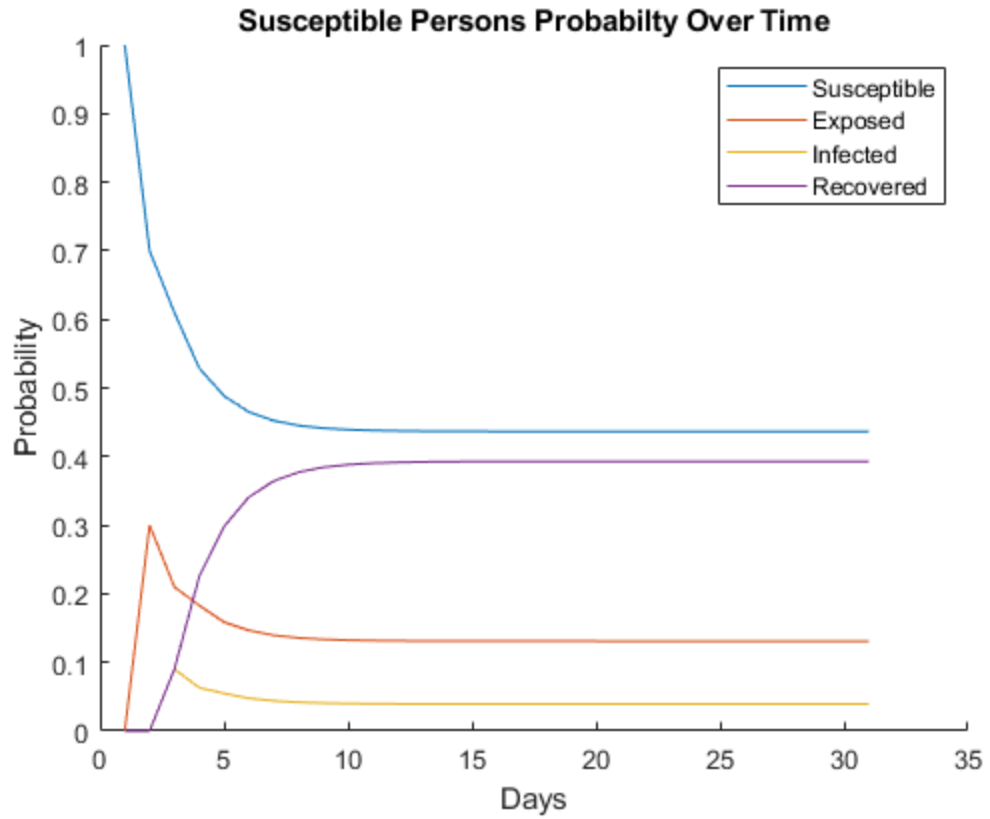
xlabel("Days")
ylabel("Probability")
title("SEIR-Im Model Using a Susceptible Person")

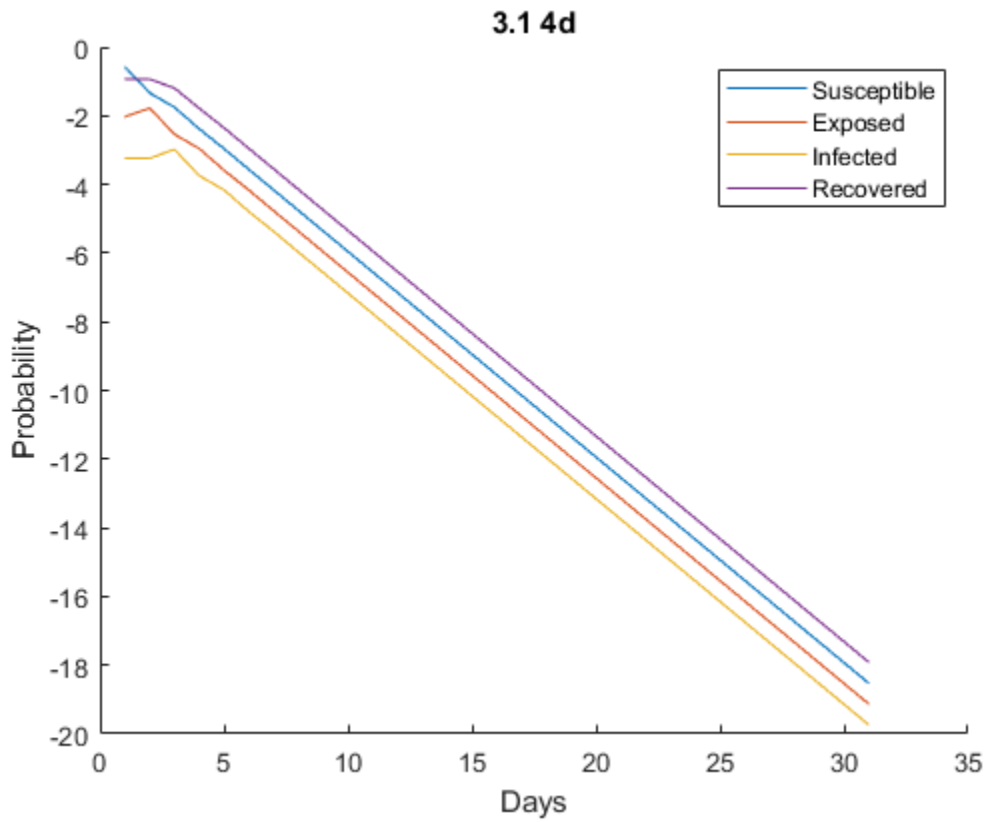
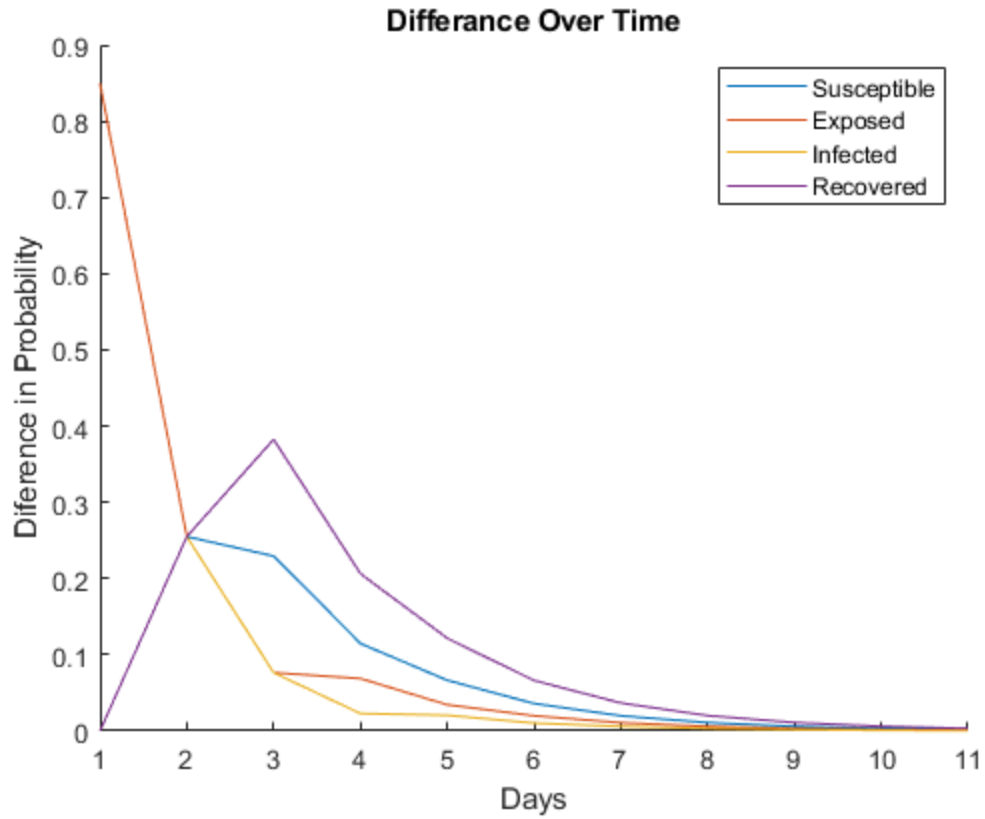
hold off

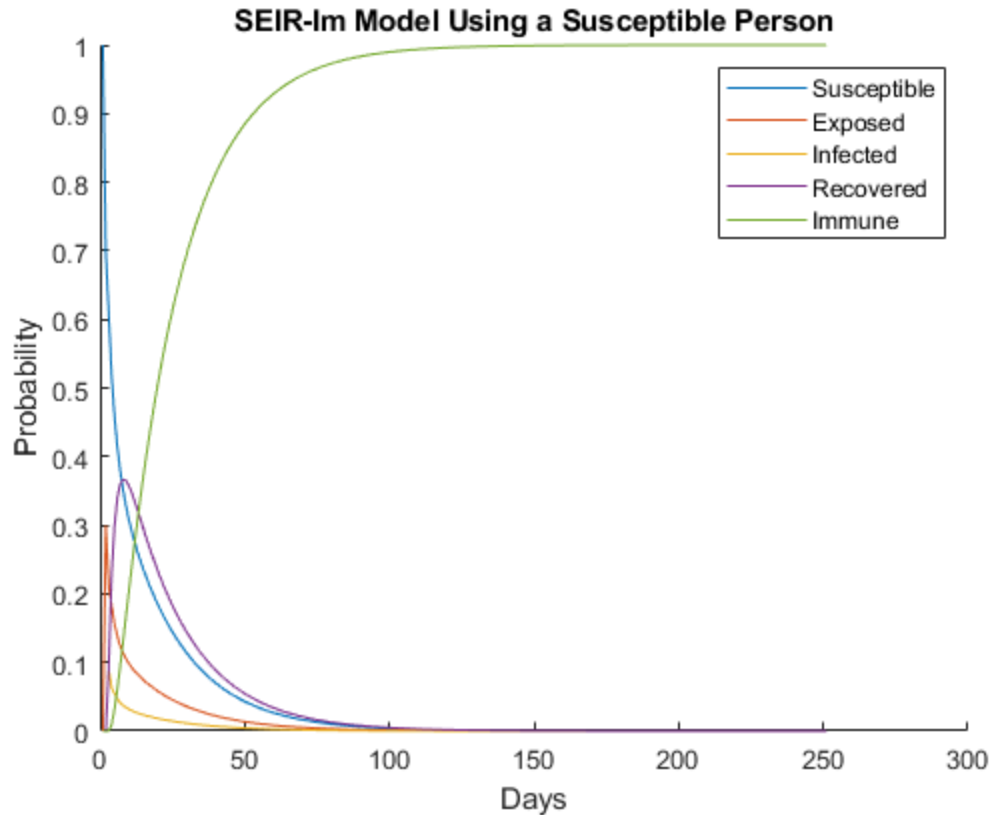
csvwrite("3[5c].csv",SEIR_IM_iteration);

Steady State Solution
    0.4367    0.1310    0.0393    0.3930

```







SEIR-VIm model

```

P_SEIR_IMV = [0.7 0.3 0 0 0 0;
              0 0 0.5 0.5 0 0;
              0 0 0 1 0 0;
              0.2 0 0 0.8 0 0;
              0 0 0 0 1 0;
              0 0 0 0 0.75 0.25];

%finding eigenvalues
EigenValues = eig(P_SEIR_IMV');

%Calulating Susceptibility

SEIRIMV_iteration = zeros(30,6);

for i=1:31
    val = [1,0,0,0,0,0]*P_SEIR_IMV^i;
    SEIRIMV_iteration(i,1:6) = val/sum(val);
end

%Graphing Probabilities
figure(5)

hold on

```

```

plot(1:31,SEIRIMV_iteration(1:31,1))
plot(1:31,SEIRIMV_iteration(1:31,2))
plot(1:31,SEIRIMV_iteration(1:31,3))
plot(1:31,SEIRIMV_iteration(1:31,4))
plot(1:31,SEIRIMV_iteration(1:31,5))
plot(1:31,SEIRIMV_iteration(1:31,6))
legend("Susceptible","Exposed","Infected","Recovered","Immune","Vaccinated")

xlabel("Days")
ylabel("Probability")
title("SEIR-ImV Model Using a Susceptible Person")

hold off
csvwrite("4[3].csv",SEIRIMV_iteration)
SEIRIMV2_iteration = zeros(30,6);

for i=1:31
    val = [.33,0,0,0,0,.67]*P_SEIR_IMV^(i-1);
    SEIRIMV2_iteration(i,1:6) = val/sum(val);
end

%Graphing Probabilities
figure(6)

hold on

plot(1:31,SEIRIMV2_iteration(1:31,1))
plot(1:31,SEIRIMV2_iteration(1:31,2))
plot(1:31,SEIRIMV2_iteration(1:31,3))
plot(1:31,SEIRIMV2_iteration(1:31,4))
plot(1:31,SEIRIMV2_iteration(1:31,5))
plot(1:31,SEIRIMV2_iteration(1:31,6))

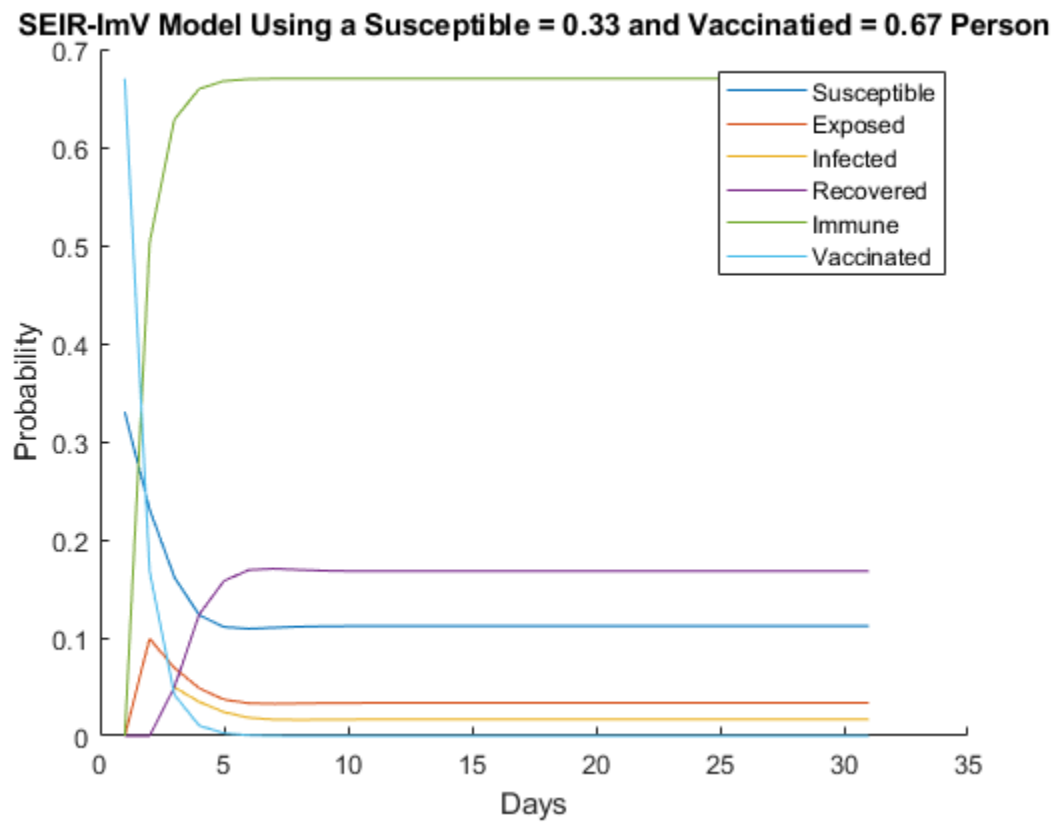
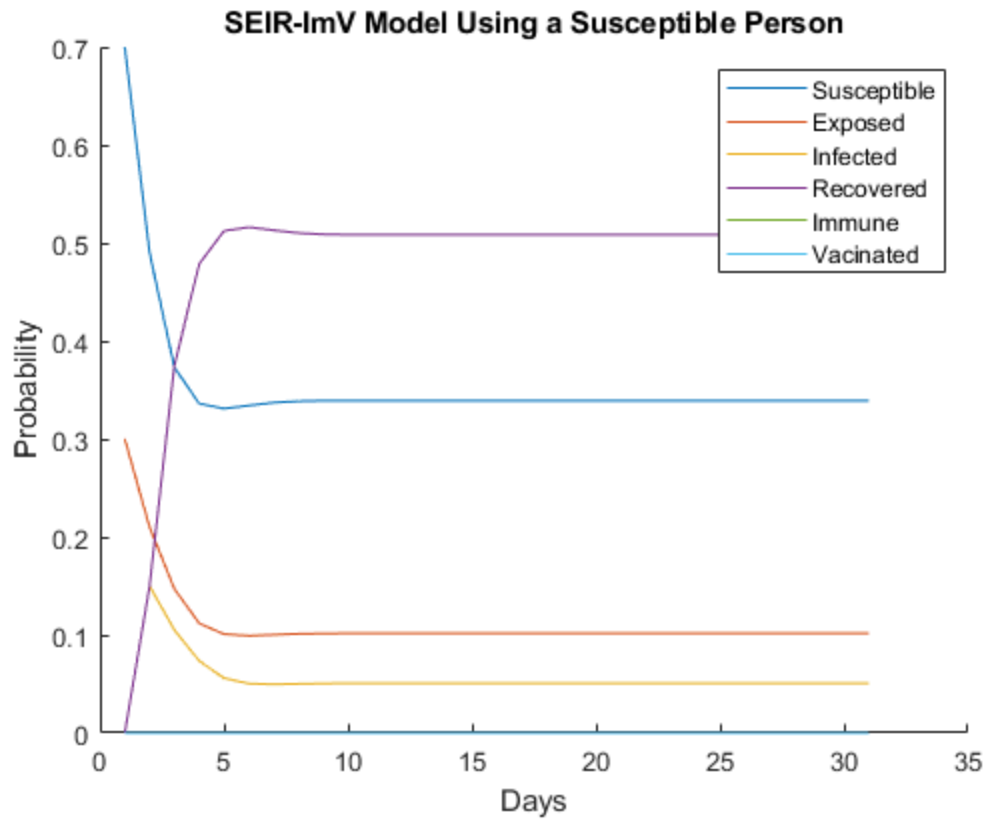
legend("Susceptible","Exposed","Infected","Recovered","Immune","Vaccinated")

xlabel("Days")
ylabel("Probability")
title("SEIR-ImV Model Using a Susceptible = 0.33 and Vaccinated =
    0.67 Person")

hold off

csvwrite("4[4].csv",SEIRIMV2_iteration)

```



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