

APPM 2360 Project 2

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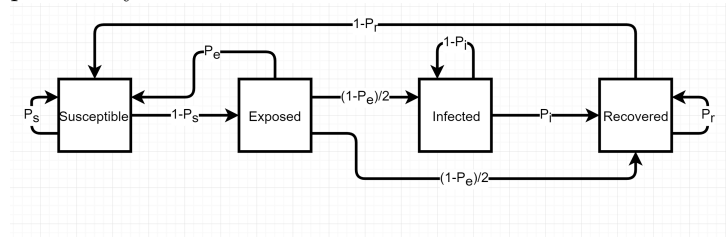
1 Introduction

A Markov Chain is a mathematical description for how a multi-state system advances from one state to another according to certain probabilistic rules. The key feature of a Markov Chain is that the next state visited in the system depends only on the current state, not on any previously visited states (the process is memoryless). This is used to model disease epidemics within small populations. For this analysis, the population experiencing the epidemic is divided into several groups:

Susceptible (S)
Exposed (E)
Infected (I)
Recovered (R)
Immune (Im)
Vaccinated (V)

2 Modeling Small Population Epidemics with Markov Chain

Graphical representation for a general susceptible, exposed, infected, recovered probability as a Markov chain:



The transition matrix for this chain is

$$\begin{matrix} & \text{SEIR} \\ \begin{bmatrix} 0.7 & 0.4 & 0 & 0.2 \\ 0.3 & 0 & 0 & 0 \\ 0 & 0.3 & 0 & 0 \\ 0 & 0.3 & 1 & 0.8 \end{bmatrix} \end{matrix}$$

An individual who is exposed to the disease will have the initial state matrix:

$$\begin{bmatrix} 0 \\ 1 \\ 0 \\ 0 \end{bmatrix}$$

and multiplying it by the transition matrix, the probability that individual will be in each state after one iteration will be:

$$\begin{bmatrix} 0.4 \\ 0 \\ 0.3 \\ 0.3 \end{bmatrix}$$

This means that after one day if someone is exposed there is a 40% chance that an exposed person becomes susceptible a 30% chance that they become infected and a 30% chance they become recovered.

If you want to know where someone who is susceptible will be in 5 days you have to multiply the transition matrix by itself five times and then by the initial matrix:

$$\begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

this will give the Matrix

$$\begin{bmatrix} 0.4650 \\ 0.1466 \\ 0.0476 \\ 0.3408 \end{bmatrix}$$

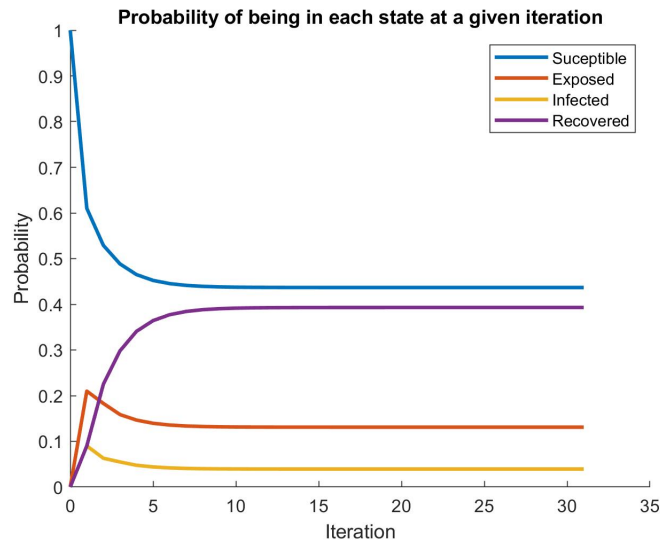
This means that after 5 days the chance a susceptible person stays that way is 46.5%, go on to be exposed 14%, go on to be infected 4.76% and become recovered is 34.08%

3 Stationary Probability Distributions

The stationary distribution is within reasonable error because when another step is taken (32 total) the values of stationary distribution do not change up to the 4th decimal point. This is therefore an accurate estimate of the true stationary distribution.

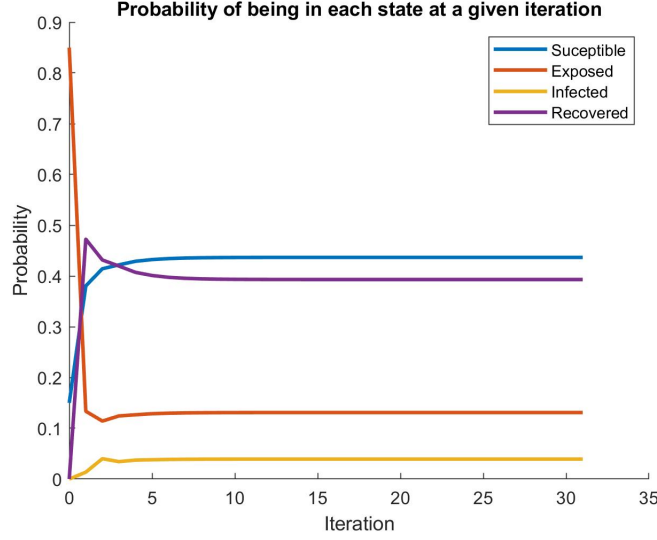
With 31 steps and an initial probability of Susceptible = 1 the stationary distribution is:

$$\begin{bmatrix} 0.4367 \\ 0.1310 \\ 0.0393 \\ 0.3930 \end{bmatrix}$$



With 31 steps and an initial probability of Susceptible = 0.15 and Exposed = 0.85 the stationary distribution is:

$$\begin{bmatrix} 0.4367 \\ 0.1310 \\ 0.0393 \\ 0.3930 \end{bmatrix}$$



The first 10 steps through the Markov Chain to calculate both plots above have a difference due to the different initial condition. The stationary distributions tend towards each other and at 31 steps, the stationary distribution of initial condition Susceptible = 1 and initial condition Susceptible = 0.15 and Exposed = 0.85 have equal stationary distributions. This is because the stationary distribution refers to the data when there is infinite steps. This shows the probabilities of each group for any arbitrary day and thus with unknown previous condition.

Initial Condition S = 1										
Step:	1	2	3	4	5	6	7	8	9	10
S	0.7	0.61	0.529	0.4885	0.46501	0.452293	0.445254	0.441394	0.439271	0.438105
E	0.3	0.21	0.183	0.1587	0.14655	0.139503	0.135688	0.133576	0.132418	0.131781
I	0	0.09	0.063	0.0549	0.04761	0.043965	0.041851	0.040706	0.040073	0.039726
R	0	0.09	0.225	0.2979	0.34083	0.364239	0.377207	0.384323	0.388238	0.390388
Initial Condition S = 0.15, E = 0.85										
Step:	1	2	3	4	5	6	7	8	9	10
S	0.445	0.3805	0.41425	0.421945	0.428979	0.432349	0.434318	0.435379	0.435966	0.436288
E	0.045	0.1335	0.11415	0.124275	0.126584	0.128694	0.129705	0.130296	0.130614	0.13079
I	0.255	0.0135	0.04005	0.034245	0.037283	0.037975	0.038608	0.038911	0.039089	0.039184
R	0.255	0.4725	0.43155	0.419535	0.407156	0.400982	0.397369	0.395414	0.394332	0.393738

The initial state vector represented as a linear combination of the eigenvectors of an arbitrary transition matrix is:

$$\vec{X}_0 = C_1 \vec{V}_1 + C_2 \vec{V}_2 + \dots + C_n \vec{V}_n$$

And when this linear combination is applied to the state vector $\vec{X}_N = P^N \vec{X}_0$ and put in terms of the transition matrix's eigenvalues/eigenvectors

$$\vec{X}_N = C_1 \lambda_1^N \vec{V}_1 + C_2 \lambda_2^N \vec{V}_2 + \dots + C_n \lambda_n^N \vec{V}_n$$

And the fact that the eigenvalues of the transition matrix are ordered $|\lambda_1| > |\lambda_2| \geq \dots \geq |\lambda_n|$ and the largest eigenvalue of the matrix is always $\lambda_1 = 1$ shows that as $n \rightarrow \infty$ all but the first term in the \vec{X}_N equation above tend toward 0. Thus:

$$\vec{X}_\infty = C_1 \vec{V}_1$$

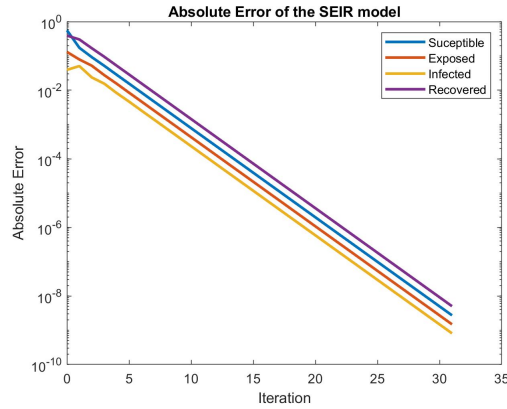
When this is applied to the SEIR model, the sum of the elements of $C_1 \vec{V}_1$ must equal 1. By dividing \vec{V}_1 by the sum of the elements of \vec{V}_1 the vector \vec{X}_∞ can be found.

$$\vec{X}_\infty = \vec{V}_1 / \Sigma \text{ elements of } \vec{V}_1 =$$

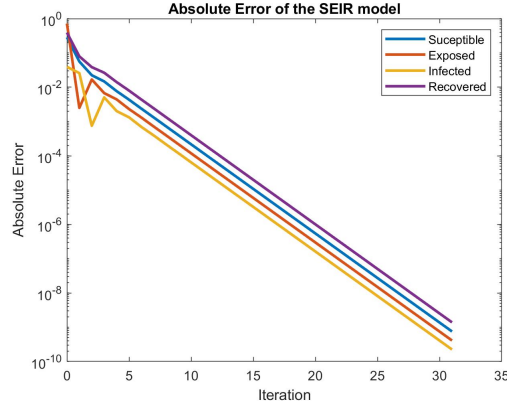
$$\begin{bmatrix} 0.4367 \\ 0.1310 \\ 0.0393 \\ 0.3930 \end{bmatrix}$$

The absolute error of each iteration of the SEIR model is calculated by: $(Abs.Error)_n = |\vec{X}_\infty - \vec{X}_n|$ with $n = \text{number of steps } (n = 1, 2, 3 \dots 31)$.

For the initial condition $S = 1$ the absolute error of each state from iteration 1 to 31 is shown in the graph below.



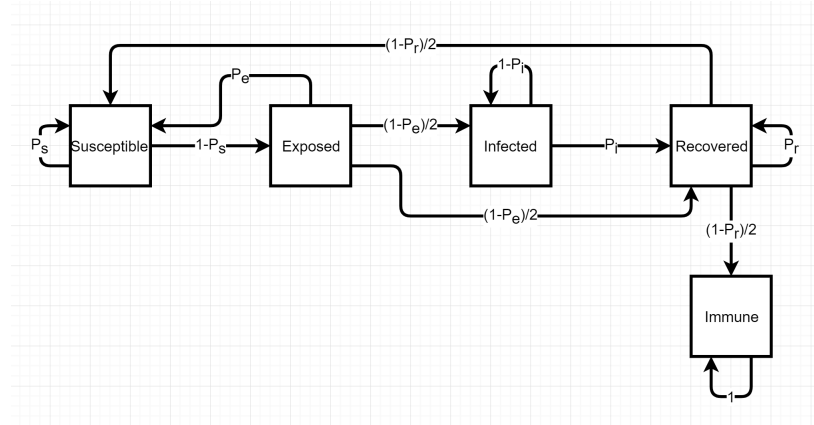
For the initial condition $S = 0.15$ $E = 0.85$ the absolute error of each state from iteration 1 to 31 is shown in the graph below.



From these graphs we can see the Markov chain converge towards the true stationary distribution at an exponential rate.

4 Adjustments to the Model

If a fifth state called "Immune (Im)" is added to the SEIR model to become a SEIR-Im model, the Markov Chain will be:

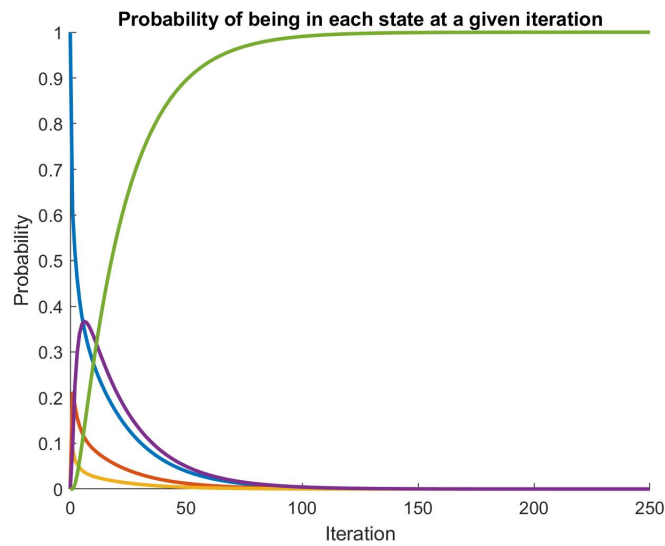


And the transition matrix for the Markov Chain will be:

$$\begin{bmatrix} 0.7 & 0.4 & 0 & 0.1 & 0 \\ 0.3 & 0 & 0 & 0 & 0 \\ 0 & 0.3 & 0 & 0 & 0 \\ 0 & 0.3 & 1 & 0.8 & 0 \\ 0 & 0 & 0 & 0.1 & 1 \end{bmatrix}$$

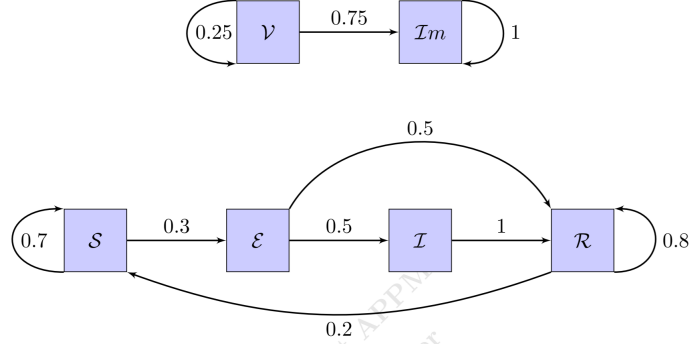
After 250 steps of the Markov chain, a stationary distribution of

$$\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 1 \end{bmatrix}$$



is calculated. The stationary distribution for the SEIR-Im model is not equal to the stationary distribution for the SEIR model because of the added group. The SEIR-Im model includes an immune group that once an individual becomes immune, they cannot move into any other group. After many Markov chain steps, which represents many days passing, eventually all individuals will become immune and the probability of being in any other group is 0.

5 Further Adjustments to the Model



The matrix for this Markov chain is:

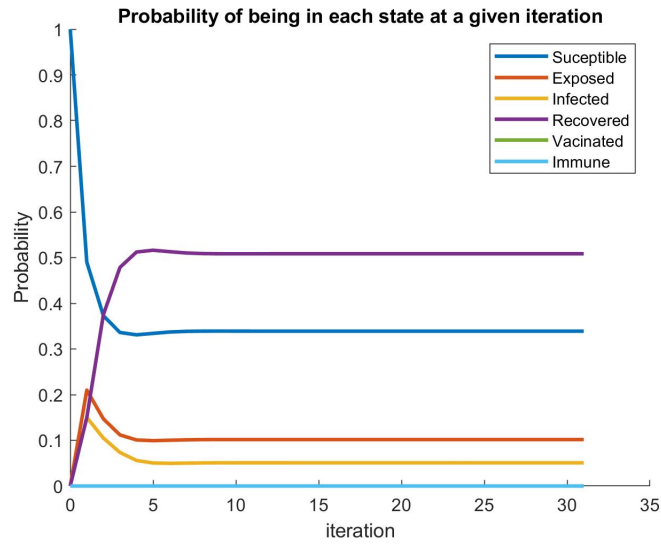
$$\begin{bmatrix} 0.7 & 0 & 0 & 0.2 & 0 & 0 \\ 0.3 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.5 & 0 & 0 & 0 & 0 \\ 0 & 0.5 & 1 & 0.8 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.25 & 0 \\ 0 & 0 & 0 & 0 & 0.75 & 1 \end{bmatrix}$$

This matrix comes in the form with two blocks of values separated by 0. This creates two sections of the matrix: rows 1-4 and rows 5-6, which are independent of each other.

This matrix has $\lambda = 1$ with multiplicity 2, this means that there can be two unique solutions, this is because the chain has two separate pieces that are not connected to each other. Which means that there are two different places that one can end up as time goes to infinity, depending on ones starting position.

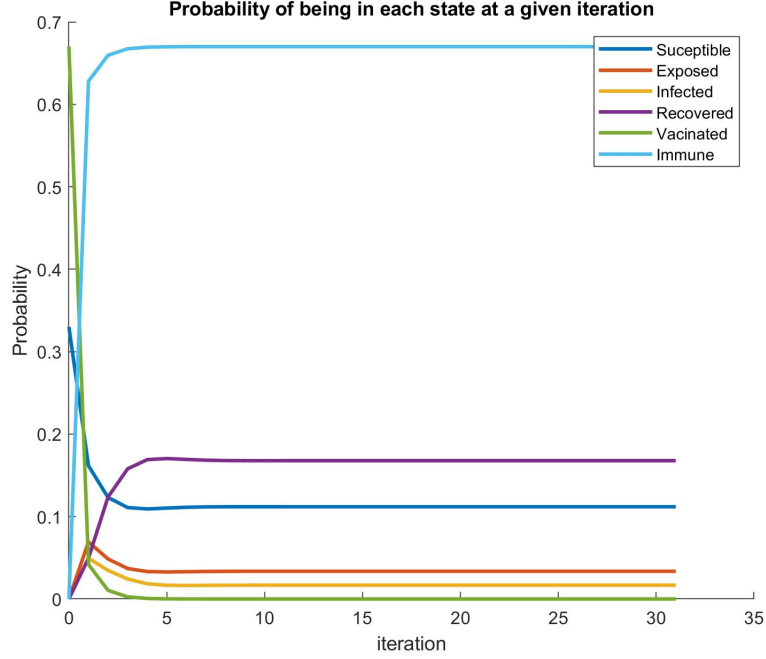
With 31 steps and an initial probability of Susceptible = 1 the stationary distribution is:

$$\begin{bmatrix} 0.3390 \\ 0.1017 \\ 0.0508 \\ 0.5085 \\ 0 \\ 0 \end{bmatrix}$$



With 31 steps and and initial probability of Susceptible = 0.33 and vaccination=0.67 the stationary distribution is:

$$\begin{bmatrix} 0.1119 \\ 0.0336 \\ 0.0168 \\ 0.1678 \\ 0.0000 \\ 0.6700 \end{bmatrix}$$



Since there are two separate chains it means that the standard distribution will not always be the same. It depends on the starting condition because there is no way for the chains to mix meaning that the total probability in each chain stays the same as what it started as.

6 Conclusion

Using Markov Chains, we found the probabilities of a population dividing into several states based on an initial probability. This can be used further to calculate the stationary distribution, showing the ultimate trend of the population. Eigenvalues/eigenvectors are also able to be used to calculate the stationary distribution ($\vec{X}_\infty = C_1 \vec{V}_1$) and probabilities of groups after N steps ($\vec{X}_N = C_1 \lambda_1^N \vec{V}_1 + C_2 \lambda_2^N \vec{V}_2 + \dots + C_n \lambda_n^N \vec{V}_n$) based on constants $C_1, C_2, C_3, \dots, C_n$ from the initial condition $\vec{X}_0 = C_1 \vec{V}_1 + C_2 \vec{V}_2 + \dots + C_n \vec{V}_n$.