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## Markov Chain Model for the Spread of an Epidemic

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MARKOV CHAIN MODEL FOR THE SPREAD OF AN  
EPIDEMIC

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submitted in partial fulfillment of the requirements for Honors in  
Mathematics at the University of Mary Washington

Fredericksburg, Virginia

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This thesis by **Abigail E. Bernhardt** is accepted in its present form as satisfying the thesis requirement for Honors in Mathematics.

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# Abstract

In this project, I analyze a mathematical model for the spread of an epidemic using techniques from statistics, probability, and differential equations to track and test the severity of an epidemic. I focus on chlamydia and use 2018 data from the Centers for Disease Control and Prevention which includes prevalence in all genders and ages within the United States. I manipulated MATLAB code for the analysis. The results are examined to understand the stochastic processes which capture the epidemic model. With this understanding, we can map the disease and raise awareness in the populations that are prone to infection, in an effort to change the outcome and rapid spread of disease.

# Contents

- 1 Stochastic Processes** **6**
- 1.1 Introduction . . . . . 6
  - 1.1.1 Discrete Random Variables . . . . . 7
- 1.2 Markov Chains . . . . . 8
- 1.3 Stochastic Matrix . . . . . 10
  
- 2 Epidemic Models** **13**
- 2.1 SI Model . . . . . 13
- 2.2 SIS Model . . . . . 15
  - 2.2.1 Examples . . . . . 17
- 2.3 SIS Differential Equations . . . . . 18
  
- 3 Simulation and Data Analysis** **20**
- 3.1 Data . . . . . 20
  - 3.1.1 Real-world Connection . . . . . 21
  
- 4 Appendices** **23**
- 4.1 MATLAB Code . . . . . 23
- References . . . . . 26

# Chapter 1

## Stochastic Processes

### 1.1 Introduction

Consider an experiment in which a coin is tossed. It may land on heads (H) or tails (T).

These are called outcomes, and together they give  $S = \{T, H\}$  which is called a sample space.

Now, if we define a function which assigns +1 for H and -1 for T, then  $X : S \rightarrow \mathbb{R}$ ,

$X(T) = -1$  and  $X(H) = 1$  is called a random variable. A collection of random variables

$\{X_t; t \in T\}$  defined on the same probability space is called a stochastic process, where  $t$

represents time. A stochastic process is a function that maps elements of an index set to

elements of a collection of random variables. Usually, the random variables are indexed by

points in time which provide the probability of an outcome to occur. Values that are assumed

by the random variable are called “states” and a collection of states is called a state-space.

An individual’s commute to work is an example of a stochastic process. Let the commute

to work consist of multiple routes, and each route represents a state in a stochastic process.

When an individual begins on one route then switches to another, this switch represents the

states transitioning in a stochastic process. Movement to the next route depends on which

route the individual is currently on, and not on past routes, just like the state of a stochastic

process depends on the current state and is independent from prior states. For each fixed  $t$ ,  $X_t(s)$  denotes a single random variable defined on  $S$ . For each fixed  $s \in S$ ,  $X_t(s)$  corresponds to a function defined on  $T$  which is called a sample path or a stochastic realization of the process [8].

This thesis focuses on applications of stochastic processes in the fields of Biology and Epidemiology. As such, the variation is due to deaths, births, immigration, and emigration. One fact about biological stochastic epidemic models is that they do eventually converge to a disease-free state [8]. Each stochastic model varies because every solution represents a single path from a unique probability distribution. Stochastic processes are quite interesting and they came to the forefront of science in the 1850s. Today, stochastic models are used to study phenomena in many disciplines.

Random variables may be discrete or continuous. They play a significant role in the study and application of stochastic processes. In this thesis, we focus on discrete random variables. A discrete random variable can only take a countable number of values and a finite or countable state-space is discrete. In a discrete model, state changes occur finitely or countably many times. For example, the number of gloves in a medical office is a discrete random variable.

### 1.1.1 Discrete Random Variables

Random variables are denoted by  $X$  and defined as a function of an outcome on a sample space. The outcome consists of numerical values of a random event, and the random variables are not the outcomes of a random event. Returning to the heads and tails example,

$X(T) = -1$  and  $X(H) = 1$  are the numerical values from the outcome, heads or tails.

One important function that goes with random variables is the probability mass function (PMF). Possible values for random variables are given by the PMF and are defined by,  $f(x) = P\{X =$



$x\}$ . This function shows the probability of the random variable taking on a value  $x$ . A simple example is tossing a fair coin twice and letting  $X$  represent the number of tails. The potential outcomes are given by  $S = \{TT, TH, HT, HH\}$ , which shows one can toss 0, 1 or 2 tails. Just looking at the PMF of tossing zero tails, we have  $P_X(0) = P(HH) = \frac{1}{4}$ . By definition, every PMF must satisfy two conditions:

$$(i) \sum_i f(x_i) = 1$$

$$(ii) 0 \leq f(x_i) \leq 1 \forall i$$

## 1.2 Markov Chains

The stochastic process  $\{X_n, n = 0, 1, 2, \dots\}$  that takes on a countable number of values is known as a Markov chain. It is denoted by the set of possible values of the process which does not include negative integers. Going back to the random variables, consider  $X_n = i$ ; this notation means the process is in state  $i$  at time  $n$ . The probability of being in state  $i$  is  $P(X = i)$ , and similarly the next state  $j$  has a probability  $P(X = j)$ . When the process is in state  $i$ , the chance of moving to state  $j$  is denoted by  $P(X_{n+1} = j / X_n = i) = p_{ij}$ . Markov stochastic processes never depend on past behavior, but instead depend solely on the present to guide the future. A few conditions come with moving states:

1.  $p_{ij} \geq 0$

2.  $i, j \geq 0$

3.  $\sum_{j=0}^{\infty} p_{ij} = 1$

4.  $i = 0, 1, 2, \dots$

The application of a Markov chain process is one of the most well-developed of all the

stochastic processes. The specific process we will be using is known as the discrete time Markov chain (DTMC) because both time and state-space are discrete.

Classification of states comes into play when dealing with the relationships between states. The first important definition is the accessibility of states from each other. We say state  $j$  is accessible from state  $i$ , denoted  $i \rightarrow j$ , if  $p_{ij}^n > 0$ . We can assume every state is accessible from itself, for example,  $p_{ii}^0 = 1$ . Another important term is communicate; denoted  $i \leftrightarrow j$ , two states  $i$  and  $j$  are said to communicate if they are accessible from each other. Markov chains can be sorted into communication classes which are made of members of the same class communicating with each other. A Markov chain is said to be irreducible if it has one communicating class, meaning all states communicate with each other. It is said to be recurrent if any time we leave the state, we return to the same state in the future with probability of 1. However, if returning to the same state is less than one, we call it transient. One simple way of showing if two states are in the same class is if both of them are either recurrent or both are transient. A communication class is closed if it is impossible to reach any state outside the set of states, from any state in the set of states, by one-step transitions.

A transition probability is when a process is in state  $i$  at time  $n$  and the next time step is  $n + 1$ . Transition probabilities are associated with various state changes, but will either stay in state  $i$  or transfer to state  $j$ . Transition probabilities that do not depend on time  $n$  are known as stationary or homogeneous, but if the transition probabilities are time dependent, they are non-stationary or non-homogeneous. In this work, we assume that states are stationary if not otherwise clarified.

### 1.3 Stochastic Matrix

A stochastic matrix is a square matrix which describes transition probabilities of moving from one state to another. The simplest matrix is a one-step transition matrix that shows the probabilities  $p_{ij}$ , demonstrated by

$$P_{ij} = \begin{pmatrix} p_{00} & p_{01} & p_{02} & \dots & p_{0j} \\ p_{10} & p_{11} & p_{12} & \dots & p_{1j} \\ \vdots & \vdots & \vdots & \dots & \vdots \\ p_{i0} & p_{i1} & p_{i2} & \dots & p_{ij} \end{pmatrix}$$

Each entry in the matrix is a non-negative real number which represents a probability, for example  $p_{12} = P(X_{n+1} = 2/X_n = 1)$ .

Transition probabilities are the probability of transitioning from one state to another in one step [5]. If the process is in state  $i$  at time  $n$ , then at the next time stamp,  $n + 1$ , it will either stay at  $i$  or move or transfer to another state. These states are explained through one-step transition probabilities. For a stochastic process, assume the change in time is minimal and only occurs from  $n$  to  $n + 1$  at any time. This concept means there is only one change in the random variable at any step in the process, and  $I_n$ , which is the number of infected and infectious individuals at time  $n$ , equals  $i$ , so  $I_{n+1}$  can be  $i$ ,  $i + 1$  or  $i - 1$ , meaning the number of infected individuals can go up or down. The transition probabilities are

$$p_{i+1,i} = Prob\{I_{n+1} = i + 1 | I_n = i\} = \frac{\beta i(N - i)}{N} \quad (1.1)$$

$$p_{i-1,i} = Prob\{I_{n+1} = i - 1 | I_n = i\} = (b + \gamma)i \quad (1.2)$$

$$p_{ii} = Prob\{I_{n+1} = i | I_n = i\} = 1 - \frac{\beta i(N - i)}{N} - (b + \gamma)i \quad (1.3)$$

$$p_{00} = 1 \quad (1.4)$$

$N$  is the total population,  $\beta$  is the number of contacts made by a single infected individual,  $b$  is the birth rate, and  $\gamma$  is the reproduction number. The state-space of  $I_n$  is  $S = \{0, 1, 2, \dots, N\}$  and  $i = 1, 2, \dots, N - 1$ .  $p_{00}$  represents the absorbing state, which is the probability the epidemic will die-off [8]. Meaning if no individuals are infected, what is the probability someone will be infected tomorrow? None.

If these probabilities do not depend on time, then they are called stationary, time-homogeneous or simply homogeneous. If the probabilities are dependent, they are said to be non-stationary or non-homogeneous. Unless a problem is stated otherwise, we will assume that the transition probabilities of DTMC are stationary. When considering the matrix, if the sets of states are finite, then  $P$  is an  $N \times N$  matrix. This stochastic matrix is a non-negative one in which every column adds up to 1. If the rows add up to one as well, the matrix is considered doubly stochastic. The matrix below displays the susceptible-infected-susceptible (SIS) model, which is an epidemic model that displays certain diseases where infected individuals return to the susceptible class. The SIS model will be described in detail later, but for now the transition matrix is formed when the states are ordered from 0 to  $N$ .

$$\begin{pmatrix} 1 & (b + \gamma) & 0 & \dots & 0 \\ 0 & 1 - \frac{\beta i(N-i)}{N} - (b + \gamma) & 2(b + \gamma) & \dots & 0 \\ 0 & \frac{\beta i(N-i)}{N} & 1 - \frac{\beta i(N-i)}{N} - 2(b + \gamma) & \dots & 0 \\ \vdots & \vdots & \vdots & \dots & \vdots \\ 0 & 0 & 0 & \dots & N(b + \gamma) \\ 0 & 0 & 0 & \dots & 1 - N(b + \gamma) \end{pmatrix}$$

This matrix shows there are two classes,  $\{0\}$  and  $\{1, 2, \dots, N\}$ . When  $p_{ij} = 0$ ,  $j \neq i-1, i, i+1$ .

The zero class represents the absorbing class, and everything else is transient. Eventually this model continues until there are no infected individuals.

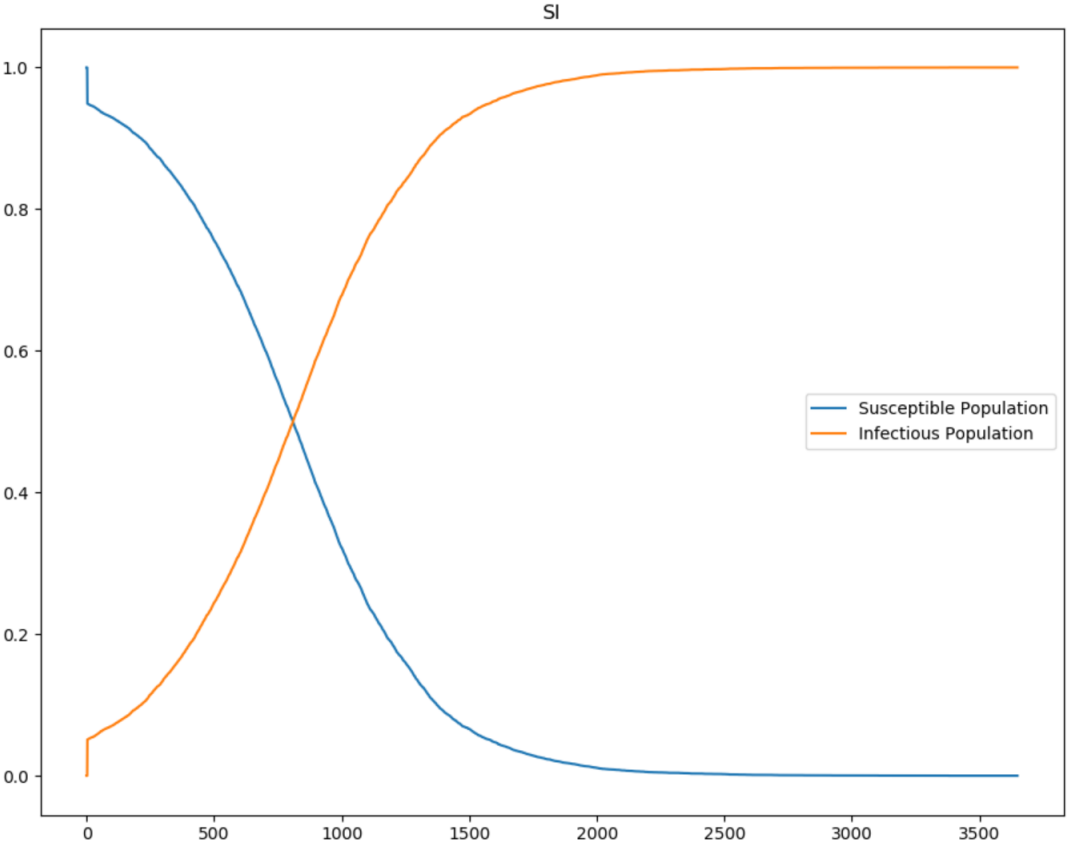
# Chapter 2

## Epidemic Models

### 2.1 SI Model

Susceptible-infectious (SI) model is the simplest form of a disease epidemic. The SI model occurs with specific infections where individuals do not develop immunity. In this case, a susceptible individual comes into contact with someone who is infected and from then on can never leave that state. This scenario results in lifelong infections that may flare up time and time again. One fact that is synonymous to all epidemics is that individuals are not born infected, but fall immediately into the susceptible class. This fact makes it easier to say that no one is born with an infectious disease. It is interesting that susceptible individuals live among the infected population without knowing who could transmit a disease to them. This model is a logistic growth model, because the number of infected individuals is continuously increasing and never decreases. The total population is represented by  $N = S + I$ , where  $N$  is the total population,  $S$  is the susceptible class, and  $I$  is the number of individuals infected with a disease.

Figure 2.1: The SI epidemic is shown. The susceptible population is shown in blue and the infectious population in orange. Every individual starts in the susceptible class since no one is born infected. More individuals become infected creating a decrease in the susceptible population. The intersection of the two curves represents an equilibrium where the number of susceptible individuals and infected individuals are equal. Post equilibrium shows the population now includes more infected individuals and fewer susceptible individuals. This pattern continues until ultimately every individual is included in the infectious population. Since this epidemic grows exponentially and it relies on no births or deaths, ultimately the whole population becomes infected.



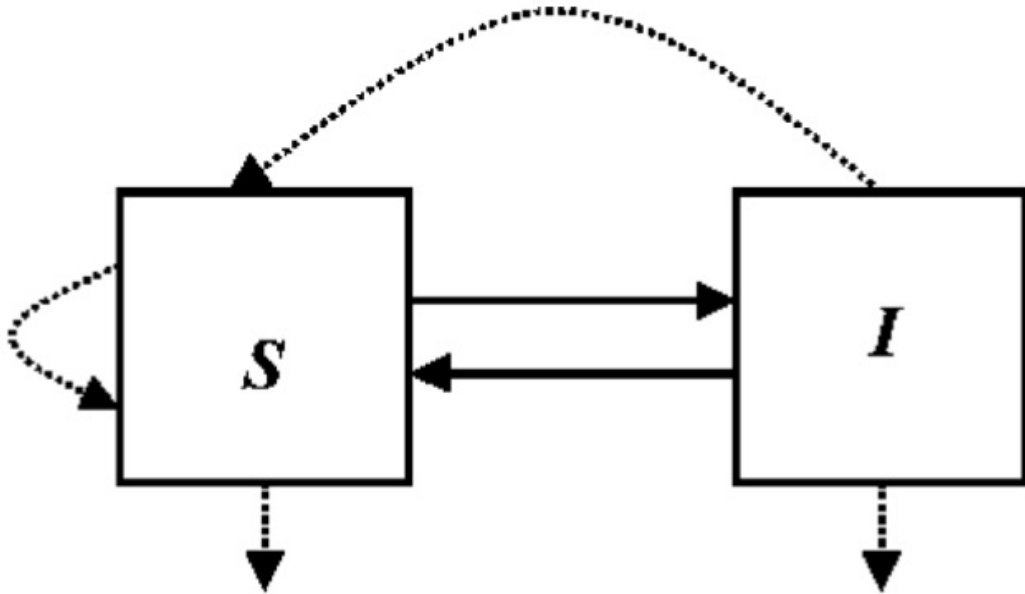
One of the most common examples of the SI epidemic is herpes. The most common human herpes virus is the herpes simplex virus (HSV). HSV can be divided into two strains, HSV-1 and HSV-2. In 2017, there were an estimated 3.7 billion individuals under the age of 50 with HSV-1, and 417 million individuals under the age of 50 worldwide infected with HSV-2 [7]. Since HSV is a viral infection, it is transmitted by skin to skin contact with infected areas, most commonly near the genitals and mouth. An infected individual with visible sores, who makes physical contact with a susceptible individual, now has infected the susceptible individual. This form of disease and epidemic is difficult to control because many individuals who are infected have no knowledge that they are infected and unknowingly spread the disease. This infection goes hand-in-hand with 2.1 because antivirals can help reduce the severity and frequency between breakouts, but there is no cure so the infected population continues to grow indefinitely.

## 2.2 SIS Model

The next model is the SIS model. Much like the SI model and most other epidemic models, the SIS model uses mathematical techniques to simplify and demonstrate an infectious disease. Individuals in this model are divided into compartments. The first compartment consists of those having recurring infections while the second compartment contains infected individuals who return to the first compartment once the disease has subsided. In this model and this type of disease, it is common to repeat infections without developing an immunity to the disease and infected individuals become immediately infectious [8]. Similar to all epidemic models, the SIS model also has no vertical transmission of the disease. This means every individual is born into the susceptible class. This is much like the SI model,  $N = S + I$ , since an individual cannot be both infected and susceptible at the same time.



Figure 2.2: This figure clearly shows the progression from susceptible (S) to infected (I) and back to susceptible (S). The solid arrows denote infection or recovery which goes back and forth from S and I, while the dotted arrows denote births or deaths, denoted by probability of  $b$ . The dotted arrows pointing down denote the two possible classes where an individual can die. The dotted arrow starting at the I and going to S denotes a female who is infected giving birth to a child who is born into the susceptible class. Finally, the arrow furthest to the left, denotes both a new mother and newborn baby in the susceptible class.



A susceptible individual becomes infected with probability  $\frac{\beta I}{N}$ , where  $\beta$  is the number of contacts made by a single infected individual over an indicated period of time. It is important to note that a new infection only occurs when  $\frac{\beta S}{N}$ , and the total number of new infections by the entire infected class is  $\frac{\beta SI}{N}$ . This model is a continuous analogue of discrete time epidemic models [8]. Many familiar diseases and illnesses fall under this epidemic model. A few examples are the common cold, chlamydia, and gonorrhea.

### 2.2.1 Examples

The simplest example of the SIS model is the common cold. The common cold is a viral infection of the upper respiratory tract, meaning the nasal area, throat, sinus, etc. This virus can last anywhere from one to three weeks and is spread through air droplets from an infected person who has sneezed, coughed or blown their nose. A susceptible individual can catch this cold if they are around a person doing any of the actions above [2]. This situation is an SIS model because most individuals get the common cold at least once a season, but then recover until the next flare up.

A more complex SIS epidemic disease is chlamydia. Chlamydia is caused by an infection from the bacterium *Chlamydia trachomatis*. It is a sexually transmitted disease (STD) that is passed through sexual contact with an infected individual. According to the Centers for Disease Control and Prevention (CDC), chlamydia is among the most prevalent of all STD's, particularly in young women. In 2018, the United States reported nearly 1.8 million cases of chlamydia, but an estimated 2.86 million cases were thought to actually occur [6]. Many individuals are asymptomatic and thus go untreated. Untreated cases can be particularly risky for women because chlamydia can result in pelvic inflammatory disease (PID) sometimes causing infertility. This silent disease may lead to the infection of more susceptible individuals. Surveys estimate only about 10% of men and anywhere from 5 to

30% of women develop symptoms [6]. One positive feature of chlamydia is it is easily cured with antibiotics. This treatment allows the infected individuals to return to the susceptible state. Since it is an SIS epidemic model, as soon as an individual returns to the susceptible class, they can unfortunately be immediately infected again. It is advised to abstain from sexual activity while on the antibiotics to prevent the spreading.

## 2.3 SIS Differential Equations

Just like statistics and probability, differential equations play a major role in describing the dynamics of the SIS epidemic model. The two main equations are

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta}{N}SI + (b + \gamma)I, \\ \frac{dI}{dt} &= \frac{\beta}{N}SI - (b + \gamma)I.\end{aligned}\tag{2.1}$$

In these equations we can assume that  $\beta > 0$  represents the contact rate,  $\gamma > 0$  represents the recovery rate,  $b \geq 0$  represents the birth rate, and the total population size is denoted by  $N = S(t) + I(t)$ . We also assume the birth and death rates are equal which makes the total population size constant,  $\frac{dN}{dt} = 0$ . Finally, the equation  $R_0 = \frac{\beta}{b + \gamma}$  represents the basic reproduction number. The basic reproduction number is extremely important in all epidemics because it is defined as the expected number of individuals with secondary infections infected by one individual in the entire susceptible population [8]. This number is not a rate, and has units of  $time^{-1}$ . If we change the numerator of the basic reproduction number equation to 1, then this new equation represents the length of time one is infected.

Let  $S(t)$ ,  $I(t)$ , and  $R(t)$  be a solution to System (2.1) above.

(1) If  $R_0 \leq 1$ , then

$$\lim_{t \rightarrow \infty} I(t) = 0$$

(disease-free equilibrium).

(2) If  $R_0 > 1$ , then

$$\lim_{t \rightarrow \infty} (S(t), I(t), R(t)) = \left( \frac{N}{R_0}, \frac{bN}{b + \gamma} \left(1 - \frac{1}{R_0}\right), \frac{\gamma N}{b + \gamma} \left(1 - \frac{1}{R_0}\right) \right)$$

(endemic equilibrium).

(3) Assume  $b = 0$ . If  $R_0 \frac{S(0)}{N} > 1$ , then there is an initial increase in the number of infected cases  $I(t)$  (epidemic), but if  $R_0 \frac{S(0)}{N} \leq 1$ , then  $I(t)$  decreases monotonically to zero (disease-free equilibrium). (In this case, the disease does eventually disappear, however if the replacement number is greater than one, then an outbreak will occur.)[8].

# Chapter 3

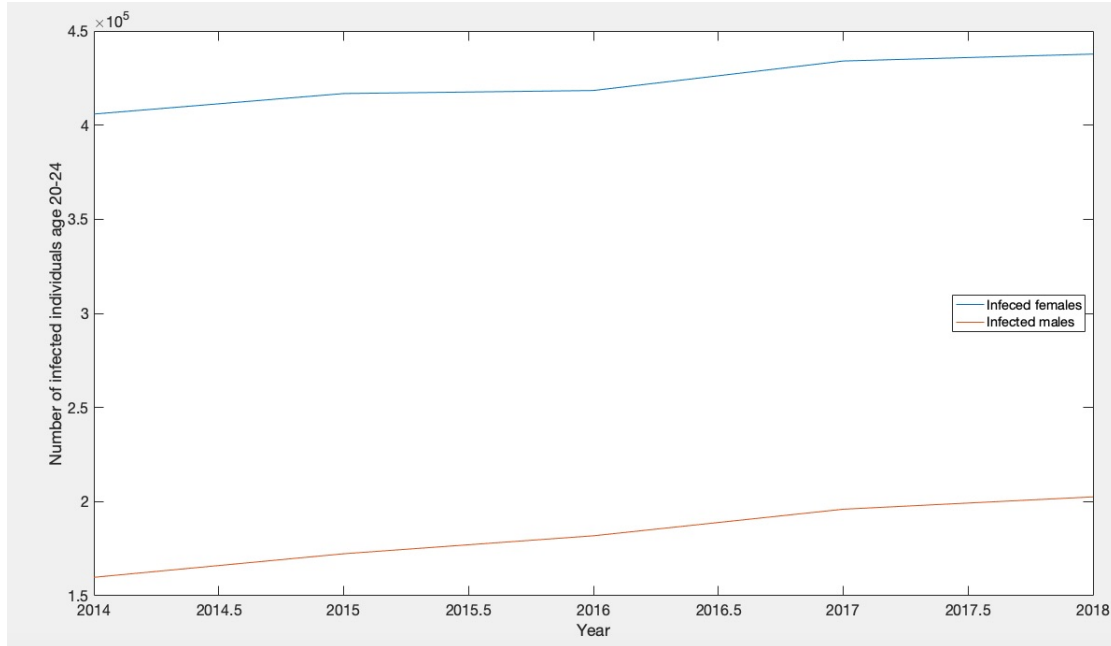
## Simulation and Data Analysis

### 3.1 Data

It was not until the year 2000 when all 50 states required the reporting of all chlamydia cases, where the individual sought medical treatment. The Healthcare Effectiveness Data and Information Set (HEDIS), found that in 2001 only 23.1% of women aged 16-24 were screened for chlamydia, but in 2017, that number had increased to 48.9% [1].

The rates of chlamydia cases are influenced by a number of variables, some being diagnostic, screening coverage, and complete reporting. In the CDC's table of reported cases of chlamydia, from 1941 to 1983, there were no cases reported at all. In 1984 testing and reporting began and there were 7,594 cases nationwide. In 1989 this number increased to over 200,000 cases reported. The spike in a short 5 year period could be due to a rise in infections throughout our population as well as an increase in our testing capabilities. In 2006, the annual cases hit 1 million and in 2018, the number was just under 2 million chlamydia cases reported. This number equates to a rate of 539.9 cases per 100,000 people [1]. As mentioned above, evidence shows females are more prone to STD's based on their higher biological risk for contraction. This observation matches the CDC data.

Figure 3.1: This figure graphs the rates per 100,000 individuals by gender. It is clear the women have a much higher rate of chlamydia than men.



Chlamydia screening has drastically increased over the past two decades. However, many individuals who are infected and at risk are still not being tested. This causes rapid infectious spread throughout the susceptible class. While we have close to 320 million people in our country, having 2 million individuals infected a year with a STD is far too many. This infection is partly due to lack of awareness and limited resources, but health officials should be educating the public about the risks of chlamydia. [1].

### 3.1.1 Real-world Connection

The world has become a very small place, most evident by the current COVID-19 pandemic and its wide-ranging contagious growth. Crafting my thesis on another transmitted infection, from my home where I am quarantined, has cemented my understanding of how easily and quickly disease can spread in today's world.

According to the Johns Hopkins Corona Virus Resource Center, there are 722,289 confirmed cases of COVID-19 in the world, with deaths and positive tests increasing by the

minute. Recently, the US surpassed all nations with 142,356 total infected individuals confirmed [4]. While we do not know when we will reach the peak of this pandemic, allowing our lives to return to some order, it is interesting to note the media's and government's reaction to this particular infectious disease as compared to others like chlamydia.

As noted, in 2018, over 1.7 million individuals were diagnosed with chlamydia and over 2.8 million individuals were estimated to be infected. While our government recently signed a 2.2 trillion dollar stimulus package to assist our citizens during this difficult time, every year over 16 billion dollars are spent in medical costs associated with sexually transmitted diseases [3]. This disparity is due to a lack of public information on prevention of chlamydia and other STD's which leads to their continued growth. While it is not a life threatening disease, chlamydia has serious consequences if left untreated.

A major lesson I have learned through the COVID-19 pandemic is that social distancing is a concept that should be practiced on many fronts. Increased public awareness of infectious diseases and ways of mitigating the spread would help keep people safe and healthy.

# Chapter 4

## Appendices

### 4.1 MATLAB Code

Discrete Time Markov Chain

SIS Epidemic Model

```
set(gca,'FontSize',18);
```

```
set(0,'DefaultAxesFontSize',18);
```

```
time=2000;
```

```
dt=0.01;
```

```
beta=1*dt;
```

```
b=0.25*dt;
```

```
gamma=0.25*dt;
```

```
N=100;
```

```
en=50;
```

```
T=zeros(N+1,N+1);
```

point in  $[0,1)$  such that  $f(q) = q$ .

```
k=0
```



$\exp(R_0)$

$R_k$

$0 \leq t_k = \exp(R_0(1 - t))$ .

$k!$

```
p=zeros(time+1,N+1);
p(1,3)=1;
bt=beta*v.*(N-v)/N; dt=(b+gama)*v;
for i=2:N
T(i,i)=1-bt(i)-dt(i);
T(i,i+1)=dt(i+1);
T(i+1,i)=bt(i);
end
T(1,1)=1;
T(1,2)=dt(2);
T(N+1,N+1)=1-dt(N+1);
for t=1:time
y=T*p(t,:);
p(t+1,:)=y;
end
pm(1,:)=p(1,:);
for t=1:time/en;
pm(t+1,:)=p(en*t,:);
end
ti=linspace(0,time,time/en+1);
```

```
st=linspace(0,N,N+1);  
mesh(st,ti,pm);  
xlabel('Number of Infectives');  
ylabel('Time Steps');  
zlabel('Probability');  
view(140,30);  
axis([0,N,0,time,0,1]);
```

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