DO WE REALLY HAVE TO TAKE ALL OUR MEDICINE? PREDICTING THE CONSEQUENCES OF LARGE-SCALE ANTIBIOTIC MISUSE

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Failure to properly complete antibiotic treatments can result in the eventual development of bacterial strains resistant to antibiotic therapy. If present trends in antibiotic misuse continue, infections that are easily treated today may not be so in the future. We consider a stochastic model and use Markov chain analysis to examine the conditions of misuse under which resistant strains will thrive. Virulence differences in the competing strains are taken into consideration, as is the possibility of superinfection. The probability of extinction is calculated for each strain. We predict the long-term effects of antibiotic misuse and consider the specific case of *Streptococcus pneumoniae*, the bacteria that cause pneumonia.

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Do we really have to take all our medicine? Predicting the consequences of large-scale antibiotic misuse.

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Abstract

Failure to properly complete antibiotic treatment can result in the eventual development of bacterial strains resistant to antibiotic therapy. If present trends in antibiotic misuse continue, infections that are easily treated today may not be so in the future. We consider a stochastic model and examine the conditions of misuse under which resistant strains will thrive. Virulence differences in the competing strains are taken into consideration as a possibility for superinfection. The probability of extinction is calculated for each strain. We predict the long-term effects of antibiotic misuse and consider the specific case of *Streptococcus pneumoniae*, the bacteria that causes pneumonia.

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1 Introduction

The rise of bacterial strains resistant to antibiotic therapy is a new problem with old roots. Since the 1940's, widespread availability of antibiotics has been a part of American life. "Miracle drugs" like penicillin transformed the medical world by turning once lethal illnesses into easily treatable infections [17]. However, until very recently, the clinicians that routinely prescribed these medications and the public that willingly consumed them were blissfully unaware that as the human race waged war on bacteria, bacteria were fighting back. Now, nearly half a century after the dawn of antibiotic salvation, humanity takes notice as our treatments begin to falter.

The lifespan of a human being exceeds that of a bacteria by orders of magnitude. As a result, a case of pneumonia that lasts two weeks in a human might represent thousands of generations of bacterial progeny. With each generation, some species evolution inevitably occurs. Treating the bacteria with antibiotics causes them to undergo selective evolution [5]. Those cells less vulnerable to the methods by which the drug attacks will outlive those that are not. As the weaker bacteria die and the bacterial community diminishes in size, the pain of the infection may subside, and the infected individual may choose to stop treatment. If this occurs before all the bacteria are eliminated, the remaining bacterial cells and their more resistant traits will be able to freely proliferate, thus increasing the reservoir of resistant genes in the population of the pathogen.

If we view this example of evolutionary pressure in the context of all cases of pneumonia treated with antibiotic therapy in the last sixty years, the magnitude of the problem of selective evolution becomes clear. We are perhaps justified in suspecting that misuse of antibiotics is a non-trivial factor in the development of resistant strains.

Since the advent of antimicrobial therapy, enthusiastic pharmaceutical companies have devoted many resources to the discovery, production, and improvement of antibiotics. However, as bacterial strains continue to evolve more sophisticated methods of resistance, the challenge of defeating them increases [10]. It has been estimated that 30% of bacterial strains are resistant to antibiotics [17]. Today, the World Health Organization reports that new drugs are no longer being produced fast enough to replace those that have lost effectiveness [18]. This is sobering news in light of the many factors currently contributing to the rise of new antibiotic resistant bacteria. The countless number of people who neglect to complete their entire course of antibiotic treatment, are not the only ones at fault. Physicians also share the blame. The Center for Disease Control estimates that twenty percent of all antibiotic prescriptions written each year are for viral infections which do not respond to antibiotics

[13]. Alarmingly, in one survey 80% of physicians questioned confessed to having prescribed antibiotics as a result of patient pressure and against their better judgment [17]. Approximately 50 million unnecessary prescriptions are prescribed annually. Industry also contributes to this epidemic of misuse. Only half of the antibiotics used each year are prescribed to humans. Many of the same medications prescribed for human treatment are distributed to animals. The animals are exposed to low dosages for long periods of time. The drugs are used for treating or preventing infection and to promote growth. These low dosages encourage growth of resistant bacteria. Antibiotics are used to control or prevent infections in agriculture. Growth of resistant strains is possible in the areas where the aerosol antibiotics become dilute, thus removing only the sensitive, non-resistant bacteria. The resistant strain can then be introduced to the intestinal tract of humans after consumption of the produce [17]. While it is interesting to consider the degree to which each of these factors contributes to the increasing trend in antibiotic resistance, we choose to focus only on the role of patient negligence.

It is our goal to examine analytically the effects of failure to complete medication, herein referred to as antibiotic misuse, on the development of antibiotic resistant strains. To do this we specifically consider the evolution of penicillin resistance in *Streptococcus pneumoniae* because it is a phenomenon already well observed in the medical community. At present, estimates of *S. pneumoniae* strains that have developed penicillin resistance range from three to thirty-five percent [14]. However, penicillin is simply one of many antibiotics found to be insufficient in treatment. Strains of *S. pneumoniae* have become resistant to numerous antibiotics including penicillin, erythromycin, macrolides, tetracycline, TMP/SMX, and Chloramphenicol [3]. This pathogen causes the pneumococcal diseases otitis media (ear infection), sinusitis, arthritis, periontitis, sepsis/bacteremia, meningitis, pneumonia, neurological sequelae and/or learning disabilities after meningitis, and deafness after recurring otitis media [13], [14]. These infections cause approximately 100,000-135,000 hospitalizations and 40,000 deaths annually in the United States [13]. Pneumonia caused by *Streptococcus pneumoniae* has become the fifth leading cause of overall deaths and is the highest cause of deaths due to infection [16]. Once an antibiotic resistant strain emerges, it may easily spread far and wide. Investigators have noted the migration of resistant strains for example, from Spain to the U.K, the U.S, South Africa, and several other countries [14]. The movement of the resistant strains creates the potential for a world-wide epidemic of untreatable pneumonia. Hence, the spread of these untreatable strains is not trivial.

To determine the role of antibiotic misuse in preventing or inducing a potentially uncontrollable *S. pneumoniae* epidemic, we develop a generalized stochastic S-I-S

model is developed in which individuals who fail to complete antibiotic treatment may develop an infection of resistant bacteria. By varying the probability that an individual fails to complete treatment we expect to account for the contribution of antibiotic misuse to the development of a resistant strain. We investigate the possibility that a resistant strain eventually replaces the treatable strain as a result of misuse by calculating the probability of extinction of each strain.

In Section 2 we propose a model for this phenomenon. In Section 3 we use continuous-time Markov chain analysis to calculate the probability of extinction for each of the two strains. In Section 4 we examine the effects of some parameters on the probability of extinction for each strain. In Section 5, we simulate the development of a resistant strain and its interactions with the non-resistant strain for varying parameter values. In section 6, we discuss the biological implications of our findings and suggest future avenues of investigation.

2 The Model

We consider a modified, two-strain, S-I-S stochastic model with superinfection to examine the development of a resistant bacterial strain (see Figure 1). The population of uninfected, susceptible individuals is represented by state S. States I_1 and I_2 represent individuals infected with non-resistant and resistant bacteria, respectively. States T_1 and T_2 consist of infected populations undergoing antibiotic treatment. We use $N = S + I_1 + T_1 + I_2 + T_2$ to represent the total population. Individuals in I_i states are assumed to be infectious. Those in T_i states are not.

Individuals infected with non-resistant bacteria will remain in an infectious state, I_1, until symptoms appear and antibiotic therapy begins, at which point they move to state T_1. The possibility of superinfection is also considered: individuals infected with non-resistant bacteria may move to state I_2 via contact with that population.

When in state T_1 individuals who complete treatment will return to the susceptible state, S. Those who do not will progress to one of three alternatives. They may (i) return to state S when the immune system eliminates remaining bacteria, (ii) return to state I_1 due to a resurgence of original bacteria, or (iii) advance to state I_2 if residual bacteria have evolved antibiotic resistance due to the selective pressure of antibiotic therapy.

Individuals who enter state I_2, either by failing to complete treatment in T_1 or by direct contact with others in I_2, will remain in that state until symptoms appear and treatment begins, at which point they move to state T_2. In T_2, individuals are treated with the same antibiotic administered to those in state T_1 but due to the nature of

I_2 infectives, this treatment will be highly ineffective in eliminating the resistant bacteria, and even individuals who complete treatment in state T_2 will return to the susceptible state at a very low rate. Those who fail to complete treatment will remain in state T_2.

We recognize that our model is very simple and does not include all the factors that contribute to the development of resistant strains. For instance, we do not include the possibility that individuals in T_2 might be treated with an alternate prescription to which the bacteria is not resistant. Consequently we neglect the possibilities that multiple resistant strains might develop simultaneously or that individuals might not have to spend such an extended period of time in the treatment state for strain 2. In addition, factors such as bacterial mutation and adaptation independent of antibiotic misuse are not specifically considered. Nonetheless, we feel that this simple model reflects some of the more important aspects of antibiotic misuse and will allow us to study the dynamics of disease.

Table 1: Parameter List

Parameters	Description
β_i	per capita contact rate of individuals in I_i
α	per capita birth rate
μ	natural mortality rate
v_i	disease induced mortality rate for strain i (dependent on virulence of strain i)
ϕ_i	rate at which infected individuals seek treatment, here considered to be the same as the rate at which first symptoms appear
γ_a	recovery rate of individuals infected with strain 1 who complete treatment
γ_b	recovery rate of individuals infected with strain 1 who do not complete treatment
γ_2	recovery rate of individuals infected with strain 2 who complete treatment
p_i	probability that an individual infected with strain i completes antibiotic treatment
q_1	probability that an individual infected with strain 1 will remain infected if treatment is not completed
q_2	probability that an individual infected with strain 1 will become infected with strain 2 as a result of failure to complete treatment

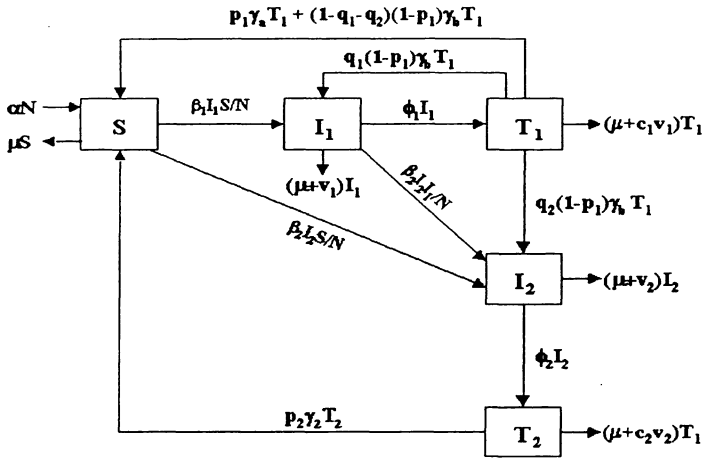

Figure 1: A model for the development of antibiotic resistant bacteria as a result of antibiotic misuse. Since this is a stochastic model, all rates are assumed to be parameters of exponential distributions.

3 Methodology

The goal of our research is to examine conditions under which the two strains coexist and under which the resistant strain replaces the non-resistant strain. To do this we first calculate the probability of extinction of each strain in terms of the parameters that will influence its extinction. This is done by finding the inverse of each strain's basic reproductive number, R_0 [4]. The basic reproductive number represents the expected number of secondary infections caused by a single infectious individual in a population of susceptible, a useful tool in predicting the future of epidemic diseases. In general, if $R_0 > 1$, the disease goes extinct with probability $\frac{1}{R_0}$ whereas it dies out with probability 1 when $R_0 \leq 1$.

As a result of the two-way interaction between states I_1 and T_1 in our model, conventional methods for calculating R_0 become complicated and alter its interpretation

as a probability of extinction. Hence, we use the method of continuous-time Markov chain analysis outlined by Hernández [4]. This method involves creating an absorbing state model (Figure 2) and using a matrix of transition probabilities to calculate R_0 for each strain (Figures 1 and 2). We use $R_0^{[1]}$ and $R_0^{[2]}$ to represent the number of secondary infections caused by an individual when infected with strain 1 and strain 2 respectively.

3.1 Absorbing State Model

To begin the absorbing state model, we separate the states S, I_1, T_1, I_2, and T_2 into three categories: active infectious states, passive infectious states, and absorbing states. An infected individual in an active infectious state infects others. In a passive infectious state the individual is infected but not infectious, yet still communicates with an active infectious state. Absorbing states mark the end of the infectious period; once entered, these states are never left [11]. We direct all possible ways of ending an infectious cycle into one absorbing state, Δ. In our model, I_1 and I_2 are actively infectious populations. Since we assume that the individuals in the T_i states are infected but not infectious, T_1 is passively infectious since it communicates with I_2, but T_2 does not communicate with an active infectious state. So, T_2 along with S and the deaths from each state make up the absorbing state. Hence the active infectious states are I_1 and I_2, the passive infectious state is T_1, and Δ consists of S, T_2, and deaths. Figure 2 illustrates a modified transition model which we use to find the expected time an individual spends in each state before going to absorbtion.

3.2 Transition Matrix

We now construct a matrix P of one-step transition probabilities where each element p_{ij} represents the probability that an individual moves directly from state i to state j. Finding $\lim_{n\to\infty} P^n$ yields a matrix with identical rows. The elements in each column are the same, indicating that as time goes to infinity the number of visits an individual makes to each state becomes independent of their state of origin. So we only concern ourselves with a single row of the matrix which we call the vector Π. From this we compute the expected time spent in state j and multiply it by β_j which illustrates the general process for calculating R_0 when dealing with one infected state.

In our model, we specifically look at two strains of bacteria causing disease and deal with two infected states. We need to calculate $R_0^{[1]}$ for strain 1 and $R_0^{[2]}$ for strain 2, which complicates the calculation of a general R_0. To do this, we must use two transition matrices, P_{I_1} and P_{I_2}, and manipulate them using the continuous-time

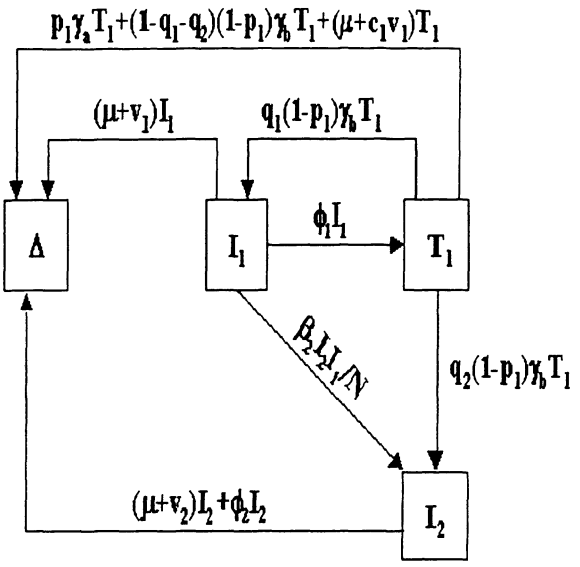

Figure 2: Absorbing state model

Markov chain process outlined in [4] (see appendix for further computation). This gives us the vector Π relating to $R_0^{[1]}$ and $\hat{\Pi}$ relating to $R_0^{[2]}$. Next, we calculate δ_{ij}, the transition rate from state i to state j, for each state in our model. Note that we only consider $i \neq j$ since $i = j \Rightarrow \delta_{ij} = 0$. Using these rates we input the transition probabilities, $p_{ij} = \frac{\delta_{ij}}{\sum_j \delta_{ij}}$, for each state into a 4×4 matrix [4] (see Equations (1) and (2)). Notice that $\delta_{I_1 I_2} = 0$ because we neglect the superinfection in our model at the beginning of the epidemic. Assuming initial conditions of the infectious states are small, we see that for large N, $\frac{I_1 I_2}{N}$ is approximately zero. Hence, we feel justified in ignoring superinfection and leave that case for future research. In addition, we assume that $\gamma_a = \gamma_b$ which simplifies the calculation of $R_0^{[1]}$, but does not affect $R_0^{[2]}$. In section (5), we consider a more realistic simulation where $\gamma_b \geq \gamma_a$. P_{I_1}, the transition matrix for $R_0^{[1]}$ is

$$
\begin{array}{c} \\ I_1 \\ T_1 \\ I_2 \\ \Delta \end{array}
\begin{array}{c}
\begin{array}{cccc} I_1 & T_1 & I_2 & \Delta \end{array} \\
\begin{pmatrix}
0 & \frac{\delta_{I_1T_1}}{\delta_{I_1T_1}+\delta_{I_1\Delta}} & 0 & \frac{\delta_{I_1\Delta}}{\delta_{I_1T_1}+\delta_{I_1\Delta}} \\
\frac{\delta_{T_1I_1}}{\delta_{T_1I_1}+\delta_{T_1I_2}+\delta_{T_1\Delta}} & 0 & \frac{\delta_{T_1I_2}}{\delta_{T_1I_1}+\delta_{T_1I_2}+\delta_{T_1\Delta}} & \frac{\delta_{T_1\Delta}}{\delta_{T_1I_1}+\delta_{T_1I_2}+\delta_{T_1\Delta}} \\
0 & 0 & 0 & 1 \\
1 & 0 & 0 & 0
\end{pmatrix}
\end{array}
\tag{1}
$$

Likewise, P_{I_2}, the transition matrix for $R_0^{[2]}$, is

$$
\begin{array}{c} \\ I_1 \\ T_1 \\ I_2 \\ \Delta \end{array}
\begin{array}{c}
\begin{array}{cccc} I_1 & T_1 & I_2 & \Delta \end{array} \\
\begin{pmatrix}
0 & \frac{\delta_{I_1T_1}}{\delta_{I_1T_1}+\delta_{I_1\Delta}} & 0 & \frac{\delta_{I_1\Delta}}{\delta_{I_1T_1}+\delta_{I_1\Delta}} \\
\frac{\delta_{T_1I_1}}{\delta_{T_1I_1}+\delta_{T_1I_2}+\delta_{T_1\Delta}} & 0 & \frac{\delta_{T_1I_2}}{\delta_{T_1I_1}+\delta_{T_1I_2}+\delta_{T_1\Delta}} & \frac{\delta_{T_1\Delta}}{\delta_{T_1I_1}+\delta_{T_1I_2}+\delta_{T_1\Delta}} \\
0 & 0 & 0 & 1 \\
0 & 0 & 1 & 0
\end{pmatrix}
\end{array}
\tag{2}
$$

where the transition rates for these matrices are

$$
\begin{aligned}
\delta_{I_1T_1} &= \phi_1 \\
\delta_{I_1\Delta} &= \mu + v_1 \\
\delta_{I_2T_2} &= \phi_2 \\
\delta_{I_2\Delta} &= \mu + v_2 \\
\delta_{T_1I_1} &= q_1(1-p_1)\gamma_b \\
\delta_{T_1I_2} &= q_2(1-p_1)\gamma_b \\
\delta_{T_1\Delta} &= p_1\gamma_a + (1-q_1-q_2)(1-p_1)\gamma_b + \mu + cv_1
\end{aligned}
$$

3.3 Calculation of $R_0^{[1]}$ and $R_0^{[2]}$

To calculate $R_0^{[1]}$ which is the number of secondary infectious caused by a single infectious individual in I_1, we first assume that every infection starts in I_1. Then in the last row of the transition matrix P_{I_1}, state Δ communicates with state I_1 with probability 1. Let $E[Z_j^{(i)}]$ be the expected time spent in state j before going to state Δ when starting in state i. In our model, the average number of infections caused by an individual starting in I_1 includes the expected time spent in either or both infectious states before complete recovery or death. Since we deal with the possibility

of becoming infected with strain 2 when an individual fails to complete treatment, $R_0^{[1]}$ may consist of secondary infected individuals from both I_1 and I_2. Thus,

$$R_0^{[1]} = \beta_1 E[z_{I_1}^{(I_1)}] + \beta_2 E[z_{I_2}^{(I_1)}]. \tag{3}$$

Using the transition matrix P_{I_1} and the Markov chain process [4], we find the stationary distribution

$$\Pi = [\pi_{I_1}, \pi_{T_1}, \pi_{I_2}, \pi_{T_2}, \pi_\Delta]$$

in order to calculate $E[Z_j^{(I_1)}]$. In analyzing the vector Π, the first element, π_{I_1}, represents the proportion of visits made to state I_1. The fifth element, π_Δ, displays the proportion of visits made to the absorbing state. Dividing π_{I_1} by π_Δ reveals the total number of visits to I_1 between two visits to Δ. A similar calculation is made for $\frac{\pi_{I_2}}{\pi_\Delta}$. Multiplying these values by the average amount of time spent in the respective infectious state during each visit gives us $E[Z_j^{(I_1)}]$, the expected time spent in state j before absorption when the first infected individual starts in state I_1. By definition [4],

$$E[Z_j^{(i)}] = \frac{\pi_j}{\pi_\Delta \delta_j}$$

where δ_j is the rate at which an individual leaves state j. In other words, $\frac{1}{\delta_j}$ is the average time spent in state j. So $\frac{1}{\delta_{I_1}} = \frac{1}{\phi_1+\mu+v_1}$ and $\frac{1}{\delta_{I_2}} = \frac{1}{\phi_2+\mu+v_2}$. Substituting these values into (1),

$$R_0^{[1]} = \beta_1 \frac{\pi_{I_1}}{\pi_\Delta \delta_{I_1}} + \beta_2 \frac{\pi_{I_2}}{\pi_\Delta \delta_{I_2}} \tag{4}$$

$$\Rightarrow R_0^{[1]} = \frac{\beta_1(\gamma_1+\mu+c_1v_1)(\phi_2+\mu+v_2) + \beta_2 q_2 \phi_1 \gamma_1 (1-p_1)}{(\phi_1+\mu+v_1)(\gamma_1+\mu+c_1v_1 - q_1\phi_1\gamma_1(1-p_1))(\phi_2+\mu+v_2)}. \tag{5}$$

Now, the calculation of $R_0^{[2]}$ involves the assumption that every infection starts in I_2. In the transition matrix P_{I_2}, Δ interacts with I_2 with probability 1. Thus, the average number of secondary infections caused by an individual starting in I_2 is

$$R_0^{[2]} = \beta_1 E[Z_{I_1}^{(I_2)}] + \beta_2 E[Z_{I_2}^{(I_2)}] \tag{6}$$

$$\Rightarrow R_0^{[2]} = \beta_2 E[Z_{I_2}^{(I_2)}]. \tag{7}$$

This definition comes from the impossibility of becoming infected with strain 1 when every infection starts as strain 2, hence $E[Z_{I_1}^{(I_2)}] = 0$. Using the transition matrix P_{I_2} and the Markov chain analysis [4] to find the stationary distribution

$$\hat{\Pi} = [\hat{\pi}_{I_1}, \hat{\pi}_{T_1}, \hat{\pi}_{I_2}, \hat{\pi}_{T_2}, \hat{\pi}_{\Delta}],$$

we calculate $E[Z_{I_2}^{(I_2)}]$ and substitute it into (5). Therefore,

$$R_0^{[2]} = \beta_2 \frac{\hat{\pi}_{I_2}}{\hat{\pi}_{\Delta}\delta_{I_2}} \tag{8}$$

$$\Rightarrow R_0^{[2]} = \frac{\beta_2}{\phi_2 + \mu + v_2}. \tag{9}$$

3.4 Probability of Extinction

Once we have the values of $R_0^{[I_1]}$ and $R_0^{[I_2]}$, the probability of extinction for each strain becomes an easy computation. Let $P_e^{(I_1)}$ be the probability of extinction of strain 1 and $P_e^{(I_2)}$ be that of strain 2. Then the probability that both strains go to extinction, P_e*, is $P_e^{(I_1)}P_e^{(I_2)}$. We use the definition of probability of extinction for strain i given in [4], $P_e[i] = \frac{1}{R_0^{[i]}}$. However, this assumes only one infected class for one strain of bacteria. We extend the definition to our model, including two infectious states for two bacterial strains and finding the probability of extinction for each strain. Therefore,

$$P_e^{(I_1)} = \frac{1}{R_0^{[1]}} = \frac{1}{\beta_1 E[z_{I_1}^{(I_1)}] + \beta_2 E[z_{I_2}^{(I_1)}]} \tag{10}$$

$$\Rightarrow P_e^{(I_1)} = \frac{(\phi_1 + \mu + v_1)(\gamma_1 + \mu + c_1 v_1 - q_1\phi_1\gamma_1(1-p_1))(\phi_2 + \mu + v_2)}{\beta_1(\gamma_1 + \mu + c_1 v_1)(\phi_2 + \mu + v_2) + \beta_2 q_2 \phi_1 \gamma_1 (1-p_1)} \tag{11}$$

$$P_e^{(I_2)} = \frac{1}{R_0^{[2]}} = \frac{1}{\beta_2 E[Z_{I_2}^{(I_2)}]} \tag{12}$$

$$\Rightarrow P_e^{(I_2)} = \frac{\phi_2 + \mu + v_2}{\beta_2} \tag{13}$$

Thus,

$$P_e* = \frac{(\phi_1 + \mu + v_1)(\gamma_1 + \mu + c_1 v_1 - q_1\phi_1\gamma_1(1-p_1))(\phi_2 + \mu + v_2)^2}{\beta_1\beta_2(\gamma_1 + \mu + c_1 v_1)(\phi_2 + \mu + v_2) + (\beta_2)^2 q_2\phi_1\gamma_1(1-p_1)} \tag{14}$$

Note that $R_0^{[i]}$ takes on a different meaning from a one-strain model because we cannot determine which of the two strains infects a typical individual. We do not have a definition for a general R_0. Hence, P_e* is only an approximation.

4 Analyzing the probability of extinction

In order to determine the significance of the probability of extinction values obtained in Section 3, we create a number of three dimensional plots. Since we are interested in examining the effects of antibiotic misuse on the rise of resistance, we focus on the parameters that describe misuse, p_1, q_1, and q_2 in our analysis. Because the probability of extinction of strain 2 is not influenced by these values, we examine it in terms of β_2 and ϕ_2.

4.1 Selecting Parameter Values

Before the three dimensional plots can be made it is necessary to select fixed numerical values for those parameters which will not be varied. A review of numerous studies has enabled us to select the following values (the sources are given below). However, when considering these numbers it is important to note that we expect them to be no more than rough approximations. In many cases, they were borrowed from studies which did not focus primarily on obtaining them. Thus, the methods by which they were originally calculated may lack rigor. Nonetheless, they will suffice to demonstrate the general behavior of our system. Note, all parameter values have units $(years)^{-1}$ unless otherwise noted.

μ - 0.0133. The life expectancy of an average person in the United States is 75 years

[15], so, $\frac{1}{\mu} = 75 \Rightarrow \mu = \frac{1}{75} = 0.0133$.

α - 0.0117. The population of the U.S. is increasing by 1.17% annually [19]. So, $(\alpha - \mu) = 0.0117 \Rightarrow \alpha = .0133 + \mu = 0.0133 + 0.0117 = 0.025$.

c_1 - 0.1. Antibiotic treatment of bacterial pneumonia has reduced disease induced morbidity by 90%, [20]. So, $c_1 v_1 = v_1 - .9v_1 \Rightarrow c_1 v_1 = (1 - .9)v_1 \Rightarrow c_1 = 0.1$.

γ_a - 36.5. A typical antibiotic treatment of bacterial pneumonia lasts 10 days, [16]. If the expected duration of treatment is $\frac{1}{\gamma_a} = 10$ days= 0.0274 years then, $\gamma_a = \frac{1}{0.0274} = 36.5$.

γ_b - 52. VanFleet [12], estimates that individuals who do not complete antibiotic therapy for bacterial pneumonia typically stop treatment after seven days, when symptioms have fully abated. The expected duration of treatmeant for these individuals is thus, $\frac{1}{\gamma_b}$= 7 days = 0.0192 years, so $\gamma_b = 52$.

q_1 - 0.07. The probability that an individual with bacterial pneumonia will experience a reccurance of the disease is 7% [7].

We were unable to find consistent and accurate values for the remaining parameters in the biological literature. When possible we estimate them using available biological data. In other cases we base our approximations on the relationships these parameters should have with respect to other known parameters. Through a series of simulations and adjustments we obtain the following values for which strain 1 will be able to sustain itself consistently in the presence of strain 2 for up to seven years (the longest period of time we consider). We feel this condition is requisite for accepting these values because a model in which strain 1 cannot exist in the presence of strain 2 for an extended period of time under normal conditions will not accurately reflect the true behavior of the system. We find:

β_1 - 146. This value indicates that a person in the non-resistant infectious state (I_1) causes 0.4 infections per day, or approximately 2 infections every five days.

β_2 - 82. This implies that a person in the resistant infectious state (I_2) will infect 0.23 persons per day, just over one person every five days. This value is biologically correct in that it reflects the less invasive, more virulent character of β_2.

v_1 - 0.15. Roughly thirty percent of untreated pneumonia cases result in death, [6]. However, through numerical simulation we found that the most realistic outcomes were obtained only when disease induced mortality was around 0.15.

v_2 - 0.2. We expect strain 2 to cause death more frequently than strain 1 due to the fact that strain 1 is more invasive, however less virulent, while strain 2 is less invasive and more virulent.

c_2 - 0.9. Treating penicillin resistant strains of *S. pneumoniae* with penicillin will not significantly reduce the impact of the infection on the carrier. We expect that treatment will not significantly reduce disease induced mortality and so estimate this value.

ϕ_i - 73. Symptoms of bacterial pneumonia may appear between 12 hours and 2 weeks after infection [9]. We found that 5 days provided realistic results. We expect individuals will seek treatment when symptoms surface, so $\frac{1}{\phi_1}$, the expected time until individuals move from I_1 to T_1, is 5 days = 0.0137 years. If $\frac{1}{\phi_1} = 0.0137$, then $\phi_1 = 73$.

ϕ_2 - 73. Resistance to penicillin will not change the rate at which bacteria multiply. We thus assume that symptoms will appear at the same rate in those infected with resistant and non-resistant strains.

γ_2 - 20. Treatment of the resistant strain will be relatively ineffective and should take a longer period of time than treating the non-resistant strain. Through trial and error we found that a value of 20 gives realistic results. This value represents an 18 day treatment period.

p_1 - $\frac{1}{3}$. Physicans [9] estimates that $\frac{1}{3}$ to $\frac{3}{4}$ patients with bacterial pneumonia complete their treatment. We found that a value of $\frac{1}{3}$ provided more realistic results for patients with strain 1.

p_2 - $\frac{3}{4}$. If $\frac{3}{4}$ of patients with strain 2 complete treatment realistic results are obtained.

q_2 - 0.01. We estimated that the probability that an individual infected with strain 1 will develop strain 2 as a result of incomplete treatment is very low.

4.2 Numerical Analysis of the Probability of Extinction

First, we analyze the probability that strain 1 will go extinct in terms of q_1, the probability that an individual who does not complete treatment goes back to strain 1, and q_2, the probability that an individual who does not complete treatment goes back to strain 2. We find that when q_1 and q_2 are both zero the probability of extinction is largest, $\frac{1}{2}$. When q_2 is one, then the probability of extinction of strain 1 is lower, therefore strain 1 benefits from secondary infections in I_2. Thus, it is best for strain 1 if they go back to I_1, it is next best if they go to I_2, and it is not so good if they go back to S. We think the reason for this strange behavior where strain 1 benefits from causing secondary infections in strain 2 has to do with the difficulty of defining a single strain R_0 in a two strain stochastic model. Strain 1 prefers to have individuals from T_1 go back to I_1 because they can infect other people. If this behavior is repeated then the probability of extinction of strain 1 is almost zero because we have a cycle between I_1 and T_1.

Next we analyze the probability of extinction of strain 1 in terms of p and q_1. The highest probability of extinction is 0.5 when $p = 1$ which means that everyone takes their medication. When this happens q_1 has no effect over the individuals. Thus, everyone becomes susceptible and they can not go back to strain 1 and infect other individuals. As p decreases, q_1 has more influence over the probability of extinction. When the values of $q_1 = 1$ and $p = 0$, the $Pe^{(I_1)}$ is zero. So, as the probability of p increases $Pe^{(I_1)}$ increases. We also analyzed the $Pe^{(I_1)}$ in terms of q_2 and p. The values of q_2 do not affect $Pe^{(I_1)}$ as much as the values of q_1. For example even when $p = 0$ and $q_2 = 1$ the $Pe^{(I_1)}$ is 0.3. This tells us that q_2 is not a strong factor in the $Pea^{(I_1)}$. Aside from this difference, q_2 causes the same kind of behavior as when we analyzed q_1 and p.

Now we analyze the same probability only with $\phi_1 = 155$(2.35 days before an individual seeks treatment). The results are generally the same but when people look for treatment after 2.5 days the disease will definitely go extinct for low values of q_1 and high values of p (see Figure 3). Also, when $p = 1$ strain 1 will go extinct for any value of q_1. When we analyze the $Pea^{(I_1)}$ in terms of p and ϕ_1 we see that for every value of ϕ_1 greater than 160(2.28 days before an individual seeks treatment) the disease always goes to extinction.

Next we analyze the probability of extinction of strain 2 in terms of ϕ_2 and β_2. We choose these parameters because the $Pe^{(I_2)}$ does not depend on p, q_1 and q_2. We notice that having our parameters $\beta_2 = 81.76$ and $\phi_2 = 73$ the disease has a very

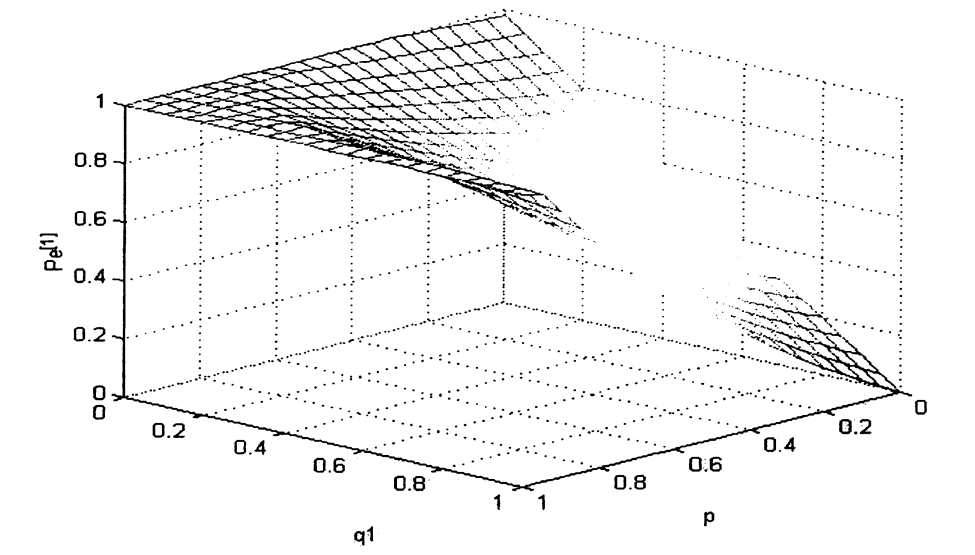

Figure 3: Probability of extinction of strain 1

high probability of extinction. When $\beta_2 < \phi_2$ we find that strain 2 will always go to extinction. In general, it looks like $Pe^{(I_2)}$ goes to one when β_2 approximately equals ϕ_2. In order for strain 2 to sustain itself β_2 has to be greater than ϕ_2 (see Figure 4).

Now we analyze the probability of extinction of both strains, Pe^*. When the values of q_1 and q_2 are equal to one, Pe^* is almost zero. This is because more people are getting infected with both strains. But we also notice that Pe^* will dramatically increase when less people are becoming infected with strain 1. In these cases q_2 does not have as much influence as q_1 on Pe^*.

When the value of q_1 decreases and p increases the probability of extinction of both strains will increase to a maximum of 0.45. Thus, Pe^* is largest when more individuals finish their medication and less individuals who do not finish their medication become infected with strain 1. If the probability that an individual takes their medication is almost zero and a large number of individuals become infected with strain 1 as a result, then the Pe^* will be almost zero. This behavior relates to $Pea^{(I_1)}$ where p, q_1 and q_2 affect Pe^* in the same way, this happens because the $Pe^{(I_2)}$ does not depend on either of these parameters. Thus under these conditions multiplying $Pe^{(I_1)}$ by $Pe^{(I_2)}$ is equivalent to multiplying it by a constant and changes only the slope of the graph, not its overall behavior (see Figure 5).

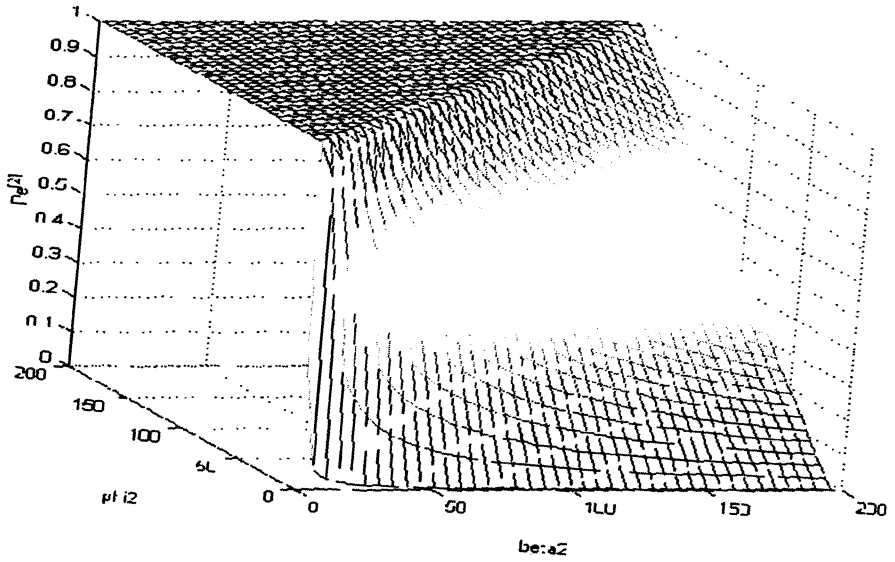

Figure 4: Probability of extinction of strain 2

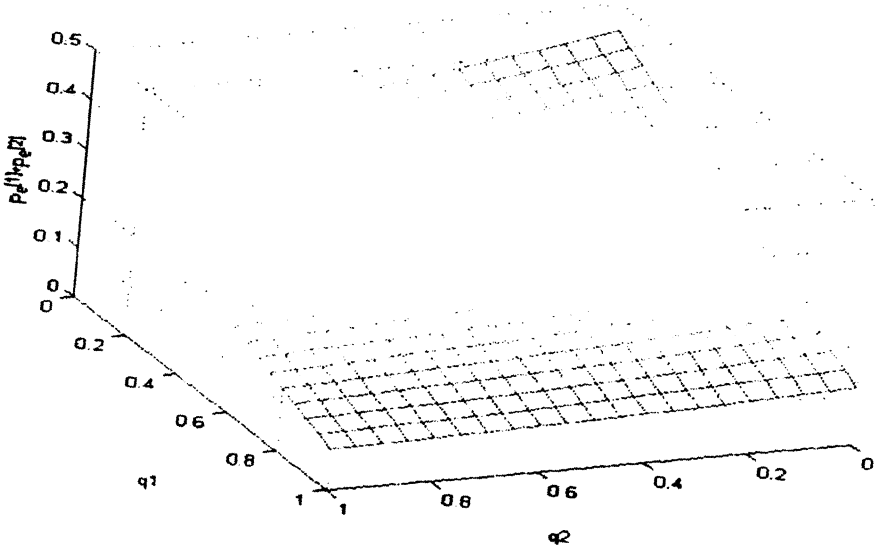

Figure 5: Probability of extinction both strains

5 Stochastic Simulations and Results

We simulate the existence and evolution of bacterial strain 1 and strain 2 introduced to a population of susceptible individuals using Matlab. Plotting the number of individuals in I_1 and T_1 versus time on one graph and the number of individuals in I_2 and T_2 versus time on another graph allows us to compare the behavior and lifespan of each strain. In our stochastic simulations we use the parameter values listed in section (4.1) unless otherwise noted.

By varying the probability that an individual completes antibiotic treatment, we take note of the relationship between the two strains over time. Since we assume that strain 1 is non-resistant and strain 2 is resistant to antibiotics, it appears that the probability that an individual infected with strain 1 finishes treatment directly influences the survival of strain 1 and indirectly influences the survival of strain 2. Through simulations, we find parameter ranges for coexistence, short-term domination of strain 2 after the extinction of strain 1, and simultaneous extinction of both strains. First, coexistence of the two strains occurs when $p_1 < 0.8$. This means that if less than 80% of people infected with strain 1 complete their medication, I_2 sustains a small endemic population with periodic outbreaks. This situation has the potential to become a problem because one of the outbreaks, shown as a peak in the graph of I_2 versus time, could jump above I_1 and cause an epidemic. Then strain 2 would get the chance to take over as strain 1 goes extinct (see Figure 6). Now, when $p_1 \geq 0.8$, the resistant strain briefly overtakes the non-resistant strain, but dies out shortly thereafter. So we see that both strains eventually go extinct and most likely will not cause a significant problem when more than 80% of the individuals in I_1 complete treatment. Also, we note that as p_1 increases to 1 from this value, it takes less time on average for strain 2 to die out. At $p_1 = 1$, I_2 dies out almost immediately which makes sense because if everyone in I_1 finishes their medication, they all go back to being susceptible, and hence, superinfection decreases dramatically (see Figure 7). Conversely, when $p_1 = 0$, the two strains coexist for a short time (less than one year) and die out together. We observe that strain 2 needs a constant or periodic influx from strain 1 to survive. While everyone fails to complete treatment, without the presence of strain 1, strain 2 cannot sustain itself and inevitably goes extinct. Here we must note that the critical value of $p_1 = 0.8$ only applies to this specific set of parameters. Varying virulence or per capita rate of contact may shift this value.

Next, we vary the parameters q_1 and q_2 which represent the probabilities that an individual being treated for strain 1 remains infected or acquires strain 2, respectively, when treatment is not completed. Similar to the previous simulations varying p_1, we find ranges for q_1 and q_2 where the two strains coexist. While $q_1 > 0.1$ and $q_2 < 0.01$

we see strong coexistence for long periods of time interjected with short, periodic outbreaks of strain 2. Over a seven year time scale, we find strain 2 dominating strain 1 for several brief periods and then receding to its low endemic population size. A greater q_1 value means more people go back to state I_1 after stopping treatment. Thus, an increased flow to I_1 easily sustains strain 2. This behavior is similar to that under our standard paramenter values (see Figure 6). Increasing q_1, we notice that the time between outbreaks of strain 2 decreases (see Figure 8). On the other hand, increasing $q_2 > 0.01$ can disrupt I_1 and cause accelerated probabilities of extinction of both strains with a short peak of strain 2 before extinction. Combining high q_2 and low p_1 values, we also see increases in the frequency of periodic outbreaks or peaks in I_2, ending with simultaneous extinction of both strains (see Figure 9). Thus, a higher probability that an individual infected with strain 1 moves to I_2 along with very few people finishing their medication results in more strain 2 outbreaks over time.

Lastly, we vary the virulence of each strain, how fast the bacteria is able to kill its host, and note other miscellaneous results. By increasing the values of v_1 and v_2 at the same rate, we observe coexistence with small, periodic outbreaks until strain 1 goes extinct. At that point, strain 2 peaks quickly and drastically before dying out (see Figure 10). Under increased virulence and as q_2 increases to 1, I_2 appears to decrease over time. Coexistence and periodic cycles still occur, but we notice a potential for strain 1 to die out and strain 2 to slowly take over. Now we consider the effect β_2, the per capita contact rate, and virulence have on each strain. Increasing β_2, v_1, and v_2 makes strain 2 more able to invade its host and both strains able to kill faster. Hence, strain 2 exists for a longer period after strain 1 goes extinct (see Figure 11).

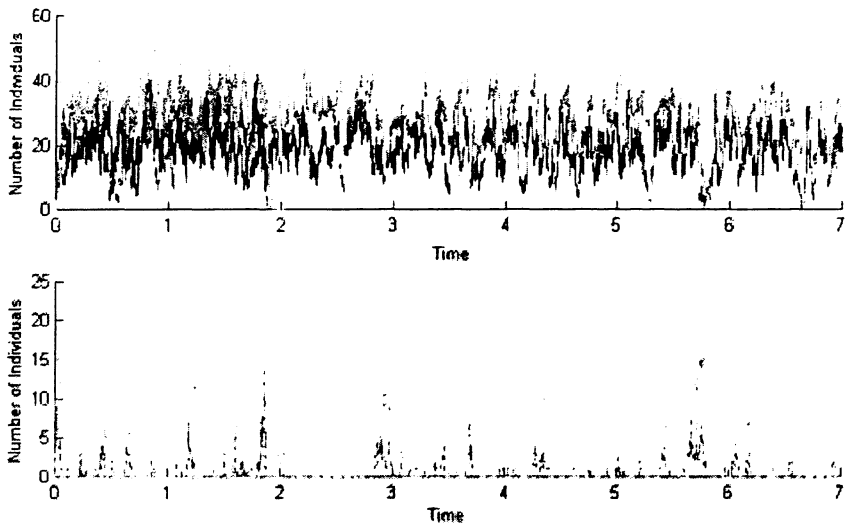

Figure 6: Coexistence under standard conditions where I_2 sustains a small endemic population, $p_1 = 0.33$.

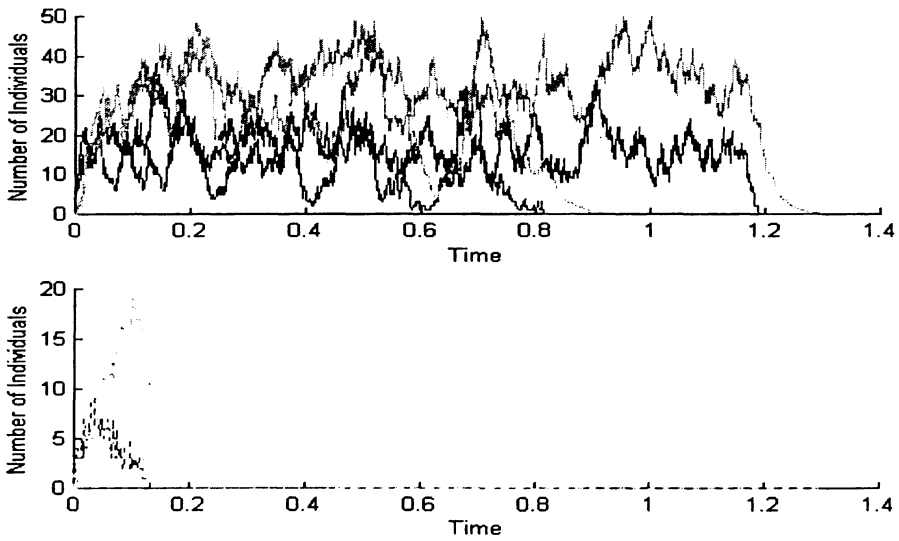

Figure 7: Strain 2 dies out quickly when everyone completes treatment, $p_1 = 1$.

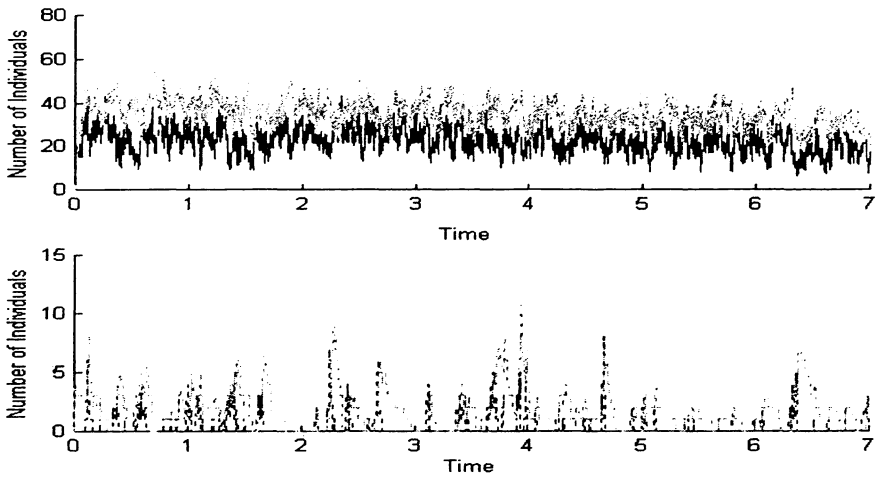

Figure 8: Increasing q_1 causes an increase in the frequency of strain 2 periodic outbreaks, $q_1 = 0.45$.

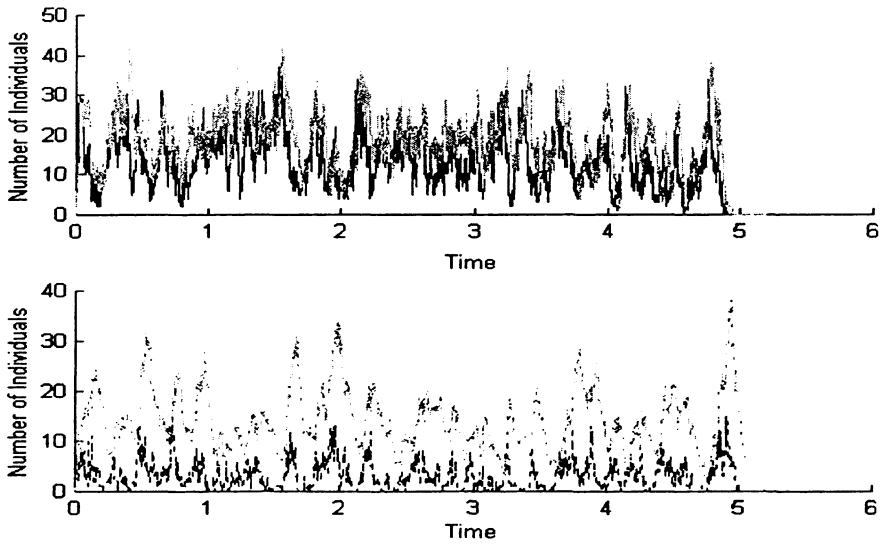

Figure 9: Increased frequency of strain 2 periodic outbreaks and simultaneous extinction of both strains, $q_2 = 0.075$ and $p_1 = 0.001$.

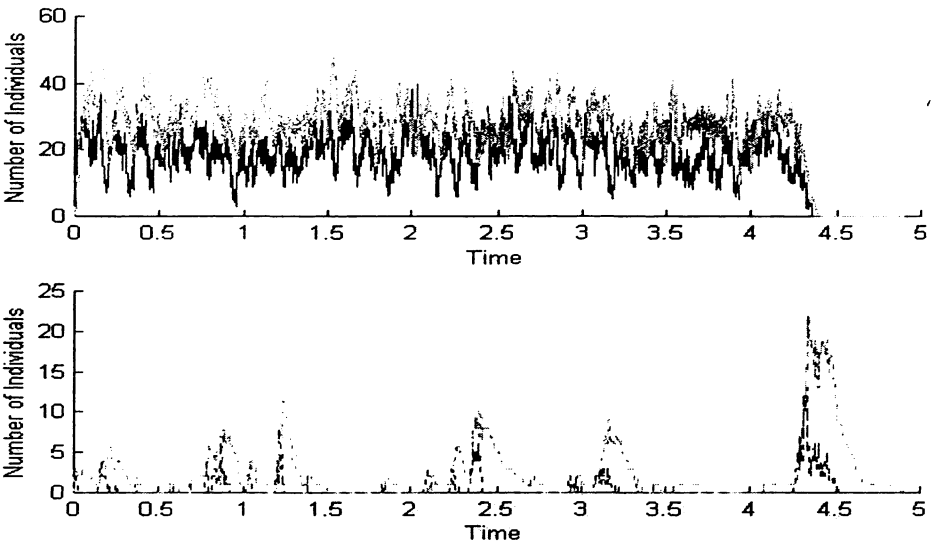

Figure 10: High virulence, $v_1 = 0.3$ and $v_2 = 0.35$.

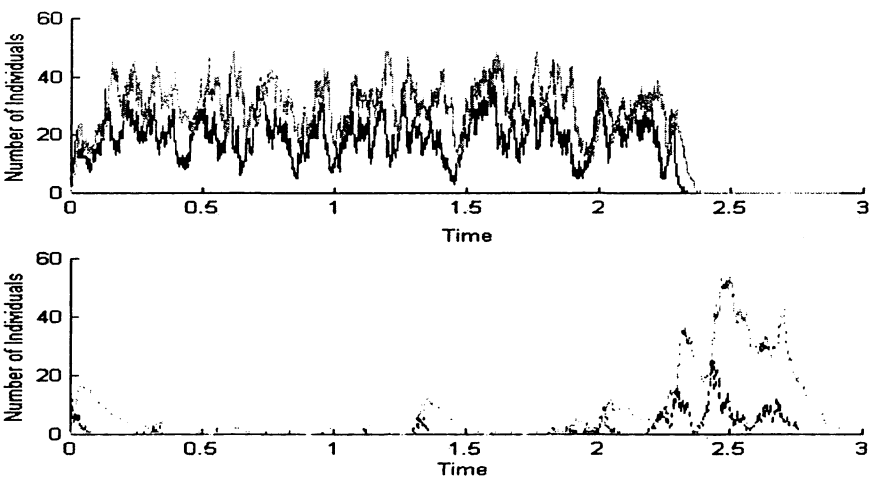

Figure 11: Strain 2 briefly takes over due to an increased per capita contact rate of individuals in I_2 and increased virulence, $\beta_2 = 110$, $v_1 = 0.25$, and $v_2 = 0.3$.

6 Discussion

Throughout this paper we study the evolution of a resistant bacterial strain in the case that an individual does not complete the course of treatment. Specifically, we consider pneumonia caused by the bacteria *Streptococcus pneumoniae*. In our research, we observed that in order for strain 2, the resistant strain to remain in a population there must be a periodic influx of strain 1, a non-resistant strain. For this reason there are four main parameters of focus: β, the contact rate; v, the virulence of the strains; q, the probability an individual will become or remain infected with a particular strain; and p, the probability an individual will complete their medication.

It is understood that because strain 2 is the resistant strain, it is able to withstand antibiotics to a greater degree if not completely. Therefore, the resistant strain can survive, grow, and reproduce while under the influence of some antibiotic, hence strain 2 is more virulent. Due to the fact that strain 2 is more virulent, it is known that it is also less invasive than strain 1. Moreover, strain 1 is the less virulent and more invasive strain. The strong invasiveness provides a high transmission rate into a host for strain 1. Once a suitable environment is established the more virulent strain carries out the infection. We showed through simulations that strain 1 has a higher contact rate per person and a lower virulence than strain 2. This implies that strain 1 may survive in a population only temporarily before its ability to grow is inhibited by an individual's immune system or medication. strain 2 may only survive in a population in the presence of strain 1 due to its poor ability to invade a host. As a result, these two cases occur coexistence of the two strains and the survival of strain 2 after strain 1 goes extinct.

These results are due to the fact that the non-resistant strains survive depending on the influence of the antibiotics, while the survival or dominance of the resistant strain is dependent on the survival of strain 1. The probability that an individual with strain 2 completes treatment is not significant due to the fact that realistically, a more effective antibiotic would be used.

We observe that the implications of the probability of extinction values found in Section 3 and analyzed in Section 4 are not entirely consistent with the results of our simulations. We suspect that this is a consequence of the complications involved in determining single strain probabilities of extinction for a two strain model. In general, the probability of extinction can be found by taking the inverse number of expected infections caused by a single, typical, infectious individual in a population of susceptible (i.e. $\frac{1}{R_0}$). Interpreting R_0 in the context of our model is not simple. First we are faced with the task of defining a 'typical' infectious individual when the possibility exists that infection could begin with either strain one or strain two.

Secondly, the precise definition of 'secondary infections' is unclear. In a single strain model there is only one type of secondary infection. Here however, the possibility exists that infections of type 1 and type 2 can result from an initial strain 1 infection. This raises the question of whether type 2 infections resulting from a type 1 infection should be considered secondary infections resulting from strain 1. Here we have chosen to do so. An implication of this, however, is that we are underestimating the probability of extinction of strain 1. Under our interpretation it is possible for an individual from strain 1 to produce no secondary strain 1 infections but still have $R_0^{[1]}$ greater than 1 because a sufficient number of strain 2 infections were produced. This would lead to predictions of a strain 1 epidemic when inn fact strain 1 was facing extinction. From a biological perspective, this is a wisely conservative error to make. It is far better to overestimate the probability of an epidemic and be adequately prepared than to underestimate the probability of an epidemic and suffer the consequences.

Another result of our R_0 interpretation is that $Pe^{(I_2)}$ does not take into account second order interactions between strain 1 and strain 2. Because strain 2 receives a periodic influx in population from members of strain 1 who do not complete treatment, it is unlikely that strain 2 will ever go completely extinct unless $p_1 = 1$. This means that even for values of β_2 and ϕ_2 for which $R_0^{[2]} < 1 \Rightarrow Pe^{(I_2)} = 1$, strain 2 will continue to exist as long as strain 1 persists. In addition, this causes the probability of extinction of strain 2 to be independent of p_1, q_1, and q_2. This is unfortunate since the effects of these parameters on $Pe^{(I_2)}$ would be of great interest in determining the effects of antibiotic misuse of the development of strain 2. As it is, $Pe^{(I_2)}$ allows us to see only the probability that strain 2 will survive on its own merit, without the assistance of influxes from strain 1. Thus, the probabilities of extinction of the two strains and their joint probability of extinction are useful in providing insight into the effects of parameter values on the model, and are highly useful in indicating which parameter values will give desirable results in our simulations. On the other hand, without the simulations we would not be able to glimpse the subtle interactions between the two competing but coexisting strains and would be unaware of the periodic cycles which allow strain 2 to survive.

7 Conclusion

In response to the question of whether or not we have to finish all prescribed medication, the answer is yes. Our research shows that as long as 80% of the population infected with a non-resistant strain of pneumonia and being treated with penicillin

complete the full course, the development of a resistant strain is hindered. We discover a high probability of extinction under these conditions, reducing the probability of an epidemic. Preventing antibiotic resistant strains from advancing is the key to the future. Once resistant strains emerge, they become much harder to kill. Despite the fact that we've achieved a great deal in this research project there is still much work to be done. Our model shows two strains of bacteria where individuals go through one kind of treatment. We simply consider one factor in the development of resistant strains, the misuse of antibiotics. Analysis of a larger number of strains with different treatments, a recovery period, and a latent state for each strain might be of future interest. Further work also includes looking at the strains for a longer period of time, depending on their latent and infectious state. It would also be interesting to investigate the parameter interactions which drive the cyclic resurgence of strain 2, and to explore other possibilities of the parameter space in general. To further understand the mechanism driving the complex interactions between these two strains it would also be useful to begin to consider new definitions for the basic reproductive number of single strains in a two strain model.

8 Acknowledgments

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9 Appendix

9.1 Simulations

The Matlab simulations used to generate the results of Section 5 were done using the program below. The parameter values used for each graph were as specified in Section 4.1 unless otherwise indicated.

```
tic;
f1=figure;
f2=figure;

R01 = beta1*(gammaB+mu+c1*v1)*(phi2+mu+v2)+beta2*q2*phi1*gammaB*(1-p1)
   /[(phi1+mu+v1)*(gammaB+mu+c1*v1)-q1*phi1*gammaB*(1-p1)]*[phi2+mu+v2];
R02 = beta2/(phi2+mu+v1);
```

```
Dx = 0;

for i = 1 :  HM

t=0;
S=Sx; I1=I1x;I2=I2 x;T1=T1x;T2=T2x;D=Dx;
N=Sx+I1x+I2x+T1x+T2x;
state=[t S I1 T1 I2 T2 D ];
TR=1;
while (t < tfinal) & (I1+I2+T1+T2 > 0)
if toc > 5
[i t ];
tic;
end;
N=S+I1+I2+T1+T2;
S_D = mu*S;
S_I1 = beta1*I1*S/N;
S_I2 = beta2*I2*S/N;
I1_T1 = phi1*I1;
I1_I2 = beta2*I2*I1/N;
I1_D = (mu+v1)*I1;
T1_I1 = q1*(1-p1)*gammaB*T1;
T1_S = p1*gammaA*T1+(1-q1-q2)*(1-p1)*gammaB*T1;
T1_I2 = q2*(1-p1)*gammaB*T1;
T1_D = (mu+c1*v1)*T1;
I2_T2 = phi2*I2;
I2_D = (mu+v2)*I2;
T2_S = p2*gamma2*T2;
T2_D = (mu+c2*v2)*T2;
BR = alpha*N;

R = [S_D S_I1 S_I2 I1_T1 I1_I2 I1_D T1_I1 T1_S T1_I2 T1_D I2_T2 I2_D T2_S T2_D
   BR];
TR = sum(R);
pr = R/TR;
prcum = cumsum(pr);
prcum=[0 prcum];
r = rand;
```

```
slot= sum(r>prcum);
if slot == 1
S=S-1; D=D+1;
elseif slot == 2
S=S-1; I1=I1+1;
elseif slot == 3
S=S-1; I2=I2+1;
elseif slot == 4
I1=I1-1; T1=T1+1;
elseif slot == 5
I1=I1-1; I2=I2+1;
elseif slot == 6
I1=I1-1; D=D+1;
elseif slot == 7
T1=T1-1; I1=I1+1;
elseif slot == 8
T1=T1-1; S=S+1;
elseif slot == 9
T1=T1-1; I2=I2+1;
elseif slot == 10
T1=T1-1; D=D+1;
elseif slot == 11
I2=I2-1; T2=T2+1;
elseif slot == 12
I2=I2-1; D=D+1;
elseif slot == 13
T2=T2-1; S=S+1;
elseif slot == 14
T2=T2-1; D=D+1;
else
S=S+1;
end;
t = t - log(rand)/TR;
c_state = [min(t,tfinal) S I1 T1 I2 T2 D];
state = [state;c_state];
end;
lastrow(i,:)=state(end,:);
x = state(:,1);
```

```
yS = state(:,2);
yI1 = state(:,3);
yT1 = state(:,4);
yI2 = state(:,5);
yT2 = state(:,6);
yD = state(:,7);
figure(f1);
hold on
plot(x,yS,'b-', x,yI1,'r-', x,yT1,'g-', x,yI2,'r:', x,yT2,'g:', x,yD,'k');
hold off
figure(f2);
hold on
subplot(2,1,1)
plot(x,yI1,'r-',x,yT1,'g-');
hold off
hold on
title([' I_1= ' num2str(I2) ', T_1= ' num2str(T2)]);
xlabel('Time')
ylabel('Number of Individuals')
hold off
hold on
subplot(2,1,2)
plot(x,yI2,'r:',x,yT2,'g:');
hold off
hold on
title([' I_2= ' num2str(I2) ', T_2= ' num2str(T2)]);
xlabel('Time')
ylabel('Number of Individuals')
hold off
end;
figure(f1)
title(['S= ' num2str(S) ', I_1= ' num2str(I1) ', I_2= ' num2str(I2) ', D=
' num2str(D) ...
', T_1= ' num2str(T1) ', T_2= ' num2str(T2) ', R_0[1] = ' num2str(R01) ',
R_0[2] = ' num2str(R02)]);
legend('S','I_1','T_1','I_2','T_2','Dead')
xlabel('Time')
ylabel('Number of Individuals')
```

```
figure(f2);
subplot(2,1,1)
legend('I_1','T_1')
title([' I_1= ' num2str(I1) ', T_1= ' num2str(T1)]);
xlabel('Time')
ylabel('Number of Individuals')
subplot(2,1,2)
legend('I_2','T_2')
title([' I_2= ' num2str(I2) ', T_2= ' num2str(T2)]);
xlabel('Time')
ylabel('Number of Individuals')
fI1=lastrow(:,2);
fI2=lastrow(:,4);
fT1=lastrow(:,3);
fT2=lastrow(:,5);
```

10 3 Dimensional Graphs

10.1 $P_e^{I_1}$

To create the Graph 3 of $P_e^{I_1}$ in terms of q_1 and p_1 the following Matlab program is used:

```
   function z = grafica(Lp1,Hp1,inc1,Lp2,Hp2,inc2,beta1,gammaA,gammaB,mu,c1,v1,pl
   ,beta2,phi2,q2); [p,q1] = meshgrid(Lp1:inc1:Hp1,Lp2:inc2:Hp2);

Z= ((phi1+mu+v1).*(p.*gammaA+(1-p).*gammaB+mu+c1.*v1)-q1.*phi1.*gammaB.*(1-p)).*
(phi2+mu+v2)./ (beta1.*(p.*gammaA+(1-p).*gammaB+mu+c1.*v1).*(phi2+mu+v2)+beta2.*(
.*phi1.*gammaB.*(1-p));

Z= min(1,Z);
mesh(p,q1,Z)

xlabel('p')
ylabel('q1')
zlabel('Pe[1]')
```

10.2 Pe^{I_2}

To create the Graph 4 of $P_e^{I_2}$ in terms of ϕ_2 and β_2 the following Matlab program is used:

```
   function z = graficaB(Lp1,Hp1,inc1,Lp2,Hp2,inc2,mu,v2);

[beta2,phi2 rbrack = meshgrid(Lp1:inc1:Hp1,Lp2:inc2:Hp2);

Z= (phi2+mu+v2)./ beta2;

Z= min(1,Z);
mesh(beta2,phi2,Z)

xlabel('beta2')
ylabel('phi2')
zlabel('Pe[2]')
```

10.3 Pe^*

To create the Graph 5 of P_e^* in terms of q_1 and q_2 the following Matlab program is used:

```
   function z =graficaC(Lp1,Hp1,inc1,Lp2,Hp2,inc2,beta1,gammaA,gammaB,mu,c1,v1,
   phi1,v2,beta2,phi2,p);

[q1,q2 ]= meshgrid(Lp1:inc1:Hp1,Lp2:inc2:Hp2);

Z= (((phi1+mu+v1).*(p.*gammaA+(1-p).*gammaB+mu+c1.*v1) q1.*phi1.*gammaB
   .*(1-p)).*(phi2+mu+v2)).*(phi2+mu+v2)./(beta2.*(beta1.*(p.*gammaA
   +(1-p).*gammaB+mu+c1.*v1).*(phi2+mu+v2)+beta2.*q2.*phi1.*gammaB.*(1-p)));

Z= min(1,Z);
mesh(q1,q2,Z)
xlabel('q1')
ylabel('q2')
zlabel('Pe*')
```

11 Markov Chain Analysis

11.1 $R_0^{[1]}$

In Maple we calculate $R_0^{[1]}$ using the continuous-time Markov chain method suggested by Hernández [4]. To begin we create the matrix of transition probabilities.

- P:=matrix(4,4,[0,phi[1]/(phi[1]+mu+v[1]),0,(mu+v[1])/(phi[1]+mu+v[1]), (q[1]*(1-p[1])*gamma[1])/(p[1]*gamma[1]+(1-p[1])*gamma[1]+mu+c[1]*v[1]),0, (q[2]*(1-p[1])*gamma[1])/(p[1]*gamma[1]+(1-p[1])*gamma[1]+mu+c[1]*v[1]), (p[1]*gamma[1]+(1-q[1]-q[2])*(1-p[1])*gamma[1]+mu+c[1]*v[1])/(p[1]*gamma[1]+ (1 p[1])*gamma[1]+mu+c[1]*v[1]),0,0,0,1,1,0,0,0]);
- J:=matrix(4,4,[1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1]);
- i:=matrix(4,4,[1,0,0,0,0,1,0,0,0,0,1,0,0,0,0,1]);

We next calculate the matrix $N = P + J - I$ where J is a matrix of all ones with zero diagonal and I is the identity matrix. Taking the inverse of this matrix will give $M = \lim_{n\to\infty} P^n$.

- N:=evalm(P+J-i);
- Inv:=inverse(N):

Because we are concerned with only one row of this matrix we multiply it by the transpose of the vector 1 to obtain the vector pi=[piI1,piT1,piI2,piT2,piD]. Dividing π_{I_1} by π_{I_Δ} and multiplying by $1/(\phi_1 + \mu + v_1)$ and β_1 will give the first term of $R_0^{[1]}$.

- L:=matrix(1,4,[1,1,1,1]);
- M3:=simplify(multiply(L,Inv)):
- eq1a:=simplify(M3[1,1]/M3[1,4]);
- R[1,a]:=collect(beta[1]*eq1a*(1/(phi[1]+mu+v[1])),gamma[1],c[1]);

We repeat these calculations using $\pi_(I_2)$ to obtain the second term of $R_0^{[1]}$.

- eq1aa:=simplify(M3[1,3]/M3[1,4]);
- R[1,b]:=collect(beta[2]*eq1aa*(1/(phi[2]+mu+v[2])),gamma[1],c[1]);

Adding the first and second terms together we find $R_0^{[1]}$.

- R[1]:=R[1,a]+R[1,b];