Modeling 2002 Outbreak of CA-MRSA in LA County Jail

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1 Abstract

In this study, we took a mathematical look into the transmission of Community Associated MRSA at a jail in LA County. We started by using the compartmental model that describes the Susceptible, Colonized and Infected populations present, along with how the inflow and outflow of inmates affects each of these populations. Afterwards, three differential equations were used to model the change in the three populations over 9 months respectively. The goal then was to create a 3D plot using the ODE45 function which takes 3 parameters including 11 variables, the time range, and our initial y_0 values. Afterwards, the plot3 function in MATLAB was used to graph our data. The next step was to approximate the solution curves for each compartment in our model consisting of the differential equations using the Runge-Kutta method. Since the parameters for male and female inmates were different, we analyzed each compartment twice, once for all the male inmates and again using the parameters for the female inmates. The last step consisted of recreating an analysis for R_0 using the matrix method, as well as the eigenvalue and weighted average approach. We also simulated R_0 values based on random samples of the varying parameter values.

2 Introduction

Methicillin-resistant Staphylococcus aureus (MRSA) is a gram-positive, non-spore forming type of bacteria that has developed resistance to many of the antibiotics that are used to treat individuals with MRSA infections. MRSA is distinguished into two main types: healthcare-associated MRSA (HA-MRSA) and community-associated MRSA (CA-MRSA). [1] These two strains have significant differences in their biology, and thus exhibit different infection models.[1] HA-MRSA was the first type to arise, and it caused mortality but was only found in hospitalized individuals. During the 1990s, CA-MRSA outbreaks began occurring among the greater community and has caused death among individuals who otherwise do not have strong risk factors in regard to their health.[3]

MRSA is typically spread through direct contact to the skin, as this is where the bacteria colonizes.[3] As such, community hot spots for MRSA occur in settings where there is higher density of individuals, more skin on skin contact, contaminated surfaces, or lower hygiene. Examples include sports teams, day-cares, homeless populations and correctional facilities. [1]

In this paper, we examine a study performed on an outbreak in one such hotbed, the Los Angeles County Jail (LACJ), which is the largest jail in the world.[1] In 2007, Emily Kajita and associates, published a study "Modelling an Outbreak of an Emerging Pathogen." In the study, they produced a mathematical model to describe the spread of the CA-MRSA bacterium among the system of the LACJ in 2002. The jail houses hundreds of thousands of individuals per year and over 20,000 at any given time. At the time the study was performed, state regulations required only 3 showers per week and 2 pairs of underwear for each inmate. The study is important to help understand the important contributing factors in spreading the disease within the jail as well as the implications this may have for the outside community, as inmates typically only reside in the jail for an average of one month, and can leave while still contagious.

We will examine the compartment model, which separates the inmates into 3 classes: Susceptible (no infection), Colonized (asymptomatic, contagious) and Infected (symptomatic infection). The model also

considers the rates at which inmates move between compartments and into/out of the outside community. We will reproduce the methods used in the study for calculating the disease reproductive number (R_0), in greater detail using the method developed by P. van den Driessche and James Watmough. [2] Further, we will implement the ODE45 software to integrate the three ordinary differential equations used in the model as well as the Runge-Katta method for examining the population dynamics.

3 Methods and Mathematical Model

Model

A compartment model is used to describe how inmates of the LA County Jail population can move between the outside community and 3 compartments: Susceptible, Colonized and Infected. See the diagram below (Figure1) for a description of the model, and it's notation, as well as the "Parameters" section of this paper.

$$\frac{dS}{dt} = \pi(1 - \gamma_C - \gamma_I) + \alpha C - \frac{c\beta_C CS}{N} - \frac{c\beta_I IS}{N} - \delta S \tag{1}$$

$$\frac{dC}{dt} = \pi\gamma_C + \frac{c\beta_C CS}{N} + \frac{c\beta_I IS}{N} - \alpha C - p\phi C - \delta C \tag{2}$$

$$\frac{dI}{dt} = \pi\gamma_I + p\phi C - \delta I \tag{3}$$

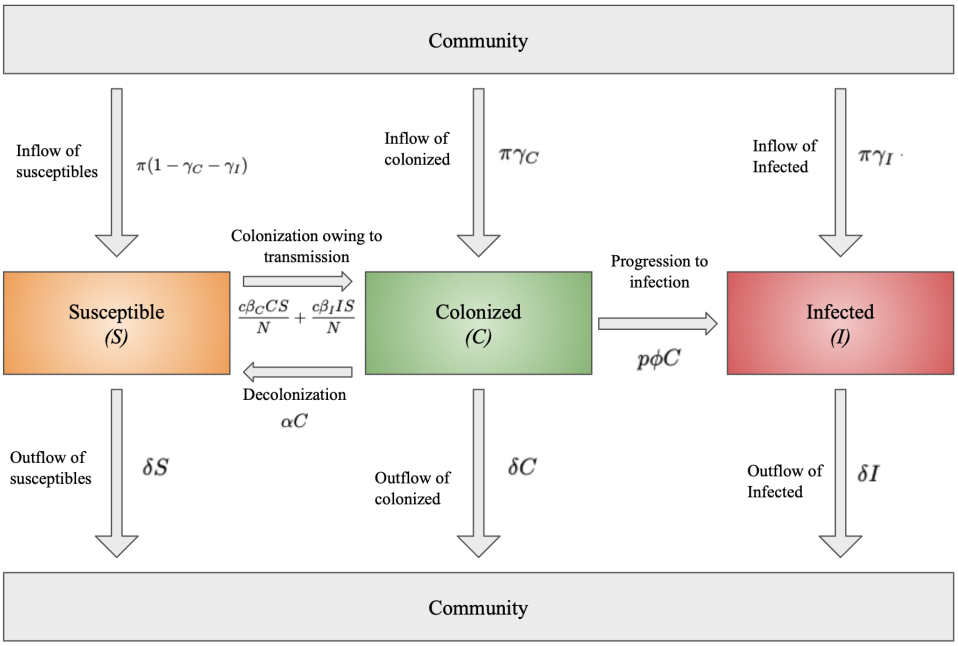

Figure 1: Community Associated MRSA: Compartment model

Parameters

Notation	Parameter
N	Total number of inmates
π	Number of individuals booked per day
$1/\delta$	Average incarceration time (days)
γ_C	Probability that an inmate enters the jail colonized with CA-MRSA
γ_I	Probability that an inmate enters the jail infected with CA-MRSA
$1/\alpha$	Average decolonization time (days)
p	Proportion of colonized individuals who progress to infected
$1/\phi$	Average time for colonized individuals to progress to infection (days)
β_C	Probability that a non-carrier individual would become colonized with CA-MRSA upon contact with a colonized individual
β_I	Probability that a non-carrier individual would become colonized with CA-MRSA upon contact with an infected individual
c	Average number of contacts per day

t_0	Males	Females
Susceptible	12,000	2,100
Colonized	50	6
Infected	50	6

Time(t)	Months
t = 1	January
...	...
t = 9	September

Note: The chart on the left highlights the initial y_0 values that were recorded in January at the start of the study. The chart on the right shows that the study took place over 9 months from January to September.

4 Data

Note: where a range of values was given, the median was used in our calculations.

Parameter	Males	Females
N	16,956	2,200
π	341 - 407	64 - 81
$1/\delta$	42 - 50	27 - 34
γ_C	$8.8\text{x}10^{-5} - 4.923\text{x}10^{-}3$	$4.43\text{x}10^{-4} - 7.77\text{x}10^{-3}$
γ_I	$8.8\text{x}10^{-5} - 4.923\text{x}10^{-}3$	$4.43\text{x}10^{-4} - 7.77\text{x}10^{-3}$
$1/\alpha$	30 - 120	30 - 120
p	0.10 - 0.30	0.10 - 0.30
$1/\phi$	4 - 15	4 - 15
β_C	$1\text{x}10^{-5} - 1.5\text{x}10^{-}3$	$1\text{x}10^{-5} - 2\text{x}10^{-3}$
β_I	$1\text{x}10^{-5} - 1.5\text{x}10^{-}3$	$1\text{x}10^{-5} - 2\text{x}10^{-3}$
c	5 - 50	5 - 50

5 Results and Discussion

5.1 Calculating R_0

In this section, we use the strategy created by van den Driessche and Watmough [2] to reproduce the basic reporduction number, R_0, as was calculated by the authors of the LA County Jail study. [1]

We start by considering the ordinary differential equations $\frac{dC}{dt}$ and $\frac{dI}{dt}$ from the model, which describe the change in the number of inmates in the Colonized and Infected states, respectively, at time t. Considering only these 2 disease-present compartments of the model, we construct the vectors F, $V \in \mathbb{R}^{2x1}$ such that

$$F = \begin{bmatrix} \text{rate of appearance of new infections in state C} \\ \text{rate of appearance of new infections in state I} \end{bmatrix} \tag{4}$$

$$= \begin{bmatrix} F_C(C,I) \\ F_I(C,I) \end{bmatrix} = \begin{bmatrix} \frac{cS}{N}(\beta_C C + \beta_I I) \\ 0 \end{bmatrix} \tag{5}$$

and

$$V = V^+ + V^- \tag{6}$$

where,

$$V^+ = \begin{bmatrix} \text{rate of transfer of transfer of individuals into state C by all other means} \\ \text{rate of transfer of transfer of individuals into state C by all other means} \end{bmatrix} \tag{7}$$

$$= \begin{bmatrix} 0 \\ p\phi C \end{bmatrix}, \tag{8}$$

$$V^- = \begin{bmatrix} \text{rate of transfer of transfer of individuals out of state C by all other means} \\ \text{rate of transfer of transfer of individuals out of state C by all other means} \end{bmatrix} \tag{9}$$

$$= \begin{bmatrix} -C(\alpha + p\phi + \delta) \\ -\delta I \end{bmatrix}. \tag{10}$$

Thus,

$$V = \begin{bmatrix} V_C \\ V_I \end{bmatrix} = \begin{bmatrix} -C(\alpha + p\phi + \delta) \\ p\phi C - \delta I \end{bmatrix} \tag{11}$$

Next, we compute the Jacobian matrices of F and V, which we will call $\mathbf{F}$ and $\mathbf{V}$, respectively.

$$\mathbf{F} = \begin{bmatrix} \frac{\partial F_C}{\partial C} & \frac{\partial F_C}{\partial I} \\ \frac{\partial F_I}{\partial C} & \frac{\partial F_I}{\partial I} \end{bmatrix} = \begin{bmatrix} \frac{cS}{N}\beta_C & \frac{cS}{N}\beta_I \\ 0 & 0 \end{bmatrix} \tag{12}$$

$$\mathbf{V} = \begin{bmatrix} \frac{\partial V_C}{\partial C} & \frac{\partial V_C}{\partial I} \\ \frac{\partial V_I}{\partial C} & \frac{\partial V_I}{\partial I} \end{bmatrix} = \begin{bmatrix} -(\alpha + p\phi + \delta) & 0 \\ p\phi & -\delta \end{bmatrix} \tag{13}$$

Now, we evaluate $\mathbf{F}$ and $\mathbf{V}$ at the disease free equilibrium (DFE). Note that at the DFE, there is no prevalence of the disease. Thus $C = I = 0$. Then, since N is constant, we know $S + C + I = N \implies S = N - (I + C) = N$. Then,

$$\mathbf{F}|_{DFE} = \begin{bmatrix} c\beta_C & c\beta_I \\ 0 & 0 \end{bmatrix} \tag{14}$$

$$\mathbf{V}|_{DFE} = \begin{bmatrix} -(\alpha + p\phi + \delta) & 0 \\ p\phi & -\delta \end{bmatrix} \tag{15}$$

Now that we have $\mathbf{F}|_{DFE}$ and $\mathbf{V}|_{DFE}$ we can find $-\mathbf{V}|_{DFE}^{-1}$

$$-\mathbf{V}|_{DFE}^{-1} = \frac{1}{-(\alpha + p\phi + \delta)(-\delta) - 0(p\phi)} \begin{bmatrix} -\delta & 0 \\ -p\phi & -(\alpha + p\phi + \delta) \end{bmatrix} = \begin{bmatrix} \frac{1}{\alpha + p\phi + \delta} & 0 \\ \frac{p\phi}{(\alpha + p\phi + \delta)\delta} & \frac{1}{\delta} \end{bmatrix} \tag{16}$$

With this result, we compute $\mathbf{F}|_{DFE} \cdot \mathbf{-V}|_{DFE}^{-1}$,

$$\mathbf{F}|_{DFE} \cdot \mathbf{(-V)}|^{-1}_{DFE} = \begin{bmatrix} c\beta_C & c\beta_I \\ 0 & 0 \end{bmatrix} \begin{bmatrix} -(\alpha + p\phi + \delta) & 0 \\ p\phi & -\delta \end{bmatrix} \tag{17}$$

$$= \begin{bmatrix} \frac{c(\beta_C\delta + \beta_I p\phi)}{\delta(\alpha + p\phi + \delta)} & \frac{c\beta_I}{\delta} \\ 0 & 0 \end{bmatrix} \tag{18}$$

For the final step, R_0 is given as the maximum eigenvalue of $\mathbf{F}|_{DFE} \cdot \mathbf{(-V)}|^{-1}_{DFE}$. Since $\mathbf{F}|_{DFE} \cdot \mathbf{(-V)}|^{-1}_{DFE} \in \mathbb{R}^{2x2}$ and has a zero, non-diagonal entry, then the eigenvalues are the two diagonal entries and the maximum eigenvalue gives:

$$R_0 = \frac{c\beta_C + p\phi c\frac{\beta_I}{S}}{\alpha + p\phi + \delta} \tag{19}$$

Biological Interpretation of R_0 .

Van den Driessche and Watmough define R_0, the basic reproduction number, as "the expected number of secondary cases produced, in a completely susceptible population by a typical infective individual." [2] That is, in the case of the LACJ and MRSA, it is the average number of inmates that one infectious inmate (Colonized or Infected), will spread the infection to, in a naive population during one disease generation. E.g. if $R_0 = 2$, one infectious inmate will lead to an additional two infectious inmates in one disease generation, leading to 4 the next generation, etc.

The result is that $R_0 = 1$ is a threshold value, where the disease maintains a constant prevalence each generation. $R_0 > 1$ means the disease is increasing its prevalence in the population, and $R_0 < 1$ implies that it is decreasing with each disease generation.

In this model, we can also derive R_0 through its biological interpretation, by examining the three ways in which inmates can exit the Colonized compartment, C, in the model. From Eqn. (2) and the table "Parameters", we see that a Colonized individual may either: 1) return to the Susceptible state by decolonizing, 2) exit the jail, or 3) enter the Infected state if the infection progresses. With this in mind, we can think of each of these three routes out of the Colonized state as having its own R_0 value, and the total R_0 as being a weighted average of the 3, as such:

$$R_0 = q_1 R_0^1 + q_2 R_0^2 + q_3 R_0^3 \tag{20}$$

We can think of q_1 as the portion of inmates who take the first route (decolonize and return to Susceptible class). Thus,

$$q_1 = \frac{\alpha}{\alpha + p\phi + \delta} \tag{21}$$

then the proportion of those who exit the jail while colonized with MRSA are represented by

$$q_2 = \frac{\delta}{\alpha + p\phi + \delta} \tag{22}$$

and the portion of those who move into to the Infected state are denoted by

$$q_3 = \frac{p\phi}{\alpha + p\phi + \delta}. \tag{23}$$

Then, we can intuitively derive R_0^i, $i = 1, 2, 3$ from the parameter definitions. Keeping in mind that R_0^i is the average number of times an individual who takes route i will spread the MRSA infection to a Susceptible individual in the population. We have

$$R_0^1 = R_0^2 = \frac{c\beta_C}{\alpha + p\phi + \delta}, \tag{24}$$

$$R_0^3 = \frac{c\beta_C}{\alpha + p\phi + \delta} + \frac{c\beta_I}{\delta} \tag{25}$$

Thus, we arrive again at the same R_0 value achieved using van den Driessche and Watmough's method, as

$$R_0 = (\frac{\alpha}{\alpha + p\phi + \delta})(\frac{c\beta_C}{\alpha + p\phi + \delta}) + (\frac{\delta}{\alpha + p\phi + \delta})(\frac{c\beta_C}{\alpha + p\phi + \delta}) + (\frac{p\phi}{\alpha + p\phi + \delta})(\frac{c\beta_C}{\alpha + p\phi + \delta} + \frac{c\beta_I}{\delta}) \quad (26)$$

$$= \frac{c\beta_C + p\phi c\frac{\beta_I}{S}}{\alpha + p\phi + \delta} \quad (27)$$

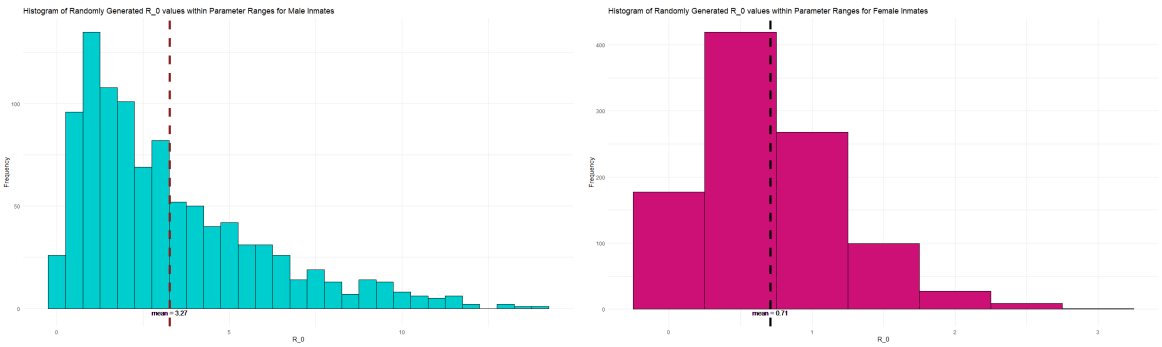

Figure 2: Histograms for Randomly Generated R_0 Values by Varying Parameter Values

In the 2007 LACJ study, the authors used sophisticated simulation and sampling techniques to simulate 1,000 R_0 values based on the varying parameter values. We used our own crude random sampling technique in order to attempt to reproduce their results, or get close. We used statistical software, R, to generate pseudo-random samples of the parameter values within their ranges, for males and females separately. In the LACJ study, they found R_0 to have a mean value of approximately 0.6 across their simulations. We had a similar result for our female simulation, which achieved a mean R_0 value of 0.71. For our Male population, however, the simulated R_0 values had much more variation and a large right tail. The mean R_0 for males in our simulation was 3.27. Figure 2 displays histograms for the frequency of simulated R_0 values for the male (left) and female (right) inmates.

5.2 ODE45 Integration Technique

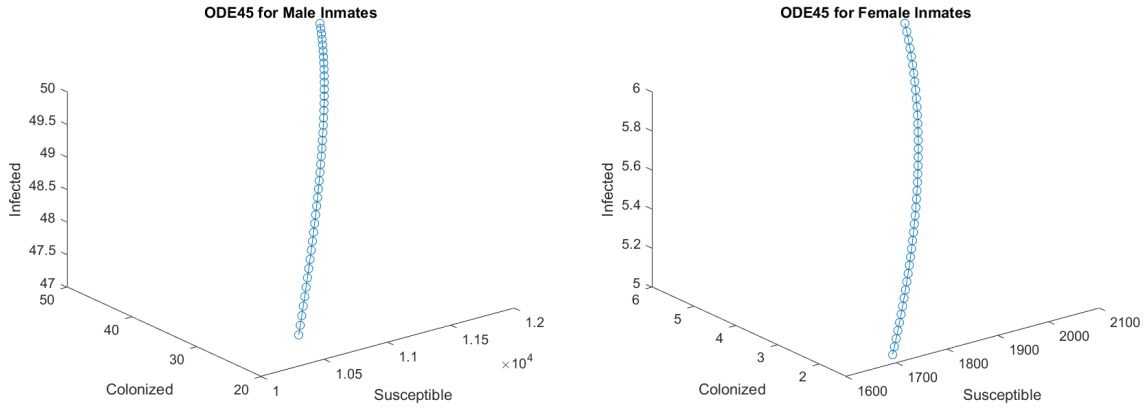

Figure 3: MATLAB ODE45 Integrations for Male and Female Inmates

The graphs in Figure 3 above shows the 3D plots that were generated as a result of our ODE45 function. We had varying parameters for male and female inmates, hence the two graphs were created independently. Each of the graphs was generated using 11 parameters, a time span, as well as some y_0 initial values consisting of the male and female population data which includes the Susceptible, Colonized and Infected populations.

5.3 Numerical Methods

In our analysis of our mathematical model, we evaluated the approximate solution curves for each differential equation through the Runge-Kutta Method. This method integrates step-wise in a recursive fashion to approximate solution curves of differential equations using specific initial values. In general, a differential equation denoted below

$$\frac{dy}{dt} = f(t, y), \quad y(t_0) = y_0. \tag{28}$$

will be integrated through the Runge-Kutta method by approximating at a step-size $h > 0$ for a function f and initial value y_0 through time t to approximate y. The method itself is as follows:

$$k_1 = f(t_n, y_n) \tag{29}$$

$$k_2 = f(t_n + \frac{h}{2}, y_n + h\frac{k_1}{2}) \tag{30}$$

$$k_3 = f(t_n + \frac{h}{2}, y_n + h\frac{k_2}{2}) \tag{31}$$

$$k_4 = f(t_n + h, y_n + hk_3) \tag{32}$$

$$y_{n+1} = y_n + \frac{h}{6}(k_1 + 2k_2 + 2k_3 + k_4) \tag{33}$$

$$t_{n+1} = t_n + h \tag{34}$$

From equations (29) through (34), we see the iterative method of evaluating the integrated equation at each step and finally we get y_{n+1}. We implemented this method into MATLAB using our three differential equations and ran it through a "for" loop for 8 iterations in order to generate 9 data points. Figures 4 and 5 below are the graphs we generated for each respective compartment in our differential equation MATLAB.

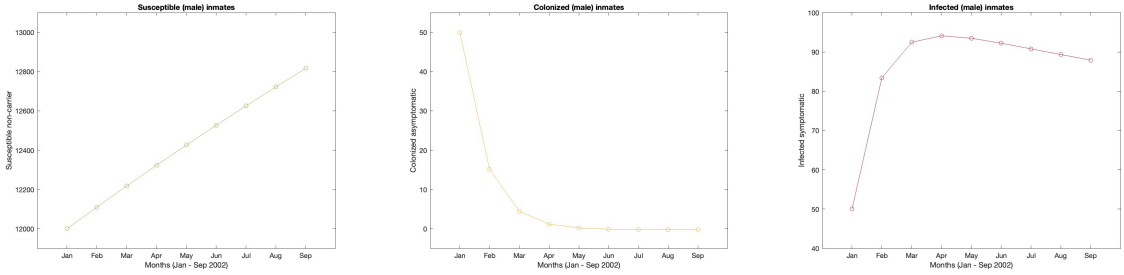

Figure 4: Runge-Kutta Numerical Method for Approximating Solution curves (Male inmates)

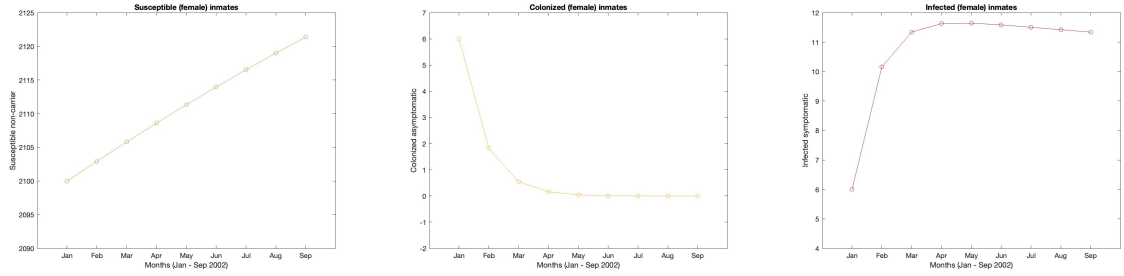

Figure 5: Runge-Kutta Numerical Method for Approximating Solution curves (Female inmates)

As we can observe, the general trends are preserved between the male and female models. Over time, inmates become more and more susceptible, and inmates decolonize and either become susceptible again or become infected. In the infected graph, we can see that there was a sharp increase in infected individuals in

the first few months and then it began to slowly decrease for subsequent months. This behavior is typical for an outbreak, and our figures exemplify that behavior.

6 Conclusion/Discussion

In this report we were able to develop an understanding of modelling disease spread with compartment models and ordinary differential equations. Examining the 2007 study[1] of a CA-MRSA outbreak in LA County Jail allowed us to reproduce and examine their methods of calculating R_0 as well as apply some other numerical methods to the equations in the model provided by Kajita, et al. Our application of the Runge-Kutta method showed us how the dynamics of the three model compartments can play out with differing levels of initial conditions. This could inform policy about the inmate on-boarding process, to ensure we are not introducing individuals into the system who are colonized or infected with CA-MRSA. From the model, we gain the insight that jails are not closed systems. In regards to CA-MRSA, individuals arrive the jail in one of 3 compartments, and will leave the same way. We want to ensure our correctional facilities are not distribution centers for antibiotic resistant bacterial infections into our communities. Policies regarding inmate booking, hygiene, crowding and access to clean clothing/facilities can have an effect on the epidemiological condition of the outside community.

7 Author Contribution

Riley Adams: Introduction, Conclusion, R_0 analysis, Parameters, Data, Methods and Mathematical Model, Figure 2
Ryan Campbell: Methods and Mathematical Model (figure), Numerical Methods: Runge-Kutta, ODE-45, Figure 4, Figure 5, Figure 1
Aditya Kurkut: Abstract, Methods and Mathematical Model, Parameters, Data, ODE-45, Figure 3
All authors consulted with each other throughout implementation of respective sections.

8 References

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2. Van den Driessche, P., and James Watmough. "Reproduction Numbers and Sub-Threshold Endemic Equilibria for Compartmental Models of Disease Transmission." Mathematical Biosciences, vol. 180, no. 1-2, 2002, pp. 29–48., https://doi.org/10.1016/s0025-5564(02)00108-6. https://www.sciencedirect.com/science/article/pii/S0025556402001086

3. Pantosti, A., and M. Venditti. "What Is MRSA?" European Respiratory Journal, vol. 34, no. 5, 2009, pp. 1190–1196., https://doi.org/10.1183/09031936.00007709. https://erj.ersjournals.com/content/34/5/1190.short

π

9 Code Appendix

9.1 R Code for R_0 Simulation (Riley Adams)

```
library(tidyverse)
#ranges for male parameters
pi_range_male <- seq(from=341,to=407,by=1)
delta_range_male <- seq(from=42,to=50,by=1)
gamma_c_range_male <- seq(from=.000088, to=.004923, by=0.00001)
gamma_i_range_male <- seq(from=.000088, to=.004923, by=0.00001)
alpha_range_male <- seq(from=30,to=120,by=1)
p_range_male <- seq(from=.1, to=.3,by=.05)
phi_range_male <- seq(from=4,to=15,by=1)
beta_c_range_male <- seq(from=.00001,to=.001,by=.000015)
beta_i_range_male <- seq(from=.00001,to=.001,by=.000015)
c_range_male <- seq(from=5,to=50,by=1)


#Male Parameter Simulations
#create 1000 samples for each parameter.
#put into dataframe
set.seed(666)
pi_male <- sample(pi_range_male,1000,replace = T)
delta_male <- sample(pi_range_male,1000,replace = T)
gamma_c_male <- sample(gamma_c_range_male,1000,replace = T)
gamma_i_male <- sample(gamma_i_range_male,1000,replace = T)
alpha_male <- sample(alpha_range_male,1000,replace = T)
p_male <- sample(p_range_male,1000,replace = T)
phi_male <- sample(phi_range_male,1000,replace = T)
beta_c_male <- sample(beta_c_range_male,1000,replace = T)
beta_i_male <- sample(beta_i_range_male,1000,replace = T)
c_male <- sample(c_range_male,1000,replace = T)


#function to calculate R_0
Rnaught <- function(delta, gamma_c, gamma_i, alpha, p, phi, beta_c, beta_i, k){
  R0 <- (k*beta_c + p*(1/phi)*k*(delta*beta_i)) / (1/alpha + p*(1/phi)+(1/delta))
  return(R0)
}

#calculate 1000 R_0 values from sampled parameters
R_nots <- numeric()
for(i in 1:1000){
  R_nots[i] <- Rnaught(delta_male[i],gamma_c_male[i], gamma_i_male[i],alpha_male[i],p_male[i],
    phi_male[i],beta_c_male[i],beta_i_male[i],c_male[i])
}

R_notsData <- as.data.frame(R_nots)
R_notsData %>%
  ggplot(aes(x=R_nots))+
  geom_histogram(binwidth = 0.5,color = 'black',fill='cyan3')+
  geom_vline(aes(xintercept=mean(R_nots)), color='firebrick4', linetype='dashed',size =2)+
  geom_text(aes(x=mean(R_nots), y=-2, label="mean = 3.27"))+
  labs(title = "Histogram of Randomly Generated R_0 values within Parameter Ranges for Male Inmates",
```

```
       x = "R_0",
       y = "Frequency")+
  theme_minimal()


#=============================================================================================================
#=============================================================================================================

#ranges for female parameters
pi_range_female <- seq(from=64,to=81,by=1)
delta_range_female <- seq(from=27,to=34,by=1)
gamma_c_range_female <- seq(from=.00043, to=.00777, by=0.0001)
gamma_i_range_female <- seq(from=.00043, to=.00777, by=0.0001)
alpha_range_female <- seq(from=30,to=120,by=1)
p_range_female <- seq(from=.1, to=.3,by=.05)
phi_range_female <- seq(from=4,to=15,by=1)
beta_c_range_female <- seq(from=.00001,to=.001,by=.000015)
beta_i_range_female <- seq(from=.00001,to=.001,by=.000015)
c_range_female <- seq(from=5,to=50,by=1)


#Female Parameter Simulations
#create 1000 samples for each parameter.
#put into dataframe
set.seed(666)
pi_female <- sample(pi_range_female,1000,replace = T)
delta_female <- sample(pi_range_female,1000,replace = T)
gamma_c_female <- sample(gamma_c_range_female,1000,replace = T)
gamma_i_female <- sample(gamma_i_range_female,1000,replace = T)
alpha_female <- sample(alpha_range_female,1000,replace = T)
p_female <- sample(p_range_female,1000,replace = T)
phi_female <- sample(phi_range_female,1000,replace = T)
beta_c_female <- sample(beta_c_range_female,1000,replace = T)
beta_i_female <- sample(beta_i_range_female,1000,replace = T)
c_female <- sample(c_range_female,1000,replace = T)


#calculate 1000 R_0 values from sampled parameters
R_nots_fem <- numeric()
for(i in 1:1000){
  R_nots_fem[i] <- Rnaught(delta_female[i],gamma_c_female[i], gamma_i_female[i],alpha_female[i],
    p_female[i],phi_female[i],beta_c_female[i],beta_i_female[i],c_female[i])
}

R_nots_fem_Data <- as.data.frame(R_nots_fem)
R_nots_fem_Data %>%
  ggplot(aes(x=R_nots_fem))+
  geom_histogram(binwidth = 0.5,color = 'black',fill='deeppink3')+
  geom_vline(aes(xintercept=mean(R_nots_fem)), color='black', linetype='dashed',size =2)+
  geom_text(aes(x=mean(R_nots_fem), y=-5, label="mean = 0.71"))+
  labs(title = "Histogram of Randomly Generated R_0 values within Parameter Ranges for Female Inmates",
       x = "R_0",
       y = "Frequency")+
  theme_minimal()
```

9.2 Runge-Kutta MATLAB code (Ryan Campbell)

```
MATLAB for MAT 124 MRSA Project
Numerical Methods
% Run this section to clear the workspace
clear;clc;
% NOTE: Parameter variable names are shared and will be overwritten
%       for each section ran. Output is y(1,:), y(2,:), and y(3,:) for male model,
%       and g(1,:), g(2,:), and g(3,:) for female model. Row 1 is S, Row 2
%       is C, and Row 3 is I.

Male Model
% Runge-Kutta method
% Parameters (midpoints if range) MALE MODEL
N = 16956;
pi = (341+407)/2;
delta = 1/((42+50)/2);
gamma_c = (8.8*10^(-5)+4.923*10^(-3))/2;
gamma_I = (8.8*10^(-5)+4.923*10^(-3))/2;
alpha = 1/((30+120)/2);
p = (0.10+0.30)/2;
phi = (4+15)/2;
beta_c = (1*10^(-5)+1.5*10^(-3))/2;
beta_I = (1*10^(-5)+1.5*10^(-3))/2;
c = (5+50)/2;

% Define function handles
% y=[R,F] <= y(1,:)=R y(2,:)=F
% y(1) = dS
% y(2) = dC
% y(3) = dI
f=@(t,y) [...
    +pi*(1-gamma_c-gamma_I)+alpha*y(2)-(c*beta_c*y(2)*y(1))/N-(c*beta_I*y(2)*y(1))/N-delta*y(1);
    +pi*(gamma_c)+(c*beta_c*y(2)*y(1))/N-(c*beta_I*y(3)*y(1))/N-alpha*y(2)-p*phi*y(2)-delta*y(2);
    +pi*(gamma_I)+p*phi*y(2)-delta*y(3)];

% Initial conditions
t(1) = 1;
y(:,1) = [12000,50,50];

% Step size
h = 1;
tfinal = 8;
M = ceil(tfinal/h);

% Update loop
for i = 1:M
    % Update time
    t(i+1) = t(i)+h;
    % Update for y
    k1 = f(t(i)    ,y(:,i)       );
    k2 = f(t(i)+h/2,y(:,i)+k1*(h/2));
    k3 = f(t(i)+h/2,y(:,i)+k2*(h/2));
    k4 = f(t(i)+h  ,y(:,i)+h  *k3);
```

```
    y(:,i+1)=y(:,i)+h/6*(k1 + 2*k2 + 2*k3 + k4);
end

% Plot the solution
figure(1); clf(1);
plot(t,y(1,:), '-o', color = '#77AC30')
xlabel('Months (Jan - Sep 2002)')
ylabel('Susceptible non-carrier')
title('Susceptible (male) inmates')
% legend('Susceptible')
xlim([0 10])
xticks([1 2 3 4 5 6 7 8 9 10])
xticklabels({'Jan', 'Feb', 'Mar', 'Apr', 'May', 'Jun', 'Jul', 'Aug', 'Sep'})
ylim([11900 13100])
ax = gca;
ax.YAxis.Exponent = 0;
% set(gca, 'Fontsize', 16)
figure(2); clf(2);
plot (t,y(2,:), '-o', color = '#EDB120' )
xlabel('Months (Jan - Sep 2002)')
ylabel('Colonized asymptomatic')
title('Colonized (male) inmates')
% legend('Colonized')
xlim([0 10])
xticks([1 2 3 4 5 6 7 8 9 10])
xticklabels({'Jan', 'Feb', 'Mar', 'Apr', 'May', 'Jun', 'Jul', 'Aug', 'Sep'})
ylim([-5 55])
% set(gca, 'Fontsize', 16)
figure(3); clf(3);
plot (t,y(3,:), '-o', color = '#A2142F')
xlabel('Months (Jan - Sep 2002)')
ylabel('Infected symptomatic')
title('Infected (male) inmates')
% legend('Infected')
xlim([0 10])
xticks([1 2 3 4 5 6 7 8 9 10])
xticklabels({'Jan', 'Feb', 'Mar', 'Apr', 'May', 'Jun', 'Jul', 'Aug', 'Sep'})
ylim([40 100])
% set(gca, 'Fontsize', 16)

Female Model
% Runge-Kutta method
% Parameters (midpoints if range) FEMALE MODEL
N = 2200;
pi = (64+81)/2;
delta = 1/((27+34)/2);
gamma_c = (4.43*10^(-4)+7.77*10^(-3))/2;
gamma_I = (4.43*10^(-4)+7.77*10^(-3))/2;
alpha = 1/((30+120)/2);
p = (0.10+0.30)/2;
phi = (4+15)/2;
beta_c = (1*10^(-5)+2*10^(-3))/2;
beta_I = (1*10^(-5)+2*10^(-3))/2;
c = (5+50)/2;
```

```
% Define function handles
% y=[R,F] <= y(1,:)=R y(2,:)=F
% y(1) = dS
% y(2) = dC
% y(3) = dI
f=@(t,g) [...
    +pi*(1-gamma_c-gamma_I)+alpha*g(2)-(c*beta_c*g(2)*g(1))/N-(c*beta_I*g(2)*g(1))/N-delta*g(1);
    +pi*(gamma_c)+(c*beta_c*g(2)*g(1))/N-(c*beta_I*g(3)*g(1))/N-alpha*g(2)-p*phi*g(2)-delta*g(2);
    +pi*(gamma_I)+p*phi*g(2)-delta*g(3)];

% Initial conditions
t(1) = 1;
g(:,1) = [2100,6,6];

% Step size
h = 1;
tfinal = 8;
M = ceil(tfinal/h);

% Update loop
for i = 1:M
    % Update time
    t(i+1) = t(i)+h;
    % Update for y
    k1 = f(t(i)    ,g(:,i)       );
    k2 = f(t(i)+h/2,g(:,i)+k1*(h/2));
    k3 = f(t(i)+h/2,g(:,i)+k2*(h/2));
    k4 = f(t(i)+h  ,g(:,i)+h  *k3);
    g(:,i+1)=g(:,i)+h/6*(k1 + 2*k2 + 2*k3 + k4);
end

% Plot the solution
figure(1); clf(1);
plot(t,g(1,:), '-o', color = '#77AC30')
xlabel('Months (Jan - Sep 2002)')
ylabel('Susceptible non-carrier')
title('Susceptible (female) inmates')
% legend('Susceptible')
xlim([0 10])
xticks([1 2 3 4 5 6 7 8 9 10])
xticklabels({'Jan', 'Feb', 'Mar', 'Apr', 'May', 'Jun', 'Jul', 'Aug', 'Sep'})
ylim([2090 2125])
ax = gca;
ax.YAxis.Exponent = 0;
% set(gca, 'Fontsize', 16)
%
figure(2); clf(2);
plot (t,g(2,:), '-o', color = '#EDB120' )
xlabel('Months (Jan - Sep 2002)')
ylabel('Colonized asymptomatic')
title('Colonized (female) inmates')
% legend('Colonized')
xlim([0 10])
```

```
xticks([1 2 3 4 5 6 7 8 9 10])
xticklabels({'Jan', 'Feb', 'Mar', 'Apr', 'May', 'Jun', 'Jul', 'Aug', 'Sep'})
ylim([-2 7])
% set(gca, 'Fontsize', 16)
%
figure(3); clf(3);
plot (t,g(3,:), '-o', color = '#A2142F')
xlabel('Months (Jan - Sep 2002)')
ylabel('Infected symptomatic')
title('Infected (female) inmates')
% legend('Infected')
xlim([0 10])
xticks([1 2 3 4 5 6 7 8 9 10])
xticklabels({'Jan', 'Feb', 'Mar', 'Apr', 'May', 'Jun', 'Jul', 'Aug', 'Sep'})
ylim([4 12])
% set(gca, 'Fontsize', 16)
```

9.3 ODE45 MATLAB Code (Aditya Kurkut)

```
% ODE45 w/ Male Inmates
clear; clc;
% Parameters (Medians were used for all of the ranges.)
N = 16956;
pi = 374;
delta = 1/46;
gamma_c = 8.8 * 10^(-5) - 4.923 * 10^(-3);
YI = 8.8 * 10^(-5) - 4.923 * 10^(-3);
alpha = 1/75;
p = 0.2;
phi = 1/9.5;
Bc = 1 * 10^(-5) - 1.5 * 10^(-3);
BI = 1 * 10^(-5) - 1.5 * 10^(-3);
c = 27.5;

% ODE45
y0 = [12000 50 50]; %initial value
tspan = [1 8]; %time span
a= 0.01;
b= 0.02;
[t,y] = ode45(@(t,y) odefcn(t,y,N,delta,gamma_c,YI,alpha,p,phi,Bc,BI,c), tspan, y0);

plot3(y(:,1),y(:,2),y(:,3),"-o") %plots 3 dimensional data
title('ODE45 for Male Inmates')
xlabel('Susceptible')
ylabel('Colonized')
zlabel('Infected')

function dydt = odefcn(~,y,N,delta,gamma_c,gamma_I,alpha,p,phi,beta_c,beta_I,c)
  dydt = zeros(3,1);
  dydt(1) = pi*(1-gamma_c-gamma_I) + alpha*y(2) - (c*beta_c*y(2).*y(1))./N - ((c*beta_I*y(3)*y(1))/N) -
  dydt(2) = pi*(gamma_c) + ((c*beta_c*y(2).*y(1))/N) + ((c*beta_I*y(3)*y(1))/N) - alpha*y(2) - p*phi*y(
  dydt(3) = pi*gamma_I + p*phi*y(2) - delta*y(3);
end
```

```
% ODE45 w/ Female Inmates
clear; clc;
% Parameters (median if range)
N = 2200;
pi = 72.5;
delta = 1/30.5;
gamma_c = 4.43 * 10^(-4) - 7.77 * 10^(-3);
YI = 4.43 * 10^(-4) - 7.77 * 10^(-3);
alpha = 1/75;
p = 0.2;
phi = 1/9.5;
Bc = 1 * 10^(-5) - 2 * 10^(-3);
BI = 1 * 10^(-5) - 2 * 10^(-3);
c = 27.5;

% ODE45
y0 = [2100 6 6]; %initial value
tspan = [1 8]; %time span
a= 0.01;
b= 0.02;
[t,y] = ode45(@(t,y) odefcn(t,y,N,delta,gamma_c,YI,alpha,p,phi,Bc,BI,c), tspan, y0);

plot3(y(:,1),y(:,2),y(:,3),"-o") %plots 3 dimensional data
title('ODE45 for Female Inmates')
xlabel('Susceptible')
ylabel('Colonized')
zlabel('Infected')

function dydt = odefcn(~,y,N,delta,gamma_c,gamma_I,alpha,p,phi,beta_c,beta_I,c)
  dydt = zeros(3,1);
  dydt(1) = pi*(1-gamma_c-gamma_I) + alpha*y(2) - (c*beta_c*y(2).*y(1))./N - ((c*beta_I*y(3)*y(1))/N) -
  dydt(2) = pi*(gamma_c) + ((c*beta_c*y(2).*y(1))/N) + ((c*beta_I*y(3)*y(1))/N) - alpha*y(2) - p*phi*y(
  dydt(3) = pi*gamma_I + p*phi*y(2) - delta*y(3);
end
```