Final Project Progress Report

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Problem Statement

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## Goals

- Develop a basic model for the transmission of Cholera within a community

- Extend the model to account for more realistic features of Cholera

- Brief discussion on how we would handle multi-stage infectious diseases

Background Discussion [1]

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### What is Cholera?

- Disease caused by bacteria (\*Vibrio cholerae\*)

- Symptoms mostly include dehydration, cramps, diarrhea, and kidney failure if left untreated

- Once recovered, immunity lasts up to two years

### Why does it occur?

- Caused by contamination of water supply with the bacteria

- Infected individuals act as incubators for bacteria and reintroduce more bacteria into water supply

- Rare in industrialized nations due to improved infrastructure

Assumptions

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- Contraction of Cholera only occurs through contact with water (generally true)

- Immunity lasts \*forever\* (valid, unless time > 2 years)

- Bacteria introduction is only from first infected

- Latent period in new infected is zero

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<img src="gen-family-standing-water.gif" height=400px width=800px />

Compartment Diagram

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Variables, Parameters, and the Derivation of Differential Equations

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$$

\begin{align\*}

\frac{dS}{dt} &= -\lambda (t) S, \\

\frac{dI}{dt} &= \lambda (t)S - \gamma I, \\

\frac{dB}{dt} &= e\_{\text{xcr}}I + (n\_b - m\_b)B, \\

\end{align\*}

$$

- $S(t)$ is the susceptible population,

- $I(t)$ is the infected population,

- $B(t)$ is the bacteria cell count,

- $\lambda (t)$ is the force of infection at time $t$,

- $n\_b - m\_b$ is the net growth rate for the cell population.

Derivation of Differential Equations (cont.)

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## What's with this $\lambda (t)$ term?

This describes how quickly susceptible individuals become infected. Since contact with water through cooking, cleaning, and eating/drinking is the only way to contract,

$$

\lambda (t) = cp(B) = c \frac{B}{k\_{50} + B},

$$

where $c$ describes the number of contacts with water, $p$ is the probability of infection given the population of bacteria, and $k\_{50}$ is the bacterial concentration at which chance of infection is 50%.

Derivation of Differential Equations (cont.)

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This leaves us with the following equations for our Cholera model,

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\begin{align\*}

\frac{dS}{dt} &= -c \frac{B}{k\_{50} + B} S, \\

\frac{dI}{dt} &= c \frac{B}{k\_{50} + B}S - \gamma I, \\

\frac{dB}{dt} &= e\_{\text{xcr}}I + (n\_b - m\_b)B, \\

\end{align\*}

$$

where $\gamma$ is the recovery rate and $e\_{\text{xcr}}$ represents the rate of excretion of the bacteria.

Code for Numerical Solution

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Here's the code I'm using to replicate Figure 5.5:

```{r, echo=T, eval=F}

graph55 <- function(t\_max) {

# Define the RK4 constants

N <- 10000;

t\_min <- 0;

t\_max <- t\_max;

h <- (t\_max - t\_min) / N;

# Define the equation constants

c <- 1; # day^-1

k50 <- 1000000; # cells / ml

gamma <- 0.2; # day^-1

exr <- 10; # cells / (ml day person)

nm <- -0.33; # day^-1

```

Code for Numerical Solution (Cont.)

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```{r, echo=T, eval=F}

# Define the diff eqs

Sp <- function(B, S) {

-1\*c\*( B / (k50+B) )\*S;

}

Ip <- function(B, S, I) {

c\*( B / (k50+B) )\*S - gamma\*I;

}

Bp <- function(B, I) {

exr\*I + nm\*B;

}

```

Code for Numerical Solution (Cont.)

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```{r, echo=T, eval=F}

# Define the arrays for the values of the functions

S <- rep(0, N);

I <- rep(0, N);

B <- rep(0, N);

t <- rep(0, N);

# Set up initial values

S[1] <- 10000;

I[1] <- 1;

B[1] <- 0;

t[1] = t\_min;

```

Code for Numerical Solution (Cont.)

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```{r, echo=T, eval=F}

# Runge-Kutta for each diff eq

for(i in 1:N) {

# dS/dt

a1 <- h\*Sp(B[i], S[i]);

b1 <- h\*Sp(B[i] + 0.5\*a1, S[i] + 0.5\*a1);

c1 <- h\*Sp(B[i] + 0.5\*b1, S[i] + 0.5\*b1)

d1 <- h\*Sp(B[i] + c1, S[i] + c1);

S[i+1] <- S[i]+(1/6)\*(a1+2\*b1+2\*c1+d1); # Next S value

```

Code for Numerical Solution (Cont.)

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```{r, echo=T, eval=F}

# Later on...

plot(t, S,

main = "Cholera Susceptible Population",

xlab = "t (days)", #x-axis label

ylab = "Population S(t)", #y-axis label

type="l",

col="blue",

xlim=c(t\_min, t\_max), #x-axis range

ylim=c(0, S[1]) #y-axis range

)

}

```

Graphs for Numerical Solution

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```{r, echo=F}

graph55 <- function(t\_max) {

# Define the RK4 constants

N <- 100000;

t\_min <- 0;

t\_max <- t\_max;

h <- (t\_max - t\_min) / N;

# Define the equation constants

c <- 1; # day^-1

k50 <- 1000000; # cells / ml

gamma <- 0.2; # day^-1

exr <- 10; # cells / (ml day person)

nm <- -0.33; # day^-1

# Define the diff eqs

Sp <- function(B, S) {

-1\*c\*( B / (k50+B) )\*S;

}

Ip <- function(B, S, I) {

c\*( B / (k50+B) )\*S - gamma\*I;

}

Bp <- function(B, I) {

exr\*I + nm\*B;

}

# Define the arrays for the values of the functions

S <- rep(0, N);

I <- rep(0, N);

B <- rep(0, N);

t <- rep(0, N);

# Set up initial values

S[1] <- 10000;

I[1] <- 1;

B[1] <- 0;

t[1] = t\_min;

# Runge-Kutta for each diff eq

for(i in 1:N) {

# dS/dt

a1 <- h\*Sp(B[i], S[i]);

b1 <- h\*Sp(B[i] + 0.5\*a1, S[i] + 0.5\*a1);

c1 <- h\*Sp(B[i] + 0.5\*b1, S[i] + 0.5\*b1)

d1 <- h\*Sp(B[i] + c1, S[i] + c1);

S[i+1] <- S[i]+(1/6)\*(a1+2\*b1+2\*c1+d1); # Next S value

# dI/dt

a2 <- h\*Ip(B[i], S[i], I[i]);

b2 <- h\*Ip(B[i] + 0.5\*a2, S[i] + 0.5\*a2, I[i] + 0.5\*a2);

c2 <- h\*Ip(B[i] + 0.5\*b2, S[i] + 0.5\*b2, I[i] + 0.5\*a2);

d2 <- h\*Ip(B[i] + c2, S[i] + c2, I[i] + c2);

I[i+1] <- I[i]+(1/6)\*(a2+2\*b2+2\*c2+d2); # Next I value

# dB/dt

a3 <- h\*Bp(B[i], I[i]);

b3 <- h\*Bp(B[i] + 0.5\*a3, I[i] + 0.5\*a3);

c3 <- h\*Bp(B[i] + 0.5\*b3, I[i] + 0.5\*b3)

d3 <- h\*Bp(B[i] + c3, I[i] + c3);

B[i+1] <- B[i]+(1/6)\*(a3+2\*b3+2\*c3+d3); # Next B value

# Update the time step

t[i+1] <- t[1] + h\*i;

}

plot(t, S,

main = "Cholera Susceptible Population",

xlab = "t (days)", #x-axis label

ylab = "Population S(t)", #y-axis label

type="l",

col="blue",

xlim=c(t\_min, t\_max), #x-axis range

ylim=c(0, S[1]) #y-axis range

)

#plot(t, I,

# main = "Cholera Infected Population",

# xlab = "t (days)", #x-axis label

# ylab = "Population I(t)", #y-axis label

# type="l",

# col="blue",

# xlim=c(t\_min, t\_max), #x-axis range

# ylim=c(0, 750) #y-axis range

# )

#plot(t, B,

# main = "Cholera Cell Population",

# xlab = "t (days)", #x-axis label

# ylab = "Population B(t)", #y-axis label

# type="l",

# col="blue",

# xlim=c(t\_min, t\_max), #x-axis range

# ylim=c(0, 17500) #y-axis range

# )

}

graph55(300)

```

Graphs for Numerical Solution (Cont.)

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```{r, echo=F}

graph55 <- function(t\_max) {

# Define the RK4 constants

N <- 100000;

t\_min <- 0;

t\_max <- t\_max;

h <- (t\_max - t\_min) / N;

# Define the equation constants

c <- 1; # day^-1

k50 <- 1000000; # cells / ml

gamma <- 0.2; # day^-1

exr <- 10; # cells / (ml day person)

nm <- -0.33; # day^-1

# Define the diff eqs

Sp <- function(B, S) {

-1\*c\*( B / (k50+B) )\*S;

}

Ip <- function(B, S, I) {

c\*( B / (k50+B) )\*S - gamma\*I;

}

Bp <- function(B, I) {

exr\*I + nm\*B;

}

# Define the arrays for the values of the functions

S <- rep(0, N);

I <- rep(0, N);

B <- rep(0, N);

t <- rep(0, N);

# Set up initial values

S[1] <- 10000;

I[1] <- 1;

B[1] <- 0;

t[1] = t\_min;

# Runge-Kutta for each diff eq

for(i in 1:N) {

# dS/dt

a1 <- h\*Sp(B[i], S[i]);

b1 <- h\*Sp(B[i] + 0.5\*a1, S[i] + 0.5\*a1);

c1 <- h\*Sp(B[i] + 0.5\*b1, S[i] + 0.5\*b1)

d1 <- h\*Sp(B[i] + c1, S[i] + c1);

S[i+1] <- S[i]+(1/6)\*(a1+2\*b1+2\*c1+d1); # Next S value

# dI/dt

a2 <- h\*Ip(B[i], S[i], I[i]);

b2 <- h\*Ip(B[i] + 0.5\*a2, S[i] + 0.5\*a2, I[i] + 0.5\*a2);

c2 <- h\*Ip(B[i] + 0.5\*b2, S[i] + 0.5\*b2, I[i] + 0.5\*a2);

d2 <- h\*Ip(B[i] + c2, S[i] + c2, I[i] + c2);

I[i+1] <- I[i]+(1/6)\*(a2+2\*b2+2\*c2+d2); # Next I value

# dB/dt

a3 <- h\*Bp(B[i], I[i]);

b3 <- h\*Bp(B[i] + 0.5\*a3, I[i] + 0.5\*a3);

c3 <- h\*Bp(B[i] + 0.5\*b3, I[i] + 0.5\*b3)

d3 <- h\*Bp(B[i] + c3, I[i] + c3);

B[i+1] <- B[i]+(1/6)\*(a3+2\*b3+2\*c3+d3); # Next B value

# Update the time step

t[i+1] <- t[1] + h\*i;

}

#plot(t, S,

# main = "Cholera Susceptible Population",

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# ylab = "Population S(t)", #y-axis label

# type="l",

# col="blue",

# xlim=c(t\_min, t\_max), #x-axis range

# ylim=c(0, S[1]) #y-axis range

# )

plot(t, I,

main = "Cholera Infected Population",

xlab = "t (days)", #x-axis label

ylab = "Population I(t)", #y-axis label

type="l",

col="blue",

xlim=c(t\_min, t\_max), #x-axis range

ylim=c(0, 750) #y-axis range

)

cat("Max number of", floor(max(I)), "infected reached on day", floor(t[which.max(I)]) );

#plot(t, B,

# main = "Cholera Cell Population",

# xlab = "t (days)", #x-axis label

# ylab = "Population B(t)", #y-axis label

# type="l",

# col="blue",

# xlim=c(t\_min, t\_max), #x-axis range

# ylim=c(0, 17500) #y-axis range

# )

}

graph55(300)

```

Graphs for Numerical Solution (Cont.)

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```{r, echo=F}

graph55 <- function(t\_max) {

# Define the RK4 constants

N <- 100000;

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# Define the equation constants

c <- 1; # day^-1

k50 <- 1000000; # cells / ml

gamma <- 0.2; # day^-1

exr <- 10; # cells / (ml day person)

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# Define the diff eqs

Sp <- function(B, S) {

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Ip <- function(B, S, I) {

c\*( B / (k50+B) )\*S - gamma\*I;

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Bp <- function(B, I) {

exr\*I + nm\*B;

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# Define the arrays for the values of the functions

S <- rep(0, N);

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B <- rep(0, N);

t <- rep(0, N);

# Set up initial values

S[1] <- 10000;

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for(i in 1:N) {

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a1 <- h\*Sp(B[i], S[i]);

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c1 <- h\*Sp(B[i] + 0.5\*b1, S[i] + 0.5\*b1)

d1 <- h\*Sp(B[i] + c1, S[i] + c1);

S[i+1] <- S[i]+(1/6)\*(a1+2\*b1+2\*c1+d1); # Next S value

# dI/dt

a2 <- h\*Ip(B[i], S[i], I[i]);

b2 <- h\*Ip(B[i] + 0.5\*a2, S[i] + 0.5\*a2, I[i] + 0.5\*a2);

c2 <- h\*Ip(B[i] + 0.5\*b2, S[i] + 0.5\*b2, I[i] + 0.5\*a2);

d2 <- h\*Ip(B[i] + c2, S[i] + c2, I[i] + c2);

I[i+1] <- I[i]+(1/6)\*(a2+2\*b2+2\*c2+d2); # Next I value

# dB/dt

a3 <- h\*Bp(B[i], I[i]);

b3 <- h\*Bp(B[i] + 0.5\*a3, I[i] + 0.5\*a3);

c3 <- h\*Bp(B[i] + 0.5\*b3, I[i] + 0.5\*b3)

d3 <- h\*Bp(B[i] + c3, I[i] + c3);

B[i+1] <- B[i]+(1/6)\*(a3+2\*b3+2\*c3+d3); # Next B value

# Update the time step

t[i+1] <- t[1] + h\*i;

}

#plot(t, S,

# main = "Cholera Susceptible Population",

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# ylab = "Population S(t)", #y-axis label

# type="l",

# col="blue",

# xlim=c(t\_min, t\_max), #x-axis range

# ylim=c(0, S[1]) #y-axis range

# )

#plot(t, I,

# main = "Cholera Infected Population",

# xlab = "t (days)", #x-axis label

# ylab = "Population I(t)", #y-axis label

# type="l",

# col="blue",

# xlim=c(t\_min, t\_max), #x-axis range

# ylim=c(0, 750) #y-axis range

# )

plot(t, B,

main = "Cholera Cell Population",

xlab = "t (days)", #x-axis label

ylab = "Population B(t)", #y-axis label

type="l",

col="blue",

xlim=c(t\_min, t\_max), #x-axis range

ylim=c(0, 17500) #y-axis range

)

cat("Max value reached on day", floor(t[which.max(B)]) );

}

graph55(300)

```

Discussion of Results

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### Observations

We can see the population of infected reaches a maximum of 400 on the 136th day, whereas the maximum bacteria count is reached three days later!

### Discussion

Why is this?

Calculating Cholera's Basic Reproduction Number

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Here, we will calculate Cholera's $R\_0$.

Extensions

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1. Waning Immunity

2. Endemic Cholera Model

3. Multi-stage Infection Model

References

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[1] https://www.cdc.gov/cholera/index.html