Mathematical modeling Cholera Model

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Introduction

Infectious diseases continue to debilitate and to cause death in humans and animals, with new disease-causing pathogens emerging and old pathogens re emerging or evolving.

For example:-

1. Virus - influenza, measles
2. Bacteria - anthrax, salmonella, chlamydia, cholera
3. Protozoa - malaria, trypanosomiasis

Introduction

Some diseases can be controlled by vaccines, antibiotics, antiviral drugs, reduction in vector populations, increased sanitation or behavioral changes.

For control of a particular diseases, it is essential to know

1. Features of pathogen
2. Mode of transmission
3. Epidemiological details

Cholera

Cholera is an infection of the small intestine caused by the bacterium *Vibrio cholerae*.

Infection causes mild diarrhea in most cases, but some cases develop severe diarrhea and vomiting, which if untreated may lead to death within a few hours due to dehydration and electrolyte imbalance.

Cholera can be transferred directly or indirectly

- Direct transmission from human to human
- Indirect transmission by infected water with bacteria shed from infected human

Type of transmission is a key factor in designing control strategies.

Mathematical modeling of SIWR model

Firstly, we identify the independent and dependent variables. The independent variable is time t, measured in days.

The set of dependent variables counts people in each of the groups, each as a function of time:

- S(t) - Susceptible population
- I(t) - Infected population
- B(t) - Concentration of bacteria in water
- R(t) - Recovered (removed) population

Assumptions of SIWR model

1. No deaths caused due to cholera, so, the total population does not change.

   $N = S + I + R = \text{constant}$

2. Non-negative initial conditions

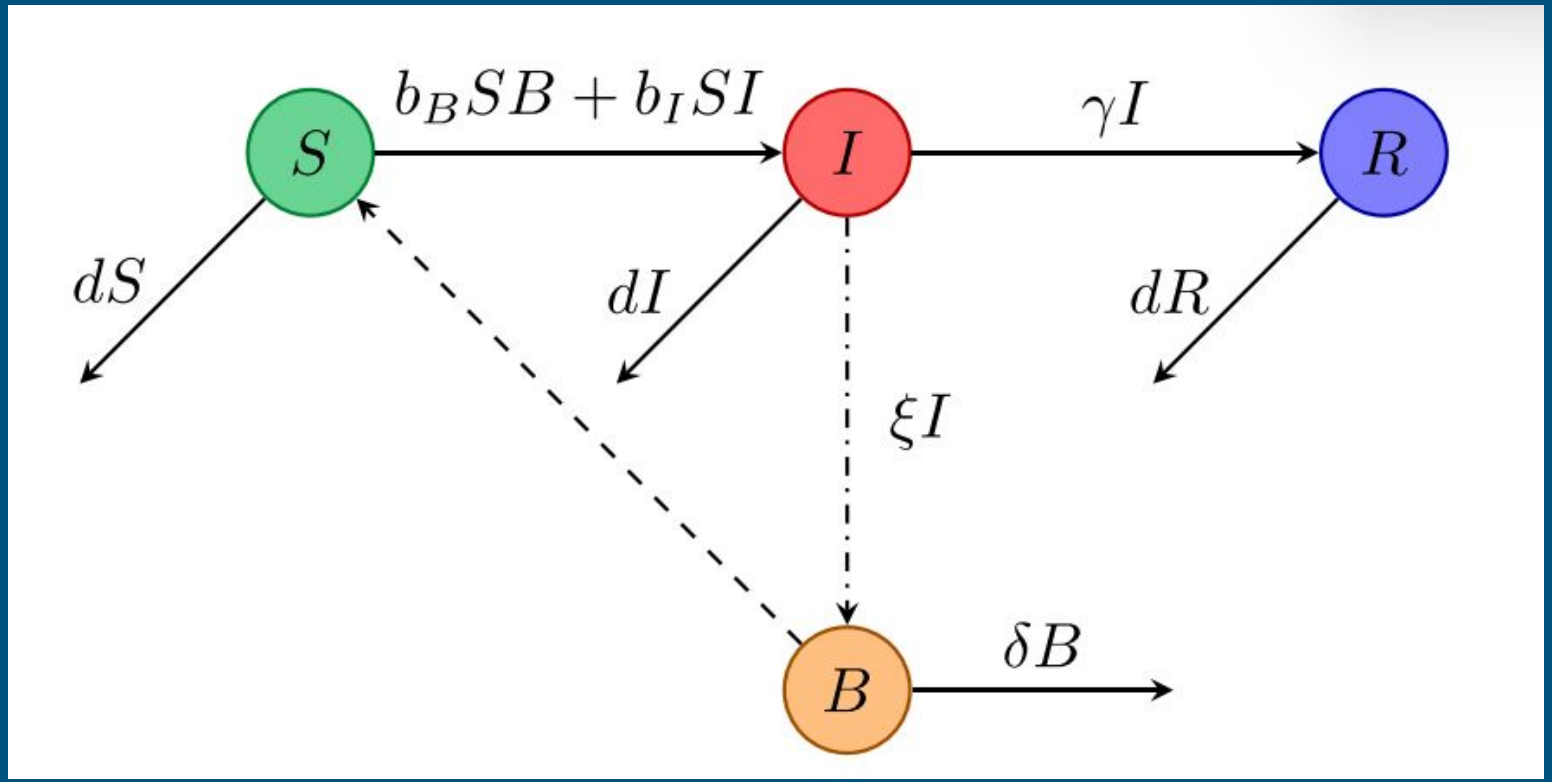
   $0 < I(0) + B(0) <<< S(0)$

   $R(0) = 0$

   $(S, I, R, B) = (N, 0, 0, 0)$

3. Shedding is not a new infection (goes into the V matrix)
4. All individuals in the population have the same probability to contract the disease.
5. Homogeneous mixing of the population : Contact of an individual with the rest of the population also follows a uniform distribution.

Schematic diagram



The equations related to model

The equations of the SIWR model is

$$\frac{dS}{dt} = dN - b_B SB - b_I SI - dS$$

$$\frac{dI}{dt} = b_B SB + b_I SI - (d + \gamma) I$$

$$\frac{dR}{dt} = \gamma I - dR$$

$$\frac{dB}{dt} = \xi I - \delta B$$

Describing the variables

$d = Natural\ birth/death\ rate$

$b_I = Person\ to\ person\ transmission\ rate$

$b_B = Person\ to\ reservoir\ contact\ rate$

$\gamma = Recovery\ rate\ of\ \ infected\ humans$

$\xi = Shedding\ rate\ (Infected\ person\ to\ resevoir\ contact\ rate)$

$\delta = pathogen\ death\ rate$

MATLAB code for equations

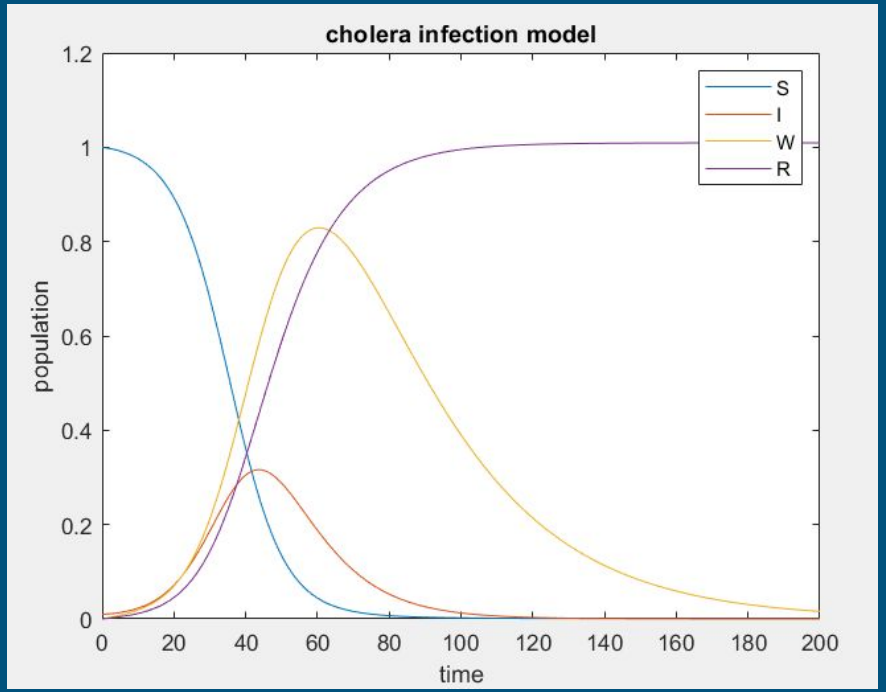
choleramodel.m | cholera.m

```
function cholera = choleramodel(t,y)
N = 10;
mu=0;
betaw=0.6217;
betai=0.6217;
gama=0.1340;
sie=0.0333;
alpha=0;

ds = mu*N -betaw*y(3)*y(1) -betai*y(1)*y(2) -mu*y(1);
di = betaw*y(3)*y(1) + betai*y(1)*y(2) -gama*y(2) -mu*y(2);
dw = alpha*y(2) -sie*y(3);
dr = gama*y(2) -mu*y(4) ;

cholera = [ds;di;dw;dr];
end
```

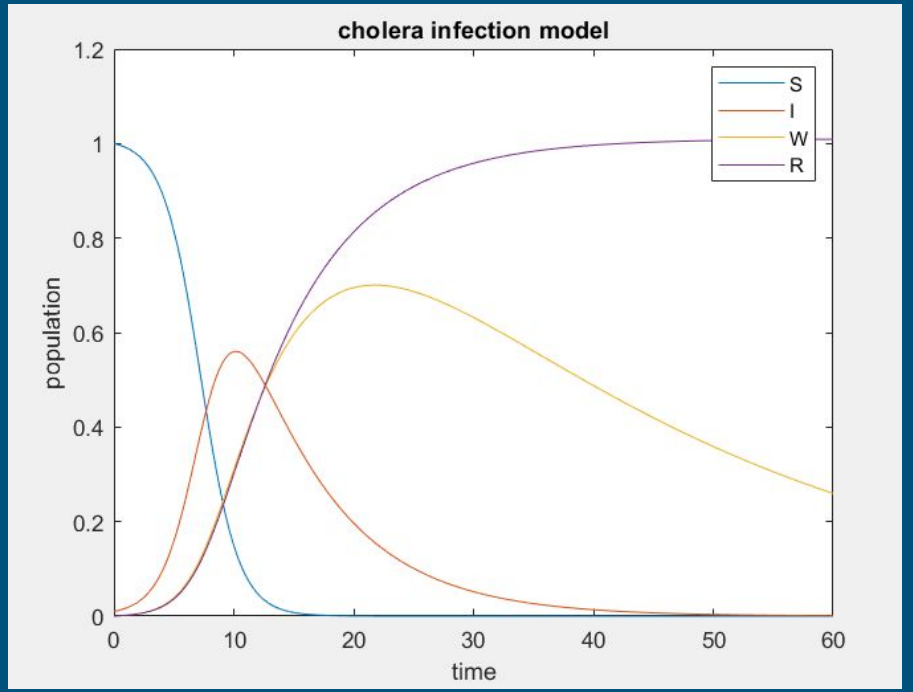
choleramodel.m | cholera.m

```
clear all; close all;
t0 = 0;
tf = 60;
tspan = t0 : 0.0001 : tf;
y0 = [1;0.01;0;0];

[t,y] = ode45(@choleramodel,tspan,y0);

figure(1)
plot(t,y)
title('cholera infection model')
xlabel('time')
ylabel('population')
legend('S','I','W','R')

figure(2)
plot(t,y(:,2))
title('plot of infected person')
xlabel('time')
ylabel('infected')
```

Plot for two different data values in zimbabwe



Plot 1



Plot 2

Reproduction Number R_0

We find the R_0 value using the next generation matrix method:

FV^{-1} is the next generation matrix.

$$R_0 = \rho(FV^{-1}),$$

where ρ denotes the spectral radius.

Further, the R_0 value is calculated at Disease Free Equilibrium (DFE) point.

Reproduction Number R_0

- In the Cholera Model (SIWR), the Infected compartments are I(t) and W(t).
- DFE at (S, I, W ,R) = (N, 0, 0, 0)
- The corresponding next generation matrix is as follows:

$$F = \begin{bmatrix} b_I N & b_B N \\ 0 & 0 \end{bmatrix} \qquad V = \begin{bmatrix} d+\gamma & 0 \\ -\xi & \delta \end{bmatrix} \qquad FV^{-1} = \begin{bmatrix} \frac{b_I N}{d+\gamma} + \frac{b_B N \xi}{\delta(d+\gamma)} & \frac{b_B N}{\gamma} \\ 0 & 0 \end{bmatrix}$$

Reproduction Number R_0

- Calculating R_0 by find spectral radius of FV^{-1}

$$R_0 = \frac{\beta_B + \beta_I}{d + \gamma}$$

$$where\ \beta_B = \frac{b_B N \xi}{\delta}\ and\ \beta_I = b_I N$$

Stability of model

- We can check the stability by using$(\lambda I - J_B^*) = 0$
- The matrix at equilibrium point(S,I,R,B) = (N,0,0,0) looks as below

$$\begin{bmatrix} \lambda + d & -b_I N & 0 & b_B N \\ 0 & \lambda - b_I N + (d + \gamma) & 0 & -b_B N \\ 0 & -\gamma & \lambda + d & 0 \\ 0 & -\xi & 0 & \lambda + \delta \end{bmatrix}$$

Stability contd...

- Final equation:

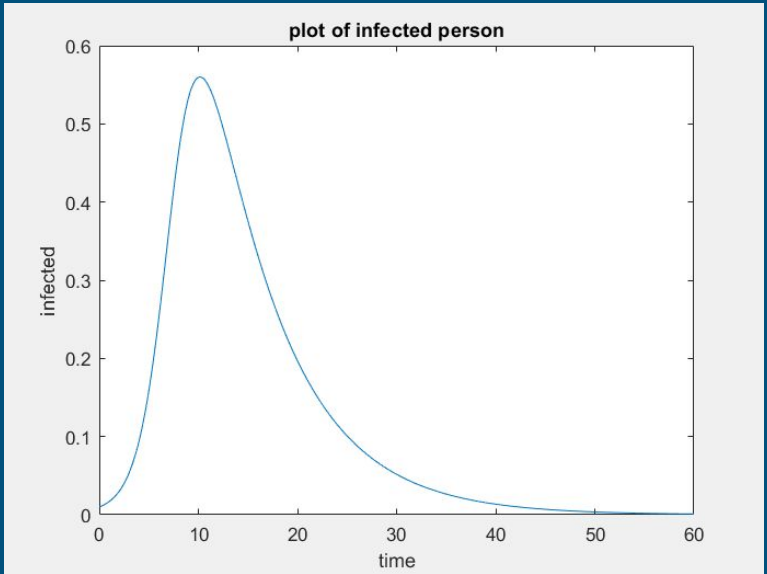
$$(\lambda + d)(\lambda + d)\left[\left(\lambda - b_I N + (d+\gamma)\right)(\lambda+\delta) - b_B N\xi\right] = 0$$

- Two eigenvalues are less than 0.
- The other part of equation stability is checked by routh's stability criterion which gives the following result.

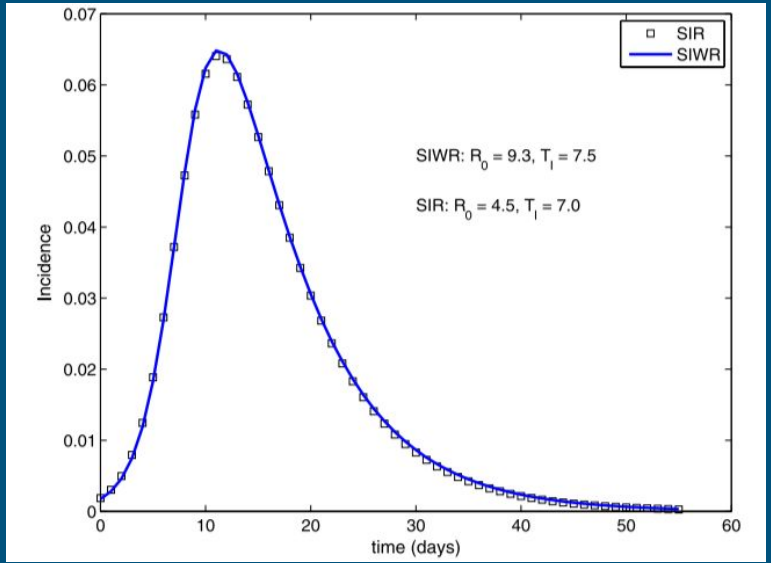
$$N < min\left(\frac{(d+\gamma)+\delta}{b_I}, \frac{(d+\gamma)\delta}{b_B\xi + b_I}\right)$$

Comparison between real data and model prediction

Plotted graph

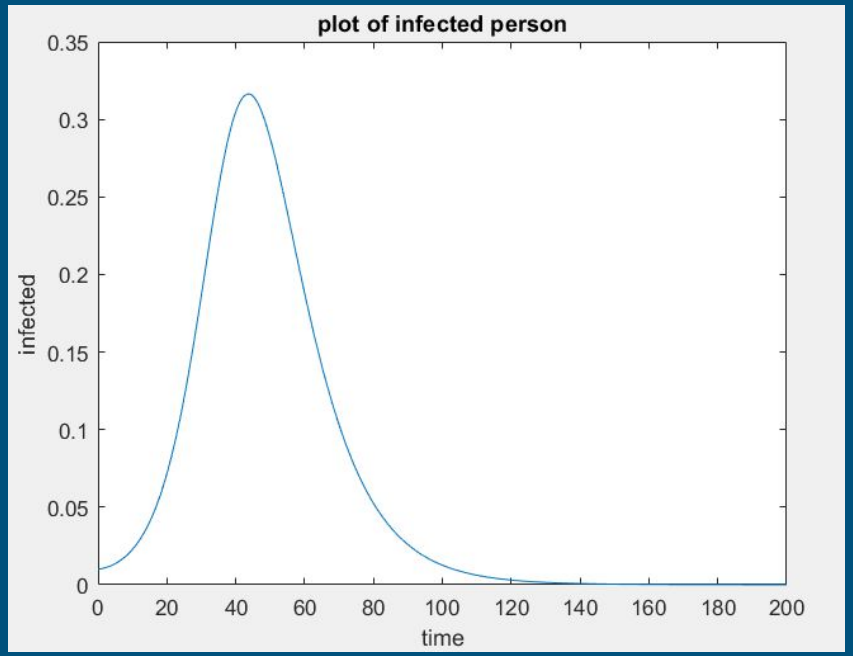


Real data from zimbabwe

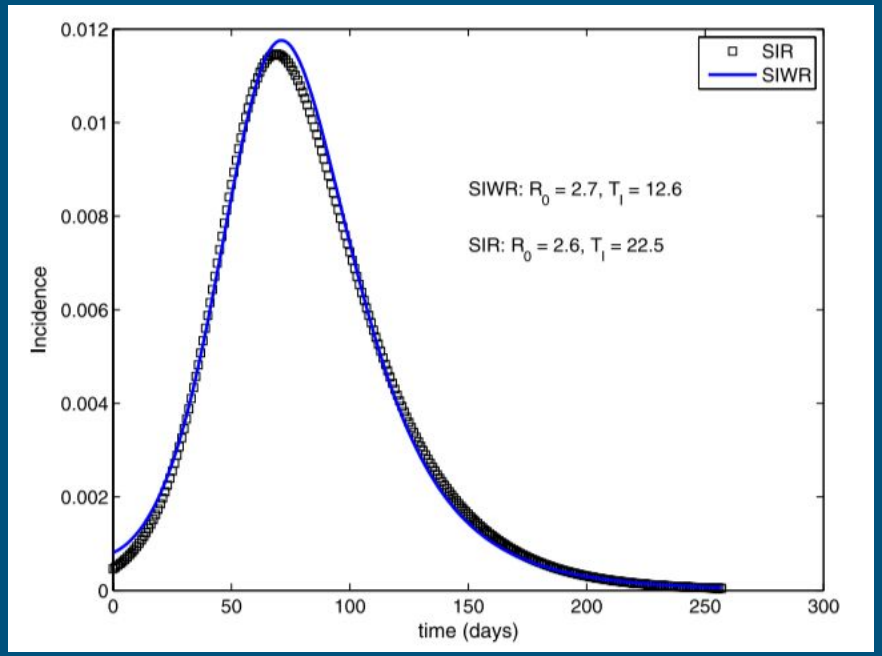


Similar but not exactly the same.

Plotted graph



Graph from real data from zimbabwe



Similar but not exactly the same.

Limitations

- Our assumptions are not exactly accurate according to real world scenario as real world have more parameters and causes.
- Estimation of parameter is done on one place data (zimbabwe), disease can have different trends according to place and situation.
- In real reproduction number is variable and changes day by day but ours can be used to calculate for one given situation.
- Some parameters like climate and weather can also affect the spread of disease which is not considered here.
- Human and water interaction cannot be exactly stated so it have a approximate value.

Conclusion

- The model's incorporation of both direct and indirect transmission modes enhances its precision and authenticity.
- The derived R_0 value gives us an idea on how each parameter effects the spread of the disease and hence is very useful when determining strategies to combat the spread.
- The model's accuracy for the given data appears to be high, based on the available evidence and analysis.
- Stability of the model depends on the population size.

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