Mathematical Modelling of Cholera Transmission in South Africa 2000/01

Done by: Nikhila Boosam (1855023)

1. Abstract

The 2000-01 cholera outbreak in South Africa, caused by the Vibrio cholerae O1 bacterium, proved to be a big challenge in public health. This report discusses the trend of the epidemic, based on the number of cholera cases and related deaths that were reported between October 2000 and April 2001. The dataset, obtained from the World Health Organization, depicts the rapid rise in the number of cases and deaths, peaking in February 2001, with over 48,000 reported infections and more than 100 deaths. Cholera is usually transmitted through contaminated water and human faeces, thus presenting a serious risk to the public health of the population, especially in conditions of poor sanitation. WHO recommended four main control measures: hygienic disposal of human faeces, adequate supply of safe drinking water, good food hygiene and, washing hands after defecation and before meals.

2. Introduction

Cholera is a severe diarrheal illness caused by the bacterium Vibrio cholerae, usually acquired from contaminated water or food. It causes fast dehydration and, if not treated, may be fatal. Cholera continues to be a major concern in areas where sanitation is poor and access to clean drinking water is limited, especially in developing regions. Starting in Indonesia in 1961, the seventh cholera pandemic spread gradually to many parts of the world. In South Africa, this outbreak started in August 2000 and then spread rapidly, with thousands being affected by the infection and a high mortality rate. This continued well into 2001, making it one of the biggest cholera epidemics ever seen in the country. Besides effective management, the strategies should ensure that such diseases are limited within a region with minimal or no infrastructure.

2.1 Background

The South African cholera outbreak of 2000/01 was a result of several factors, including contaminated water sources, poor sanitation, and the

rapid spread of the Vibrio cholerae bacterium. In many regions of South Africa, especially in underdeveloped areas, access to safe drinking water and proper sanitation was limited, which created an environment conducive to the spread of cholera. Public health authorities responded with measures such as improving water quality, promoting hygiene practices, and educating the public about the importance of safe water and sanitation.

2.2 Data Description

The data for this project is drawn from the World Health Organization (WHO) archives, covering the period from October 2000 to April 2001. It includes the total reported cholera cases and related deaths at various points during the outbreak. Below is a summary of the progression of the epidemic:

- In October 2000, there were 2,175 reported cases and 22 deaths.
- By March 2001, the number of cases had risen to over 78,000, with 163 deaths.
- The outbreak peaked in early 2001, with thousands of new cases reported weekly.

Date	Cases (total)	Deaths (total)
Oct 13, 2000	2175	22
Oct 18, 2000	3075	26
Oct 19, 2000	3279	27
Oct 26, 2000	3806	33
Nov 02, 2000	4270	32
Nov 09, 2000	4583	33
Nov 19, 2000	5285	35
Nov 27, 2000	5876	35

Dec 05, 2000	6548	35
Dec 19, 2000	8137	41
Dec 29,2000	11183	51
Jan 09, 2001	15983	60
Jan 14, 2001	19499	66
Jan 25, 2001	27431	74
Feb 04, 2001	37204	85
Feb 14, 2001	48647	108
Feb 22, 2001	56092	120
Mar 03, 2001	62607	131
Mar 14, 2001	69761	139
Mar 28, 2001	78140	163
Apr 16, 2001	86107	181

Table 1: Cholera outbreak in South Africa 2000/01

2.3 Problem Statement

The cholera outbreak represented a major public health crisis, with rapid transmission and a high number of fatalities. The epidemic led to thousands of reported cases and deaths, raising urgent questions about the effectiveness of public health measures, such as improved water hygiene, sanitation, and food safety practices.

This project focuses on understanding the dynamics of the outbreak and addressing the following questions:

1. Modelling the epidemic without any control mechanism.
2. Including the recommended control mechanism in the model and seeing if we can find a better fit to the data.
3. Using the model to determine which of the given control mechanism is the most effective.
4. Predicting the further development of the disease provided that all the control mechanisms are in place.

3. Formulation of the Mathematical Model

The cholera outbreak is modelled using a compartmental framework that divides the population and environmental factors into several compartments. An extended version for the general SIR model has been taken to fit the symptomatic and asymptomatic cases along with the bacteria and deaths (due to disease) compartments.

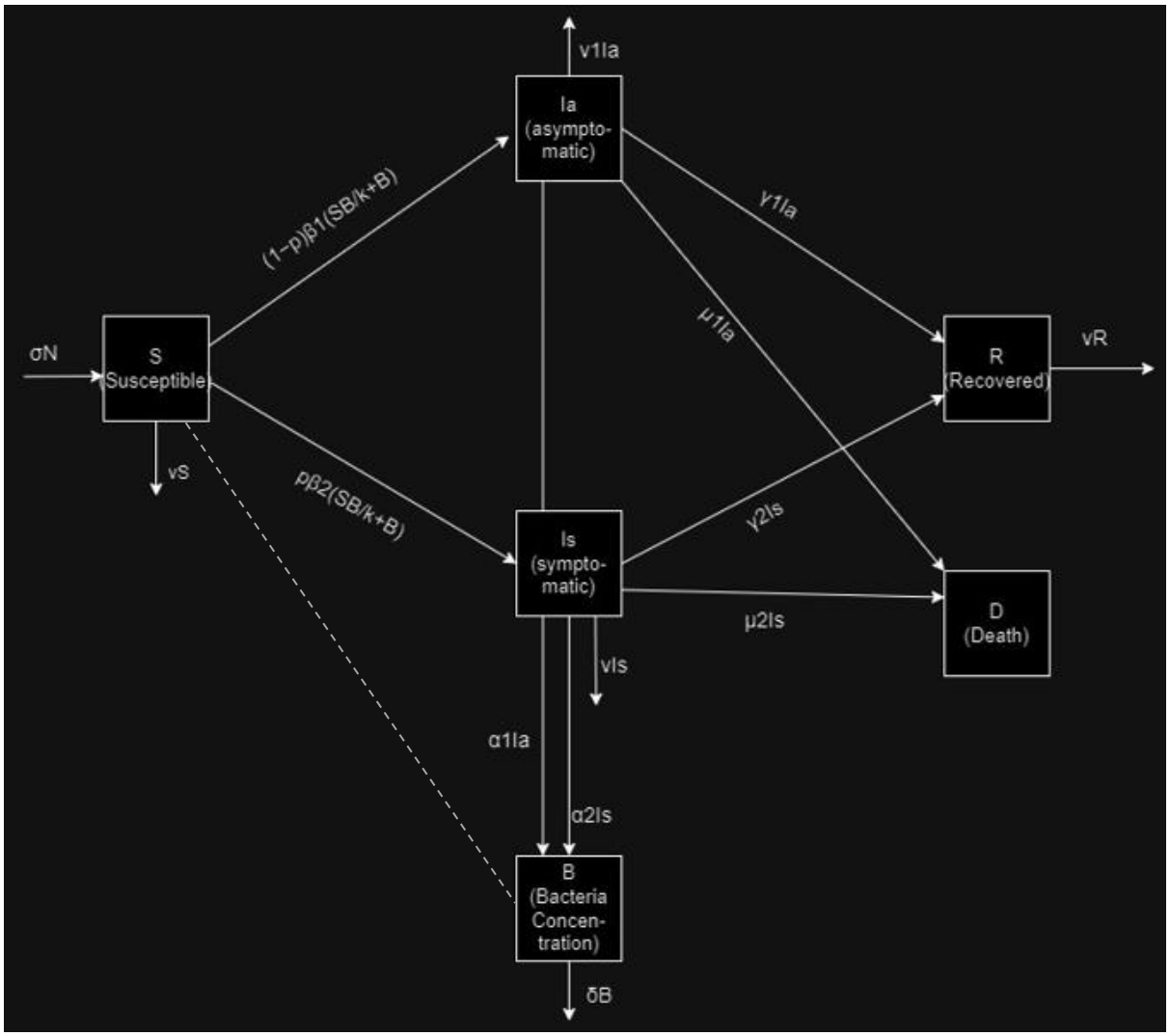

Figure 1: Mathematical Model

The model shows the interplay between susceptible population(S), infected individuals (asymptomatic (I_a) and symptomatic (I_s)), recovered individuals(R), deaths(D), and the concentration of bacteria in the environment (B).

3.1 Model Description

Susceptible Population (S):

The susceptible compartment (S) consists of individuals who are at risk of contracting cholera. These individuals can be infected through contact with contaminated water or food that contains the bacteria. The rate at which susceptible individuals become infected depends on the concentration of bacteria in the environment (B) and the transmission rate (β), which governs the probability of infection upon exposure. The susceptible population is also replenished through natural births at a rate σ, and it decreases due to infection, natural deaths at rate ν, and transitions to the infected compartments (I_a and I_s).

Asymptomatic Infected (I_a):

The asymptomatic infected individuals (I_a) are those who carry the cholera bacteria but do not show any severe symptoms. These individuals are still infectious, contributing to the environmental contamination through the bacteria they shed, which can further infect susceptible individuals. The rate of transition from susceptible to asymptomatic infected individuals is determined by the infection rate and bacteria concentration. Although they do not exhibit symptoms, these individuals eventually recover, either through natural recovery or through the resolution of the infection, and can contribute to the pool of recovered individuals (R). Asymptomatic individuals can also die due to cholera at rate μ_1 and contribute to the overall mortality rate.

Symptomatic Infected (I_s):

The symptomatic compartment (Is) represents individuals who develop severe symptoms of cholera, such as diarrhea and dehydration. These individuals are more likely to transmit the disease to others due to their higher bacterial shedding rates, and they significantly contribute to environmental contamination. Symptomatic individuals have a higher

death rate from cholera (μ_2) compared to asymptomatic carriers. They recover at a rate γ2. The transition into symptomatic infection depends on the exposure to bacteria and the severity of the disease.

Recovered Population (R):

The recovered compartment (R) includes individuals who have survived the infection and developed temporary immunity to cholera. While recovered individuals are not infectious, they are considered immune for some time, reducing their risk of reinfection. The recovery from both asymptomatic and symptomatic infection occurs at rates γ1 and γ2, respectively.

Bacteria Concentration:

The bacteria concentration (B) represents the environmental presence of bacteria in water sources where it can infect susceptible individuals. The bacteria concentration is influenced by the shedding of bacteria from both asymptomatic ($\alpha_1 I_a$) and symptomatic ($\alpha_2 I_s$) infected individuals. This concentration naturally decays over time at a rate δ, reflecting the environmental cleanup or bacterial die-off. The level of bacteria in the environment is critical for sustaining the infection cycle and triggering new infections.

Deaths (D):

The death compartment (D) tracks the cumulative number of individuals who have died due to cholera. Deaths occur from both asymptomatic ($\mu_1 I_a$) and symptomatic ($\mu_2 I_s$) infections. These individuals transition from the infected compartments to the death compartment as a result of the disease's fatal progression.

3.2 Model Equations

$$\frac{dS}{dt} = \sigma N - (1-p)\beta_1 S\left(\frac{B}{k+B}\right) - P\beta_2 S\left(\frac{B}{k+B}\right) - \nu S$$

$$\frac{dI_a}{dt} = (1-p)\beta_1 S\left(\frac{B}{k+B}\right) - \gamma_1 I_a - \alpha_1 I_a - \mu_1 I_a - \nu I_a$$

$$\frac{dI_s}{dt} = p\beta_2 S\left(\frac{B}{k+B}\right) - \gamma_2 I_s - \alpha_2 I_s - \mu_2 I_s - \nu I_s$$

$$\frac{dR}{dt} = \gamma_1 I_a + \gamma_2 I_s - \nu R$$

$$\frac{dB}{dt} = \alpha_1 I_a + \alpha_2 I_s - \delta B$$

$$\frac{dD}{dt} = \mu_1 I_a + \mu_2 I_s$$

3.3 Parameters

The parameter values for the model were estimated using a combination of empirical data and literature-based assumptions. For rates like birth, death, and recovery, values were drawn from demographic and health data specific to the population or region of interest. Transmission parameters, such as the rate at which individuals shed bacteria and the decay rate of the bacteria in the environment, were estimated based on previous studies of cholera outbreaks and environmental conditions. The proportion of

symptomatic versus asymptomatic cases (denoted by p) was taken from the data given in the question. Additionally, parameters such as immunity waning rate (v) were estimated from studies of cholera immunity dynamics. Sensitivity analysis was performed to assess how variations in these parameters might impact model predictions.

Parameter	Description	Estimated Value
σ	Birth rate	0.0001/day
β_1	Bacteria transmission rate for asymptomatic individuals	0.002/day
β_2	Bacteria transmission rate for symptomatic individuals	0.005/day
k	Half saturation constant	1×10^3
p	Proportion of infected individuals who show symptoms	0.2
γ_1	Recovery rates for asymptomatic individuals	0.1/day
γ_2	Recovery rates for symptomatic individuals	0.2/day
μ_1	Death rates due to cholera for asymptomatic individuals	0.0005/day
μ_2	Death rates due to cholera for symptomatic individuals	0.002/day
α_1	Rates of bacteria contribution by asymptomatic individuals	0.03/day
α_2	Rates of bacteria contribution by symptomatic individuals	0.08/day
δ	Decay rate of bacteria	0.01/day
ν	Natural death rate	0.0001/day

3.4 Model Assumptions

1. **Population Dynamics:** The population is assumed to be closed, meaning there is no immigration or emigration. Births and deaths

occur at constant rates, and the model assumes a sufficiently large population to ignore random fluctuations.

2. **Cholera Infection:** Cholera is transmitted through contaminated water or food, not directly from person to person. People are divided into two groups: asymptomatic (I_a) and symptomatic (I_s).
3. **Environmental Contamination:** The concentration of cholera bacteria (Vibrio cholerae) in the environment is influenced by bacterial shedding from both asymptomatic and symptomatic individuals. The bacteria naturally decay over time at a constant rate, and the model assumes there is no external source of contamination.
4. **Homogeneous Mixing:** The model assumes that the population mixes homogeneously, meaning that every individual has an equal chance of being exposed to contaminated water or food. It does not account for any spatial or social factors that could affect exposure.

3.5 Restrictions

- The model uses constant parameters over time, while in reality, interventions, immunity levels and environmental factors may lead to variations.
- Homogeneous mixing is incapable of fully modelling localized dynamics or the clustering of the infections.
- The model does not take into consideration other external sources of bacteria.

4. Model Simulations

The model simulation numerically solves differential equations to track the spread of cholera, population changes, and environmental contamination over time. It divides the population into compartments (susceptible, asymptomatic, symptomatic, and recovered) and accounts for bacterial shedding and decay. Using estimated parameter values, the simulation predicts how infections and environmental contamination evolve, helping to explore disease dynamics and the potential impact of interventions.

4.1 Initial Model without any intervention

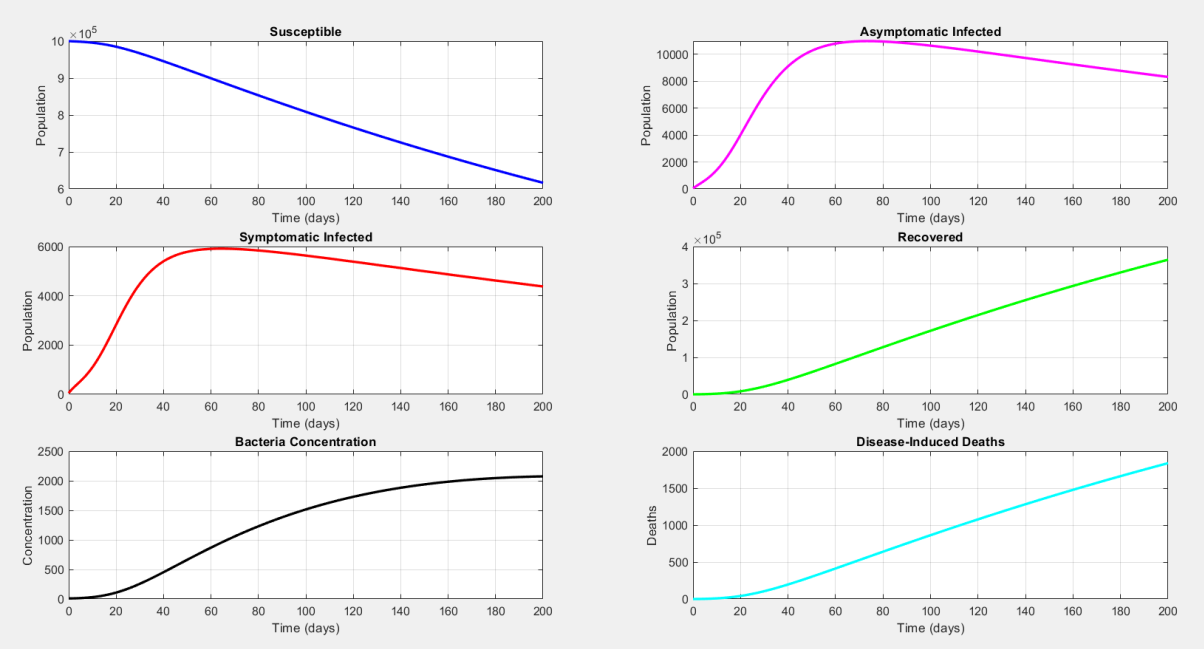

Figure 2: Initial model without any control mechanism

Results obtained from the model represent how the cholera progresses through the population over time. The susceptible population, driven by interactions with bacteria and infected individuals, shows a sharp decline. The asymptomatic infected group (Ia) rises early on, reflecting individuals who contract the disease but exhibit no symptoms, while the symptomatic group (I_s) peaks later, indicating the burden of symptomatic cases on the population. Recovery (R) grows steadily as individuals recover from both asymptomatic and symptomatic states, eventually stabilizing when disease transmission slows. The bacterial concentration B, increases initially because of the interaction of bacteria with infected individuals but decays with time due to natural processes. Finally, the disease induced deaths D are accumulated and show the toll of the disease.

4.1.1 Residual Analysis

The residual analysis is used to compare the model's predictions with actual data. It helps assess the model's fit, identify any assumptions that may be violated, and guide improvements for more accurate predictions.

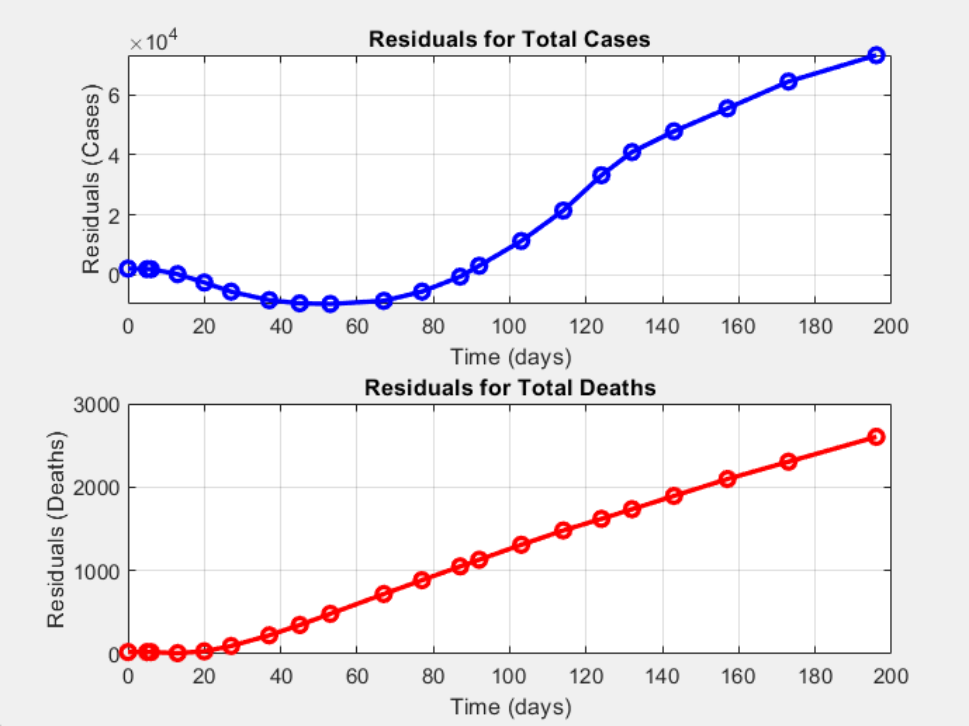

Figure 3: Residual Analysis for cases and deaths

From the residual analysis, we can see that the model is a pretty good fit to the given data, taking into consideration the limitations of the data. The observed and predicted values for cases and deaths are mostly aligning with each other.

4.1.2 Sensitivity Analysis

Sensitivity analysis is used to evaluate how changes in model parameters affect the model's outcomes. By systematically varying parameters (such as transmission rates, recovery rates, or immunity duration), sensitivity analysis helps identify which parameters have the most significant impact on disease dynamics. This allows us to prioritize key factors, assess uncertainty in predictions, and better understand the robustness of the model under different scenarios. It is also useful for exploring how model predictions change with different input values, guiding decision-making and public health interventions.

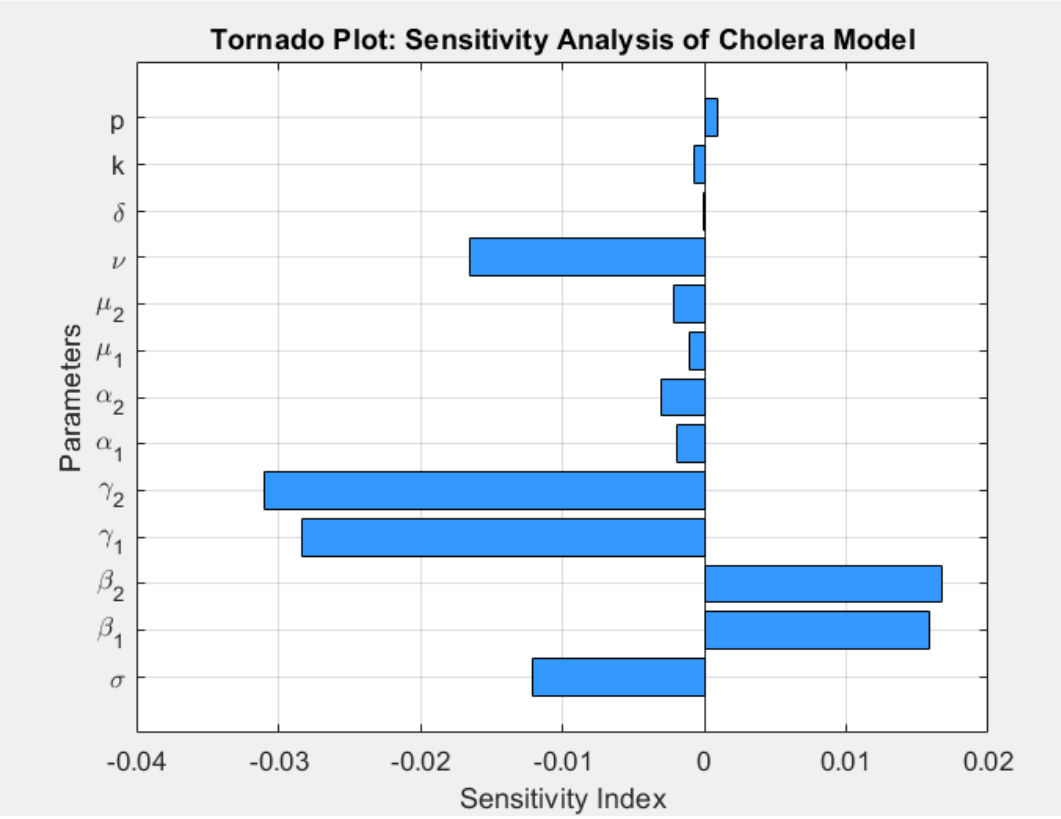

Figure 4: Sensitivity analysis of the parameters

4.2 Model with Control Mechanism 1

Control Mechanism 1: Hygienic disposal of human faeces

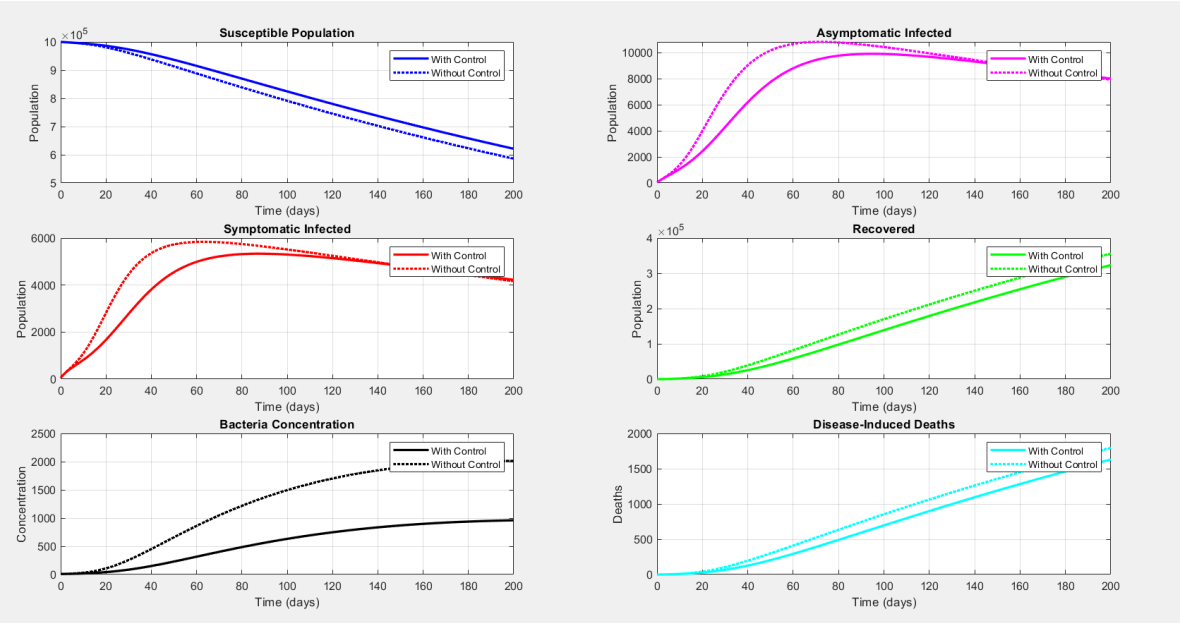

Figure 5: Simulation of model with control mechanism 1

For this, we make changes to the parameter which is likely to reduce the effect of the bacteria according to the control mechanism. The “hygienic disposal of human faeces” mainly affects the α parameter. So, we reduce α by (1-u) in the equations and then perform the simulations to get the output.

$$\alpha = \alpha(1 - \boldsymbol{u_1})$$

In this plot, there is a visible effect of the control mechanism to the model which proves its importance.

4.3 Model with Control Mechanism 2

Control Mechanism 2: Adequate supply of safe drinking water

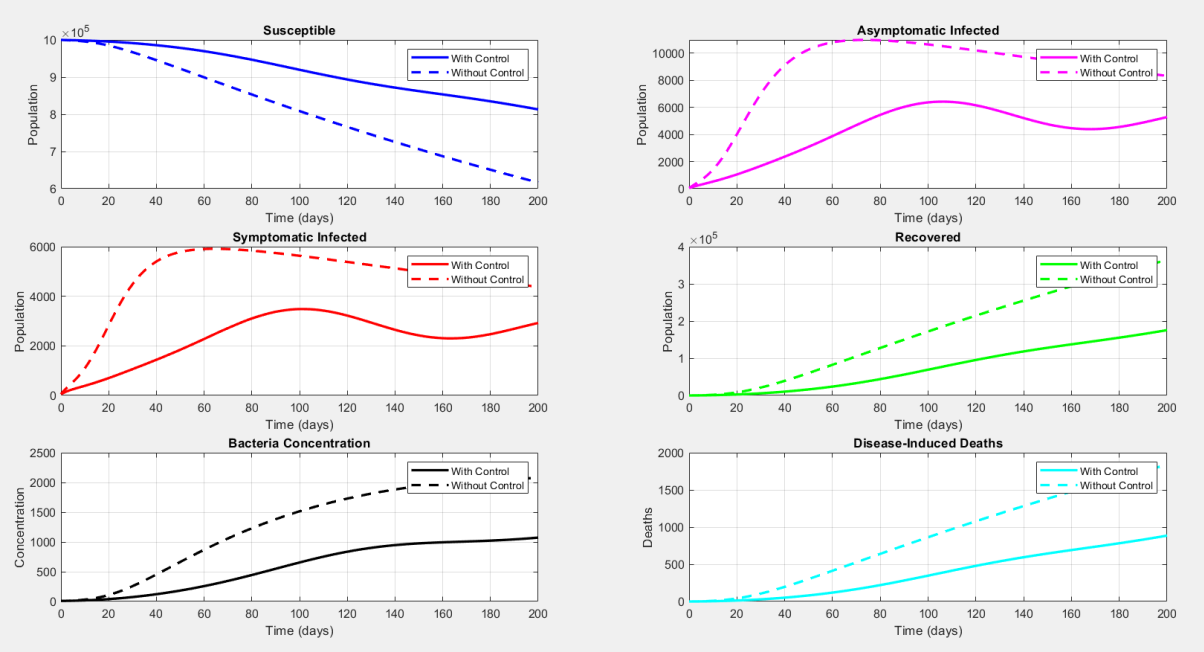

Figure 6: Simulation of model with control mechanism 2

For this, we make changes to the parameter which is likely to reduce the effect of the bacteria according to the control mechanism. The “adequate supply of safe drinking water” mainly affects the β parameter. So, we reduce β by (1-u) in the equations and then perform the simulations to get the output.

$$\beta = \beta(1 - \boldsymbol{u_2})$$

In this plot, it can be observed that the bacteria and deaths are decreased by a lot, showing significant effect of the control mechanism.

4.4 Model with Control Mechanism 3

Control Mechanism 3: Good food hygiene and cooking

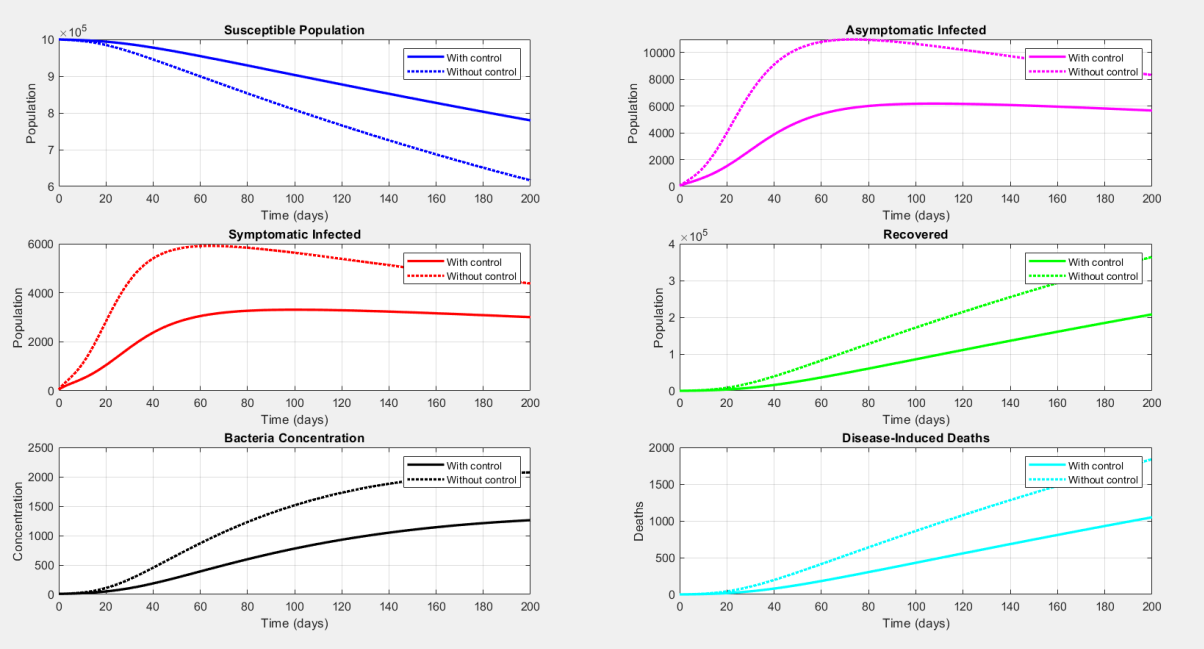

Figure 7: Simulation of model with control mechanism 3

The "good food hygiene and cooking" also affects the β parameter. So, we reduce β by (1 - u_1) (1 - u_2) in the equations and then perform the simulations to get the output. We again change the same parameter since both the safe drinking water and the good food hygiene affect the same parameter.

In this plot, it shows significant effect of the control mechanism but a bit less than the previous one i.e., control mechanism 2.

$$\beta = \beta(1 - \boldsymbol{u_2})\,(1 - \boldsymbol{u_3})$$

4.5 Model with Control Mechanism 4

Control Mechanism 4: Washing hands after defecation and before meals

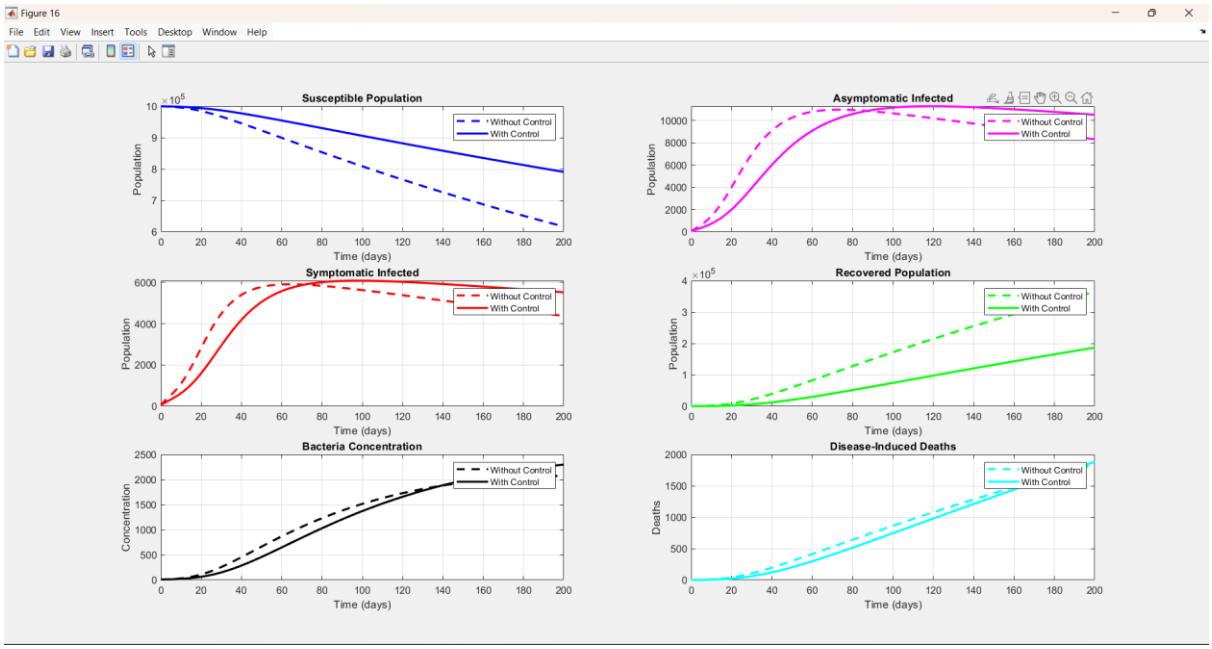

Figure 8: Simulation of model with control mechanism 4

This control mechanism, "washing hands after defecation and before meals" mainly affects the γ parameter. So, we reduce γ by (1 - u) in the equations and then perform the simulations to get the output.

$$\gamma = \gamma(1 - \boldsymbol{u_4})$$

In this plot, there is not much visible effect to the model. So, we can conclude that this control mechanism will not be much helpful in clearing out the disease alone.

4.6 Model with intervention of all control mechanism

The simulation shows that implementing all control measures—hygienic faeces disposal, adequate supply of safe drinking water, good food hygiene and cooking, and washing hands after defecation and before meals—drastically mitigates the spread and impact of the disease. These measures significantly reduce the peak of both symptomatic and asymptomatic infections, lower environmental bacterial concentrations, and delay the

outbreak's progression, making it more manageable. Furthermore, they result in a substantial reduction in disease-induced deaths and promote quicker recovery rates. The susceptible population declines more gradually, preserving a larger portion of the population from infection. Overall, the combined application of these measures is highly effective in controlling the outbreak, minimizing mortality, and ensuring sustainable recovery for the population.

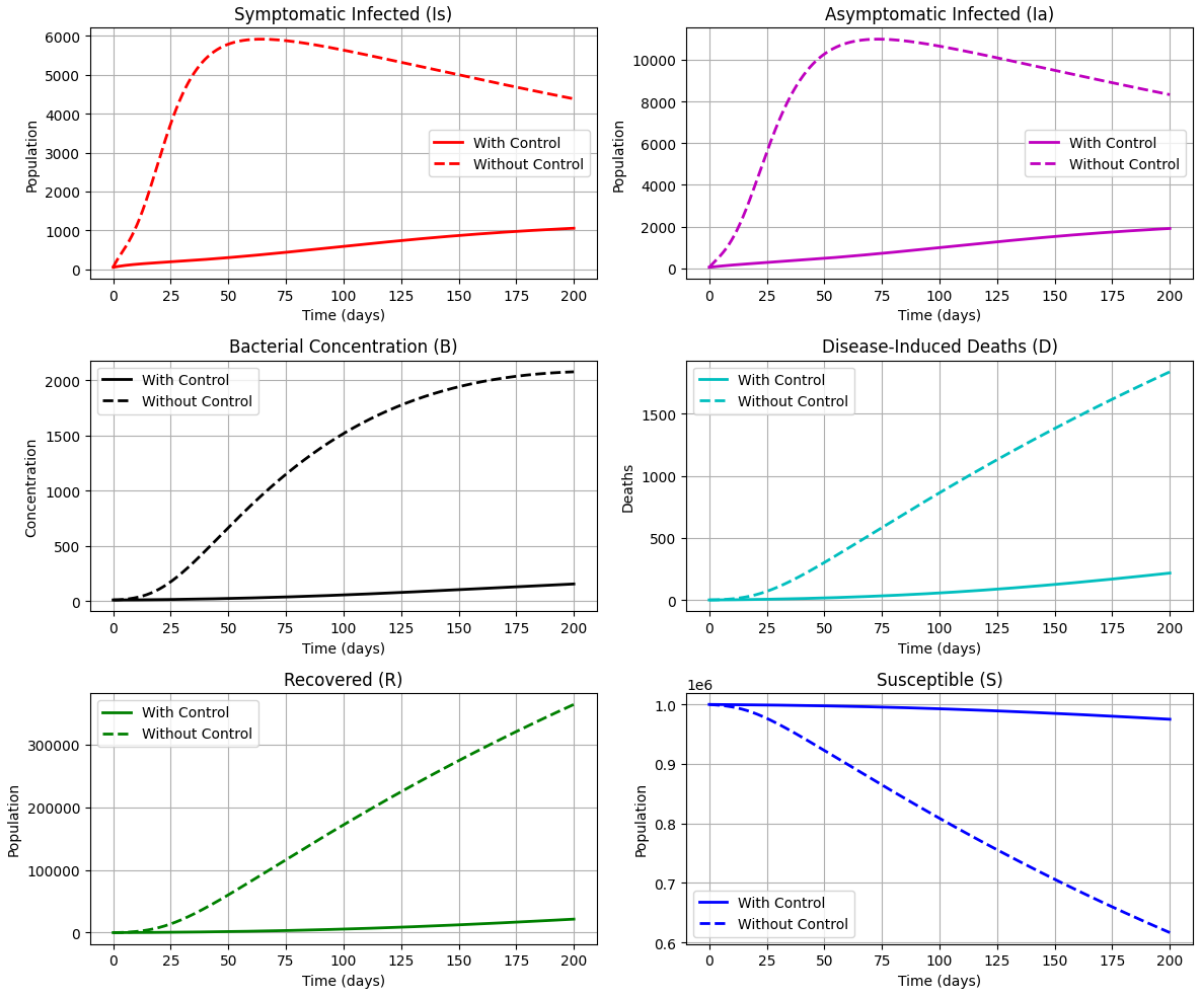

Figure 9: Simulation of model with intervention of all 4 control mechanisms

5. Results

These simulations further support the fact that comprehensive control measures are vital in handling cholera, especially since it has environmental influence. The absence of control measures is accompanied by a wild spread of the disease, leading to an explosive growth in both symptomatic and asymptomatic cases, high bacterial loads and massive disease induced mortality. The population becomes highly vulnerable on the whole, with a decline in the susceptible group and slow recoveries.

However, this balance dramatically changes in dynamics when the control measures are introduced, such as hygienic faeces disposal, safe drinking water, food hygiene, and hand washing. These interventions reduce infection peaks, slow the rate of disease transmission, and minimize bacterial contamination. Consequently, there is a drastic reduction in the number of deaths, while the rate of recovery accelerates and preserves health within the population. The susceptible population also decreases more gradually, enabling a more manageable progression of the disease over time.

Of the various control measures, adequate supply of safe drinking water has the most immediate affect on reducing transmission over short term, while the combination of all the measures provides the best long-term results. The results underline the need for a multifaceted approach to control the disease, one that encompasses not only the direct infection transmission but also environmental modification which contributes to disease transmission.

In the end, the simulations confirm that integrated public health interventions are effective in containing outbreaks. These findings underscore the need for an integrated approach that incorporates immediate and long-term measures to reduce disease burden, prevent large-scale outbreaks, and promote sustainable health recovery within populations.

6. Further Development

Further development of this project could involve expanding the model to account for varying population demographics, behaviours, and regional differences as it would make it more applicable to diverse settings. Additionally, integrating more complex control measures like vaccination, quarantine, and medical treatments, as well as simulating the effects of behavioural change, could enhance the model's utility. Introducing spatial dynamics, economic impact assessments, and stochastic elements would provide a more comprehensive understanding of disease spread and control. Modelling long-term disease evolution and healthcare system stress would also be beneficial. Ultimately, the integration of global disease spread simulations and policy comparisons could make this project a valuable tool for public health planning and decision-making.

7. References

1. Wang, J. (2022). Mathematical Models for Cholera Dynamics—A Review.

Microorganisms, 10(12), 2358.
https://pmc.ncbi.nlm.nih.gov/articles/PMC9783556/

2. Maliki, O. S., & Chibuike, O. C. (2021). A Mathematical Model for the Control of Cholera Epidemic without Natural Recovery. Applied Mathematics, 12(08), 655–668.

https://doi.org/10.4236/am.2021.128046

3. Hartley, D. M., Morris, J. G., & Smith, D. L. (2005). Hyperinfectivity: A Critical

Element in the Ability of V. cholerae to Cause Epidemics? PLoS Medicine, 3(1), e7. https://doi.org/10.1371/journal.pmed.0030007 World Health Organization: WHO & World Health Organization: WHO. (2024, December 5). Cholera.

https://www.who.int/news-room/fact-sheets/detail/cholera

4. Chao, D. L., Longini, I. M., & Morris, J. G. (2013). Modelling Cholera Outbreaks. Current Topics in Microbiology and Immunology, 195–209.

https://pmc.ncbi.nlm.nih.gov/articles/PMC4238032/

5. *Item*. (2000, November 3). https://www.who.int/emergencies/disease-outbreak-news/item/2000_11_03a-en

6. Hntsa, K. H., & Kahsay, B. N. (2020). Analysis of Cholera Epidemic Controlling Using Mathematical Modelling. International Journal of Mathematics and Mathematical Sciences, 2020, 1–13. https://doi.org/10.1155/2020/7369204 World Health Organization: WHO & World Health Organization: WHO. (2024, December 5). Cholera.

https://www.who.int/news-room/fact-sheets/detail/cholera

7. Brhane, K. W., Ahmad, A. G., Hina, H., & Emadifar, H. (2024). Mathematical modelling of cholera dynamics with intrinsic growth considering constant interventions. Scientific Reports, 14(1). https://doi.org/10.1038/s41598-024-55240-0

8. World Health Organization: WHO & World Health Organization: WHO. (2024,

December 5). Cholera. https://www.who.int/news-room/fact-sheets/detail/cholera

8. Appendices

8.1 MATLAB code for initial model

```
% Parameters
sigma = 0.0001;   % Birth rate
beta1 = 0.002;    % Transmission rate for asymptomatic
beta2 = 0.005;    % Transmission rate for symptomatic
gamma1 = 0.1;     % Recovery rate for asymptomatic
gamma2 = 0.2;     % Recovery rate for symptomatic
alpha1 = 0.001;   % Bacterial interaction for asymptomatic
alpha2 = 0.003;   % Bacterial interaction for symptomatic
mu1 = 0.0005;     % Death rate for asymptomatic
mu2 = 0.001;      % Death rate for symptomatic
nu = 0.0001;      % Natural death rate
delta = 0.01;     % Bacteria decay rate
```

```
k = 100;         % Half-saturation constant
p = 0.3;         % Proportion of symptomatic cases
N = 1e6;         % Total population size

% Initial conditions
S0 = N - 100;    % Initial susceptibles
Ia0 = 50;        % Initial asymptomatic infected
Is0 = 50;        % Initial symptomatic infected
R0 = 0;          % Initial recovered
B0 = 10;         % Initial bacterial concentration
D0 = 0;          % Initial deaths

% Time span
tspan = [0, 200]; % Time in days
y0 = [S0, Ia0, Is0, R0, B0, D0];

% Define ODE system
ode = @(t, y) [
   sigma * N - p * beta2 * y(1) * y(5) / (y(5) + k) - (1-p) * beta1 * y(1) * y(5) / (y(5) + k) - nu * y(1);  % dS/dt
   (1-p) * beta1 * y(1) * y(5) / (y(5) + k) - gamma1 * y(2) - alpha1 * y(2) - mu1 * y(2) - nu * y(2);      % dIa/dt
   p * beta2 * y(1) * y(5) / (y(5) + k) - gamma2 * y(3) - alpha2 * y(3) - mu2 * y(3) - nu * y(3); % dIs/dt
   gamma1 * y(2) + gamma2 * y(3) - nu * y(4);                                    % dR/dt
   alpha1 * y(2) + alpha2 * y(3) - delta * y(5);                                 % dB/dt
   mu1 * y(2) + mu2 * y(3)                                                       % dD/dt
];

% Solve ODE system
```

```
[t, y] = ode45(ode, tspan, y0);
% Extract results
S = y(:, 1);
Ia = y(:, 2);
Is = y(:, 3);
R = y(:, 4);
B = y(:, 5);
D = y(:, 6);

% Plot results
figure;
subplot(3, 2, 1);
plot(t, S, 'b', 'LineWidth', 2);
title('Susceptible');
xlabel('Time (days)');
ylabel('Population');
grid on;
subplot(3, 2, 2);
plot(t, Ia, 'm', 'LineWidth', 2);
title('Asymptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
grid on;
subplot(3, 2, 3);
plot(t, Is, 'r', 'LineWidth', 2);
title('Symptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
grid on;
```

```
subplot(3, 2, 4);
plot(t, R, 'g', 'LineWidth', 2);
title('Recovered');
xlabel('Time (days)');
ylabel('Population');
grid on;
subplot(3, 2, 5);
plot(t, B, 'k', 'LineWidth', 2);
title('Bacteria Concentration');
xlabel('Time (days)');
ylabel('Concentration');
grid on;
subplot(3, 2, 6);
plot(t, D, 'c', 'LineWidth', 2);
title('Disease-Induced Deaths');
xlabel('Time (days)');
ylabel('Deaths');
grid on;
```

8.2 MATLAB code for model with control mechanism 1

```
% Parameters
sigma = 0.0001;   % Birth rate
beta1 = 0.002;    % Transmission rate for asymptomatic
beta2 = 0.005;    % Transmission rate for symptomatic
gamma1 = 0.1;     % Recovery rate for asymptomatic
gamma2 = 0.2;     % Recovery rate for symptomatic
alpha1 = 0.001;   % Bacterial interaction for asymptomatic
alpha2 = 0.003;   % Bacterial interaction for symptomatic
```

```
mu1 = 0.0005;     % Death rate for asymptomatic

mu2 = 0.001;      % Death rate for symptomatic

nu = 0.0001;      % Natural death rate

delta = 0.01;     % Bacteria decay rate

k = 100;          % Half-saturation constant

p = 0.3;          % Proportion of symptomatic cases

N = 1e6;          % Total population size


% Control parameters: hygienic disposal of human feces

u1_with_control = 0.5;  % Control effort (50% effectiveness)

u1_without_control = 0; % No control (u1 = 0)


% Initial conditions

S0 = N - 100;     % Initial susceptibles

Ia0 = 50;         % Initial asymptomatic infected

Is0 = 50;         % Initial symptomatic infected

R0 = 0;           % Initial recovered

B0 = 10;          % Initial bacterial concentration

D0 = 0;           % Initial deaths


% Time span for simulation

tspan = [0, 200]; % Time in days

y0 = [S0, Ia0, Is0, R0, B0, D0];  % Initial state vector


% Define the system of ODEs with control (hygienic disposal of human feces)

ode_with_control = @(t, y) [

   -sigma * N - p * beta2 * y(1) * y(5) / (y(5) + k) - (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - nu *
y(1);  % dS/dt

   (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - gamma1 * y(2) - alpha1 * (1 - u1_with_control) *
y(2) - mu1 * y(2) - nu * y(2);  % dIa/dt
```

```
    p * beta2 * y(1) * y(5) / (y(5) + k) - gamma2 * y(3) - alpha2 * (1 - u1_with_control) * y(3) - mu2 * y(3) - nu * y(3);  % dIs/dt

    gamma1 * y(2) + gamma2 * y(3) - nu * y(4);  % dR/dt

    alpha1 * (1 - u1_with_control) * y(2) + alpha2 * (1 - u1_with_control) * y(3) - delta * y(5);  % dB/dt

    mu1 * y(2) + mu2 * y(3);  % dD/dt

];


ode_without_control = @(t, y) [

    -sigma * N - p * beta2 * y(1) * y(5) / (y(5) + k) - (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - nu * y(1);  % dS/dt

    (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - gamma1 * y(2) - alpha1 * (1 - u1_without_control) * y(2) - mu1 * y(2) - nu * y(2);  % dIa/dt

    p * beta2 * y(1) * y(5) / (y(5) + k) - gamma2 * y(3) - alpha2 * (1 - u1_without_control) * y(3) - mu2 * y(3) - nu * y(3);  % dIs/dt

    gamma1 * y(2) + gamma2 * y(3) - nu * y(4);  % dR/dt

    alpha1 * (1 - u1_without_control) * y(2) + alpha2 * (1 - u1_without_control) * y(3) - delta * y(5);  % dB/dt

    mu1 * y(2) + mu2 * y(3);  % dD/dt

];


% Solve the system of ODEs with control

[t_with_control, y_with_control] = ode45(ode_with_control, tspan, y0);


% Solve the system of ODEs without control

[t_without_control, y_without_control] = ode45(ode_without_control, tspan, y0);


% Extract the results

S_with_control = y_with_control(:, 1);

Ia_with_control = y_with_control(:, 2);

Is_with_control = y_with_control(:, 3);
```

```
R_with_control = y_with_control(:, 4);
B_with_control = y_with_control(:, 5);
D_with_control = y_with_control(:, 6);

S_without_control = y_without_control(:, 1);
Ia_without_control = y_without_control(:, 2);
Is_without_control = y_without_control(:, 3);
R_without_control = y_without_control(:, 4);
B_without_control = y_without_control(:, 5);
D_without_control = y_without_control(:, 6);

% Plot the comparison with and without control (dotted lines for no control)
figure;

subplot(3, 2, 1);
plot(t_with_control, S_with_control, 'b', 'LineWidth', 2); hold on;
plot(t_without_control, S_without_control, 'b:', 'LineWidth', 2); % Dotted line for no control
title('Susceptible Population');
xlabel('Time (days)');
ylabel('Population');
grid on;
legend('With Control', 'Without Control');

subplot(3, 2, 2);
plot(t_with_control, Ia_with_control, 'm', 'LineWidth', 2); hold on;
plot(t_without_control, Ia_without_control, 'm:', 'LineWidth', 2); % Dotted line for no
control
title('Asymptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
```

```
grid on;
legend('With Control', 'Without Control');

subplot(3, 2, 3);
plot(t_with_control, Is_with_control, 'r', 'LineWidth', 2); hold on;
plot(t_without_control, Is_without_control, 'r:', 'LineWidth', 2); % Dotted line for no control
title('Symptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
grid on;
legend('With Control', 'Without Control');

subplot(3, 2, 4);
plot(t_with_control, R_with_control, 'g', 'LineWidth', 2); hold on;
plot(t_without_control, R_without_control, 'g:', 'LineWidth', 2); % Dotted line for no control
title('Recovered');
xlabel('Time (days)');
ylabel('Population');
grid on;
legend('With Control', 'Without Control');

subplot(3, 2, 5);
plot(t_with_control, B_with_control, 'k', 'LineWidth', 2); hold on;
plot(t_without_control, B_without_control, 'k:', 'LineWidth', 2); % Dotted line for no control
title('Bacteria Concentration');
xlabel('Time (days)');
ylabel('Concentration');
grid on;
legend('With Control', 'Without Control');
```

```
subplot(3, 2, 6);
plot(t_with_control, D_with_control, 'c', 'LineWidth', 2); hold on;
plot(t_without_control, D_without_control, 'c:', 'LineWidth', 2); % Dotted line for no control
title('Disease-Induced Deaths');
xlabel('Time (days)');
ylabel('Deaths');
grid on;
legend('With Control', 'Without Control');
```

8.3 MATLAB code for model with control mechanism 2

```
% Parameters
sigma = 0.0001;   % Birth rate
beta1 = 0.002;    % Transmission rate for asymptomatic
beta2 = 0.005;    % Transmission rate for symptomatic
gamma1 = 0.1;     % Recovery rate for asymptomatic
gamma2 = 0.2;     % Recovery rate for symptomatic
alpha1 = 0.001;   % Bacterial interaction for asymptomatic
alpha2 = 0.003;   % Bacterial interaction for symptomatic
mu1 = 0.0005;     % Death rate for asymptomatic
mu2 = 0.001;      % Death rate for symptomatic
nu = 0.0001;      % Natural death rate
delta = 0.01;     % Bacteria decay rate
k = 100;          % Half-saturation constant
p = 0.3;          % Proportion of symptomatic cases
N = 1e6;          % Total population size

% Initial conditions
S0 = N - 100;     % Initial susceptibles
```

```
Ia0 = 50;        % Initial asymptomatic infected
Is0 = 50;        % Initial symptomatic infected
R0 = 0;          % Initial recovered
B0 = 10;         % Initial bacterial concentration
D0 = 0;          % Initial deaths

% Time span
tspan = [0, 200]; % Time in days
y0 = [S0, Ia0, Is0, R0, B0, D0];

% Define time-dependent control variable u2 (safe drinking water)
u2 = @(t) min(1, max(0, 0.5 + 0.1 * sin(0.05 * t)));  % Time-varying control (between 0 and 1)

% Define ODE system with control for safe drinking water (u2)
ode_with_control = @(t, y) [
   sigma * N - p * beta2 * (1 - u2(t)) * y(1) * y(5) / (y(5) + k) - (1 - p) * beta1 * (1 - u2(t)) * y(1) * y(5) / (y(5) + k) - nu * y(1);  % dS/dt
   (1 - p) * beta1 * (1 - u2(t)) * y(1) * y(5) / (y(5) + k) - gamma1 * y(2) - alpha1 * y(2) - mu1 * y(2) - nu * y(2);       % dIa/dt
   p * beta2 * (1 - u2(t)) * y(1) * y(5) / (y(5) + k) - gamma2 * y(3) - alpha2 * y(3) - mu2 * y(3) - nu * y(3);          % dIs/dt
   gamma1 * y(2) + gamma2 * y(3) - nu * y(4);                                          % dR/dt
   alpha1 * y(2) + alpha2 * y(3) - delta * y(5);                                       % dB/dt
   mu1 * y(2) + mu2 * y(3)                                                             % dD/dt
];

% Define ODE system without control (no reduction in beta1 or beta2)
ode_without_control = @(t, y) [
   sigma * N - p * beta2 * y(1) * y(5) / (y(5) + k) - (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - nu * y(1);  % dS/dt
```

```
    (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - gamma1 * y(2) - alpha1 * y(2) - mu1 * y(2) - nu * y(2);      % dIa/dt
    p * beta2 * y(1) * y(5) / (y(5) + k) - gamma2 * y(3) - alpha2 * y(3) - mu2 * y(3) - nu * y(3);  % dIs/dt
    gamma1 * y(2) + gamma2 * y(3) - nu * y(4);                                                      % dR/dt
    alpha1 * y(2) + alpha2 * y(3) - delta * y(5);                                                   % dB/dt
    mu1 * y(2) + mu2 * y(3)                                                                         % dD/dt
];

% Solve ODE system with control
[t_with_control, y_with_control] = ode45(ode_with_control, tspan, y0);

% Solve ODE system without control
[t_without_control, y_without_control] = ode45(ode_without_control, tspan, y0);

% Extract results for both cases
S_with_control = y_with_control(:, 1);
Ia_with_control = y_with_control(:, 2);
Is_with_control = y_with_control(:, 3);
R_with_control = y_with_control(:, 4);
B_with_control = y_with_control(:, 5);
D_with_control = y_with_control(:, 6);

S_without_control = y_without_control(:, 1);
Ia_without_control = y_without_control(:, 2);
Is_without_control = y_without_control(:, 3);
R_without_control = y_without_control(:, 4);
B_without_control = y_without_control(:, 5);
D_without_control = y_without_control(:, 6);
```

```
% Plot results comparing with and without control
figure;

subplot(3, 2, 1);
plot(t_with_control, S_with_control, 'b', 'LineWidth', 2); hold on;
plot(t_without_control, S_without_control, 'b--', 'LineWidth', 2);
title('Susceptible');
xlabel('Time (days)');
ylabel('Population');
legend('With Control', 'Without Control');
grid on;

subplot(3, 2, 2);
plot(t_with_control, Ia_with_control, 'm', 'LineWidth', 2); hold on;
plot(t_without_control, Ia_without_control, 'm--', 'LineWidth', 2);
title('Asymptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
legend('With Control', 'Without Control');
grid on;

subplot(3, 2, 3);
plot(t_with_control, Is_with_control, 'r', 'LineWidth', 2); hold on;
plot(t_without_control, Is_without_control, 'r--', 'LineWidth', 2);
title('Symptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
legend('With Control', 'Without Control');
grid on;
```

```
subplot(3, 2, 4);
plot(t_with_control, R_with_control, 'g', 'LineWidth', 2); hold on;
plot(t_without_control, R_without_control, 'g--', 'LineWidth', 2);
title('Recovered');
xlabel('Time (days)');
ylabel('Population');
legend('With Control', 'Without Control');
grid on;

subplot(3, 2, 5);
plot(t_with_control, B_with_control, 'k', 'LineWidth', 2); hold on;
plot(t_without_control, B_without_control, 'k--', 'LineWidth', 2);
title('Bacteria Concentration');
xlabel('Time (days)');
ylabel('Concentration');
legend('With Control', 'Without Control');
grid on;

subplot(3, 2, 6);
plot(t_with_control, D_with_control, 'c', 'LineWidth', 2); hold on;
plot(t_without_control, D_without_control, 'c--', 'LineWidth', 2);
title('Disease-Induced Deaths');
xlabel('Time (days)');
ylabel('Deaths');
legend('With Control', 'Without Control');
grid on;
```

8.4 MATLAB code for model with control mechanism 3

```
% Parameters
sigma = 0.0001;   % Birth rate
beta1 = 0.002;    % Transmission rate for asymptomatic
beta2 = 0.005;    % Transmission rate for symptomatic
gamma1 = 0.1;     % Recovery rate for asymptomatic
gamma2 = 0.2;     % Recovery rate for symptomatic
alpha1 = 0.001;   % Bacterial interaction for asymptomatic
alpha2 = 0.003;   % Bacterial interaction for symptomatic
mu1 = 0.0005;     % Death rate for asymptomatic
mu2 = 0.001;      % Death rate for symptomatic
nu = 0.0001;      % Natural death rate
delta = 0.01;     % Bacteria decay rate
k = 100;          % Half-saturation constant
p = 0.3;          % Proportion of symptomatic cases
N = 1e6;          % Total population size

% Control variables (interventions)
u2 = 0.25;        % Food hygiene control (0 = no control, 1 = maximum control)
u3 = 0.25;        % Cooking control (0 = no control, 1 = maximum control)

% Initial conditions
S0 = N - 100;     % Initial susceptibles
Ia0 = 50;         % Initial asymptomatic infected
Is0 = 50;         % Initial symptomatic infected
R0 = 0;           % Initial recovered
B0 = 10;          % Initial bacterial concentration
D0 = 0;           % Initial deaths

% Time span
```

```
tspan = [0, 200]; % Time in days

y0 = [S0, Ia0, Is0, R0, B0, D0];


% Define ODE system with control

ode_with_control = @(t, y) [

   sigma * N - p * beta2 * y(1) * y(5) / (y(5) + k) * (1 - u2) * (1 - u3) - (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) * (1 - u2) * (1 - u3) - nu * y(1);  % dS/dt

   (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) * (1 - u2) * (1 - u3) - gamma1 * y(2) - alpha1 * y(2) - mu1 * y(2) - nu * y(2);  % dIa/dt

   p * beta2 * y(1) * y(5) / (y(5) + k) * (1 - u2) * (1 - u3) - gamma2 * y(3) - alpha2 * y(3) - mu2 * y(3) - nu * y(3);  % dIs/dt

   gamma1 * y(2) + gamma2 * y(3) - nu * y(4);  % dR/dt

   alpha1 * y(2) + alpha2 * y(3) - delta * y(5);  % dB/dt

   mu1 * y(2) + mu2 * y(3)  % dD/dt

];


% Define ODE system without control (u2 = 0 and u3 = 0)

ode_without_control = @(t, y) [

   sigma * N - p * beta2 * y(1) * y(5) / (y(5) + k) - (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - nu * y(1);  % dS/dt

   (1 - p) * beta1 * y(1) * y(5) / (y(5) + k) - gamma1 * y(2) - alpha1 * y(2) - mu1 * y(2) - nu * y(2);  % dIa/dt

   p * beta2 * y(1) * y(5) / (y(5) + k) - gamma2 * y(3) - alpha2 * y(3) - mu2 * y(3) - nu * y(3);  % dIs/dt

   gamma1 * y(2) + gamma2 * y(3) - nu * y(4);  % dR/dt

   alpha1 * y(2) + alpha2 * y(3) - delta * y(5);  % dB/dt

   mu1 * y(2) + mu2 * y(3)  % dD/dt

];


% Solve ODE system with control

[t_with_control, y_with_control] = ode45(ode_with_control, tspan, y0);
```

```
S_with_control = y_with_control(:, 1);
Ia_with_control = y_with_control(:, 2);
Is_with_control = y_with_control(:, 3);

% Solve ODE system without control
[t_without_control, y_without_control] = ode45(ode_without_control, tspan, y0);
S_without_control = y_without_control(:, 1);
Ia_without_control = y_without_control(:, 2);
Is_without_control = y_without_control(:, 3);

% Plot results
figure;

% Susceptible population plot
subplot(3, 2, 1);
plot(t_with_control, S_with_control, 'b', 'LineWidth', 2); % With control (solid)
hold on;
plot(t_without_control, S_without_control, 'b:', 'LineWidth', 2); % Without control (dotted)
title('Susceptible Population');
xlabel('Time (days)');
ylabel('Population');
legend('With control', 'Without control');
grid on;

% Asymptomatic infected population plot
subplot(3, 2, 2);
plot(t_with_control, Ia_with_control, 'm', 'LineWidth', 2); % With control (solid)
hold on;
plot(t_without_control, Ia_without_control, 'm:', 'LineWidth', 2); % Without control (dotted)
```

```
title('Asymptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
legend('With control', 'Without control');
grid on;

% Symptomatic infected population plot
subplot(3, 2, 3);
plot(t_with_control, Is_with_control, 'r', 'LineWidth', 2); % With control (solid)
hold on;
plot(t_without_control, Is_without_control, 'r:', 'LineWidth', 2); % Without control (dotted)
title('Symptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
legend('With control', 'Without control');
grid on;

% Recovered population plot
subplot(3, 2, 4);
plot(t_with_control, y_with_control(:, 4), 'g', 'LineWidth', 2); % With control (solid)
hold on;
plot(t_without_control, y_without_control(:, 4), 'g:', 'LineWidth', 2); % Without control
(dotted)
title('Recovered');
xlabel('Time (days)');
ylabel('Population');
legend('With control', 'Without control');
grid on;

% Bacteria concentration plot
```

```
subplot(3, 2, 5);
plot(t_with_control, y_with_control(:, 5), 'k', 'LineWidth', 2); % With control (solid)
hold on;
plot(t_without_control, y_without_control(:, 5), 'k:', 'LineWidth', 2); % Without control (dotted)
title('Bacteria Concentration');
xlabel('Time (days)');
ylabel('Concentration');
legend('With control', 'Without control');
grid on;

% Disease-induced deaths plot
subplot(3, 2, 6);
plot(t_with_control, y_with_control(:, 6), 'c', 'LineWidth', 2); % With control (solid)
hold on;
plot(t_without_control, y_without_control(:, 6), 'c:', 'LineWidth', 2); % Without control (dotted)
title('Disease-Induced Deaths');
xlabel('Time (days)');
ylabel('Deaths');
legend('With control', 'Without control');
grid on;
```

8.5 MATLAB code for model with control mechanism 4

```
% Plot results
figure;
% Susceptible Population
subplot(3, 2, 1);
plot(t_no_control, S_no_control, 'b--', 'LineWidth', 2); % Without control (dashed line in blue)
```

```
hold on;
plot(t_with_control, S_with_control, 'b-', 'LineWidth', 2); % With control (solid line in blue)
title('Susceptible Population');
xlabel('Time (days)');
ylabel('Population');
legend('Without Control', 'With Control');
grid on;

% Asymptomatic Infected
subplot(3, 2, 2);
plot(t_no_control, Ia_no_control, 'm--', 'LineWidth', 2); % Without control (dashed line in pink)
hold on;
plot(t_with_control, Ia_with_control, 'm-', 'LineWidth', 2); % With control (solid line in pink)
title('Asymptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
legend('Without Control', 'With Control');
grid on;

% Symptomatic Infected
subplot(3, 2, 3);
plot(t_no_control, Is_no_control, 'r--', 'LineWidth', 2); % Without control (dashed line in orange)
hold on;
plot(t_with_control, Is_with_control, 'r-', 'LineWidth', 2); % With control (solid line in orange)
title('Symptomatic Infected');
xlabel('Time (days)');
ylabel('Population');
```

```
legend('Without Control', 'With Control');
grid on;

% Recovered Population
subplot(3, 2, 4);
plot(t_no_control, R_no_control, 'g--', 'LineWidth', 2); % Without control (dashed line in green)
hold on;
plot(t_with_control, R_with_control, 'g-', 'LineWidth', 2); % With control (solid line in green)
title('Recovered Population');
xlabel('Time (days)');
ylabel('Population');
legend('Without Control', 'With Control');
grid on;

% Bacteria Concentration
subplot(3, 2, 5);
plot(t_no_control, B_no_control, 'k--', 'LineWidth', 2); % Without control (dashed line in black)
hold on;
plot(t_with_control, B_with_control, 'k-', 'LineWidth', 2); % With control (solid line in black)
title('Bacteria Concentration');
xlabel('Time (days)');
ylabel('Concentration');
legend('Without Control', 'With Control');
grid on;

% Disease-Induced Deaths
subplot(3, 2, 6);
```

```
plot(t_no_control, D_no_control, 'c--', 'LineWidth', 2); % Without control (dashed line in light blue)

hold on;

plot(t_with_control, D_with_control, 'c-', 'LineWidth', 2); % With control (solid line in light blue)

title('Disease-Induced Deaths');

xlabel('Time (days)');

ylabel('Deaths');

legend('Without Control', 'With Control');

grid on;
```

8.6 MATLAB code for residual analysis

```
% Parameters

sigma = 0.0001;   % Birth rate

beta1 = 0.002;    % Transmission rate for asymptomatic

beta2 = 0.005;    % Transmission rate for symptomatic

gamma1 = 0.1;     % Recovery rate for asymptomatic

gamma2 = 0.2;     % Recovery rate for symptomatic

alpha1 = 0.001;   % Bacterial interaction for asymptomatic

alpha2 = 0.003;   % Bacterial interaction for symptomatic

mu1 = 0.0008;     % Adjusted death rate for asymptomatic

mu2 = 0.0015;     % Adjusted death rate for symptomatic

nu = 0.0001;      % Natural death rate

delta = 0.01;     % Bacteria decay rate

k = 100;          % Half-saturation constant

p = 0.3;          % Proportion of symptomatic cases

N = 1e6;          % Total population size


% Initial conditions

S0 = N - 100;     % Initial susceptibles
```

```
Ia0 = 50;        % Initial asymptomatic infected

Is0 = 50;        % Initial symptomatic infected

R0 = 0;          % Initial recovered

B0 = 10;         % Initial bacterial concentration

D0 = 0;          % Initial deaths

y0 = [S0, Ia0, Is0, R0, B0, D0];


% Observed data

time_data = [0, 5, 6, 13, 20, 27, 37, 45, 53, 67, 77, 87, 92, 103, 114, 124, 132, 143, 157, 173,
196]; % Days

cases_observed = [2175, 3075, 3279, 3806, 4270, 4583, 5285, 5876, 6548, 8137, 11183,
15983, ...
   19499, 27431, 37204, 48647, 56092, 62607, 69761, 78140, 86107]; % Total cases

deaths_observed = [22, 26, 27, 33, 32, 33, 35, 35, 35, 41, 51, 60, 66, 74, 85, 108, 120, 131,
139, 163, 181]; % Total deaths


% Time span for simulation

tspan = [0, max(time_data)];


% Define ODE system

ode = @(t, y) [
   sigma * N - p * beta2 * y(1) * y(5) / (y(5) + k) - (1-p) * beta1 * y(1) * y(5) / (y(5) + k) - nu *
y(1);  % dS/dt
   (1-p) * beta1 * y(1) * y(5) / (y(5) + k) - gamma1 * y(2) - alpha1 * y(2) - mu1 * y(2) - nu *
y(2);      % dIa/dt
   p * beta2 * y(1) * y(5) / (y(5) + k) - gamma2 * y(3) - alpha2 * y(3) - mu2 * y(3) - nu * y(3);
% dIs/dt
   gamma1 * y(2) + gamma2 * y(3) - nu * y(4);                                    % dR/dt
   alpha1 * y(2) + alpha2 * y(3) - delta * y(5);                                 % dB/dt
   mu1 * y(2) + mu2 * y(3)                                                       % dD/dt
];
```

```
% Solve ODE system
[t, y] = ode45(ode, tspan, y0);

% Extract total cases (Ia + Is) and deaths
total_cases_predicted = y(:, 2) + y(:, 3); % Ia + Is
total_deaths_predicted = y(:, 6); % D

% Interpolate to match observed time points
cases_predicted = interp1(t, total_cases_predicted, time_data);
deaths_predicted = interp1(t, total_deaths_predicted, time_data);

% Compute residuals
cases_residuals = cases_observed - cases_predicted;
deaths_residuals = deaths_observed - deaths_predicted;

% Plot residuals
figure;

subplot(2, 1, 1);
plot(time_data, cases_residuals, 'bo-', 'LineWidth', 2);
xlabel('Time (days)');
ylabel('Residuals (Cases)');
title('Residuals for Total Cases');
grid on;

subplot(2, 1, 2);
plot(time_data, abs(deaths_residuals), 'ro-', 'LineWidth', 2);  % Plot absolute values for deaths residuals
xlabel('Time (days)');
```

```
ylabel('Residuals (Deaths)');
title('Residuals for Total Deaths');
grid on;

% Residual diagnostics
figure;

% Histogram for case residuals
subplot(2, 2, 1);
histogram(cases_residuals, 10, 'FaceColor', 'b');
xlabel('Residuals (Cases)');
ylabel('Frequency');
title('Histogram of Case Residuals');
grid on;

% Histogram for death residuals (absolute values)
subplot(2, 2, 2);
histogram(abs(deaths_residuals), 10, 'FaceColor', 'r');  % Absolute values for histogram
xlabel('Residuals (Deaths)');
ylabel('Frequency');
title('Histogram of Death Residuals');
grid on;

% Autocorrelation for case residuals
subplot(2, 2, 3);
autocorr(cases_residuals);
title('Autocorrelation of Case Residuals');

% Autocorrelation for death residuals (absolute values)
```

```
subplot(2, 2, 4);
autocorr(abs(deaths_residuals));  % Absolute values for autocorrelation
title('Autocorrelation of Death Residuals');
```

8.7 MATLAB code for sensitivity analysis

```
function cholera_sensitivity_analysis_with_tornado
    % Initial Conditions and Parameters
    sigma = 0.1; beta1 = 0.5; beta2 = 0.6; gamma1 = 0.3; gamma2 = 0.3;
    alpha1 = 0.02; alpha2 = 0.03; mu1 = 0.01; mu2 = 0.02; nu = 0.05; delta = 0.1; k = 0.01;
    p = 0.5; % Proportion symptomatic

    % Define Initial Values for S, Ia, Is, R, B, D
    S0 = 50000; Ia0 = 1; Is0 = 0; R0 = 0; B0 = 0.01; D0 = 0;
    y0 = [S0, Ia0, Is0, R0, B0, D0];  % Initial conditions vector

    % Time span for simulation
    tspan = [0 200];  % Time from 0 to 200 days

    % Define model parameters
    params = [sigma, beta1, beta2, gamma1, gamma2, alpha1, alpha2, mu1, mu2, nu, delta, k,
p];

    % Solve the system of ODEs
    [t, y] = ode45(@(t, y) cholera_model(t, y, params), tspan, y0);

    % Output: Sensitivity analysis and tornado plot
    sensitivity_analysis_and_tornado(params, y, t);
end
```

```
% Cholera model equations
function dydt = cholera_model(t, y, params)
    S = y(1); Ia = y(2); Is = y(3); R = y(4); B = y(5); D = y(6);

    sigma = params(1); beta1 = params(2); beta2 = params(3); gamma1 = params(4); gamma2 = params(5);
    alpha1 = params(6); alpha2 = params(7); mu1 = params(8); mu2 = params(9); nu = params(10);
    delta = params(11); k = params(12); p = params(13);

    dSdt = -sigma * S - p * beta2 * S * (B / (B + k)) - (1 - p) * beta1 * S * (B / (B + k)) - nu * S;
    dIadt = (1 - p) * beta1 * S * (B / (B + k)) - gamma1 * Ia - alpha1 * Ia - mu1 * Ia - nu * Ia;
    dIsdt = p * beta2 * S * (B / (B + k)) - gamma2 * Is - alpha2 * Is - mu2 * Is - nu * Is;
    dRdt = gamma1 * Ia + gamma2 * Is - nu * R;
    dBdt = alpha1 * Ia + alpha2 * Is - delta * B;
    dDdt = mu1 * Ia + mu2 * Is;

    dydt = [dSdt; dIadt; dIsdt; dRdt; dBdt; dDdt];
end

% Sensitivity Analysis Function and Tornado Plot
function sensitivity_analysis_and_tornado(params, y, t)
    % Output Variables of Interest (Infected Individuals and Bacteria)
    total_infected = y(:, 2) + y(:, 3);  % Ia + Is (total infected individuals)
    total_bacteria = y(:, 5);  % Bacteria concentration

    % Compute baseline infected total and bacteria concentration
    baseline_infected = sum(total_infected);
    baseline_bacteria = sum(total_bacteria);
```

```
% Perturb each parameter by 10%
perturb_factor = 0.1;
n_params = length(params);
sensitivity_indices = zeros(n_params, 1);

for i = 1:n_params
    % Perturb one parameter
    perturbed_params = params;
    perturbed_params(i) = perturbed_params(i) * (1 + perturb_factor);

    % Solve the model with the perturbed parameter
    [t_perturbed, y_perturbed] = ode45(@(t, y) cholera_model(t, y, perturbed_params), t,
y(1, :));

    % Get the new infected total and bacteria concentration
    total_infected_perturbed = y_perturbed(:, 2) + y_perturbed(:, 3);
    total_bacteria_perturbed = y_perturbed(:, 5);

    % Compute the new sums of infected and bacteria concentration
    perturbed_infected = sum(total_infected_perturbed);
    perturbed_bacteria = sum(total_bacteria_perturbed);

    % Sensitivity indices for infected and bacteria concentration
    sensitivity_infected = (perturbed_infected - baseline_infected) / baseline_infected;
    sensitivity_bacteria = (perturbed_bacteria - baseline_bacteria) / baseline_bacteria;

    % Store the sensitivity indices
    sensitivity_indices(i) = sensitivity_infected; % You can choose either infected or bacteria
end
```

```
    % Create a Tornado Plot (Bar Chart) for Sensitivity Indices
    parameter_names = {'\sigma', '\beta_1', '\beta_2', '\gamma_1', '\gamma_2', ...
                       '\alpha_1', '\alpha_2', '\mu_1', '\mu_2', '\nu', '\delta', 'k', 'p'};

    % Plotting
    figure;
    barh(sensitivity_indices, 'FaceColor', [0.2, 0.6, 1], 'EdgeColor', 'black');
    set(gca, 'yticklabel', parameter_names);
    title('Tornado Plot: Sensitivity Analysis of Cholera Model');
    xlabel('Sensitivity Index');
    ylabel('Parameters');
    grid on;
end
```