

# Mathematical Modeling and Analysis of the SEIR Epidemic System

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# Introduction

## Context

The study of mathematical modeling is an important step in the study of mathematics, being an integral tool of applied mathematics. Modeling allows for the transformation of real-world data into quantitative models for prediction and analysis. In the field of biology, understanding nonlinear interactions between different population groups is crucial in predicting the impact of and methods of intervention in the system. The study of diseases relies heavily on differential equation models to describe the spread of infectious diseases and to identify the conditions under which outbreaks may disappear.

## Problem Statement

The problem considered in this study describes the dynamic behavior of an infectious disease in a closed population model. We aim to analyze the disease-free state and the threshold conditions for disease spread. Using the SEIR model to answer these questions:

1. Under what parameter conditions does the disease-free equilibrium become unstable?
2. How does the basic reproduction number,  $R_0$ , function as a bifurcation parameter?
3. Can numerical simulation validate the theoretical predictions of stability analysis?

## Objectives

The primary goal of this project is to apply the modeling strategies learned in MTH4201 to a biological system. The specific objectives are:

- Formulation: To derive the system of nonlinear ordinary differential equations (ODEs) governing the SEIR model.
- Analysis: To perform stability analysis using linearization and Jacobian matrix evaluation for a 3\*3 subsystem.
- Simulation: To implement the model in MATLAB using numerical solvers to generate time-series and 3D phase plane visualizations.
- Synthesis: To connect the numerical results with theoretical concepts of bifurcation and stability.

# Literature Review

## Classical Algorithms

The study of deterministic models began with McKendrick and Kermack in 1927, their work laid the foundation for compartmental modeling, dividing populations into categories based on their disease status. Standard texts in mathematical biology, such as J.D. Murray's Mathematical Biology and R. Haberman's Mathematical Models, explore these systems extensively.

From a computational perspective, these models are systems of nonlinear ODEs. Classical numerical algorithms for solving such systems typically use Euler's method for approximations and Runge-Kutta methods for increased accuracy. In modern mathematics, the standard method to ensure numerical stability and accuracy during simulation is adaptive step-size solvers like the Dormand-Prince.

## Applications

The SIR model and its modifications (SEIR, SIRS) are widely used in healthcare. They have been applied to:

- Historical Analysis:
  - Modeling the Great Plague of London and the 1918 Influenza pandemic.
- Modern Epidemiology:
  - Predicting hospital loads during the COVID-19 pandemic and analyzing the effectiveness of vaccination campaigns or social distancing measures.
- Ecological Modeling:
  - Similar predator-prey dynamics are observed in ecological systems, making the mathematical techniques transferable across disciplines.

## Methodology

### Mathematical Formulation

To increase the biological realism beyond the standard SIR model used in the midterm, this project implements the SEIR framework. This model incorporates an "Exposed" compartment (E), representing individuals who have contracted the pathogen but are not yet infectious (latent period). We also include vital dynamics.

$$\frac{dS}{dt} = \mu - \beta SI - \mu S$$

$$\frac{dE}{dt} = \beta SI - (\sigma + \mu)E$$

$$\frac{dI}{dt} = \sigma E - (\gamma + \mu)I$$

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

Where:

- $\beta$ : Transmission rate.
- $\sigma$ : Incubation rate ( $1/\sigma$  is the average latent period).
- $\gamma$ : Recovery rate.
- $\mu$ : Natural birth/death rate.

The total population is normalized  $S+E+I+R=1$ .

### Stability Analysis and Linearization:

Since the total population is constant ( $S+E+I+R=1$ ), the variable R is redundant ( $R = 1 - S - E - I$ ). Therefore, the system dynamics are fully determined by the 3D subsystem involving S, E, and I. The Jacobian matrix J for this subsystem is:

$$J = \begin{bmatrix} -\beta I - \mu & 0 & -\beta S \\ \beta I & -\sigma - \mu & \beta S \\ 0 & \sigma & -\gamma - \mu \end{bmatrix}$$

Evaluating at the DFE (1,0,0):

$$J_{DFE} = \begin{bmatrix} -\mu & 0 & -\beta \\ 0 & -\sigma - \mu & \beta \\ 0 & \sigma & -\gamma - \mu \end{bmatrix}$$

The eigenvalues are  $\lambda_1 = -\mu$  (always stable). The remaining block determines the epidemic threshold.

The Basic Reproduction Number for SEIR is derived as:

$$R_0 = \frac{\beta\sigma}{(\sigma + \mu)(\gamma + \mu)}$$

If  $R_0 < 1$ , the DFE is stable (epidemic dies out).

If  $R_0 > 1$ , the DFE is unstable, and the system moves toward an endemic state.

Endemic Equilibrium (EE): Solving the algebraic system for  $I \neq 0$ : From steady state equations, we derive:

$$S^* = \frac{(\sigma + \mu)(\gamma + \mu)}{\beta\sigma} = \frac{1}{R_0}$$

$$S^* = \frac{\mu}{\gamma + \mu} \left(1 - \frac{1}{R_0}\right)$$

$$E^* = \frac{\gamma + \mu}{\sigma} I^*$$

For the EE, the characteristic equation of the Jacobian typically yields complex conjugate eigenvalues with negative real parts, indicating a Stable Spiral trajectory.

To mathematically validate these oscillations, we computed the eigenvalues of the Jacobian matrix at the endemic equilibrium. The resulting values are  $\lambda_1 \approx -0.2298, \lambda_{2,3} \approx -0.0173 \pm 0.0389i$ . The imaginary part confirms the spiral nature of the trajectory. The negative real part ( $-0.0173$ ) confirms asymptotic stability.

Complexity vs. Midterm: Unlike the 2D midterm model, the inclusion of the Exposed class introduces a delay in transmission. This delay often destabilizes the approach to equilibrium, causing more pronounced spiral oscillations before settling.

## Implementation

The model was implemented in MATLAB. The system of differential equations was defined as a function vector and solved using the `ode45` solver over a time span of  $t = [0, 300]$ .

- Inputs: Parameters  $\beta, \sigma, \gamma, \mu$  and initial state vector  $y_0 = [0.9, 0.09, 0.01, 0]$ .
- Outputs: Time vector  $t$  and solution matrix containing  $S(t), E(t), I(t)$ , and  $R(t)$ .
- Visualization: The code generates two primary figures: a time-series plot of population fractions and a phase plane plot of  $S$  versus  $E$  versus  $I$  to visualize the system trajectories.

## Results and Discussion

### Experimental Setup

We simulate a disease with a long incubation period (like Chickenpox or Measles) to highlight the SEIR dynamics.

$\beta = 0.5$  (High transmission)

$\sigma = 0.1$  (Latent period  $\sim 10$  days)

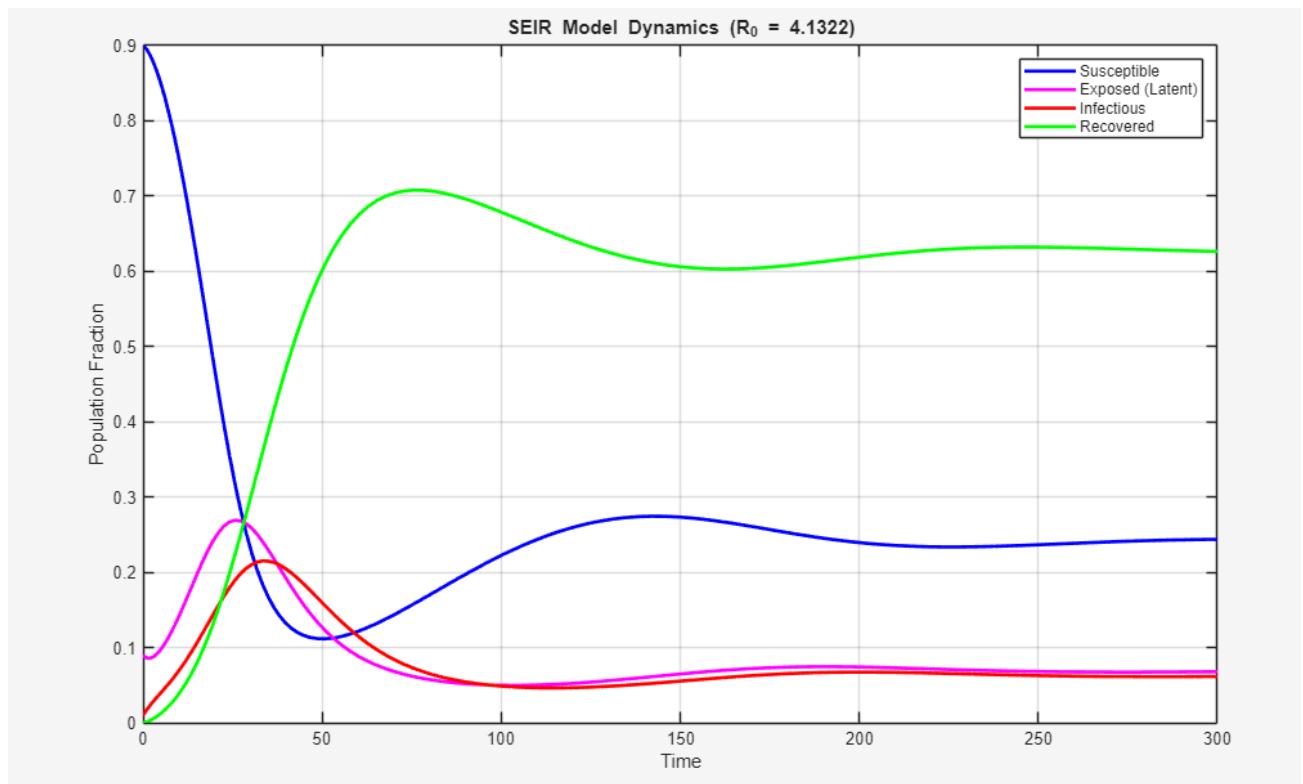
$\gamma = 0.1$  (Infectious period  $\sim 10$  days)

$\mu = 0.01$  (Vital dynamics)

Resulting  $R_0 \approx 4.1322$  (This indicates a super-critical scenario where a severe epidemic is expected)

### Visualization

Figure 1: SEIR Epidemic Model Simulation (Time Series)



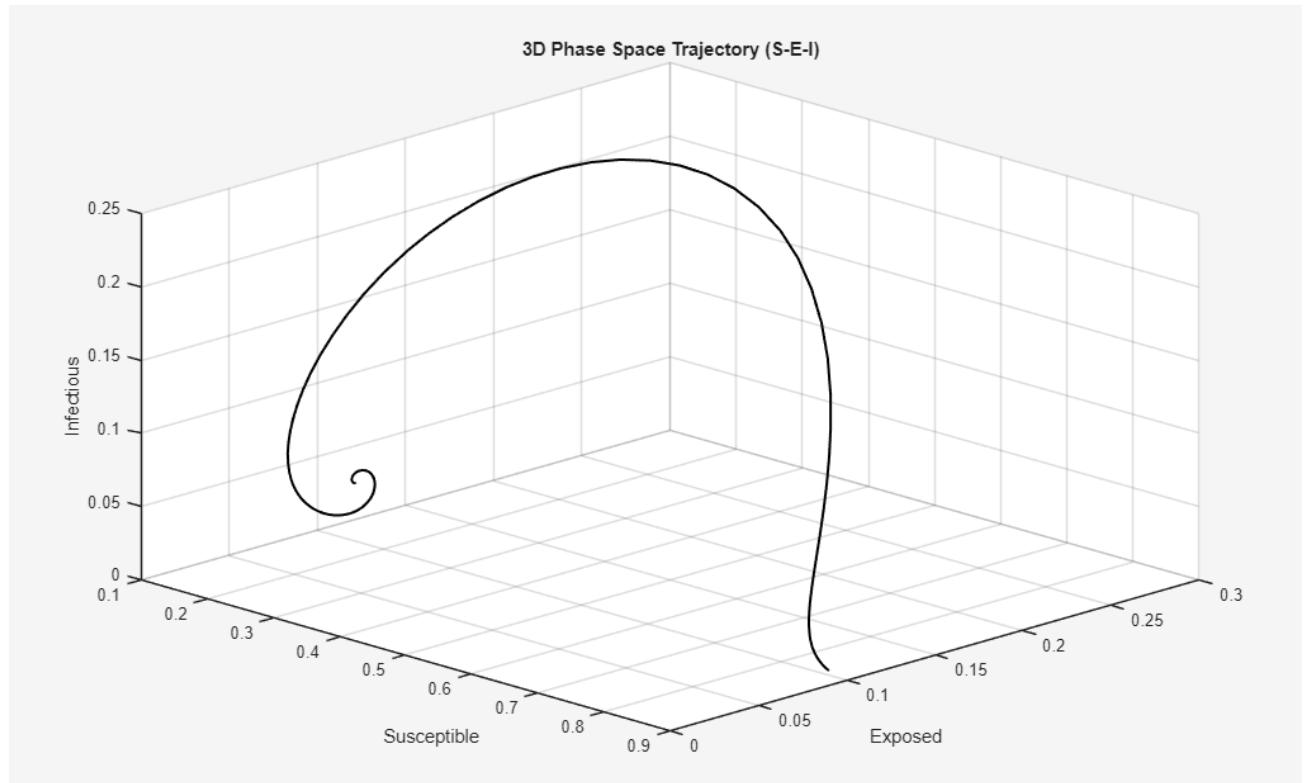
### Analysis:

The time-series graph (Figure 1) demonstrates the interaction between system components.

1. Unlike the SIR model, the Infectious population (Red) does not rise immediately. It follows the rise of the Exposed population (Pink). This lag represents the incubation period.

2. The system clearly shows damped oscillations; the number of infected individuals reaches a peak, then decreases, and then rises again in a damped wave before reaching an endemic equilibrium.
3. The Susceptible population (Blue) drops sharply at the beginning, fueling the first wave of Exposed individuals.

Figure 2: Phase Plane Analysis (S-E-I)

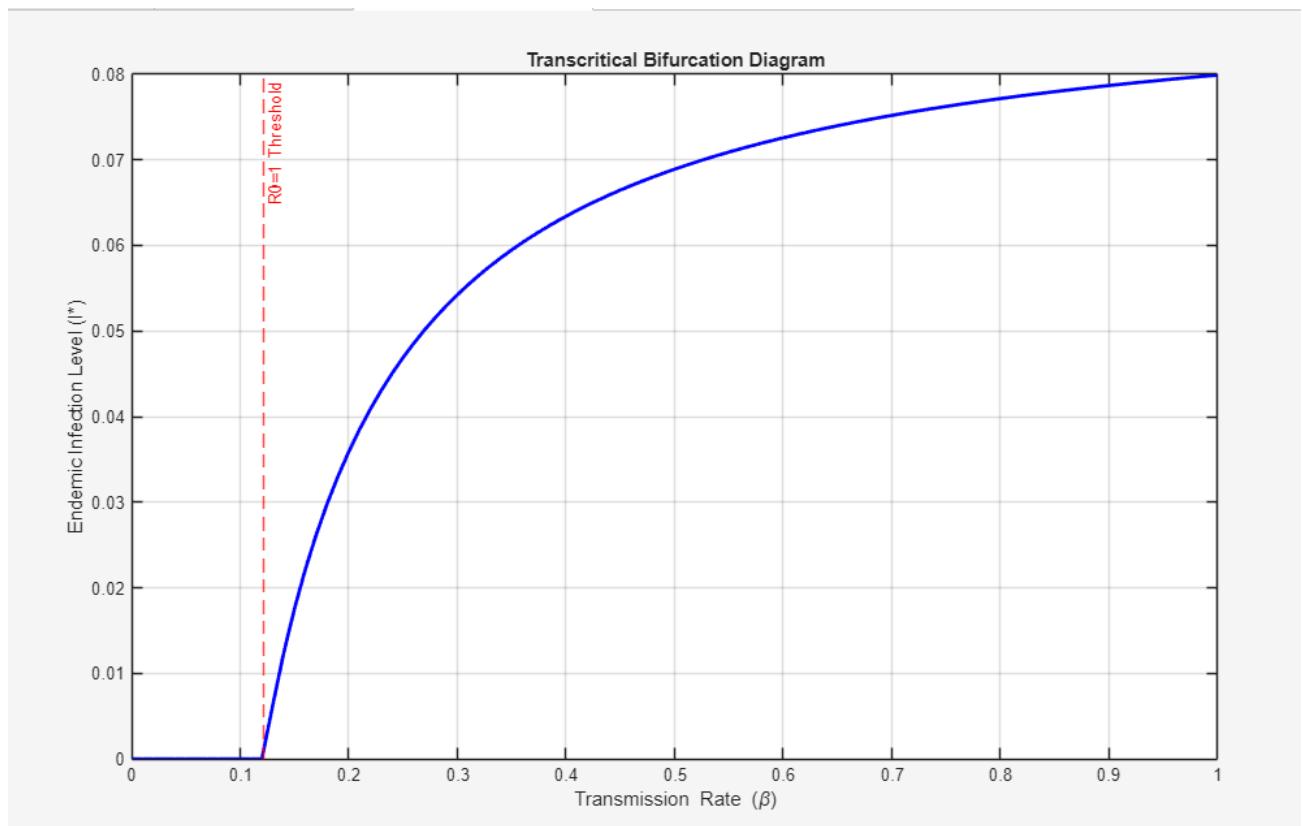


Analysis:

The 3D phase space plot (Figure 2) illustrates the trajectory of the system in the (S, E, I) space.

- The curve starts at (0.9, 0.09, 0.01) and spirals outward and upward as the epidemic begins.
- The trajectory forms a clear spiral, converging toward the interior endemic equilibrium point.
- This visualization confirms that the endemic equilibrium acts as a stable spiral sink in the 3D space, a more complex stability feature than the 2D centers observed in simple SIR models.

Figure 3: Transcritical Bifurcation Diagram ( $I^*$  vs  $\beta$ )



#### Analysis:

The bifurcation diagram illustrates the dependence of the endemic equilibrium level of infected individuals on the transmission rate parameter.

- The dashed red line marks the critical infection transmission rate, effectively dividing the system into two different stability regimes.
- To the left of the threshold, the infection rate is insufficient to sustain an epidemic. The system has a single stable equilibrium at  $I^* = 0$ , meaning that any outbreak naturally dies out.
- When  $\beta$  increases beyond the critical value, the disease-free equilibrium becomes unstable. A new stable branch appears (solid blue curve), representing the endemic equilibrium.

## Discussion

The results of the numerical simulation confirm the analytical conclusion obtained in the first part of the project. Since the reproduction number exceeded one, the system operates significantly above the endemic threshold. This confirms the existence of a state where the disease-free equilibrium loses stability, forcing the system to transition to an endemic state. The analysis also confirms the presence of a transcritical bifurcation at  $R_0 = 1$ . As  $\beta$  crosses the critical value, the disease-free equilibrium loses stability, and a stable endemic equilibrium emerges, indicating the onset of a sustained epidemic. The dynamic influence of  $E$  is also important. Unlike the standard SIR model analyzed in the midterm project, the SEIR model accounts for the biological delay during disease incubation. This delay creates inertia and prevents a monotonic approach to equilibrium. Mathematically, this indicates the presence of complex eigenvalues in the Jacobian matrix. Geometrically, this manifests as a stable spiral attractor in the phase space. Thus, the project applies key course topics such as stability analysis of high-dimension nonlinear systems, interpretation of the Jacobian, and visualization of phase trajectories.

## Conclusion

The project successfully applied methods for analyzing the SEIR epidemic system model. After formulating the problem as a system of four nonlinear ODEs and applying stability analysis, the conditions for an epidemic outbreak were rigorously determined. The derivation of  $R_0$  provided a precise metric for predicting system behavior. The MATLAB simulations and 3D phase plane analysis confirmed these theoretical findings, demonstrating the methods of applied mathematics in providing predictive insights into complex biological phenomena.

## References

- Hethcote, H. W. "The Mathematics of Infectious Diseases." *SIAM Review*, 2000.
- Kermack, W. O., and McKendrick, A. G. (1927). "A Contribution to the Mathematical Theory of Epidemics." *Proceedings of the Royal Society A*.
- Haberman, R. (1998). *Mathematical Models: Mechanical Vibrations, Population Dynamics, and Traffic Flow*. SIAM.
- Murray, J. D. (2002). *Mathematical Biology: I. An Introduction*. Springer, 3rd Edition.

## Appendix A – MATLAB code

```
clear; close all; clc;
beta = 0.5;
sigma = 0.1;
gamma = 0.1;
mu = 0.01;
R0 = (beta * sigma) / ((sigma + mu) * (gamma + mu));
fprintf('Basic Reproduction Number R0 = %.4f\n', R0);
S0 = 0.90;
E0 = 0.09;
I0 = 0.01;
R0_init = 0;
y0 = [S0 E0 I0 R0_init];
tspan = [0 300];
[t, sol] = ode45(@(t,y) seir_equations(t,y,beta,sigma,gamma,mu), tspan, y0);
S = sol(:,1);
E = sol(:,2);
I = sol(:,3);
R = sol(:,4);
figure;
plot(t, S, 'b', 'LineWidth', 2); hold on;
plot(t, E, 'm', 'LineWidth', 2);
plot(t, I, 'r', 'LineWidth', 2);
plot(t, R, 'g', 'LineWidth', 2);
legend('Susceptible','Exposed (Latent)','Infectious','Recovered');
xlabel('Time');
ylabel('Population Fraction');
title(['SEIR Model Dynamics (R_0 = ' num2str(R0) ')']);
grid on;
figure;
plot3(S, E, I, 'k', 'LineWidth', 1.5);
xlabel('Susceptible');
ylabel('Exposed');
zlabel('Infectious');
title('3D Phase Space Trajectory (S-E-I)');
grid on;
view(45, 30);
beta_vals = 0:0.01:1;
I_star = zeros(size(beta_vals));
threshold_beta = 0;
for k = 1:length(beta_vals)
    b = beta_vals(k);
    R0_curr = (b * sigma) / ((sigma + mu) * (gamma + mu));
    if R0_curr <= 1
        I_star(k) = 0;
    else
```

```

I_star(k) = (mu * (R0_curr - 1)) / b;
end
if abs(R0_curr - 1) < 0.05 && threshold_beta == 0
    threshold_beta = b;
end
end
figure;
plot(beta_vals, I_star, 'b-', 'LineWidth', 2); hold on;
beta_crit = ((sigma + mu) * (gamma + mu)) / sigma;
xline(beta_crit, 'r--', 'LineWidth', 1.5, 'Label', 'R0=1 Threshold');
xlabel('Transmission Rate (\beta)');
ylabel('Endemic Infection Level (I*)');
title('Transcritical Bifurcation Diagram');
grid on;
function dydt = seir_equations(t, y, beta, sigma, gamma, mu)
S = y(1); E = y(2); I = y(3); R = y(4);
dS = mu - beta*S*I - mu*S;
dE = beta*S*I - (sigma + mu)*E;
dI = sigma*E - (gamma + mu)*I;
dR = gamma*I - mu*R;
dydt = [dS; dE; dI; dR];
end

```

## Code 2(Computing eigenvalues)

```

beta = 0.5; sigma = 0.1; gamma = 0.1; mu = 0.01;
R0 = (beta*sigma)/((sigma+mu)*(gamma+mu));
S_star = 1/R0;
I_star = (mu/(gamma+mu)) * (1 - 1/R0);
E_star = (gamma+mu)/sigma * I_star;
J_EE = [ -beta*I_star - mu, 0, -beta*S_star;
         beta*I_star, -(sigma+mu), beta*S_star;
         0, sigma, -(gamma+mu) ];
eigenvalues = eig(J_EE)

```