

Numerical Modeling of Spatiotemporal Epidemic Dynamics: A Reaction–Diffusion SIR System with Stability Analysis

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Abstract

This work investigates a spatial SIR epidemic model with diffusion, described by a system of nonlinear reaction–diffusion equations. The stability of the system is analyzed using the basic reproduction number R_0 , distinguishing between the disease-free ($R_0 < 1$) and endemic ($R_0 > 1$) regimes. For the numerical solution, a finite difference method is used for spatial discretization, while time integration is performed using the explicit Euler method and the Milne predictor–corrector scheme. The Milne method, initialized via Runge–Kutta, provides improved accuracy in capturing transient dynamics. The numerical results confirm convergence to the expected equilibrium states and demonstrate that the proposed methods preserve key qualitative properties such as positivity and boundedness.

1 Introduction

1.1 The Classic SIR Model (Kermack–McKendrick)

The mathematical modeling of infectious diseases began in earnest with the seminal work of W. O. Kermack and A. G. McKendrick in 1927 [5]. They introduced the compartmental SIR model to explain the rapid rise and fall of epidemic outbreaks, such as the plague in Bombay (1905–1906). The SIR system partitions a closed population into three mutually exclusive classes:

- $S(t)$ – Susceptible: individuals who can catch the disease.
- $I(t)$ – Infectious: individuals who have the disease and can transmit it.

- $R(t)$ – Recovered: individuals who are immune and no longer contribute to transmission.

The dynamics are governed by the following ordinary differential equations (ODEs):

$$\begin{aligned}\frac{dS}{dt} &= -\beta \frac{SI}{N}, \\ \frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I, \\ \frac{dR}{dt} &= \gamma I,\end{aligned}\tag{1.1}$$

where $N = S + I + R$ is the total constant population.

Parameters:

- β – transmission rate (rate at which two individuals come into contact and the disease spreads).
- γ – recovery rate ($1/\gamma$ is the mean infectious period).

Motivation for spatial extension. The classical SIR model assumes a well-mixed population, where individuals interact uniformly in space. However, in realistic settings, populations are spatially distributed and individuals move locally. To capture this behavior, diffusion terms are introduced, leading to a system of partial differential equations. This transforms the model from a finite-dimensional dynamical system into an infinite-dimensional one, where the state variables depend on both time and space.

2. SIR System with Diffusion Terms

The classical SIR model assumes perfect mixing – every individual is equally likely to contact any other. In reality, populations are spatially distributed. Pathogens spread through local movement (e.g., infected individuals traveling, rodents dispersing, or airborne particles diffusing).

To incorporate spatial effects, we introduce diffusion terms to the SIR system. The resulting reaction-diffusion model describes how susceptible, infected, and recovered individuals move across a spatial domain $\Omega \subset \mathbb{R}^n$:

In the classical SIR model, the total population satisfies $N = S + I + R$ and remains constant over time. However, when birth and death terms are introduced, this is no longer the case. Indeed,

$$\frac{d}{dt}(S + I + R) = b - d_1(S + I + R),$$

so the total population varies in time and approaches the steady state $N = \frac{b}{d_1}$. Therefore, the reduction $R = N - S - I$ is not valid in the presence of demographic effects.

$$\begin{cases} \frac{\partial S}{\partial t} = d_S \Delta S + b - \beta SI - d_1 S, & t > 0, \mathbf{x} \in \Omega, \\ \frac{\partial I}{\partial t} = d_I \Delta I + \beta SI - \gamma I - d_1 I, & t > 0, \mathbf{x} \in \Omega, \\ \frac{\partial R}{\partial t} = d_R \Delta R + \gamma I - d_1 R, & t > 0, \mathbf{x} \in \Omega, \end{cases} \quad (1.2)$$

where:

- $\Omega \subset \mathbb{R}^n$ is a bounded domain with smooth boundary $\partial\Omega$,
- Δ denotes the Laplacian operator (spatial diffusion),
- $\beta > 0$: transmission rate,
- $\gamma > 0$: recovery rate,
- $b > 0$: birth/recruitment rate (new individuals entering the susceptible class per unit time),
- $d_1 > 0$: natural death rate (assumed equal for all compartments),
- $d_S, d_I, d_R > 0$: diffusion coefficients for susceptible, infectious, and recovered individuals, respectively.

We impose homogeneous Neumann (no-flux) boundary conditions:

$$\frac{\partial S}{\partial \nu} = \frac{\partial I}{\partial \nu} = \frac{\partial R}{\partial \nu} = 0 \quad \text{on } \partial\Omega, \quad (1.3)$$

where ν is the outward unit normal vector. These conditions ensure that no individuals cross the boundary, reflecting a closed population with respect to migration.

Remark on total population. In contrast to the classical SIR model, the inclusion of birth and death terms implies that the total population is no longer constant. Indeed,

$$\frac{d}{dt}(S + I + R) = b - d_1(S + I + R),$$

so the total population varies in time and approaches the steady state $N = \frac{b}{d_1}$. Consequently, the reduction $R = N - S - I$ is not valid in this setting.

2 Equilibrium states and their stability

Before analyzing the stability of SIR model with diffusive terms, it is better to gain the general idea by first considering the stability analysis on the basic SIR model. Since R does not appear in the first two equations and $R = N - S - I$, the system reduces to the two-dimensional system:

$$\begin{aligned}\frac{dS}{dt} &= -\beta \frac{SI}{N}, \\ \frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I.\end{aligned}\tag{2.1}$$

2.1 Equilibrium Points

Let's consider the following definition:

Definition 2.1. *Consider the autonomous differential system*

$$\frac{d\mathbf{X}}{dt} = \mathbf{F}(\mathbf{X}),$$

where $\mathbf{X}(t) \in \mathbb{R}^n$ and $\mathbf{F} : \mathbb{R}^n \rightarrow \mathbb{R}^n$ is a vector field. An **equilibrium solution** (also called a **steady state** or **fixed point**) is a constant solution $\mathbf{X}^*$ satisfying

$$\mathbf{F}(\mathbf{X}^*) = \mathbf{0}.$$

Equilibrium solutions satisfy $\frac{dS}{dt} = 0$ and $\frac{dI}{dt} = 0$. From (2.1):

$$-\beta \frac{SI}{N} = 0,\tag{2.2}$$

$$\beta \frac{SI}{N} - \gamma I = 0.\tag{2.3}$$

From (2.2), the equilibrium equation

$$-\beta \frac{SI}{N} = 0,$$

it follows that $SI = 0$. Since the product of two real numbers is zero if and only if at least one of them is zero, we conclude that either $S = 0$ or $I = 0$. The case $S = 0$ corresponds to a situation where no susceptible individuals remain in the population, meaning that all individuals have already been infected or removed. This scenario is typically unrealistic in epidemiological modeling during the course of an epidemic.

Case 1: $I = 0$. Then (2.3) is automatically satisfied. Thus, any point of the form $(S, 0)$ with $0 \leq S \leq N$ is an equilibrium. These are **disease-free equilibria** (DFE).

For an endemic equilibrium to be biologically meaningful, we require $I^* > 0$. This condition is equivalent to $R_0 = \frac{\beta}{\gamma} > 1$, which ensures that the infection can persist in the population.

Case 2: $I \neq 0$. Then from (2.3):

$$\beta \frac{S}{N} - \gamma = 0 \quad \Rightarrow \quad S = \frac{\gamma N}{\beta}.$$

Substituting into (2.2) gives no further restriction. However, from the reduced system, we also require $I > 0$ and $S + I \leq N$. This yields the **endemic equilibrium**:

$$S^* = \frac{\gamma N}{\beta}, \quad I^* = N - S^* = N \left(1 - \frac{\gamma}{\beta} \right) = N \left(1 - \frac{1}{R_0} \right),$$

where $R_0 = \beta/\gamma$ is the basic reproduction number. Note that $I^* > 0$ if and only if $R_0 > 1$.

2.2 The Basic Reproduction Number

Definition 2.2. *The **basic reproduction number** R_0 is defined as*

$$R_0 = \frac{\beta}{\gamma}.$$

It represents the average number of secondary infections caused by a single infectious individual in a completely susceptible population.

The existence and stability of equilibria are determined by R_0 :

- If $R_0 < 1$: Only the disease-free equilibrium exists.
- If $R_0 > 1$: Both the disease-free and endemic equilibria exist.
- If $R_0 = 1$: A transcritical bifurcation occurs.

2.3 Linearization and Jacobian Matrix

To analyze stability, we linearize the system (2.1) around an equilibrium point (S^*, I^*) . Let

$$u = S - S^*, \quad v = I - I^*,$$

where u and v are small perturbations. The linearized system is

$$\frac{d}{dt} \begin{pmatrix} u \\ v \end{pmatrix} = J(S^*, I^*) \begin{pmatrix} u \\ v \end{pmatrix},$$

where J is the Jacobian matrix:

$$J(S, I) = \begin{pmatrix} \frac{\partial}{\partial S} (-\beta \frac{SI}{N}) & \frac{\partial}{\partial I} (-\beta \frac{SI}{N}) \\ \frac{\partial}{\partial S} (\beta \frac{SI}{N} - \gamma I) & \frac{\partial}{\partial I} (\beta \frac{SI}{N} - \gamma I) \end{pmatrix}.$$

Computing the partial derivatives:

$$\frac{\partial}{\partial S} \left(-\beta \frac{SI}{N} \right) = -\beta \frac{I}{N}, \quad (2.4)$$

$$\frac{\partial}{\partial I} \left(-\beta \frac{SI}{N} \right) = -\beta \frac{S}{N}, \quad (2.5)$$

$$\frac{\partial}{\partial S} \left(\beta \frac{SI}{N} - \gamma I \right) = \beta \frac{I}{N}, \quad (2.6)$$

$$\frac{\partial}{\partial I} \left(\beta \frac{SI}{N} - \gamma I \right) = \beta \frac{S}{N} - \gamma. \quad (2.7)$$

Thus,

$$J(S, I) = \begin{pmatrix} -\beta \frac{I}{N} & -\beta \frac{S}{N} \\ \beta \frac{I}{N} & \beta \frac{S}{N} - \gamma \end{pmatrix}.$$

2.4 Stability of the Disease-Free Equilibrium

At a disease-free equilibrium $(S^*, I^*) = (S_0, 0)$ where $S_0 \in [0, N]$, the Jacobian becomes:

$$J(S_0, 0) = \begin{pmatrix} 0 & -\beta \frac{S_0}{N} \\ 0 & \beta \frac{S_0}{N} - \gamma \end{pmatrix}.$$

Since the Jacobian matrix is lower triangular, its eigenvalues are given by the diagonal entries:

$$\lambda_1 = 0, \quad \lambda_2 = \beta \frac{S_0}{N} - \gamma.$$

The zero eigenvalue reflects the fact that there is not a single disease-free equilibrium, but

rather a continuum of equilibria forming the line $I = 0$. Therefore, perturbations along this direction neither grow nor decay, leading to neutral stability. The stability in the I -direction is determined by λ_2 :

- If $\lambda_2 < 0$, i.e., $\beta S_0/N < \gamma$ or $S_0 < \gamma N/\beta$, perturbations in I decay.
- If $\lambda_2 > 0$, i.e., $S_0 > \gamma N/\beta$, perturbations in I grow.

For the biologically relevant case where the initial susceptible population is the total population $S_0 = N$ (before disease introduction), we have:

$$\lambda_2 = \beta - \gamma = \gamma(R_0 - 1).$$

Theorem 2.1 (Stability of the Disease-Free Equilibrium). *Consider the SIR model (2.1) with initial condition $(S(0), I(0)) = (N, I_0)$ where $I_0 > 0$ is small.*

- If $R_0 < 1$, then $\lambda_2 < 0$ and the disease-free equilibrium is **stable**. The disease dies out.
- If $R_0 > 1$, then $\lambda_2 > 0$ and the disease-free equilibrium is **unstable**. The disease invades the population.

2.5 Stability of the Endemic Equilibrium

The endemic equilibrium exists only when $R_0 > 1$ and is given by:

$$S^* = \frac{N}{R_0}, \quad I^* = N \left(1 - \frac{1}{R_0} \right).$$

Evaluating the Jacobian at (S^*, I^*) :

$$J(S^*, I^*) = \begin{pmatrix} -\beta \frac{I^*}{N} & -\beta \frac{S^*}{N} \\ \beta \frac{I^*}{N} & \beta \frac{S^*}{N} - \gamma \end{pmatrix}.$$

Substitute $S^* = N/R_0$ and $I^* = N(1 - 1/R_0)$:

$$\beta \frac{S^*}{N} = \beta \cdot \frac{1}{R_0} = \frac{\beta}{R_0} = \gamma,$$

since $R_0 = \beta/\gamma$. Also,

$$\beta \frac{I^*}{N} = \beta \left(1 - \frac{1}{R_0} \right) = \beta - \frac{\beta}{R_0} = \beta - \gamma.$$

Thus,

$$J^* = \begin{pmatrix} -(\beta - \gamma) & -\gamma \\ \beta - \gamma & 0 \end{pmatrix}.$$

The trace and determinant are:

$$\text{tr}(J^*) = -(\beta - \gamma) = -\gamma(R_0 - 1), \quad (2.8)$$

$$\det(J^*) = 0 \cdot (-(\beta - \gamma)) - (-\gamma)(\beta - \gamma) = \gamma(\beta - \gamma) = \gamma^2(R_0 - 1). \quad (2.9)$$

The eigenvalues satisfy the characteristic equation:

$$\lambda^2 - \text{tr}(J^*)\lambda + \det(J^*) = 0,$$

which gives:

$$\lambda^2 + \gamma(R_0 - 1)\lambda + \gamma^2(R_0 - 1) = 0.$$

For $R_0 > 1$, we have $\text{tr}(J^*) < 0$ and $\det(J^*) > 0$. Both eigenvalues have negative real parts, implying:

Theorem 2.2 (Stability of the Endemic Equilibrium). *For $R_0 > 1$, the endemic equilibrium $(S^*, I^*) = \left(\frac{N}{R_0}, N\left(1 - \frac{1}{R_0}\right)\right)$ is **locally asymptotically stable**. That is, small perturbations decay, and the disease persists at an endemic level.*

The stability analysis reveals that the basic reproduction number R_0 serves as a threshold parameter:

R_0	Disease-Free Equilibrium	Endemic Equilibrium
$R_0 < 1$	Stable	Does not exist
$R_0 = 1$	Transcritical bifurcation	Emerges
$R_0 > 1$	Unstable	Stable

Table 1: Summary of equilibrium stability for the SIR model.

This threshold behavior is fundamental to epidemiological theory: if $R_0 < 1$, in models with demographic effects, the disease may persist and approach a stable endemic equilibrium where a fraction of the population remains infected indefinitely (in the absence of interventions).

3 Equilibrium points and Stability Analysis of SIR system with diffusion

3.1 Equilibrium Points

An equilibrium is a state of the system in which all time derivatives are set to zero, meaning that the spread of the infection no longer changes over time. In other words, the number of infected individuals remains constant, neither increasing nor decreasing. Studying equilibrium points is essential for understanding the long-term behavior of the epidemic. If the equilibrium level of infection is zero or very small, the disease eventually dies out. In contrast, if the equilibrium corresponds to a positive number of infected individuals, the disease persists in the population, leading to an endemic state.

To find equilibrium points, we neglect spatial variation (i.e., $\Delta S = \Delta I = \Delta R = 0$) and set time derivatives equal to zero:

$$\frac{\partial S}{\partial t} = 0, \quad \frac{\partial I}{\partial t} = 0, \quad \frac{\partial R}{\partial t} = 0.$$

This gives the algebraic system:

$$0 = b - \beta SI - d_1 S, \tag{E1}$$

$$0 = \beta SI - (\gamma + d_1)I, \tag{E2}$$

$$0 = \gamma I - d_1 R. \tag{E3}$$

Disease-Free Equilibrium (DFE)

From equation (E2), we have:

$$I(\beta S - (\gamma + d_1)) = 0.$$

The disease-free case corresponds to:

$$I = 0.$$

Substituting $I = 0$ into (E1):

$$0 = b - d_1 S \quad \Rightarrow \quad S^* = \frac{b}{d_1}.$$

Substituting $I = 0$ into (E3):

$$0 = -d_1 R \quad \Rightarrow \quad R^* = 0.$$

Thus, the disease-free equilibrium is:

$$E_{df} = \left(\frac{b}{d_1}, 0, 0 \right).$$

Endemic Equilibrium

For the endemic case, we assume $I \neq 0$. Then from (E2):

$$\beta S = \gamma + d_1 \quad \Rightarrow \quad S^* = \frac{\gamma + d_1}{\beta}.$$

Substitute S^* into (E1):

$$0 = b - \beta S^* I - d_1 S^*.$$

Using $\beta S^* = \gamma + d_1$, we get:

$$0 = b - (\gamma + d_1) I - d_1 S^*.$$

Solve for I :

$$(\gamma + d_1) I = b - d_1 S^*$$

$$I^* = \frac{b - d_1 S^*}{\gamma + d_1}.$$

Substitute $S^* = \frac{\gamma + d_1}{\beta}$:

$$I^* = \frac{b - d_1 \frac{\gamma + d_1}{\beta}}{\gamma + d_1} = \frac{b\beta - d_1(\gamma + d_1)}{\beta(\gamma + d_1)}.$$

Now from (E3):

$$R^* = \frac{\gamma}{d_1} I^*.$$

Thus,

$$R^* = \frac{\gamma}{d_1} \cdot \frac{b\beta - d_1(\gamma + d_1)}{\beta(\gamma + d_1)}.$$

Endemic Equilibrium Point

$$E_e = \left(\frac{\gamma + d_1}{\beta}, \frac{b\beta - d_1(\gamma + d_1)}{\beta(\gamma + d_1)}, \frac{\gamma}{d_1} \cdot \frac{b\beta - d_1(\gamma + d_1)}{\beta(\gamma + d_1)} \right).$$

3.2 Stability of disease-free equilibrium point

Stability of the disease-free equilibrium.

The Jacobian matrix evaluated at the disease-free equilibrium $E_{df} = \left(\frac{b}{d_1}, 0, 0 \right)$ is given by

$$J(E_{df}) = \begin{bmatrix} -d_1 & -\beta \frac{b}{d_1} & 0 \\ 0 & \beta \frac{b}{d_1} - (\gamma + d_1) & 0 \\ 0 & \gamma & -d_1 \end{bmatrix}. \quad (3.1)$$

The eigenvalues are

$$\lambda_1 = -d_1, \quad \lambda_2 = \beta \frac{b}{d_1} - (\gamma + d_1), \quad \lambda_3 = -d_1.$$

Thus, the disease-free equilibrium is locally asymptotically stable if

$$\beta \frac{b}{d_1} < \gamma + d_1.$$

Defining the basic reproduction number

$$R_0 = \frac{\beta b}{d_1(\gamma + d_1)},$$

we conclude that the disease-free equilibrium is stable if $R_0 < 1$ and unstable if $R_0 > 1$.

3.3 Stability of endemic equilibrium point

To analyze the stability of the equilibrium points, we consider small perturbations around the equilibrium state. Let the equilibrium point be denoted by (S^*, I^*) . We introduce small perturbations $s(t, \mathbf{x})$ and $i(t, \mathbf{x})$ such that:

$$S(t, \mathbf{x}) = S^* + s(t, \mathbf{x}), \quad I(t, \mathbf{x}) = I^* + i(t, \mathbf{x}), \quad (3.2)$$

Remark on notation. Here, $S(t, \mathbf{x})$ and $I(t, \mathbf{x})$ denote the full state variables, while $s(t, \mathbf{x})$ and $i(t, \mathbf{x})$ represent small perturbations around the equilibrium. Later, coefficients such as S_k and I_k will denote Fourier mode amplitudes corresponding to spatial wave number k .

where $|s| \ll 1$ and $|i| \ll 1$. Substituting these expressions into the diffusive SIR system with demographics:

$$\begin{cases} \frac{\partial S}{\partial t} = d_S \Delta S + b - \beta SI - d_1 S, \\ \frac{\partial I}{\partial t} = d_I \Delta I + \beta SI - \gamma I - d_1 I, \end{cases} \quad (3.3)$$

we linearize the system by neglecting higher-order terms. Since $|s| \ll 1$ and $|i| \ll 1$, the product si is of second order and therefore much smaller than the linear terms. Hence, terms like si are neglected in the linear approximation.

Substituting $S = S^* + s$ and $I = I^* + i$ into the S equation:

$$\frac{\partial(S^* + s)}{\partial t} = d_S \Delta(S^* + s) + b - \beta(S^* + s)(I^* + i) - d_1(S^* + s). \quad (3.4)$$

Since S^* and I^* are constants, $\partial S^*/\partial t = 0$ and $\Delta S^* = 0$. Expanding the nonlinear term:

$$(S^* + s)(I^* + i) = S^* I^* + S^* i + s I^* + si. \quad (3.5)$$

The term si is nonlinear (product of perturbations) and will be neglected in the linearization. Thus, equation (3.4) becomes:

$$\frac{\partial s}{\partial t} = d_S \Delta s + b - \beta(S^* I^* + S^* i + s I^*) - d_1 S^* - d_1 s. \quad (3.6)$$

At equilibrium, the steady-state conditions satisfy:

$$b - \beta S^* I^* - d_1 S^* = 0. \quad (3.7)$$

Using this to simplify, we obtain:

$$\begin{aligned} \frac{\partial s}{\partial t} &= d_S \Delta s + b - \beta S^* I^* - \beta S^* i - \beta I^* s - d_1 S^* - d_1 s \\ &= d_S \Delta s + b - \beta S^* I^* - d_1 S^* - \beta S^* i - \beta I^* s - d_1 s \\ &= d_S \Delta s - (\beta I^* + d_1) s - \beta S^* i. \end{aligned} \quad (3.8)$$

Therefore, the linearized S equation can be written as:

$$\frac{\partial s}{\partial t} = a_{11}s + a_{12}i + d_S \Delta s, \quad (3.9)$$

where the coefficients are defined as:

$$\boxed{a_{11} = -(\beta I^* + d_1)}, \quad \boxed{a_{12} = -\beta S^*}. \quad (3.10)$$

Now substitute $S = S^* + s$ and $I = I^* + i$ into the I equation:

$$\frac{\partial(I^* + i)}{\partial t} = d_I \Delta(I^* + i) + \beta(S^* + s)(I^* + i) - \gamma(I^* + i) - d_1(I^* + i). \quad (3.11)$$

Again, $\partial I^*/\partial t = 0$ and $\Delta I^* = 0$. Expanding the nonlinear term and neglecting the product si :

$$(S^* + s)(I^* + i) = S^* I^* + S^* i + s I^* + si. \quad (3.12)$$

Thus:

$$\begin{aligned} \frac{\partial i}{\partial t} &= d_I \Delta i + \beta(S^* I^* + S^* i + s I^*) - \gamma I^* - \gamma i - d_1 I^* - d_1 i \\ &= d_I \Delta i + \beta S^* I^* + \beta S^* i + \beta I^* s - \gamma I^* - \gamma i - d_1 I^* - d_1 i. \end{aligned} \quad (3.13)$$

At equilibrium, the steady-state condition for I gives:

$$\beta S^* I^* - \gamma I^* - d_1 I^* = 0 \quad \Rightarrow \quad \beta S^* I^* = (\gamma + d_1) I^*. \quad (3.14)$$

Using this to simplify equation (3.13):

$$\begin{aligned} \frac{\partial i}{\partial t} &= d_I \Delta i + \beta S^* I^* + \beta S^* i + \beta I^* s - \gamma I^* - \gamma i - d_1 I^* - d_1 i \\ &= d_I \Delta i + \beta S^* I^* + \beta S^* i + \beta I^* s - (\gamma + d_1) I^* - (\gamma + d_1) i \\ &= d_I \Delta i + \beta S^* i + \beta I^* s - (\gamma + d_1) I^* + \beta S^* I^* - (\gamma + d_1) i \\ &= d_I \Delta i + \beta I^* s + [\beta S^* - (\gamma + d_1)] i. \end{aligned} \quad (3.15)$$

Therefore, the linearized I equation can be written as:

$$\frac{\partial i}{\partial t} = a_{21} s + a_{22} i + d_I \Delta i, \quad (3.16)$$

where the coefficients are defined as:

$$\boxed{a_{21} = \beta I^*}, \quad \boxed{a_{22} = \beta S^* - \gamma - d_1}. \quad (3.17)$$

Collecting the linearized equations, we obtain the following system:

$$\begin{cases} \frac{\partial s}{\partial t} = a_{11}s + a_{12}i + d_S \Delta s, \\ \frac{\partial i}{\partial t} = a_{21}s + a_{22}i + d_I \Delta i, \end{cases} \quad (3.18)$$

where the coefficients a_{ij} are given by:

$$\boxed{\begin{aligned} a_{11} &= -(\beta I^* + d_1), \\ a_{12} &= -\beta S^*, \\ a_{21} &= \beta I^*, \\ a_{22} &= \beta S^* - \gamma - d_1. \end{aligned}} \quad (3.19)$$

These coefficients depend on the equilibrium point (S^*, I^*) under consideration.

Restriction to one-dimensional domain. For simplicity, we restrict the spatial domain to the one-dimensional interval $\Omega = (0, L) \subset \mathbb{R}$. In this case, the Laplacian reduces to the second derivative with respect to x , and the eigenfunctions satisfying Neumann boundary conditions are cosine functions. For a bounded domain Ω with homogeneous Neumann (no-flux) boundary conditions:

$$\frac{\partial S}{\partial \nu} = \frac{\partial I}{\partial \nu} = 0 \quad \text{on } \partial\Omega, \quad (3.20)$$

the appropriate eigenfunctions of the Laplacian are cosine functions. Thus, representing the solutions in the form of Fourier expansion: [2, 6]:

$$S(t, x) = \sum_k S_k e^{\lambda t} \cos(kx), \quad I(t, x) = \sum_k I_k e^{\lambda t} \cos(kx), \quad (3.21)$$

where:

- λ is the growth rate of perturbations. The stability of the equilibrium is determined by the sign of $\text{Re}(\lambda)$: if $\text{Re}(\lambda) < 0$, perturbations decay; if $\text{Re}(\lambda) > 0$, perturbations grow,
- k is the wavenumber, given by $k = \frac{n\pi}{L}$ for $n = 0, 1, 2, \dots$ on a domain of length L ,
- $\cos(kx)$ satisfies the Neumann boundary conditions: $\frac{d}{dx} \cos(kx) = -k \sin(kx) = 0$ at the boundaries.

The spatial derivatives (Laplacian) are computed as:

$$\Delta S = \frac{\partial^2 S}{\partial x^2} = \sum_k S_k e^{\lambda t} \cdot (-k^2) \cos(kx), \quad \Delta I = \sum_k I_k e^{\lambda t} \cdot (-k^2) \cos(kx). \quad (3.22)$$

Substituting (3.21) and (3.22) into the linearized system:

$$\begin{cases} \frac{\partial S}{\partial t} = a_{11}S + a_{12}I + d_S \Delta S, \\ \frac{\partial I}{\partial t} = a_{21}S + a_{22}I + d_I \Delta I, \end{cases} \quad (3.23)$$

we obtain:

$$\begin{aligned} \sum_k \lambda S_k e^{\lambda t} \cos(kx) &= a_{11} \sum_k S_k e^{\lambda t} \cos(kx) + a_{12} \sum_k I_k e^{\lambda t} \cos(kx) \\ &\quad + d_S \sum_k S_k e^{\lambda t} (-k^2) \cos(kx). \end{aligned} \quad (3.24)$$

Rearranging terms:

$$\sum_k (a_{11} - d_S k^2 - \lambda) S_k e^{\lambda t} \cos(kx) + \sum_k a_{12} I_k e^{\lambda t} \cos(kx) = 0. \quad (3.25)$$

Since the cosine functions $\{\cos(kx)\}$ form an orthogonal basis under Neumann boundary conditions, each mode must satisfy the equation independently, the coefficients for each k must vanish, yielding:

$$(a_{11} - d_S k^2 - \lambda) S_k + a_{12} I_k = 0. \quad (3.26)$$

Similarly, for the I equation:

$$\begin{aligned} \sum_k \lambda I_k e^{\lambda t} \cos(kx) &= a_{21} \sum_k S_k e^{\lambda t} \cos(kx) + a_{22} \sum_k I_k e^{\lambda t} \cos(kx) \\ &\quad + d_I \sum_k I_k e^{\lambda t} (-k^2) \cos(kx). \end{aligned} \quad (3.27)$$

Rearranging:

$$\sum_k a_{21} S_k e^{\lambda t} \cos(kx) + \sum_k (a_{22} - d_I k^2 - \lambda) I_k e^{\lambda t} \cos(kx) = 0. \quad (3.28)$$

Thus, for each mode k :

$$a_{21}S_k + (a_{22} - d_I k^2 - \lambda) I_k = 0. \quad (3.29)$$

Equations (3.26) and (3.29) form a homogeneous linear system for each wavenumber k :

$$\begin{cases} (a_{11} - d_S k^2 - \lambda) S_k + a_{12} I_k = 0, \\ a_{21} S_k + (a_{22} - d_I k^2 - \lambda) I_k = 0. \end{cases} \quad (3.30)$$

This can be written in matrix form as:

$$\begin{bmatrix} a_{11} - d_S k^2 - \lambda & a_{12} \\ a_{21} & a_{22} - d_I k^2 - \lambda \end{bmatrix} \begin{bmatrix} S_k \\ I_k \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}. \quad (3.31)$$

The system (3.31) is a homogeneous linear system. Such a system admits nontrivial solutions $(S_k, I_k) \neq (0, 0)$ if and only if the determinant of the coefficient matrix is zero.

For nontrivial solutions $(S_k, I_k) \neq (0, 0)$, the determinant of the variational matrix must be zero:

$$\det \begin{pmatrix} a_{11} - d_S k^2 - \lambda & a_{12} \\ a_{21} & a_{22} - d_I k^2 - \lambda \end{pmatrix} = 0. \quad (3.32)$$

Expanding the determinant gives the characteristic equation:

$$(a_{11} - d_S k^2 - \lambda) (a_{22} - d_I k^2 - \lambda) - a_{12} a_{21} = 0. \quad (3.33)$$

This expands to the quadratic dispersion relation:

$$\lambda^2 + \xi_1(k)\lambda + \xi_2(k) = 0, \quad (3.34)$$

where:

$$\xi_1(k) = d_S k^2 + d_I k^2 - (a_{11} + a_{22}), \quad (3.35)$$

$$\xi_2(k) = (d_S k^2 - a_{11})(d_I k^2 - a_{22}) - a_{12} a_{21}. \quad (3.36)$$

This relation is called the dispersion relation and determines how perturbations with wave number k evolve in time through the growth rate λ .

The stability of the system is determined by the roots of the characteristic equation (3.34).

In particular, the equilibrium is said to be *locally asymptotically stable* if all eigenvalues λ have negative real parts.

For a quadratic polynomial of the form:

$$\lambda^2 + a_1\lambda + a_2 = 0,$$

the Routh–Hurwitz criterion states that all roots have negative real parts if and only if [3]:

$$a_1 > 0 \quad \text{and} \quad a_2 > 0. \quad (3.37)$$

Applying this result to equation (3.34), we obtain the following stability conditions:

$$\xi_1(k) > 0, \quad \xi_2(k) > 0. \quad (3.38)$$

The first condition:

$$\xi_1(k) = (d_S + d_I)k^2 - (a_{11} + a_{22}) > 0, \quad (3.39)$$

ensures that the sum of eigenvalues has a negative real part. The second condition:

$$\xi_2(k) = (d_S k^2 - a_{11})(d_I k^2 - a_{22}) - a_{12}a_{21} > 0, \quad (3.40)$$

ensures that the product of eigenvalues is positive, preventing the existence of a positive real eigenvalue.

Unlike ordinary differential equation systems, the stability conditions here depend on the spatial wave number k . Therefore, stability must be verified for all admissible values of k .

- If conditions (3.38) hold for all k , the equilibrium is stable.
- If there exists some k such that $\xi_1(k) > 0$ but $\xi_2(k) < 0$, then at least one eigenvalue has a positive real part, and the system becomes unstable.

When $k = 0$, the system reduces to the non-spatial (ODE) case:

$$\xi_1(0) = -(a_{11} + a_{22}), \quad (3.41)$$

$$\xi_2(0) = a_{11}a_{22} - a_{12}a_{21}. \quad (3.42)$$

These correspond to the classical stability conditions for the Jacobian matrix of the reaction system without diffusion.

The presence of diffusion introduces the terms $d_S k^2$ and $d_I k^2$, which may alter stability. In particular, it is possible for the system to be stable at $k = 0$ but unstable for some $k > 0$. This phenomenon is known as *diffusion-driven instability* or *Turing instability*.

Thus, the Routh–Hurwitz criterion provides a simple and effective way to determine stability by checking the positivity of the coefficients $\xi_1(k)$ and $\xi_2(k)$ for all relevant spatial modes.

4 Basic Reproduction Number

In this section, we derive the basic reproduction number R_0 for the reaction–diffusion epidemic system

$$\frac{\partial S}{\partial t} = d_S \Delta S + b - \beta SI - d_1 S, \quad (4.1)$$

$$\frac{\partial I}{\partial t} = d_I \Delta I + \beta SI - (\gamma + d_1) I. \quad (4.2)$$

The basic reproduction number R_0 represents the average number of secondary infections generated by a single infected individual introduced into a completely susceptible population.

To derive R_0 , we consider the spatially homogeneous case (i.e., neglecting diffusion terms) and analyze the behavior near the disease-free equilibrium. Setting the time derivatives to zero and assuming $I = 0$, we obtain

$$S^* = \frac{b}{d_1}.$$

Substituting $S = S^*$ into the equation for I , we obtain

$$\frac{dI}{dt} = \left(\beta \frac{b}{d_1} - (\gamma + d_1) \right) I.$$

The infection will grow if the coefficient of I is positive. This motivates the definition of the basic reproduction number as

$$R_0 = \frac{\beta \frac{b}{d_1}}{\gamma + d_1}.$$

Hence, we obtain the expression

$$\boxed{R_0 = \frac{\beta b}{d_1(\gamma + d_1)}}. \quad (4.3)$$

The value of R_0 determines the qualitative behavior of the system. In particular,

- if $R_0 < 1$, the infection cannot invade the population and the disease-free equilibrium is locally asymptotically stable;
- if $R_0 > 1$, the infection persists and an endemic equilibrium exists.

Indeed, for the endemic equilibrium to exist (i.e., $I^* > 0$), it is required that

$$b\beta - d_1(\gamma + d_1) > 0,$$

which is equivalent to the condition $R_0 > 1$.

5 Numerical Methods and Analysis

In this section, we develop a finite difference method (FDM) to numerically approximate the solutions of the diffusive SIR system.

Recall the diffusive SIR model with demographic processes:

$$\begin{cases} \frac{\partial S}{\partial t} = d_S \Delta S + b - \beta SI - d_1 S, & t > 0, x \in [0, L], \\ \frac{\partial I}{\partial t} = d_I \Delta I + \beta SI - \gamma I - d_1 I, & t > 0, x \in [0, L], \\ \frac{\partial R}{\partial t} = d_R \Delta R + \gamma I - d_1 R, & t > 0, x \in [0, L], \end{cases} \quad (5.1)$$

with homogeneous Neumann (no-flux) boundary conditions:

$$\frac{\partial S}{\partial x}(t, 0) = \frac{\partial S}{\partial x}(t, L) = 0, \quad \frac{\partial I}{\partial x}(t, 0) = \frac{\partial I}{\partial x}(t, L) = 0, \quad \frac{\partial R}{\partial x}(t, 0) = \frac{\partial R}{\partial x}(t, L) = 0, \quad (5.2)$$

and initial conditions:

$$S(0, x) = S_0(x), \quad I(0, x) = I_0(x), \quad R(0, x) = R_0(x), \quad x \in [0, L]. \quad (5.3)$$

5.1 Spatial Discretization

This section presents the space discretization of model (2.1). The computational domain is partitioned into a two-dimensional grid in time and space, with spatial step size defined as

$$\Delta x = \frac{L}{N} \quad (5.4)$$

along the x -axis and temporal step size as

$$\Delta t = \frac{T}{K}. \quad (5.5)$$

The grid points are given by

$$x_i = i\Delta x, \quad i = 0, 1, 2, \dots, N, \quad (5.6)$$

and

$$t_n = n\Delta t, \quad n = 0, 1, 2, \dots, K, \quad (5.7)$$

denoted as (x_i, t_n) .

Spatial discretization is carried out using the finite difference method, which yields the following semi-discrete formulation:

$$\begin{cases} \frac{dS_i}{dt} = \frac{d_S}{(\Delta x)^2} (S_{i+1} - 2S_i + S_{i-1}) + b - \beta S_i I_i - d_1 S_i, \\ \frac{dI_i}{dt} = \frac{d_I}{(\Delta x)^2} (I_{i+1} - 2I_i + I_{i-1}) + \beta S_i I_i - \gamma I_i - d_1 I_i. \end{cases} \quad (5.8)$$

5.2 Temporal Discretization

After performing the spatial discretization, we obtain a system of ordinary differential equations in time. To fully discretize the system, we now approximate the time derivatives using the forward difference scheme.

For each grid point $i = 0, 1, \dots, N$ and time level $t_n = n\Delta t$, we introduce the approximations:

$$\frac{dS_i}{dt} \approx \frac{S_i^{n+1} - S_i^n}{\Delta t}, \quad \frac{dI_i}{dt} \approx \frac{I_i^{n+1} - I_i^n}{\Delta t}. \quad (5.9)$$

Substituting these expressions into the semi-discrete system (64), we obtain the fully discrete scheme:

$$\begin{cases} \frac{S_i^{n+1} - S_i^n}{\Delta t} = \frac{d_S}{(\Delta x)^2} (S_{i+1}^n - 2S_i^n + S_{i-1}^n) + b - \beta S_i^n I_i^n - d_1 S_i^n, \\ \frac{I_i^{n+1} - I_i^n}{\Delta t} = \frac{d_I}{(\Delta x)^2} (I_{i+1}^n - 2I_i^n + I_{i-1}^n) + \beta S_i^n I_i^n - \gamma I_i^n - d_1 I_i^n. \end{cases} \quad (5.10)$$

Rearranging the above equations, we obtain the explicit update formulas:

$$\begin{cases} S_i^{n+1} = S_i^n + \Delta t \left[\frac{d_S}{(\Delta x)^2} (S_{i+1}^n - 2S_i^n + S_{i-1}^n) + b - \beta S_i^n I_i^n - d_1 S_i^n \right], \\ I_i^{n+1} = I_i^n + \Delta t \left[\frac{d_I}{(\Delta x)^2} (I_{i+1}^n - 2I_i^n + I_{i-1}^n) + \beta S_i^n I_i^n - \gamma I_i^n - d_1 I_i^n \right]. \end{cases} \quad (5.11)$$

This scheme provides the numerical approximation of the system at each time step t_{n+1} using the known values at time t_n .

5.3 Stability Analysis

We study the stability of the proposed finite difference scheme using the Von Neumann method [7].

Von Neumann Stability Criterion. A finite difference scheme is said to be stable if, for a Fourier mode of the form

$$u_i^n = f(t^n) e^{i\xi x_i},$$

the amplification factor satisfies

$$\left| \frac{f(t + \Delta t)}{f(t)} \right| \leq 1 + \chi \Delta t,$$

where χ is a constant independent of Δt .

Assume a Fourier expansion of the form

$$S_i^n = f(t) e^{i\xi x_i}, \quad I_i^n = f(t) e^{i\xi x_i}.$$

After substitution into the scheme, the amplification factor satisfies

$$\left| \frac{f(t + \Delta t)}{f(t)} \right|^2 \leq 1 + \chi \Delta t,$$

where χ is a constant.

Theorem 5.1. *If*

$$\left| -\frac{4d_S \Delta t}{(\Delta x)^2} \sin^2 \left(\frac{\xi h}{2} \right) + (1 - d_1 \Delta t) \right| \leq 1$$

and

$$\left| -\frac{4d_I \Delta t}{(\Delta x)^2} \sin^2 \left(\frac{\xi h}{2} \right) + (1 - (d_1 + \gamma) \Delta t) \right| \leq 1,$$

then the proposed finite difference scheme is stable with $(n+1)\Delta t = T$.

Proof. Consider

$$S_i^{n+1} = \frac{d_S \Delta t}{(\Delta x)^2} (S_{i+1}^n - 2S_i^n + S_{i-1}^n) + (1 - d_1 \Delta t) S_i^n.$$

Substituting

$$S_i^n = f(t) e^{i\xi x_i},$$

we obtain

$$f(t + \Delta t) e^{i\xi x_i} = \frac{d_S \Delta t}{(\Delta x)^2} (e^{i\xi(x_i+h)} + e^{i\xi(x_i-h)} - 2e^{i\xi x_i}) f(t) + (1 - d_1 \Delta t) f(t) e^{i\xi x_i}.$$

Factoring out $f(t) e^{i\xi x_i}$ gives

$$\frac{f(t + \Delta t)}{f(t)} = \frac{d_S \Delta t}{(\Delta x)^2} (e^{i\xi h} + e^{-i\xi h} - 2) + (1 - d_1 \Delta t).$$

Using

$$e^{i\xi h} + e^{-i\xi h} = 2 \cos(\xi h),$$

we get

$$\frac{f(t + \Delta t)}{f(t)} = \frac{d_S \Delta t}{(\Delta x)^2} (2 \cos(\xi h) - 2) + (1 - d_1 \Delta t).$$

Using the identity

$$\cos(\theta) = 1 - 2 \sin^2 \left(\frac{\theta}{2} \right),$$

we obtain

$$\frac{f(t + \Delta t)}{f(t)} = -\frac{4d_S \Delta t}{(\Delta x)^2} \sin^2 \left(\frac{\xi h}{2} \right) + (1 - d_1 \Delta t).$$

Thus,

$$\left| \frac{f(t + \Delta t)}{f(t)} \right| = \left| -\frac{4d_S \Delta t}{(\Delta x)^2} \sin^2 \left(\frac{\xi h}{2} \right) + (1 - d_1 \Delta t) \right|.$$

Similarly,

$$I_i^{n+1} = \frac{d_I \Delta t}{(\Delta x)^2} (I_{i+1}^n - 2I_i^n + I_{i-1}^n) + (1 - (d_1 + \gamma) \Delta t) I_i^n.$$

Proceeding in the same way, we obtain

$$\left| \frac{f(t + \Delta t)}{f(t)} \right| = \left| -\frac{4d_I \Delta t}{(\Delta x)^2} \sin^2 \left(\frac{\xi h}{2} \right) + (1 - (d_1 + \gamma) \Delta t) \right|.$$

Conclusion.

If

$$\left| -\frac{4d_S\Delta t}{(\Delta x)^2} \sin^2\left(\frac{\xi h}{2}\right) + (1 - d_1\Delta t) \right| \leq 1$$

and

$$\left| -\frac{4d_I\Delta t}{(\Delta x)^2} \sin^2\left(\frac{\xi h}{2}\right) + (1 - (d_1 + \gamma)\Delta t) \right| \leq 1,$$

then

$$\left| \frac{f(t + \Delta t)}{f(t)} \right| \leq 1,$$

which proves the stability of the scheme. □

5.4 Consistency Analysis

We analyze the consistency of the proposed finite difference scheme by comparing it with the continuous system using Taylor series expansion [8].

Definition (Consistency). A finite difference scheme is said to be consistent if the local truncation error tends to zero as $\Delta t, \Delta x \rightarrow 0$, i.e., the scheme approximates the original PDE.

Theorem 5.2. *The proposed finite difference scheme for the system is consistent with the corresponding partial differential equations.*

Proof. We illustrate the consistency for the S -equation. The same arguments apply to the I -equation.

Consider the continuous equation

$$\frac{\partial S}{\partial t} = d_S \frac{\partial^2 S}{\partial x^2} + (\text{reaction terms}).$$

The corresponding finite difference scheme is

$$\frac{S_i^{n+1} - S_i^n}{\Delta t} = d_S \frac{S_{i+1}^n - 2S_i^n + S_{i-1}^n}{(\Delta x)^2} + (\text{reaction terms}).$$

Expanding S_i^{n+1} about (x_i, t^n) , we obtain

$$S_i^{n+1} = S_i^n + \frac{\partial S}{\partial t} \Delta t + \frac{\partial^2 S}{\partial t^2} \frac{(\Delta t)^2}{2} + \mathcal{O}((\Delta t)^3).$$

Thus,

$$\frac{S_i^{n+1} - S_i^n}{\Delta t} = \frac{\partial S}{\partial t} + \frac{\partial^2 S}{\partial t^2} \frac{\Delta t}{2} + \mathcal{O}((\Delta t)^2).$$

Expanding S_{i+1}^n and S_{i-1}^n , we get

$$S_{i+1}^n = S_i^n + \frac{\partial S}{\partial x} \Delta x + \frac{\partial^2 S}{\partial x^2} \frac{(\Delta x)^2}{2} + \frac{\partial^3 S}{\partial x^3} \frac{(\Delta x)^3}{6} + \mathcal{O}((\Delta x)^4),$$

$$S_{i-1}^n = S_i^n - \frac{\partial S}{\partial x} \Delta x + \frac{\partial^2 S}{\partial x^2} \frac{(\Delta x)^2}{2} - \frac{\partial^3 S}{\partial x^3} \frac{(\Delta x)^3}{6} + \mathcal{O}((\Delta x)^4).$$

Adding these expansions:

$$S_{i+1}^n - 2S_i^n + S_{i-1}^n = \frac{\partial^2 S}{\partial x^2} (\Delta x)^2 + \mathcal{O}((\Delta x)^4).$$

Thus,

$$\frac{S_{i+1}^n - 2S_i^n + S_{i-1}^n}{(\Delta x)^2} = \frac{\partial^2 S}{\partial x^2} + \mathcal{O}((\Delta x)^2).$$

Substituting the expansions into the finite difference scheme:

$$\frac{\partial S}{\partial t} + \frac{\partial^2 S}{\partial t^2} \frac{\Delta t}{2} + \mathcal{O}((\Delta t)^2) = d_S \left(\frac{\partial^2 S}{\partial x^2} + \mathcal{O}((\Delta x)^2) \right) + (\text{reaction terms}).$$

Rearranging, we obtain

$$\frac{\partial S}{\partial t} = d_S \frac{\partial^2 S}{\partial x^2} + (\text{reaction terms}) + \mathcal{O}(\Delta t) + \mathcal{O}((\Delta x)^2).$$

As $\Delta t \rightarrow 0$ and $\Delta x \rightarrow 0$, the truncation error vanishes, and the finite difference scheme converges to the original PDE. Hence, the scheme is consistent.

The same analysis applies to the I -equation, which completes the proof. □

5.5 Numerical Results and Discussion

In this section, we present the numerical results obtained by applying the implicit finite difference scheme to the diffusive SIR model with demographic processes. The simulations are performed on a one-dimensional domain of length $L = 5.0$ with homogeneous Neumann boundary conditions. The parameters used in the simulation are summarized in Table 2.

The basic reproduction number R_0 is a crucial threshold parameter that determines the long-term dynamics of the epidemic. For our model, R_0 is given by:

Parameter	Description	Value
L	Domain length	5.0
T	Total simulation time	1200.0
N_x	Number of spatial grid points	100
d_S	Diffusion coefficient for susceptible	0.1
d_I	Diffusion coefficient for infected	0.05
β	Transmission rate	0.8
γ	Recovery rate	0.8
d_1	Natural death rate	0.1
b	Birth/recruitment rate	0.01

Table 2: Numerical parameters used for the virus-free equilibrium simulation.

$$R_0 = \frac{\beta b}{d_1(\gamma + d_1)}. \quad (5.12)$$

Substituting the parameter values from Table 2:

$$R_0 = \frac{0.8 \times 0.01}{0.1 \times (0.8 + 0.1)} = \frac{0.008}{0.1 \times 0.9} = \frac{0.008}{0.09} \approx 0.0889. \quad (5.13)$$

Since $R_0 \approx 0.0889 < 1$, the system is expected to exhibit **virus-free equilibrium**, meaning that the infection will eventually die out over time.

Virus-Free Equilibrium Figure 3 and Figure 4 are plotted using the implicit finite difference scheme described in Section 3 with the parameters given in Table 2.

Figure 3 shows the dynamics of the susceptible population over time and space. From the figure, we observe that the number of susceptible individuals decreases gradually from its initial distribution and eventually stabilizes. The spatial variation of the susceptible population diminishes over time due to diffusion.

Figure 4 displays the infected population dynamics. It is evident that the infected population decreases monotonically over time and approaches zero. The infection does not spread throughout the domain; instead, it decays due to the recovery process and natural death, without any new outbreaks. The spatial peak of infection, initially centered in the middle of the domain, spreads slightly due to diffusion but ultimately vanishes.

All graphs in Figures 3 and 4 demonstrate that the numerical scheme preserves the essential properties of the continuous model, including:

- **Positivity:** Both $S(t, x)$ and $I(t, x)$ remain non-negative throughout the simulation,
- **Boundedness:** The solutions remain within physically meaningful bounds,

- **Convergence:** The solutions approach the virus-free equilibrium $(S^*, I^*) = (b/d_1, 0) = (0.1, 0)$ as $t \rightarrow \infty$.

These results confirm that for $R_0 < 1$, the disease-free equilibrium is stable, and the virus eventually disappears from the population. This behavior is consistent with the theoretical stability analysis presented in Section 4.

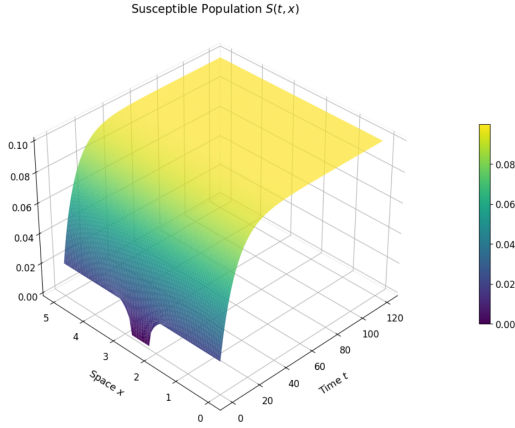


Figure 1: Susceptible population $S(t, x)$ - 3D view

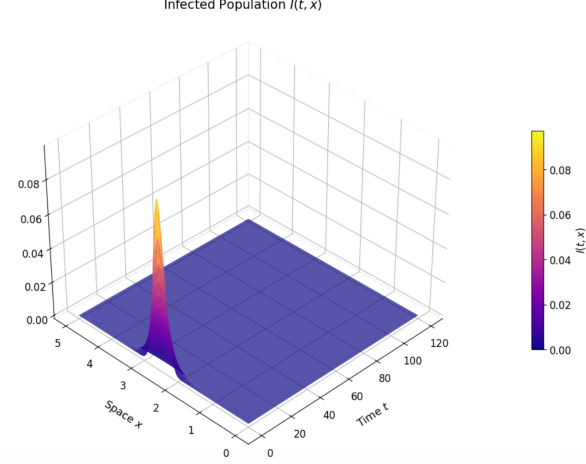


Figure 2: Infected population $I(t, x)$ - 3D view

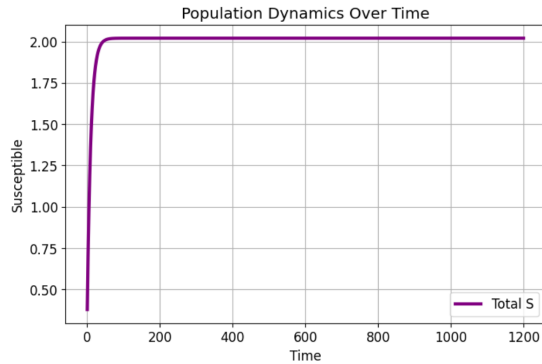


Figure 3: Susceptible population $S(t, x)$ - 2D contour

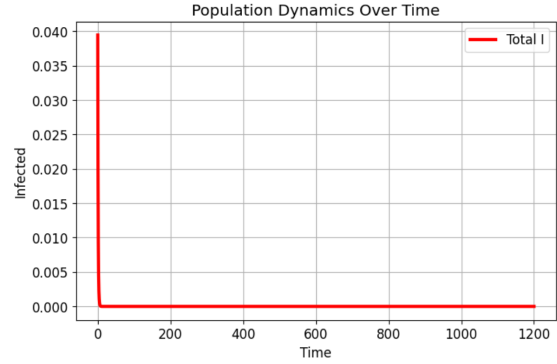


Figure 4: Infected population $I(t, x)$ - 2D contour

Figure 5: Numerical solution at virus-free equilibrium ($R_0 \approx 0.0889 < 1$). (a) 3D surface plot of susceptible population showing decrease over time. (b) 3D surface plot of infected population showing decay to zero. (c) 2D contour plot of susceptible population. (d) 2D contour plot of infected population. The scheme preserves positivity and boundedness.

The numerical simulations clearly demonstrate that when the basic reproduction number is less than unity ($R_0 < 1$), the epidemic cannot sustain itself. The infected population

decays monotonically to zero, while the susceptible population approaches the demographic equilibrium b/d_1 . This confirms the theoretical result that the disease-free equilibrium is locally asymptotically stable under the condition $R_0 < 1$. The implicit finite difference scheme successfully captures this behavior while preserving positivity and boundedness of the solution.

Endemic Equilibrium Case ($R_0 > 1$) In this section, we investigate the behavior of the diffusive SIR model when the basic reproduction number exceeds unity. The numerical simulations are performed on the same spatial domain and using the same implicit finite difference scheme as in the previous subsection. However, the parameter values are modified to ensure that $R_0 > 1$.

The parameters used in this simulation are summarized in Table 3.

Parameter	Description	Value
L	Domain length	5.0
T	Total simulation time	120.0
N_x	Number of spatial grid points	100
d_S	Diffusion coefficient for susceptible	0.01
d_I	Diffusion coefficient for infected	0.05
β	Transmission rate	5.0
γ	Recovery rate	0.8
d_1	Natural death rate	0.1
b	Birth/recruitment rate	5.0

Table 3: Numerical parameters used for the endemic equilibrium simulation.

Using the same formula as in (5.12), we compute:

$$R_0 = \frac{\beta b}{d_1(\gamma + d_1)}. \quad (5.14)$$

Substituting the parameter values:

$$R_0 = \frac{5.0 \times 5.0}{0.1 \times (0.8 + 0.1)} = \frac{25}{0.1 \times 0.9} = \frac{25}{0.09} \approx 277.78. \quad (5.15)$$

Since $R_0 \approx 277.78 \gg 1$, the system is expected to exhibit a **persistent infection** and converge to a non-trivial endemic equilibrium.

The numerical results are presented in Figures 8 and 9.

Figure 8 shows the evolution of the susceptible population over time and space. Initially, the susceptible population decreases rapidly due to infection transmission. However, due to the presence of the birth term b , the susceptible population is continuously replenished. As a result, the system stabilizes and approaches a steady-state distribution.

Figure 9 illustrates the dynamics of the infected population. Unlike the virus-free case, the infected population increases from its initial condition and approaches a positive steady-state value. The infection persists across the spatial domain, indicating the establishment of an endemic state.

The endemic equilibrium for the non-spatial system is given by:

$$S^* = \frac{\gamma + d_1}{\beta}, \quad I^* = \frac{b}{\gamma + d_1} - \frac{d_1}{\beta}. \quad (5.16)$$

Substituting the parameter values, we obtain:

$$S^* = \frac{0.8 + 0.1}{5.0} = \frac{0.9}{5.0} = 0.18, \quad (5.17)$$

$$I^* = \frac{5.0}{0.8 + 0.1} - \frac{0.1}{5.0} = \frac{5.0}{0.9} - 0.02 \approx 5.56 - 0.02 = 5.54. \quad (5.18)$$

The numerical results are consistent with these theoretical predictions, confirming the stability of the endemic equilibrium when $R_0 > 1$.

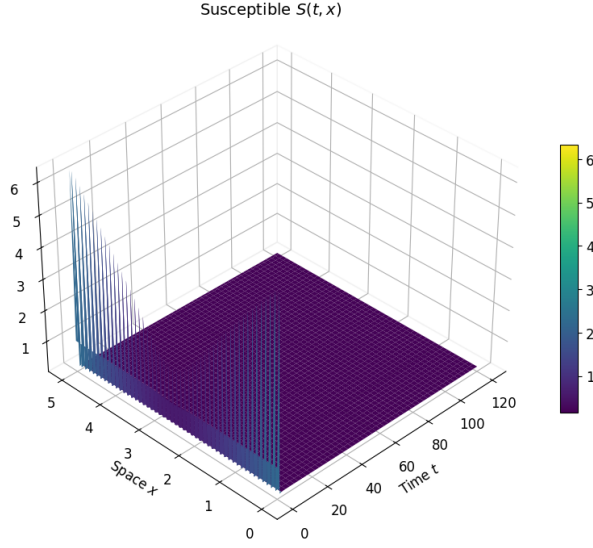


Figure 6: Susceptible population $S(t, x)$ - 3D view

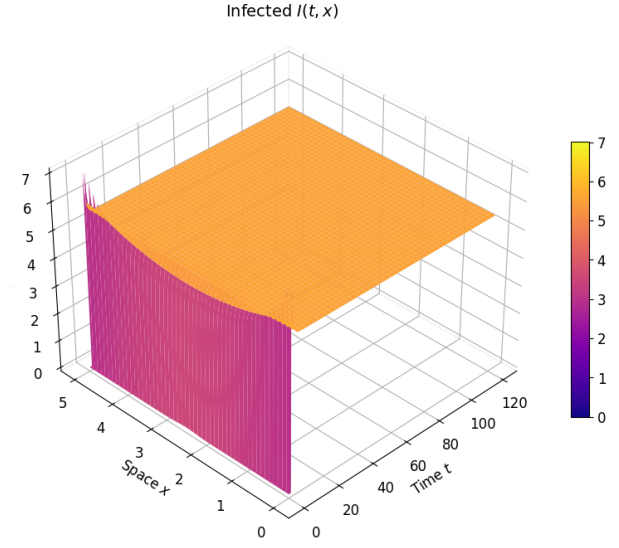


Figure 7: Infected population $I(t, x)$ - 3D view

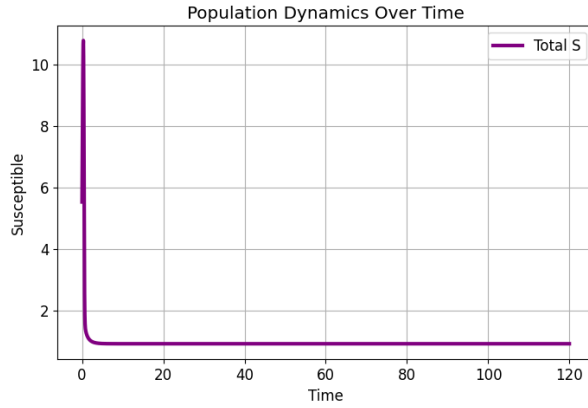


Figure 8: Susceptible population $S(t, x)$ - 2D contour

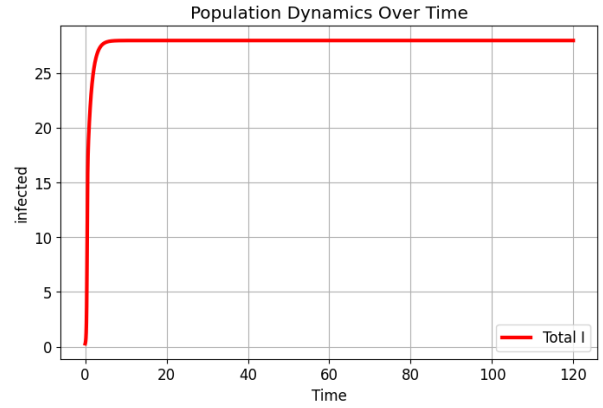


Figure 9: Infected population $I(t, x)$ - 2D contour

Figure 10: Numerical solution at endemic equilibrium ($R_0 > 1$). (a) The susceptible population decreases initially and stabilizes due to demographic effects. (b) The infected population increases and converges to a positive steady state, indicating persistence of the disease. (c)-(d) Contour plots illustrating spatial diffusion and convergence to equilibrium.

The numerical simulations demonstrate that when $R_0 > 1$, the infection persists in the population and converges to a non-zero steady state. Unlike the virus-free case, the infected population does not decay to zero but instead stabilizes at a positive level. This confirms that the endemic equilibrium is locally asymptotically stable when the basic reproduction number exceeds unity. The numerical scheme successfully captures this behavior while preserving positivity, boundedness, and convergence of the solution.

5.6 Milne Predictor–Corrector Method

In this section, the Milne Simpson method (also known as Milne’s predictor-corrector method) is employed for time discretization [4].

The Milne method is a multistep predictor–corrector scheme used for the numerical solution of ordinary differential equations of the form

$$\frac{dy}{dt} = f(t, y).$$

The **predictor** (explicit Milne formula) is given by:

$$y_{n+1}^{(p)} = y_{n-3} + \frac{4h}{3} (2f_{n-2} - f_{n-1} + 2f_n), \quad (5.19)$$

where h is the time step and $f_k = f(t_k, y_k)$.

The **corrector** (Simpson-type formula) is:

$$y_{n+1}^{(c)} = y_{n-1} + \frac{h}{3} (f_{n-1} + 4f_n + f_{n+1}^{(p)}), \quad (5.20)$$

where $f_{n+1}^{(p)} = f(t_{n+1}, y_{n+1}^{(p)})$ is evaluated using the predicted value.

Since the Milne method is a multistep scheme, it requires initial values at the first few time levels, which are typically obtained using a one-step method such as the Runge–Kutta method.

Applying this to the spatially discretized system, we obtain the following time-discretized equations:

Milne Time Discretization of the Semi-Discrete System

After applying finite difference discretization in space, the reaction–diffusion system reduces to a system of ordinary differential equations in time:

$$\begin{cases} \frac{dS_i}{dt} = d_S \frac{S_{i+1} - 2S_i + S_{i-1}}{(\Delta x)^2} + b - \beta S_i I_i - d_1 S_i, \\ \frac{dI_i}{dt} = d_I \frac{I_{i+1} - 2I_i + I_{i-1}}{(\Delta x)^2} + \beta S_i I_i - \gamma I_i - d_1 I_i. \end{cases} \quad (5.21)$$

Let us denote:

$$f_i^n = \frac{d_S}{(\Delta x)^2} (S_{i+1}^n - 2S_i^n + S_{i-1}^n) - d_1 S_i^n.$$

$$g_i^n = \frac{d_I}{(\Delta x)^2} (I_{i+1}^n - 2I_i^n + I_{i-1}^n) - \gamma I_i^n - d_1 I_i^n.$$

where f and g correspond to the right-hand sides of the equations for S and I , respectively.

Predictor Step

The Milne predictor formulas for S_i and I_i are given by:

$$S_i^{n+1,(p)} = S_i^{n-3} + \frac{4\Delta t}{3} (2f_i^{n-2} - f_i^{n-1} + 2f_i^n), \quad (5.22)$$

$$I_i^{n+1,(p)} = I_i^{n-3} + \frac{4\Delta t}{3} (2g_i^{n-2} - g_i^{n-1} + 2g_i^n). \quad (5.23)$$

Corrector Step

Using the predicted values, the corrected solutions are computed as:

$$S_i^{n+1} = S_i^{n-1} + \frac{\Delta t}{3} (f_i^{n-1} + 4f_i^n + f_i^{n+1,(p)}), \quad (5.24)$$

$$I_i^{n+1} = I_i^{n-1} + \frac{\Delta t}{3} (g_i^{n-1} + 4g_i^n + g_i^{n+1,(p)}), \quad (5.25)$$

where

$$f_i^{n+1,(p)} = f(S_i^{n+1,(p)}, I_i^{n+1,(p)}), \quad g_i^{n+1,(p)} = g(S_i^{n+1,(p)}, I_i^{n+1,(p)}).$$

Remark

Since the Milne method is a multistep scheme, initial values at the first time levels ($n = 0, 1, 2, 3$) are required. These values are obtained using a one-step method such as the Runge-Kutta method:

$$\begin{aligned} k_1^S &= f(S_i^n, I_i^n), & k_1^I &= g(S_i^n, I_i^n), \\ k_2^S &= f\left(S_i^n + \frac{\Delta t}{2}k_1^S, I_i^n + \frac{\Delta t}{2}k_1^I\right), & k_2^I &= g\left(S_i^n + \frac{\Delta t}{2}k_1^S, I_i^n + \frac{\Delta t}{2}k_1^I\right), \\ k_3^S &= f\left(S_i^n + \frac{\Delta t}{2}k_2^S, I_i^n + \frac{\Delta t}{2}k_2^I\right), & k_3^I &= g\left(S_i^n + \frac{\Delta t}{2}k_2^S, I_i^n + \frac{\Delta t}{2}k_2^I\right), \\ k_4^S &= f(S_i^n + \Delta t k_3^S, I_i^n + \Delta t k_3^I), & k_4^I &= g(S_i^n + \Delta t k_3^S, I_i^n + \Delta t k_3^I). \end{aligned}$$

The solution is then updated by:

$$S_i^{n+1} = S_i^n + \frac{\Delta t}{6} (k_1^S + 2k_2^S + 2k_3^S + k_4^S), \quad (5.26)$$

$$I_i^{n+1} = I_i^n + \frac{\Delta t}{6} (k_1^I + 2k_2^I + 2k_3^I + k_4^I). \quad (5.27)$$

5.7 Stability Analysis of the Milne Scheme

In this section, we introduce the stability analysis of the Milne method, following the approach presented in [1].

Predictor Step

The Milne predictor is given by:

$$\bar{S}_i^{n+1} = S_i^{n-3} + \frac{4\Delta t}{3} (2F_i^{n-2} - F_i^{n-1} + 2F_i^n), \quad (5.28)$$

where

$$F_i^n = \frac{d_S}{(\Delta x)^2} (S_{i+1}^n - 2S_i^n + S_{i-1}^n) - d_1 S_i^n. \quad (5.29)$$

Expanded Predictor

Substituting F_i^n explicitly:

$$\bar{S}_i^{n+1} = S_i^{n-3} + \frac{4\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} (S_{i+1}^{n-2} - 2S_i^{n-2} + S_{i-1}^{n-2}) - d_1 S_i^{n-2} \right. \quad (5.30)$$

$$\left. - \left(\frac{d_S}{(\Delta x)^2} (S_{i+1}^{n-1} - 2S_i^{n-1} + S_{i-1}^{n-1}) - d_1 S_i^{n-1} \right) \right. \quad (5.31)$$

$$\left. + \frac{d_S}{(\Delta x)^2} (S_{i+1}^n - 2S_i^n + S_{i-1}^n) - d_1 S_i^n \right]. \quad (5.32)$$

Substitution into Corrector

Substituting $\bar{S}_i^{n+1}$ into the corrector yields

$$S_i^{n+1} = S_i^{n-1} + \frac{\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} (S_{i+1}^{n-1} - 2S_i^{n-1} + S_{i-1}^{n-1}) - d_1 S_i^{n-1} \right. \quad (5.33)$$

$$\left. + 4 \left(\frac{d_S}{(\Delta x)^2} (S_{i+1}^n - 2S_i^n + S_{i-1}^n) - d_1 S_i^n \right) \right. \quad (5.34)$$

$$\left. + \frac{d_S}{(\Delta x)^2} \left(S_{i+1}^{n+1} - 2 \left(S_i^{n-3} + \frac{4\Delta t}{3} [\dots] \right) + S_{i-1}^{n+1} \right) \right. \quad (5.35)$$

$$\left. - d_1 \left(S_i^{n-3} + \frac{4\Delta t}{3} [\dots] \right) \right]. \quad (5.36)$$

Fourier Representation

We assume a Fourier mode of the form

$$S_i^n = e^{at_n} e^{\hat{i}kx_i}, \quad \phi = k\Delta x. \quad (5.37)$$

Substituting into the scheme gives the fully expanded relation:

$$\begin{aligned}
e^{a(t_n+\Delta t)}e^{\hat{ik}x_i} &= e^{a(t_n-\Delta t)}e^{\hat{ik}x_i} + \frac{\Delta t}{3} \left[\frac{dS}{(\Delta x)^2} \left(e^{a(t_n-\Delta t)}e^{\hat{ik}(x_i+\Delta x)} - 2e^{a(t_n-\Delta t)}e^{\hat{ik}x_i} + e^{a(t_n-\Delta t)}e^{\hat{ik}(x_i-\Delta x)} \right) \right. \\
&\quad - d_1 e^{a(t_n-\Delta t)}e^{\hat{ik}x_i} + 4 \left(\frac{dS}{(\Delta x)^2} \left(e^{at_n}e^{\hat{ik}(x_i+\Delta x)} - 2e^{at_n}e^{\hat{ik}x_i} + e^{at_n}e^{\hat{ik}(x_i-\Delta x)} \right) - d_1 e^{at_n}e^{\hat{ik}x_i} \right) \\
&\quad + \frac{dS}{(\Delta x)^2} \left(e^{a(t_n+\Delta t)}e^{\hat{ik}(x_i+\Delta x)} - 2 \left(e^{a(t_n-3\Delta t)}e^{\hat{ik}x_i} + \frac{4\Delta t}{3} \left[\frac{dS}{(\Delta x)^2} \left(e^{a(t_n-2\Delta t)}e^{\hat{ik}(x_i+\Delta x)} \right. \right. \right. \\
&\quad - 2e^{a(t_n-2\Delta t)}e^{\hat{ik}x_i} + e^{a(t_n-2\Delta t)}e^{\hat{ik}(x_i-\Delta x)} - d_1 e^{a(t_n-2\Delta t)}e^{\hat{ik}x_i} \\
&\quad - \left(\frac{dS}{(\Delta x)^2} \left(e^{a(t_n-\Delta t)}e^{\hat{ik}(x_i+\Delta x)} - 2e^{a(t_n-\Delta t)}e^{\hat{ik}x_i} + e^{a(t_n-\Delta t)}e^{\hat{ik}(x_i-\Delta x)} \right) - d_1 e^{a(t_n-\Delta t)}e^{\hat{ik}x_i} \right) \\
&\quad \left. \left. \left. + \left(\frac{dS}{(\Delta x)^2} \left(e^{at_n}e^{\hat{ik}(x_i+\Delta x)} - 2e^{at_n}e^{\hat{ik}x_i} + e^{at_n}e^{\hat{ik}(x_i-\Delta x)} \right) - d_1 e^{at_n}e^{\hat{ik}x_i} \right) \right] \right) \right) \right. \\
&\quad \left. + e^{a(t_n+\Delta t)}e^{\hat{ik}(x_i-\Delta x)} \right) - d_1 \left(e^{a(t_n-3\Delta t)}e^{\hat{ik}x_i} + \frac{4\Delta t}{3} \left[\frac{dS}{(\Delta x)^2} \left(e^{a(t_n-2\Delta t)}e^{\hat{ik}(x_i+\Delta x)} \right. \right. \right. \\
&\quad - 2e^{a(t_n-2\Delta t)}e^{\hat{ik}x_i} + e^{a(t_n-2\Delta t)}e^{\hat{ik}(x_i-\Delta x)} - d_1 e^{a(t_n-2\Delta t)}e^{\hat{ik}x_i} \\
&\quad - \left(\frac{dS}{(\Delta x)^2} \left(e^{a(t_n-\Delta t)}e^{\hat{ik}(x_i+\Delta x)} - 2e^{a(t_n-\Delta t)}e^{\hat{ik}x_i} + e^{a(t_n-\Delta t)}e^{\hat{ik}(x_i-\Delta x)} \right) - d_1 e^{a(t_n-\Delta t)}e^{\hat{ik}x_i} \right) \\
&\quad \left. \left. \left. + \left(\frac{dS}{(\Delta x)^2} \left(e^{at_n}e^{\hat{ik}(x_i+\Delta x)} - 2e^{at_n}e^{\hat{ik}x_i} + e^{at_n}e^{\hat{ik}(x_i-\Delta x)} \right) - d_1 e^{at_n}e^{\hat{ik}x_i} \right) \right] \right) \right) \right].
\end{aligned}
\tag{5.38}$$

Multiplying both sides of relation (5.38) by $e^{-at_n}e^{-\hat{i}kx_i}$, we obtain the following expression:

$$\begin{aligned}
e^{a\Delta t} = e^{-a\Delta t} &+ \frac{\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} \left(e^{-a\Delta t} e^{\hat{i}\phi} - 2e^{-a\Delta t} + e^{-a\Delta t} e^{-\hat{i}\phi} \right) - d_1 e^{-a\Delta t} + 4 \left(\frac{d_S}{(\Delta x)^2} \left(e^{\hat{i}\phi} - 2 + e^{-\hat{i}\phi} \right) - d_1 \right) \right. \\
&+ \frac{d_S}{(\Delta x)^2} \left(e^{a\Delta t} e^{\hat{i}\phi} - 2 \left(e^{-3a\Delta t} + \frac{4\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} \left(e^{-2a\Delta t} e^{\hat{i}\phi} - 2e^{-2a\Delta t} + e^{-2a\Delta t} e^{-\hat{i}\phi} \right) \right. \right. \right. \\
&\quad \left. \left. - d_1 e^{-2a\Delta t} - \left(\frac{d_S}{(\Delta x)^2} \left(e^{-a\Delta t} e^{\hat{i}\phi} - 2e^{-a\Delta t} + e^{-a\Delta t} e^{-\hat{i}\phi} \right) - d_1 e^{-a\Delta t} \right) \right. \right. \\
&\quad \left. \left. + \left(\frac{d_S}{(\Delta x)^2} \left(e^{\hat{i}\phi} - 2 + e^{-\hat{i}\phi} \right) - d_1 \right) \right] \right) + e^{a\Delta t} e^{-\hat{i}\phi} \right) \\
&- d_1 \left(e^{-3a\Delta t} + \frac{4\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} \left(e^{-2a\Delta t} e^{\hat{i}\phi} - 2e^{-2a\Delta t} + e^{-2a\Delta t} e^{-\hat{i}\phi} \right) \right. \right. \\
&\quad \left. \left. - d_1 e^{-2a\Delta t} - \left(\frac{d_S}{(\Delta x)^2} \left(e^{-a\Delta t} e^{\hat{i}\phi} - 2e^{-a\Delta t} + e^{-a\Delta t} e^{-\hat{i}\phi} \right) - d_1 e^{-a\Delta t} \right) \right. \right. \\
&\quad \left. \left. + \left(\frac{d_S}{(\Delta x)^2} \left(e^{\hat{i}\phi} - 2 + e^{-\hat{i}\phi} \right) - d_1 \right) \right] \right) \right].
\end{aligned} \tag{5.39}$$

Using the identities

$$e^{\hat{i}\phi} + e^{-\hat{i}\phi} = 2 \cos(\phi), \quad e^{\hat{i}\phi} - e^{-\hat{i}\phi} = 2i \sin(\phi),$$

and

$$e^{\hat{i}\phi} - 2 + e^{-\hat{i}\phi} = 2(\cos \phi - 1),$$

the previous relation (5.39) can be rewritten as

$$\begin{aligned}
e^{a\Delta t} = e^{-a\Delta t} &+ \frac{\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} (2e^{-a\Delta t}(\cos \phi - 1)) - d_1 e^{-a\Delta t} + 4 \left(\frac{d_S}{(\Delta x)^2} (2(\cos \phi - 1)) - d_1 \right) \right. \\
&+ \frac{d_S}{(\Delta x)^2} \left(e^{a\Delta t} e^{i\phi} - 2 \left(e^{-3a\Delta t} + \frac{4\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} (2e^{-2a\Delta t}(\cos \phi - 1)) - d_1 e^{-2a\Delta t} \right. \right. \right. \\
&\quad \left. \left. \left. - \left(\frac{d_S}{(\Delta x)^2} (2e^{-a\Delta t}(\cos \phi - 1)) - d_1 e^{-a\Delta t} \right) \right. \right. \right. \\
&\quad \left. \left. \left. + \left(\frac{d_S}{(\Delta x)^2} (2(\cos \phi - 1)) - d_1 \right) \right] \right) \right] + e^{a\Delta t} e^{-i\phi} \right) \\
&- d_1 \left(e^{-3a\Delta t} + \frac{4\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} (2e^{-2a\Delta t}(\cos \phi - 1)) - d_1 e^{-2a\Delta t} \right. \right. \\
&\quad \left. \left. - \left(\frac{d_S}{(\Delta x)^2} (2e^{-a\Delta t}(\cos \phi - 1)) - d_1 e^{-a\Delta t} \right) \right. \right. \\
&\quad \left. \left. + \left(\frac{d_S}{(\Delta x)^2} (2(\cos \phi - 1)) - d_1 \right) \right] \right) \right].
\end{aligned} \tag{5.40}$$

Simplifying the equation (5.40) we obtain the amplication factor that equal to

$$\begin{aligned}
e^{a\Delta t} \left[1 - \frac{2d_S \Delta t}{3(\Delta x)^2} \cos \phi \right] &= e^{-a\Delta t} + \frac{\Delta t}{3} \left[\frac{2d_S}{(\Delta x)^2} e^{-a\Delta t} (\cos \phi - 1) - d_1 e^{-a\Delta t} \right. \\
&+ 4 \left(\frac{2d_S}{(\Delta x)^2} (\cos \phi - 1) - d_1 \right) \\
&- \frac{2d_S}{(\Delta x)^2} \left(e^{-3a\Delta t} + \frac{4\Delta t}{3} \left[\frac{2d_S}{(\Delta x)^2} e^{-2a\Delta t} (\cos \phi - 1) - d_1 e^{-2a\Delta t} \right. \right. \\
&\quad \left. \left. - \left(\frac{2d_S}{(\Delta x)^2} e^{-a\Delta t} (\cos \phi - 1) - d_1 e^{-a\Delta t} \right) \right. \right. \\
&\quad \left. \left. + \left(\frac{2d_S}{(\Delta x)^2} (\cos \phi - 1) - d_1 \right) \right] \right) \\
&- d_1 \left(e^{-3a\Delta t} + \frac{4\Delta t}{3} \left[\frac{2d_S}{(\Delta x)^2} e^{-2a\Delta t} (\cos \phi - 1) - d_1 e^{-2a\Delta t} \right. \right. \\
&\quad \left. \left. - \left(\frac{2d_S}{(\Delta x)^2} e^{-a\Delta t} (\cos \phi - 1) - d_1 e^{-a\Delta t} \right) \right. \right. \\
&\quad \left. \left. + \left(\frac{2d_S}{(\Delta x)^2} (\cos \phi - 1) - d_1 \right) \right] \right) \right].
\end{aligned} \tag{5.41}$$

Define

$$G = e^{a\Delta t}, \quad r = e^{-a\Delta t}, \quad \lambda = \frac{d_S \Delta t}{(\Delta x)^2}.$$

Then the left-hand side becomes

$$G \left(1 - \frac{2\lambda}{3} \cos \phi \right).$$

We repeatedly encounter the expression

$$\frac{2d_S}{(\Delta x)^2} (\cos \phi - 1) - d_1.$$

Define

$$A := \frac{2d_S}{(\Delta x)^2} (\cos \phi - 1) - d_1.$$

Then

$$\frac{2d_S}{(\Delta x)^2} e^{-a\Delta t} (\cos \phi - 1) - d_1 e^{-a\Delta t} = Ar.$$

Rewrite each term:

$$e^{-a\Delta t} = r,$$

$$\frac{2d_S}{(\Delta x)^2} e^{-a\Delta t} (\cos \phi - 1) - d_1 e^{-a\Delta t} = Ar,$$

$$4 \left(\frac{2d_S}{(\Delta x)^2} (\cos \phi - 1) - d_1 \right) = 4A.$$

Big repeated block:

$$\frac{2d_S}{(\Delta x)^2} e^{-2a\Delta t} (\cos \phi - 1) - d_1 e^{-2a\Delta t} = Ar^2,$$

$$\frac{2d_S}{(\Delta x)^2} e^{-a\Delta t} (\cos \phi - 1) - d_1 e^{-a\Delta t} = Ar,$$

$$\frac{2d_S}{(\Delta x)^2} (\cos \phi - 1) - d_1 = A.$$

Hence, the inner bracket simplifies to

$$Ar^2 - Ar + A.$$

Now our equation becomes:

$$G \left(1 - \frac{2\lambda}{3} \cos \phi \right) = r + \frac{\Delta t}{3} \left[Ar + 4A - \frac{2d_S}{(\Delta x)^2} \left(r^3 + \frac{4\Delta t}{3} (Ar^2 - Ar + A) \right) - d_1 \left(r^3 + \frac{4\Delta t}{3} (Ar^2 - Ar + A) \right) \right]. \quad (5.42)$$

The aim of this analysis is to provide a general characterization of the necessary conditions for stability. Due to the complexity of the resulting expressions, we adopt the simplifications introduced in Remark 3.1 for the sake of clarity and readability. Under these assumptions, we obtain a linear stability condition, which can be interpreted as a necessary condition for the stability of the proposed scheme.

To gain further insight, we begin the analysis by considering two extreme cases of the phase angle, namely $|\phi| = \pi$ and $\phi = 0$.

Case 1. For $|\phi| = \pi$, we have

$$\cos \phi = -1, \quad \sin^2 \left(\frac{\phi}{2} \right) = 1.$$

Substituting into A , we obtain

$$A = \frac{2d_S}{(\Delta x)^2}(-2) - d_1 = -\frac{4d_S}{(\Delta x)^2} - d_1.$$

Hence, the amplification factor becomes

$$G \left(1 + \frac{2\lambda}{3} \right) = r + \frac{\Delta t}{3} \left[Ar + 4A - \left(\frac{2d_S}{(\Delta x)^2} + d_1 \right) \left(r^3 + \frac{4\Delta t}{3} (Ar^2 - Ar + A) \right) \right]. \quad (5.43)$$

The squared modulus of the amplification factor gives

$$|e^{a\Delta t}|^2 = \left| \frac{e^{-a\Delta t} + \frac{\Delta t}{3} (\text{all terms above})}{1 + \frac{2d_S\Delta t}{3(\Delta x)^2}} \right|^2. \quad (5.44)$$

Since all diffusion terms contribute negatively and dominate for sufficiently large Δt ,

there exist parameter values such that

$$|e^{a\Delta t}| > 1.$$

Thus, the scheme is **unconditionally unstable** for $|\phi| = \pi$.

Case 2: $\phi = 0$

In this case, $\cos \phi = 1$. Recall,

$$A = \frac{2d_S}{(\Delta x)^2}(\cos \phi - 1) - d_1,$$

we obtain

$$A = \frac{2d_S}{(\Delta x)^2}(1 - 1) - d_1 = -d_1.$$

Substituting $\phi = 0$ into the amplification factor equation

$$G\left(1 - \frac{2\lambda}{3}\cos \phi\right) = r + \frac{\Delta t}{3}[\dots],$$

yields

$$G\left(1 - \frac{2\lambda}{3}\right) = r + \frac{\Delta t}{3}[\dots].$$

Using $A = -d_1$, we simplify the repeated terms:

$$Ar + 4A = -d_1r - 4d_1,$$

and

$$Ar^2 - Ar + A = -d_1(r^2 - r + 1).$$

Hence,

$$r^3 + \frac{4\Delta t}{3}(Ar^2 - Ar + A) = r^3 - \frac{4\Delta t}{3}d_1(r^2 - r + 1).$$

Moreover, the diffusion term

$$\frac{2d_S}{(\Delta x)^2}(\cos \phi - 1)$$

vanishes at $\phi = 0$, so all spatial contributions disappear.

Therefore, the right-hand side reduces to

$$r\left(1 - \frac{2\lambda}{3}\right),$$

and we obtain

$$G\left(1 - \frac{2\lambda}{3}\right) = r\left(1 - \frac{2\lambda}{3}\right).$$

Assuming $1 - \frac{2\lambda}{3} \neq 0$, we conclude

$$\boxed{G(0) = r = e^{-a\Delta t}}.$$

The magnitude of the amplification factor at $\phi = 0$ is

$$|G(0)| = e^{-a\Delta t} \leq 1.$$

Thus, the scheme is stable for the zero mode. Moreover, for $a > 0$, we have

$$|G(0)| < 1$$

Thus, the numerical scheme is stable.

Case 3: $0 < |\phi| \ll \pi$.

Using the Taylor expansion around $\phi = 0$ and neglecting higher-order terms, we obtain

$$\cos \phi \approx 1 - \frac{\phi^2}{2}.$$

$$G = G_{\text{const}} + G_{\phi^2} \phi^2 \tag{5.45}$$

Squaring both sides, we obtain

$$|G|^2 = G^2 = (G_{\text{const}})^2 + 2G_{\text{const}}G_{\phi^2} \phi^2. \tag{5.46}$$

Constant part:

$$\begin{aligned} G_{\text{const}} = & \frac{1}{1 - \frac{2\lambda}{3}} \left[r + \frac{\Delta t}{3} \left((-d_1)r + 4(-d_1) \right. \right. \\ & - \frac{2d_S}{(\Delta x)^2} \left(r^3 + \frac{4\Delta t}{3} [(-d_1)r^2 - (-d_1)r + (-d_1)] \right) \\ & \left. \left. - d_1 \left(r^3 + \frac{4\Delta t}{3} [(-d_1)r^2 - (-d_1)r + (-d_1)] \right) \right) \right]. \end{aligned} \tag{5.47}$$

Coefficient of ϕ^2 :

$$\begin{aligned}
G_{\phi^2} = & \frac{1}{1 - \frac{2\lambda}{3}} \cdot \frac{\Delta t}{3} \left[\left(\frac{d_S}{(\Delta x)^2} \right) r + 4 \left(\frac{d_S}{(\Delta x)^2} \right) \right. \\
& - \frac{2d_S}{(\Delta x)^2} \left(\frac{4\Delta t}{3} \left[\left(\frac{d_S}{(\Delta x)^2} \right) r^2 - \left(\frac{d_S}{(\Delta x)^2} \right) r + \left(\frac{d_S}{(\Delta x)^2} \right) \right] \right) \\
& \left. - d_1 \left(\frac{4\Delta t}{3} \left[\left(\frac{d_S}{(\Delta x)^2} \right) r^2 - \left(\frac{d_S}{(\Delta x)^2} \right) r + \left(\frac{d_S}{(\Delta x)^2} \right) \right] \right) \right].
\end{aligned} \tag{5.48}$$

Thus,

$$|G|^2 = (G_{\text{const}})^2 + 2G_{\text{const}}G_{\phi^2}\phi^2. \tag{5.49}$$

Stability condition:

$$|G|^2 < 1. \tag{5.50}$$

Introduce ε (with $0 \leq \varepsilon < 1$):

$$|G_{\text{const}}| \leq \varepsilon, \quad |2G_{\text{const}}G_{\phi^2}|\phi \leq 1 - \varepsilon. \tag{5.51}$$

This implies

$$-\varepsilon \leq G_{\text{const}} \leq \varepsilon, \tag{5.52}$$

$$-(1 - \varepsilon) \leq 2G_{\text{const}}G_{\phi^2}\phi \leq 1 - \varepsilon. \tag{5.53}$$

Multiplying the inequalities, we obtain

$$|G_{\text{const}}| \cdot |2G_{\text{const}}G_{\phi^2}|\phi \leq \varepsilon(1 - \varepsilon). \tag{5.54}$$

Hence,

$$2|G_{\text{const}}|^2 |G_{\phi^2}| \phi \leq \varepsilon(1 - \varepsilon). \tag{5.55}$$

Multiplying by $|\phi|$, we finally obtain

$$\boxed{2|G_{\text{const}}|^2 |G_{\phi^2}| \phi^2 \leq \varepsilon(1 - \varepsilon)}. \tag{5.56}$$

With this work, we conclude the following lemma:

Lemma 5.1. *A necessary condition for stability of the proposed numerical scheme is*

$$2 \left| \frac{r + \frac{\Delta t}{3} \left[-d_1 r - 4d_1 - \frac{2d_S}{(\Delta x)^2} \left(r^3 + \frac{4\Delta t}{3} (-d_1 r^2 + d_1 r - d_1) \right) - d_1 \left(r^3 + \frac{4\Delta t}{3} (-d_1 r^2 + d_1 r - d_1) \right) \right]}{1 - \frac{2\lambda}{3}} \right|^2 \times \left| \frac{\frac{\Delta t}{3} \left[\frac{d_S}{(\Delta x)^2} r + \frac{4d_S}{(\Delta x)^2} - \frac{2d_S}{(\Delta x)^2} \left(\frac{4\Delta t}{3} \left(\frac{d_S}{(\Delta x)^2} r^2 - \frac{d_S}{(\Delta x)^2} r + \frac{d_S}{(\Delta x)^2} \right) \right) - d_1 \left(\frac{4\Delta t}{3} \left(\frac{d_S}{(\Delta x)^2} r^2 - \frac{d_S}{(\Delta x)^2} r + \frac{d_S}{(\Delta x)^2} \right) \right) \right]}{1 - \frac{2\lambda}{3}} \right| \phi^2 \leq \varepsilon(1 - \varepsilon), \quad (5.57)$$

where

$$\lambda = \frac{d_S \Delta t}{(\Delta x)^2}, \quad r = e^{-a\Delta t}, \quad \phi = k\Delta x,$$

and $0 \leq \varepsilon < 1$, with $k \neq 0$ the wave number.

5.8 Milne Method: Numerical Results

In this section, the Milne predictor–corrector method is applied to the spatial SIR reaction–diffusion system. The method is initialized using a Runge–Kutta scheme and then advanced using the multistep Milne formulation. The numerical results are presented for both $R_0 < 1$ and $R_0 > 1$ cases.

Case $R_0 < 1$

For $R_0 < 1$, the numerical results confirm the convergence toward the disease-free equilibrium. As shown in Figure 11, the infected population $I(t)$ decreases monotonically and approaches zero, indicating that the infection dies out over time.

In contrast, the susceptible population $S(t)$ stabilizes at a positive constant level, determined by the balance between the recruitment term b and the natural death rate d_1 . The absence of oscillations in this case reflects the stability of the disease-free equilibrium.

The following parameters were used:

Parameter	Value
d_S	0.01
d_I	0.05
β	0.8
b	0.01
γ	0.8
d_1	0.1
$R_0 = \frac{\beta b}{d_1(\gamma + d_1)}$	< 1

Table 4: Parameter values for the disease-free case ($R_0 < 1$).

The Milne method accurately captures this behavior, preserving the positivity and boundedness of the solution while correctly reproducing the theoretical prediction that the infection vanishes when $R_0 < 1$.

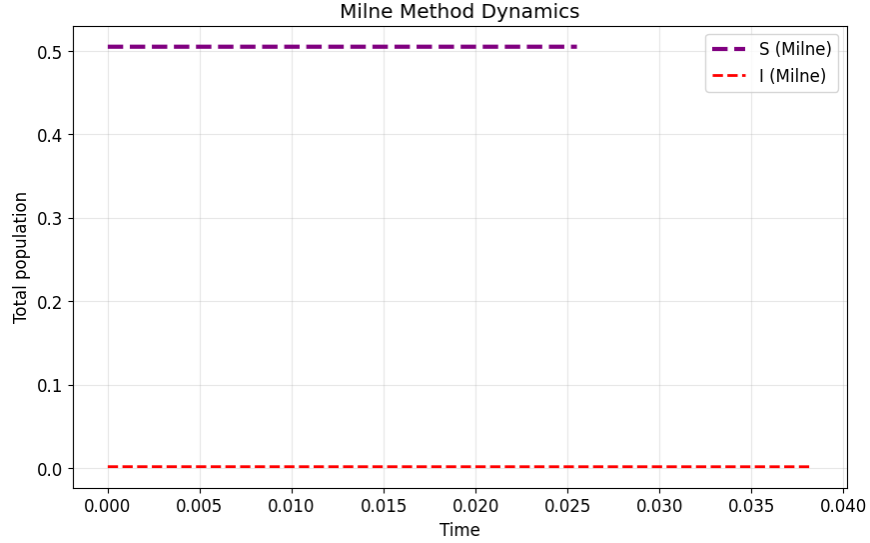


Figure 11: Temporal dynamics of the susceptible and infected populations obtained using the Milne method for $R_0 < 1$. The infected population rapidly decays to zero, while the susceptible population converges to a positive steady state.

Case $R_0 > 1$

For $R_0 > 1$, the numerical results show the emergence of an endemic equilibrium. The infected population initially grows rapidly, reaches a peak, and then stabilizes at a positive

level. Meanwhile, the susceptible population decreases due to infection and later converges to a lower steady state. The following parameters were used:

Parameter	Value
d_S	0.01
d_I	0.05
β	5.0
b	5.0
γ	0.8
d_1	0.1
$R_0 = \frac{\beta b}{d_1(\gamma + d_1)}$	> 1

Table 5: Parameter values for the endemic case ($R_0 > 1$).

The obtained results are consistent with the theoretical predictions. The Milne method accurately captures both the rapid growth phase and the long-term stabilization. Compared to the Euler method, the transient dynamics are more pronounced, with a sharper infection peak and smoother convergence.

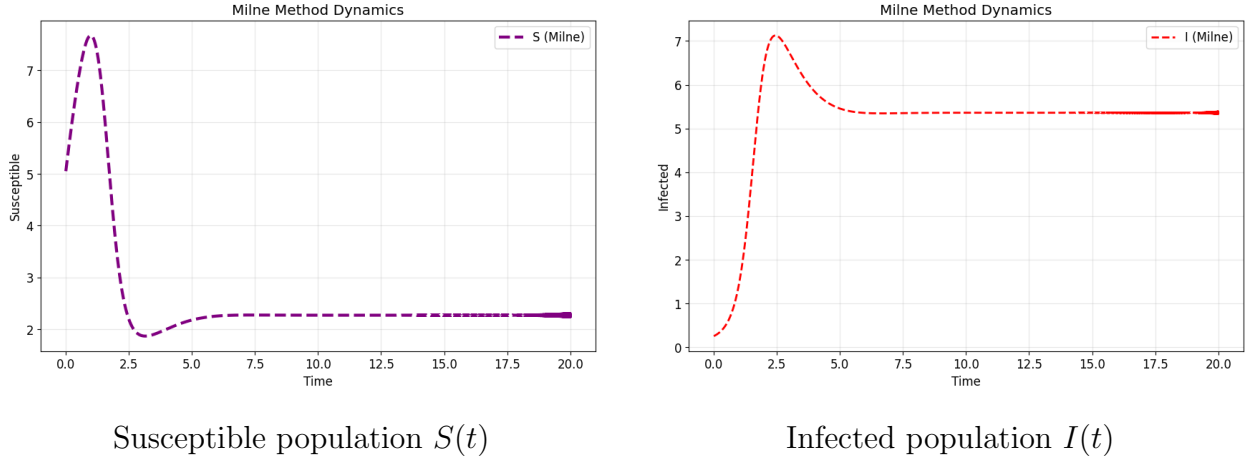


Figure 12: Temporal dynamics of the susceptible and infected populations obtained using the Milne method for $R_0 > 1$. The infected population increases, reaches a peak, and converges to a positive steady state, while the susceptible population decreases and stabilizes at a lower level.

Discussion

Overall, the Milne method provides higher accuracy in approximating the temporal dynamics of the system compared to the Euler scheme. In particular, it better resolves transient behavior such as peaks and rapid changes. However, the method is more sensitive to the choice of time step and may exhibit oscillations if the step size is not sufficiently small.

Despite this, the numerical simulations confirm that the method preserves the qualitative properties of the model, including positivity, boundedness, and convergence to the correct equilibrium states in both regimes.

6 Numerical Implementation

In this section, we present the numerical implementation used to simulate the reaction–diffusion SIR system. The spatial discretization is performed using the finite difference method, while time integration is carried out using different schemes such as the explicit Euler method and the Milne predictor–corrector method.

All simulations were implemented in Python using NumPy and Matplotlib libraries.

6.1 Finite Difference Scheme (Explicit Euler)

The following Python code was used to simulate the system using the explicit Euler method:

```
1 S_history = []
2 I_history = []
3 S_total = []
4 I_total = []
5 time = []
6
7 for n in range(Nt):
8     for i in range(1, Nx-1):
9         lap_S = (S[i+1] - 2*S[i] + S[i-1]) / dx**2
10        lap_I = (I[i+1] - 2*I[i] + I[i-1]) / dx**2
11
12        S_new[i] = S[i] + dt * (dS * lap_S + b- beta * S[i]*I[i] -
13                               d1*S[i])
14        I_new[i] = I[i] + dt * (dI * lap_I + beta * S[i]*I[i] -
15                               gamma*I[i] - d1*I[i])
16
17    # Neumann BC
```

```

16     S_new[0] = S_new[1]
17     S_new[-1] = S_new[-2]
18     I_new[0] = I_new[1]
19     I_new[-1] = I_new[-2]
20
21     S_new = np.maximum(S_new, 0)
22     I_new = np.maximum(I_new, 0)
23
24     S[:] = S_new
25     I[:] = I_new
26
27     # Store data
28     S_history.append(S.copy())
29     I_history.append(I.copy())
30     S_total.append(np.sum(S) * dx)
31     I_total.append(np.sum(I) * dx)
32     time.append(n * dt)
33
34 S_history = np.array(S_history)
35 I_history = np.array(I_history)

```

Listing 1: Explicit Euler Scheme for the Reaction–Diffusion SIR Model

6.2 Milne Predictor–Corrector Scheme

To improve accuracy, the Milne predictor–corrector method was implemented. Initial values were computed using the fourth-order Runge–Kutta method, followed by the multistep Milne scheme.

```

1 def compute_rhs(S, I):
2     fS = np.zeros_like(S)
3     fI = np.zeros_like(I)
4
5     for i in range(1, Nx-1):
6         lap_S = (S[i+1] - 2*S[i] + S[i-1]) / dx**2
7         lap_I = (I[i+1] - 2*I[i] + I[i-1]) / dx**2
8
9         fS[i] = dS * lap_S + b - beta * S[i]*I[i] - d1*S[i]
10        fI[i] = dI * lap_I + beta * S[i]*I[i] - gamma*I[i] - d1*I[i]

```

```

11
12     # Neumann BC
13     fS[0] = fS[1]
14     fS[-1] = fS[-2]
15     fI[0] = fI[1]
16     fI[-1] = fI[-2]
17
18     return fS, fI
19
20
21
22 def rk4_step(S, I):
23     k1S, k1I = compute_rhs(S, I)
24     k2S, k2I = compute_rhs(S + 0.5*dt*k1S, I + 0.5*dt*k1I)
25     k3S, k3I = compute_rhs(S + 0.5*dt*k2S, I + 0.5*dt*k2I)
26     k4S, k4I = compute_rhs(S + dt*k3S, I + dt*k3I)
27
28     S_new = S + (dt/6)*(k1S + 2*k2S + 2*k3S + k4S)
29     I_new = I + (dt/6)*(k1I + 2*k2I + 2*k3I + k4I)
30
31     return S_new, I_new
32
33
34
35 S_vals = [S.copy()]
36 I_vals = [I.copy()]
37
38 for _ in range(2): # need 3 starting points
39     S, I = rk4_step(S, I)
40     S_vals.append(S.copy())
41     I_vals.append(I.copy())
42
43
44
45 for n in range(2, Nt-1):
46
47     f_n2_S, f_n2_I = compute_rhs(S_vals[n-2], I_vals[n-2])
48     f_n1_S, f_n1_I = compute_rhs(S_vals[n-1], I_vals[n-1])

```

```

49     f_n_S, f_n_I = compute_rhs(S_vals[n], I_vals[n])
50
51
52     S_pred = S_vals[n-2] + (4*dt/3)*(2*f_n2_S - f_n1_S + 2*f_n_S)
53     I_pred = I_vals[n-2] + (4*dt/3)*(2*f_n2_I - f_n1_I + 2*f_n_I)
54
55
56     f_pred_S, f_pred_I = compute_rhs(S_pred, I_pred)
57
58
59     S_next = S_vals[n-1] + (dt/3)*(f_n1_S + 4*f_n_S + f_pred_S)
60     I_next = I_vals[n-1] + (dt/3)*(f_n1_I + 4*f_n_I + f_pred_I)
61
62
63     S_next = np.maximum(S_next, 0)
64     I_next = np.maximum(I_next, 0)
65
66     S_vals.append(S_next.copy())
67     I_vals.append(I_next.copy())
68
69
70
71 S_history = np.array(S_vals)
72 I_history = np.array(I_vals)
73 time = np.arange(len(S_history)) * dt

```

Listing 2: Milne Predictor–Corrector Implementation

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