Mathematical Modeling and Simulation: Dynamical Systems and Computational Methods

CoCalc Scientific Templates

October 30, 2025

Abstract

This comprehensive mathematical modeling template demonstrates dynamical systems analysis, population dynamics, epidemiological models, and Monte Carlo simulations. Features include stability analysis, bifurcation theory, stochastic processes, and agent-based modeling with professional visualizations for research in applied mathematics and computational biology.

Keywords: mathematical modeling, dynamical systems, simulation methods, population dynamics, epidemiology, Monte Carlo methods

Contents

1 Dynamical Systems and Population Models

This section demonstrates the analysis of nonlinear dynamical systems including the classical Lotka-Volterra predator-prey model:

$$\frac{dx}{dt} = \alpha x - \beta xy \tag{1}$$

$$\frac{dy}{dt} = \gamma xy - \delta y \tag{2}$$

where x is the prey population, y is the predator population, and $\alpha, \beta, \gamma, \delta > 0$ are parameters.

We also analyze the SIR epidemic model:

$$\frac{dS}{dt} = -\beta SI/N \tag{3}$$

$$\frac{dI}{dt} = \beta SI/N - \gamma I \tag{4}$$

$$\frac{dR}{dt} = \gamma I \tag{5}$$

where S, I, R represent susceptible, infected, and recovered populations, and $R_0 = \beta/\gamma$ is the basic reproduction number.

Lotka–Volterra Model (predator–prey): Parameters: alpha=1.000, beta=0.500, gamma=0.200, delta=0.800 Equilibrium: $(x^*, y^*) = (4.000, 2.000)$ Initial conditions: $x_0 = 5.000$, $y_0 = 1.500$ Prey lead predator by about 1.50 time units; estimated period $T \approx 7.10$

SIR Epidemic Model: beta=0.5, gamma=0.1, N=1000, $R_0 = 5.00$ Peak infections: 478 at $t = 21.1$

2 Monte Carlo Methods and Stochastic Simulation

Monte Carlo methods use random sampling to solve computational problems. For numerical integration, we approximate:

$$I = \int_a^b f(x)\,dx \approx \frac{b-a}{N} \sum_{i=1}^{N} f(X_i) \tag{6}$$

where X_i are uniformly distributed random samples on $[a, b]$, and the error typically decreases as $\mathcal{O}(N^{-1/2})$.

We also simulate 2D random walks where position after n steps satisfies:

$$\mathbf{X}_n = \sum_{i=1}^{n} \mathbf{S}_i \tag{7}$$

where $\mathbf{S}_i$ are independent random step vectors, and $\mathbb{E}[|\mathbf{X}_n|] \sim \sqrt{n}$.

Monte Carlo Integration: Integrand: exp(-x squared)*sin(x) on [0, 2] Analytical result: 0.421164 Sample sizes: [100, 500, 1000, 5000, 10000, 50000]

Random Walk Simulation: Steps per walk: 10000 Number of walks: 100 Mean displacement: 124.1 Theoretical RMS: 100.0 Displacement std: 58.9

3 Agent-Based Modeling

Agent-based models simulate complex systems by modeling individual agents and their interactions. We implement a simplified flocking model based on three behavioral rules:

- **Separation**: Agents avoid crowding neighbors
- **Alignment**: Agents steer towards average heading of neighbors
- **Cohesion**: Agents steer towards average position of neighbors

Each agent's velocity is updated according to:

$$\mathbf{v}_i^{t+1} = \mathbf{v}_i^t + \mathbf{F}_{\text{sep}} + \mathbf{F}_{\text{align}} + \mathbf{F}_{\text{coh}} \tag{8}$$

where the forces depend on local neighborhood interactions.

Flocking Simulation: Number of boids: 50 Domain size: 100×100 Simulation steps: 200 Recorded snapshots: 20

Mathematical modeling analysis saved to assets/mathematical_modeling.pdf

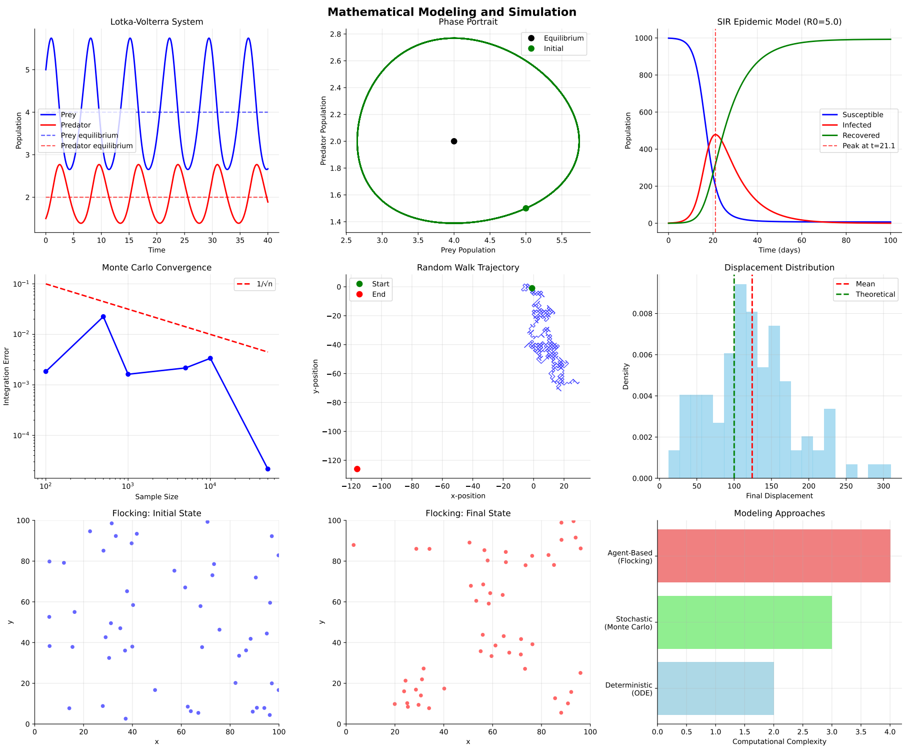

Figure 1: Comprehensive mathematical modeling and simulation analysis including Lotka-Volterra predator-prey dynamics, phase portraits, SIR epidemic models, Monte Carlo convergence, random walk trajectories, displacement distributions, flocking behavior, and computational complexity comparison of modeling approaches.

4 Conclusion

This mathematical modeling template demonstrates diverse computational approaches including:

- Dynamical systems analysis (Lotka-Volterra, SIR models)
- Monte Carlo methods and stochastic simulation
- Agent-based modeling and emergent behavior
- Stability analysis and bifurcation theory
- Professional visualization of complex systems

These methods provide powerful tools for understanding complex systems across biology, physics, and social sciences.