Stochastic Epidemic Simulation Using Monte Carlo

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Introduction

Deterministic epidemic models, like the SIR and SEIR systems built earlier, describe the *average* behavior of an outbreak. In reality, however, epidemics are shaped by chance: who meets whom, when an infection happens, and whether a chain of transmission dies out early or explodes.

This project asks:

How does randomness affect outbreak outcomes in an SIR model?

To answer this, we construct a stochastic SIR model and run many Monte Carlo simulations. Instead of a single epidemic curve, we obtain a *distribution* of possible outbreaks, revealing how variable epidemic size can be even under identical parameters.

Methods

Stochastic SIR Framework

We keep the same compartments as before:

- $S(t)$: Susceptible
- $I(t)$: Infected
- $R(t)$: Recovered

But instead of differential equations, we model **daily transitions** as random events:

- New infections are drawn from a binomial distribution based on the probability that a susceptible individual is infected by the current infectious pool.
- Recoveries are drawn from a binomial distribution based on the probability that an infected individual recovers on a given day.

This yields a discrete-time, stochastic SIR process. Each simulation run is one possible realization of the epidemic.

Monte Carlo Simulation

We fix:

- population size N,
- transmission parameter β,
- recovery rate γ,
- initial infected I_0.

We then:

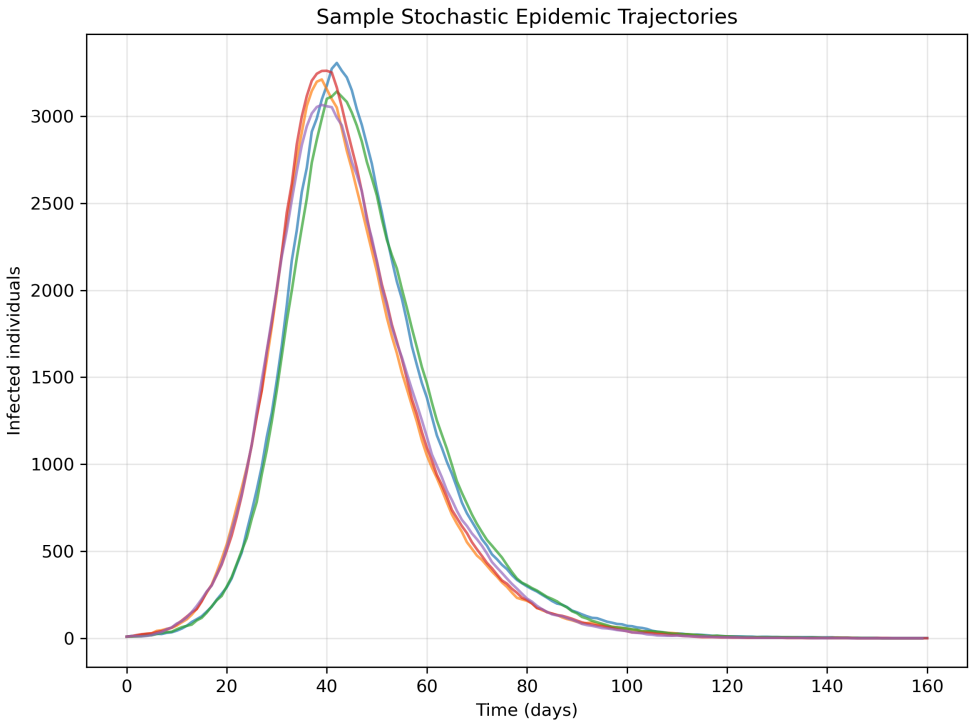
1. Simulate the epidemic day by day until a fixed horizon or until infections die out.
2. Record the full trajectory $S(t), I(t), R(t)$.
3. Repeat this process many times (e.g., 200 runs).

From these runs, we extract:

- sample infection trajectories,
- the final outbreak size $R(T)$ for each run,
- the distribution of final sizes.

Results

Sample Stochastic Trajectories

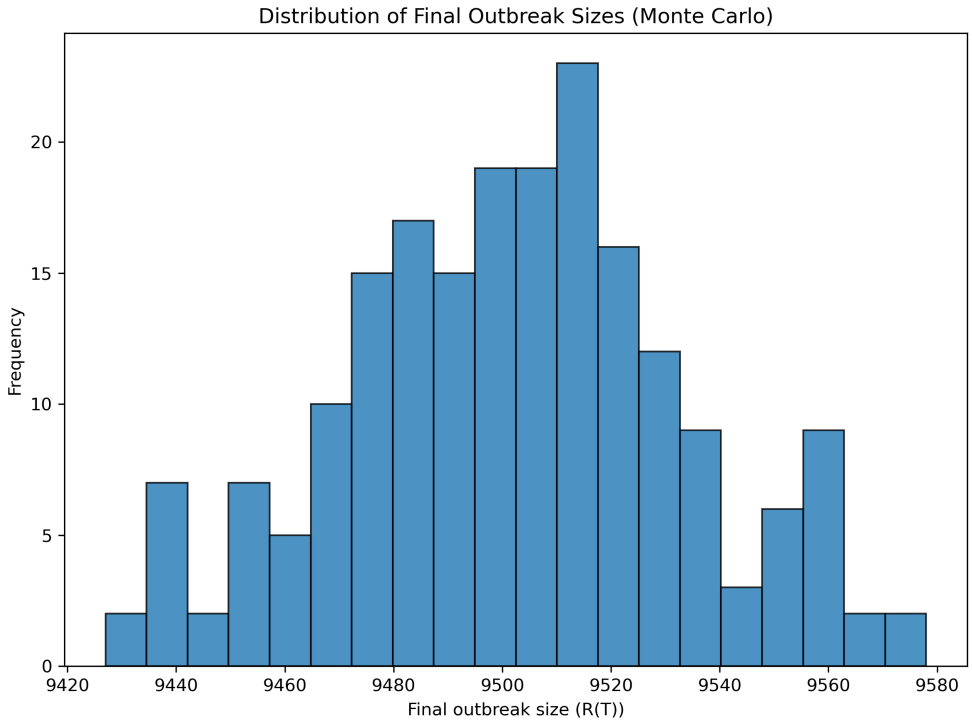


Each line represents one possible epidemic under the same parameters and initial conditions. Several patterns are visible:

- Some outbreaks grow quickly and reach a high peak.
- Others grow more slowly or peak at a lower level.
- A few may fade out relatively early if chance events break transmission chains.

This variability is **not** captured by deterministic models, which always produce the same smooth curve.

Distribution of Final Outbreak Sizes



The histogram shows the distribution of final outbreak sizes across all Monte Carlo runs. Even with identical parameters:

- Some simulations result in relatively small outbreaks.
- Others infect a large fraction of the population.

This spread reflects the inherent randomness in who gets infected and when.

Discussion

This project highlights a crucial point in infectious disease modeling:

> **Deterministic models describe the average epidemic, but real epidemics are single stochastic realizations.**

Key insights:

- **Randomness can prevent or trigger large outbreaks.** Even when the basic reproduction number suggests a major epidemic is likely, chance can still lead to early extinction.
- **Policy decisions must account for variability.** Planning for only the "average" outcome can underestimate risk.
- **Monte Carlo simulation is a natural extension of compartmental models.** It connects clean mathematical structure with realistic uncertainty.

From a portfolio perspective, this project shows that you can move beyond ODEs into stochastic processes and simulation-based inference—exactly the kind of depth employers look for in modeling roles.

Conclusion

By simulating many stochastic SIR epidemics, this project reveals how outbreak outcomes can vary widely under fixed parameters. The deterministic SIR curve is just one point in a broader distribution of possibilities.

Together with your previous SIR vaccination and age-structured SEIR projects, this work forms a coherent infectious disease modeling series that demonstrates:

- mathematical modeling skills,
- numerical implementation,
- stochastic thinking,
- and clear scientific storytelling.