

Deterministic and Stochastic SIR Models

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1 Introduction

Deterministic models, like the Susceptible, Infected, Recovered (SIR) model, are powerful tools in the field of epidemiology. These models can be enhanced to account for various factors, such as different transmission rates among age groups or the structure of the population. They can also include compartments for individuals who are isolated, quarantined, or vaccinated, and can factor in births and deaths.

Stochastic models introduce randomness into the simulation of epidemics, allowing for more realistic outcomes, especially in smaller populations. One method of stochastic simulation is through Stochastic Differential Equations (SDE). SDE are similar to ordinary differential equations (ODE) used in deterministic models, but they include an extra stochastic component. The advantage of SDE is that they run nearly as fast as deterministic models while allowing for assessments of outbreak probabilities and final epidemic sizes. However, they may occasionally yield unrealistic results, such as the number of susceptibles increasing, which should not happen without new births or reinfections. Like deterministic models, SDE also struggle with accurately depicting networked populations and other essential transmission dynamics.

The SIR model is one of the simplest compartmental models, and many models are derivatives of this basic form. The model consists of three compartments:

Susceptible(S): The number of susceptible individuals. When a susceptible and an infec-

tious individual come into "infectious contact", the susceptible individual contracts the disease and transitions to the infectious compartment.

Infectious(I): The number of infectious individuals. These are individuals who have been infected and are capable of infecting susceptible individuals.

Recovered(R): The number of removed (and immune) or deceased individuals. These are individuals who have been infected and have either recovered from the disease and entered the removed compartment, or died. It is assumed that the number of deaths is negligible with respect to the total population. This compartment may also be called recovered.

1.1 Deterministic SIR Model

The Deterministic SIR Model is a classic mathematical model used in epidemiology to describe the spread of infectious diseases within a population. The model divides the population into three compartments:

Susceptible(S): Individuals who are not infected but are at risk of contracting the disease.

Infected(I): Individuals who have the disease and can transmit it to susceptible individuals.

Recovered(R): Individuals who have recovered from the disease.

1.1.1 Mathematical Model

1. $N = S + I + R$
2. $\frac{dS}{dt} = -\beta \frac{SI}{N}$
3. $\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$
4. $\frac{dR}{dt} = \gamma I$

1.1.2 Model Parameters

1. **N**: Total population
2. **β (Beta)**: Transmission rate per susceptible and infected individual.
3. **γ (gamma)**: Recovery rate of infected individuals.

1.2 Agent-based Epidemic Model

In this model, agents (people) can be in one of three states: Susceptible (S), Infected (I), or Recovered (R). The code incorporates infection spread, recovery, and potential loss of immunity, simulating the dynamics of an infectious disease over time with random movements of agents within a constrained area.

1.2.1 Model Parameters

1. **R-circle**: Defines the radius of the circular boundary in which agents move.
2. **r-infection**: Sets the distance within which an infected agent can spread the infection to susceptible agents.
3. **σ (sigma)**: Controls the randomness of agent movement (standard deviation for random walk).
4. **α (alpha)**: Probability of infection if a susceptible agent comes within the infection radius of an infected agent.
5. **β (beta)**: Probability of recovery for infected agents in each time step.

6. **γ (gamma)**: Probability of losing immunity for recovered agents.
7. **N**: Total number of agents.
8. **T**: Total number of time steps in the simulation.
9. **S_0, I_0, R_0** : Initial counts of Susceptible, Infected, and Recovered agents.

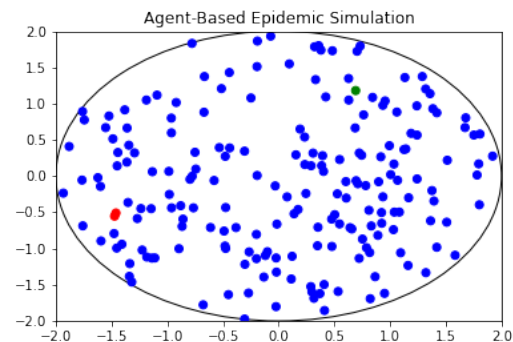


Figure 1: Agent-Based Epidemic Simulation

1.3 Probabilistic Epidemic Model

The probabilistic epidemic model described in your document is a mathematical framework that models the spread of an epidemic by using probability and state transitions, instead of deterministic differential equations like in SIR models. Here's a breakdown of the main elements.

Susceptible(S): Individuals who have not yet contracted the disease but are at risk.

Infected(I): Individuals who have contracted the disease and can spread it.

Recovered(R): Individuals who have recovered and are assumed to have immunity for some time.

1.3.1 Assumptions:

1. **Constant Population**: The model assumes no one dies from the disease; the sum of all states (S, I, R) remains constant.

2. **Well-Mixed Population:** Every individual has an equal chance of interacting with every other individual in the population.
3. **Large Population Size:** Allows modeling proportions instead of discrete individuals, simplifying probability calculations.

1.3.2 Transition Probabilities:

The model uses three main parameters to define the probabilities of transitioning between states:

1. **Infection Probability(α):**
The probability that a susceptible individual becomes infected.
2. **Recovery Probability(β):**
The probability that an infected individual recovers.
3. **Immunity Loss Probability(γ)**
The probability that a recovered individual becomes susceptible again (immunity loss)

Transition Matrix :

$$P = \begin{bmatrix} 1 - \alpha & \alpha & 0 \\ 0 & 1 - \beta & \beta \\ \gamma & 0 & 1 - \gamma \end{bmatrix}$$

2 Results and comparison

2.1 Deterministic SIR model

The below diagram represents the SIR model of an epidemic using a deterministic approach. This model illustrates the progression of a disease within a population over time, displaying changes in the proportions of individuals in each of the three compartments: Susceptible (S), Infected (I), and Recovered (R).

At the beginning of the epidemic (Day 0), the entire population is nearly susceptible, represented by the blue curve starting close

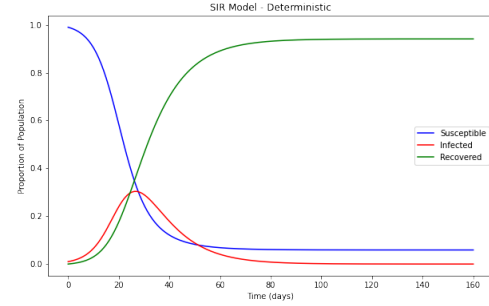


Figure 2: SIR model deterministic

to 1 on the y-axis. This indicates that almost everyone is at risk of infection since very few individuals, if any, are initially infected or immune. The infection rate is low because there are very few infected individuals to spread the disease.

As time progresses, more susceptible individuals (blue curve) contract the infection. This leads to an increase in the proportion of infected individuals, represented by the red curve, which rises quickly. Simultaneously, the susceptible population starts to decrease as more individuals become infected. The rapid growth of the infection indicates the beginning of an outbreak phase.

The red curve, which represents the infected population, reaches its peak between Days 20 and 40. At this point, a significant portion of the population is infected, and the number of new infections is at its highest. This peak signifies the epidemic's most intense phase, where the disease is spreading the fastest, fueled by the large number of both susceptible and infected individuals interacting.

After reaching the peak, the number of infected individuals begins to decrease as people recover and move into the recovered compartment. The green curve representing the recovered population starts rising sharply. This decline in infection indicates that the epidemic is slowing down, as the pool of susceptible individuals decreases and immunity within the population grows.

Eventually, the susceptible (blue) and infected (red) curves flatten as the proportions

stabilize. The blue curve reaches a low, steady level, indicating that only a small fraction of the population remains susceptible. Meanwhile, the green curve reaches a high, stable proportion, showing that most of the population has recovered and is now immune. The red curve approaches zero, indicating that the number of active infections has nearly vanished, marking the epidemic's end.

2.2 Agent-Based Epidemic Model

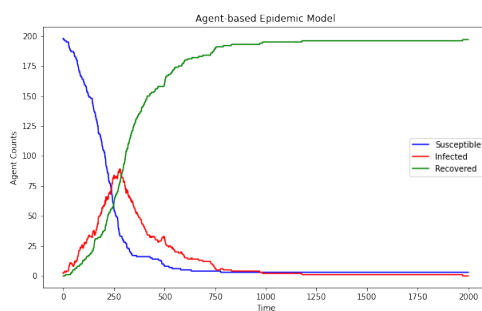


Figure 3: Agent Based Epidemic Model

The diagram represents an Agent-based Epidemic Model, which simulates the spread of a disease within a population of individual agents over time. Each curve in the plot represents the counts of agents in each of the three states: Susceptible (S), Infected (I), and Recovered (R), showing the dynamic changes as the infection spreads and recedes.

At the start, most of the agents are in the susceptible state, indicated by the high blue curve. There are few to no infected individuals initially, so the red curve for infected agents starts close to zero. Over time, some susceptible agents come into contact with infected ones, leading to an increase in infections.

As the infection spreads, the number of infected agents (red curve) rises, showing the onset of an epidemic. Simultaneously, the number of susceptible agents (blue curve) drops as they transition into the infected state. This increase in infections represents the rapid transmission of the disease within the agent-based population.

The red curve reaches its peak around the 200 – 300 time units, where the infection rate is at its highest. During this period, many agents are infected, resulting in a sharp drop in the susceptible agent count and a noticeable rise in the recovered count (green curve) as agents begin to recover from the infection.

After the peak, the infection curve (red) declines as more agents recover, moving into the recovered state. This decline suggests that the epidemic is slowing down, as fewer susceptible agents remain, reducing the chances of transmission. The green curve for recovered agents rises significantly, indicating that a large proportion of the population has acquired immunity.

Toward the right side of the plot, all three curves stabilize. The blue curve for susceptibles remains close to zero, suggesting that almost everyone has been infected or has recovered. The red curve approaches zero, indicating that very few, if any, agents are still infected. The green curve flattens at its highest level, showing that most agents are in the recovered state, marking the epidemic's end.

2.3 Probabilistic Epidemic Model

In Probabilistic Epidemic Model, which simulates the progression of an epidemic where each individual's transition between states (Susceptible, Infected, and Recovered) is governed by probabilistic rules rather than fixed rates. The curves depict how the proportions of susceptible (blue), infected (red), and recovered (green) individuals change over time, reflecting the epidemic dynamics with a stochastic approach.

At the beginning of the simulation, the population is mostly susceptible (blue curve), with only a few individuals infected (red curve). This initial state shows a high risk of infection spread, as most of the population is vulnerable to the disease.

As time progresses, the infection spreads among the susceptible individuals. The red curve rises sharply as more individuals become infected, while the blue curve for sus-

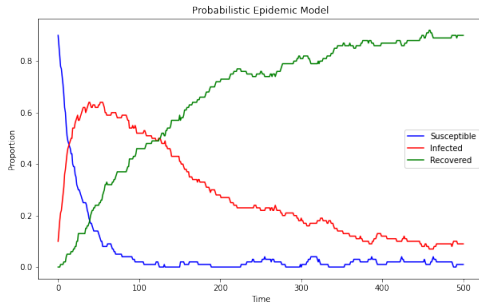


Figure 4: Probabilist Epidemic Model

ceptible individuals declines. This phase illustrates the rapid spread of the epidemic, as many susceptible individuals encounter infected ones and transition into the infected state. The random interactions and probabilistic transitions contribute to the fluctuations in both curves, making them less smooth than in a deterministic model.

The infected population reaches a peak around the 50–100 time units, with the red curve at its highest point. During this phase, the number of new infections is balanced by recoveries, leading to slight fluctuations rather than a smooth peak. This variability reflects the stochastic nature of the probabilistic model, where each individual's transition to the next state is influenced by chance rather than fixed rates.

After the peak, the infection rate declines as more individuals recover, and the green curve for recovered individuals rises. The blue curve for susceptible individuals remains low, as most have either become infected or recovered. This decline in infections represents the slowing down of the epidemic, as fewer susceptible individuals remain to propagate the disease. The green recovery curve continues to increase as the epidemic progresses, with fluctuations showing the probabilistic nature of recoveries over time.

Towards the end, the infected (red) curve stabilizes at a low level, close to zero, indicating that very few active infections remain. The recovered population (green

curve) reaches a high, stable proportion, while the susceptible population (blue) remains low. The epidemic reaches an equilibrium state where the disease no longer spreads significantly, marking the end of the epidemic.

3 Agent-based Epidemic Model with Lockdown and Vaccination

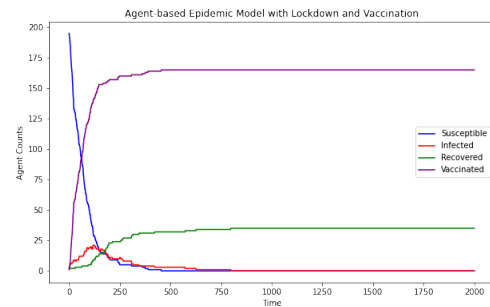


Figure 5: Agent based epidemic model with lockdown and vaccination

In the beginning, the Susceptible (Blue) group, which includes everyone who hasn't yet been infected or vaccinated, is quite large. But as the disease starts spreading, this group shrinks quickly, meaning that many people are either catching the infection or getting vaccinated.

The Infected (Red) line spikes quickly at first, showing a rapid spread of the disease. However, this spike doesn't last long—thanks to lockdowns, which reduce people's contact with each other, and vaccinations, which protect people from catching the infection. As a result, the number of infected people drops sharply and eventually approaches zero, indicating the outbreak is being controlled.

The Recovered (Green) line rises as infected people recover from the disease and gain immunity. After a while, this group reaches a stable level, which suggests that the disease has stopped spreading significantly, and there aren't many new cases.

The Vaccinated (Purple) line shows the number of people who get vaccinated over

time. Early in the outbreak, this number increases quickly, as a large portion of the population gets vaccinated to prevent further spread of the disease. Eventually, the vaccinated group stabilizes at a high level, showing that most people in the population are protected, either through vaccination or recovery from the disease.

In the deterministic SIR model, the disease spreads freely, causing a large infection peak and requiring most people to recover from infection to stop the outbreak. In contrast, the agent-based model in the figure includes lockdowns and vaccinations, which reduce infections by converting susceptible people directly to vaccinated. This leads to a much lower infection peak and faster control of the outbreak, with fewer people needing to recover from the disease. Overall, the agent-based model shows how interventions like vaccination and lockdowns can quickly and effectively contain an epidemic, unlike the traditional SIR model.

4 Comparison of Models

4.1 Deterministic and Agent based model

4.1.1 Stochastic Nature:

In this agent-based model, there are fluctuations in the curves, especially noticeable in the infection curve, due to the random interactions between agents. This is in contrast to the smooth, predictable curves in the deterministic SIR model, which assumes uniform mixing in the population.

4.1.2 Granularity:

The agent-based model provides a more granular view, tracking individual agents and their state transitions, while the deterministic SIR model uses aggregate population proportions, which simplifies the dynamics.

4.1.3 Time Scale Variability:

The time scale in the agent-based model can be much more extended (up to 2000 time units in this plot) compared to the shorter time scale seen in the deterministic model. This variation depends on individual interactions, which can delay or speed up the epidemic progression.

4.1.4 Noise and Realism:

The agent-based model captures random variations that mimic real-world unpredictability, such as clusters of infections or random recoveries, providing a more realistic view of how an epidemic might spread unevenly in different parts of a population.

4.2 Deterministic and Probabilistic Epidemic Model

4.2.1 Stochastic Variability:

Unlike the deterministic SIR model, the probabilistic model shows significant fluctuations in all curves, particularly in the infected and recovered populations. These fluctuations arise from the randomness in individual transitions, making the model more representative of real-world epidemic patterns, where randomness and chance interactions play a major role.

4.2.2 Non-Smooth Transitions:

In the probabilistic model, the curves are not smooth and show random oscillations, unlike the smooth, predictable trajectories of the deterministic SIR model. This irregularity captures the uncertainties in individual behaviors and interactions, which are absent in the deterministic approach.

4.2.3 Realistic Dynamics:

The probabilistic model provides a more realistic view of an epidemic, accounting for the unpredictability of real-life interactions and recoveries. This randomness makes the

model suitable for analyzing smaller populations or heterogeneous environments, where individual behaviors and random events significantly impact the epidemic's progression.

5 Future Scope

5.1 Deterministic Models

5.1.1 Multi-Scale Modeling

Deterministic models could be expanded to operate on multiple scales, from individual to community and regional levels. These models can then predict the spread at different population sizes and help coordinate local and global interventions.

5.1.2 Application to Zoonotic Diseases:

Deterministic models could be tailored to study zoonotic diseases, where the transmission involves different species. Incorporating parameters for animal-to-human transmission would be particularly relevant for diseases originating from wildlife.

5.1.3 Predictive Policy Simulations:

Deterministic models can become powerful tools for government and healthcare decision-making. By simulating various intervention scenarios (e.g., lockdown, vaccination, testing), the models could help optimize strategies for different regions and situations.

5.2 Agent-Based Models

5.2.1 Behavioral Adaptation Modeling:

Future agent-based models could simulate behavioral adaptations, such as social distancing, mask-wearing, and vaccination acceptance. Modeling individual responses to government interventions would provide valuable insights into behavioral dynamics during an epidemic.

5.2.2 AI-Enhanced Agent Behavior:

Using AI techniques, agents can be programmed with adaptive, intelligent behavior, allowing them to change based on their experiences. For example, agents can simulate "learning" from past outbreaks or observing others' health status, creating even more realistic epidemic simulations.

5.2.3 Application in Vaccination Strategy Optimization:

Agent-based models can be used to simulate and optimize vaccination strategies in diverse populations, considering factors such as age, mobility, and contact frequency. This approach would aid in creating more effective immunization policies, especially in heterogeneous populations.

6 Conclusion

In this study, we explored three types of epidemic models: the deterministic SIR model, the agent-based epidemic model, and the probabilistic epidemic model.

The deterministic SIR model provides a smooth and predictable approach to understanding epidemic dynamics. However, it may oversimplify complex social interactions and lacks the variability that real-world epidemics often display.

The agent-based model introduces a high level of detail by simulating each individual's behavior, incorporating randomness in movement, and modeling infections on a local scale. This model better reflects social structures and is particularly useful for studying disease spread in smaller or structured populations. However, it is computationally intensive and may be harder to scale.

The probabilistic epidemic model bridges these two approaches by incorporating randomness into state transitions while still working at the population level. This adds variability to the epidemic's progression, which makes it useful for smaller populations

or scenarios where chance plays a larger role in disease transmission.

In comparing the models, the deterministic model is ideal for fast, large-scale simulations; the agent-based model is suited for detailed, individual-based studies; and the probabilistic model provides a balanced approach, adding realism without excessive complexity. Each model has a role in epidemiology, with the choice largely depending on the specific research goals and available computational resources.

7 References

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