MARKOV SIMULATION: A Comprehensive Analysis of the Markovian SIR Epidemic Model for Comparative City Simulations

Introduction

The study of epidemic dynamics is crucial for public health planning and intervention strategies. As a student in a field that involves epidemiology related questions, I was very excited to read papers on this and work on my using Markov Simulation to answer some of these questions. This notebook employs a grid-based Susceptible-Infected-Recovered (SIR) model, where I have incorporated demographic factors, infection zones, and Markov Chains, to simulate and compare disease outbreaks in two hypothetical cities: Mumbai and Jorhat. Mumbai represents a young, densely populated urban center, while Jorhat symbolizes an older, sparsely populated rural community. By contrasting these two cities, the simulation aims to imagine how demographic differences influence epidemic progression. This is my try to see to use this example for generalization of similar city types we see elsewhere. Furthermore, the model explores the impact of varying disease characteristics, specifically comparing a mild, common disease like the flu with a highly contagious one like measles. Finally, the simulation visualizes how vaccines when incorporated the target for an age group which was the situation in India in the initial vaccination stages for Covid-19 where you had to be of a certain age group to first receive the vaccine. This approach provides valuable insights into the complexities of disease transmission and the potential benefits of targeted public health measures.

Applications for the SIR Model and Markov Chains in Epidemiology:

The main theory that I am using here involves dividing the group we are working with into one of three states: Susceptible (S), those who can contract the disease (which here everyone initially

is); Infected (I), those currently carrying and transmitting the disease; and Recovered (R), those who have had the disease and are now immune. This model has broad applications, including:

1. Predicting Outbreak Trajectories: The SIR model helped us see through the graph, the peak of an epidemic, the total number of infected individuals, and the duration of the outbreak.
2. Evaluating Intervention Strategies: The model allowed me to insert in the simulation a public health intervention, which was vaccination campaigns. Then see how that changed the peaks of infection.
3. Comparative Epidemiology: As demonstrated in this notebook, the SIR model can be used to compare disease spread across different populations or settings.

Advantages and Disadvantages of the Implementation

The implementation in the notebook offers several advantages:

1. Integration of Spatial Dynamics and Markov Chains: The model uniquely combines a spatial grid-based simulation with a theoretical Markov Chain approach. This allows for a comparison of how local interactions and population-level dynamics influence disease spread. It is one step closer towards visualizing how disease spread
2. Demographic Heterogeneity: The inclusion of age structure and varying population densities provides a more realistic representation of real-world scenarios.
3. Vaccination Simulation: The ability to simulate targeted vaccination campaigns for different age groups helps to see the benefit it does.

4. Visualizations: The use of plots to display the Susceptible, Infected, and Recovered curves for both the simulation and the Markov Chain model facilitates a clear understanding of the results.

However, the implementation also has some disadvantages:

1. Simplifications: The SIR model itself is a simplification of reality. This model was not able to incorporate a lot of factors which might occur in real time disease spread.
2. Grid-Based Limitations: The grid-based simulation imposes a spatial structure that did a fair job but might not be the best representation of the real world..

Methodology for Code Functionality Confirmation:

1. Unit Testing: Individual functions, such as “apply_vaccination” and “run_simulation”, could were tested in isolation with various inputs to verify their correctness.
2. Visual Inspection: The plots generated by the code are visually inspected to ensure they exhibit expected trends. For instance, the number of susceptible individuals should decrease over time, while the number of recovered individuals should increase. Which helped me conclude that the model is working.
3. Documentation and Comments: Clear documentation and comments within the code make it easier to understand, debug, and maintain.
4. Modular Design: Breaking the code into smaller, reusable simplifies testing.

Explanation of Formulas Used

This showed the transition between each stage(these are the formulas I got from the research papers and incorporated into google colab

Susceptible:

$$S_{t+1} = S_t - \beta \times S_t \times I_t$$

The number of susceptible individuals decreases as they get infected.

Infected:

$$I_{t+1} = I_t + \beta \times S_t \times I_t - \gamma \times I_t$$

The infected group grows as more people get infected and shrinks as they recover.

Recovered:

$$R_{t+1} = R_t + \gamma \times I_t$$

The recovered group increases as infected individuals recover.

Where:

- S_t, I_t, R_t = number of susceptible, infected, and recovered individuals at time t
- β (beta) = transmission rate (how easily the disease spreads)
- γ (gamma) = recovery rate (how quickly people recover)

Markov Chain Transition Matrix:

This matrix models the probabilities of transitioning from one state (S, I, R) to another in a **single time step**:

$$P = \begin{bmatrix} 1 - p_{\text{infection}} & p_{\text{infection}} & 0 \\ 0 & 1 - p_{\text{recovery}} & p_{\text{recovery}} \\ p_{\text{loss\_immunity}} & 0 & 1 - p_{\text{loss\_immunity}} \end{bmatrix}$$

Each row represents the **current state**, and each column represents the **next state**.

Where:

- p_infection = chance that a S person becomes I
- p_recovery = chance that a I person becomes R
- p_loss_immunity = chance that a R becomes S again

Markov Chain State Update Formula

This formula updates the fractions of people in each group using matrix multiplication with every “step”:

$$[S_{t+1}, I_{t+1}, R_{t+1}] = [S_t, I_t, R_t] \times P$$

Graph Interpretation

By comparing the left and right subplots, we can observe the differences between the two simulations, first the spatial simulation and then the theoretical Markov Chain prediction. Reflecting this into real life scenario although possible to some extent not fully a generalization may arise due to the simplifications made in the Markov model, such as the assumption of homogeneous mixing. The graphs also allow us to analyze the impact of different parameters and city demographics on the epidemic's trajectory. For example, we can compare the peak infection rate and the total number of infected individuals between Mumbai and Jorhat for both the flu and measles scenarios. The effects of vaccination can be assessed by comparing simulations with and without vaccination, and by varying the target age group and coverage.

Conclusion

This notebook provides a valuable framework for simulating and analyzing epidemic dynamics in different urban and rural settings. We are seeing through this how diseases spread looks different when a place is highly crowded and when a place is lower in population. This shows the effectiveness of measures like social distancing and quarantine like we saw during covid. By integrating a grid-based SIR model with Markov Chains and incorporating demographic factors and vaccination interventions, the simulation offers an understanding to the complexities of disease transmission. The comparative analysis of Mumbai and Jorhat where one is was my effort of trying to visualize my hometown and the comparing to one of the busiest cities in my country with a "downtown" like crowded environment in the heart of that city shows the importance of considering population structure in epidemic modeling and public health planning. While the model has limitations due to its nature of being simple, it provides valuable insights into the potential impact of various factors on epidemic outcomes at least at the very foundational level.

Citations:

1. Linda. "An Introduction to Stochastic Epidemic Models." *Lecture Notes in Mathematics*, 1 Jan. 2008, pp. 81–130, https://doi.org/10.1007/978-3-540-78911-6_3.

2. Xu, Zhaobin, et al. "A Continuous Markov-Chain Model for the Simulation of COVID-19 Epidemic Dynamics." *Biology*, vol. 11, no. 2, 26 Jan. 2022, p. 190, https://doi.org/10.3390/biology11020190. Accessed 16 Nov. 2022.3.
3. "Welcome to Zscaler Directory Authentication." *Ieee.org*, 2025, ieeexplore.ieee.org/abstract/document/9435414. Accessed 13 May 2025.