

Sabancı University
**Faculty of Engineering and Natural
Sciences CS414 – Network Science**

ASSIGNMENT 2

SI AND SIR MODELS

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Introduction

In this assignment, we explore agent-based modeling of epidemic spreading on networks using the SI and SIR models. The aim is to understand how network structure and model parameters affect the dynamics of infection spread. We use synthetic social networks generated via well-known models such as Erdős-Rényi, Barabási-Albert, and Watts-Strogatz. The simulation is implemented in Python using NetworkX for graph generation, and Matplotlib for visualization. All simulations follow the structure provided in the assignment template without modification to the base logic flow.

SI Model

Model Description

The SI (Susceptible-Infected) model consists of two states:

- **S (Susceptible)**: can become infected if connected to an infected neighbour.
- **I (Infected)**: remains infected forever.

In each timestep:

- Each infected node has a probability μ to infect its susceptible neighbours.
- No recovery is possible.

Implementation Details

The SimulationSI class maintains agent states and the network. At each step:

- Infected agents attempt to infect their neighbours with probability μ .
- State counts are updated and stored for plotting.

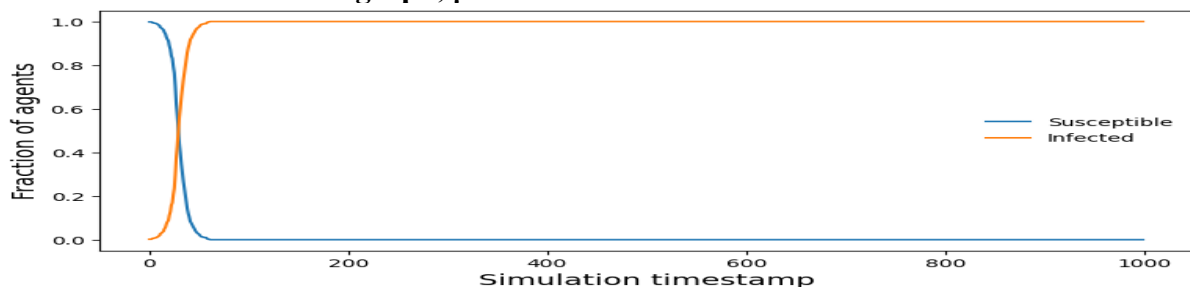
Simulation was run with:

- $n\text{Agents} = 500$
- $\mu = 0.01, 0.1, 0.05$
- Network: Erdős-Rényi (initial)

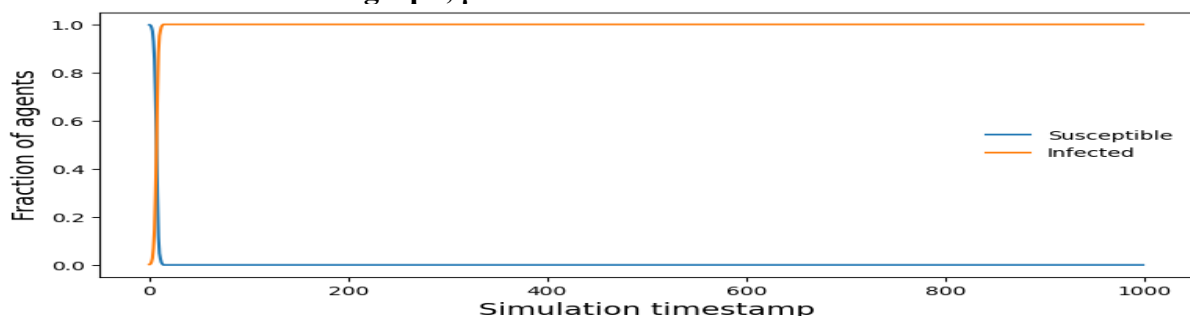
Results and Observations

Below are plots for the fraction of Susceptible and Infected agents over time.

Plot of SI Model - ER graph, $\mu=0.01$



Plot of SI Model - ER graph, $\mu=0.05$



Key observations:

- The number of susceptible agents steadily decreases while infections rise.
- Infection saturates when no more susceptible neighbours exist.
- Increasing μ leads to faster saturation.

Parameter Variation: μ

We experimented with different transmission probabilities:

- $\mu = 0.01$
- $\mu = 0.05$
- $\mu = 0.1$

Observations:

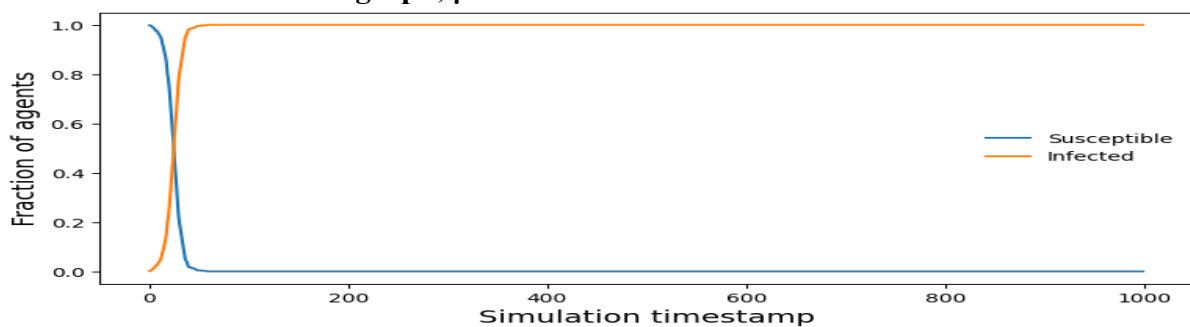
- Lower μ results in slower spread.
- At higher μ , infection approaches full saturation rapidly (within fewer time steps).

Topology Variation

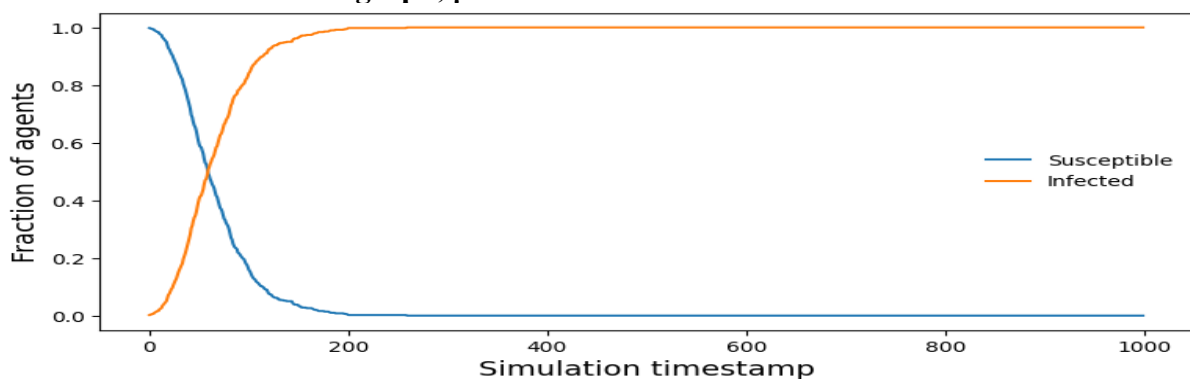
We tested with the following network types:

- Erdős-Rényi (ER)
- Barabási-Albert (BA)

Plot of SI Model - ER graph, $\mu=0.01$



Plot of SI Model - BA graph, $\mu=0.01$



Observations:

- ER networks tend to spread infection faster than BA.
 - BA networks show slower infection than ER due to hubs (depending on rewiring prob).
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2. SIR Model

Model Description

The SIR model extends SI with a third state:

- **R (Recovered)**: infected agents can recover with probability γ .

At each time step:

- Infected agents infect susceptible neighbours with probability μ .
- Infected agents recover with probability γ .

Implementation Details

The SimulationSIR class includes recovery dynamics. Key features:

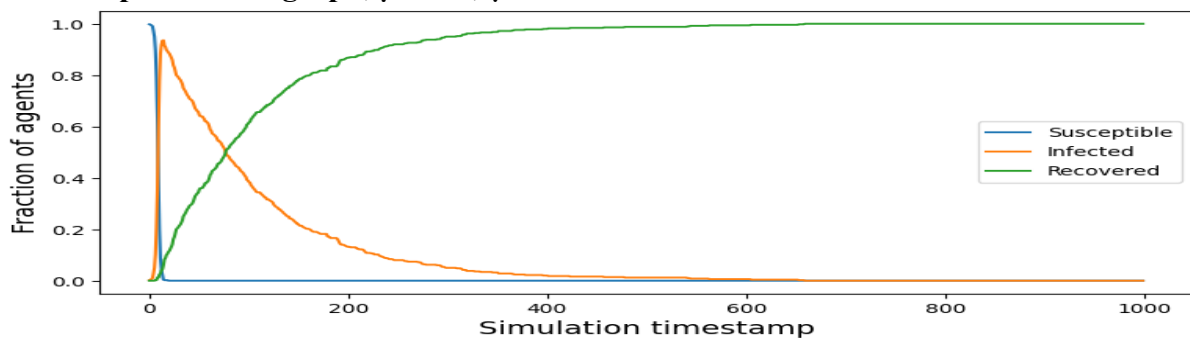
- Both new infections and recoveries are applied in each step.
- State counts include "S", "I", and "R".

The simulation used:

- $\mu = 0.05$
- $\gamma = 0.01$
- Erdős-Rényi network (initial)

Results and Observations

SIR plot for ER graph, $\mu=0.05$, $\gamma=0.01$



We observe:

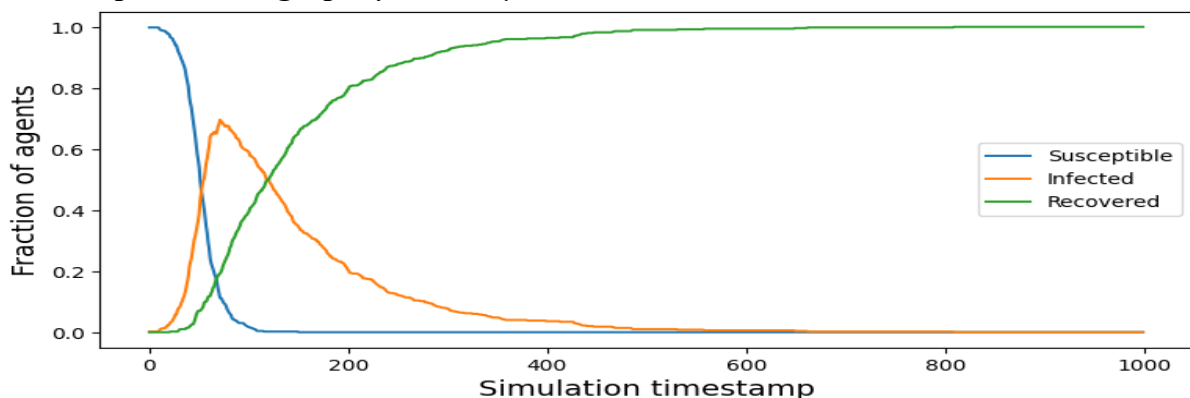
- The infection rises, peaks, and declines.
- The recovered population increases steadily.
- Susceptible decrease, but not to zero — some avoid infection entirely.

Parameter Variation: μ and γ

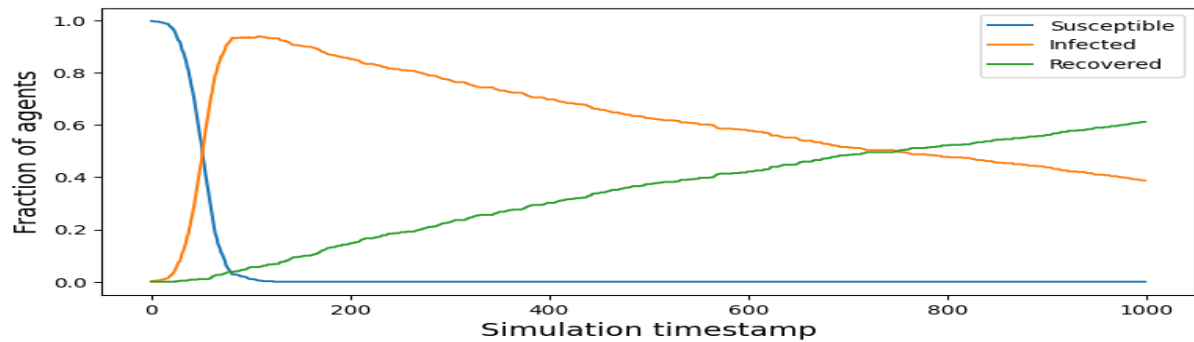
We explored different values of μ and γ :

- $\mu \in \{0.02, 0.05, 0.005\}$
- $\gamma \in \{0.01, 0.001, 0.05\}$

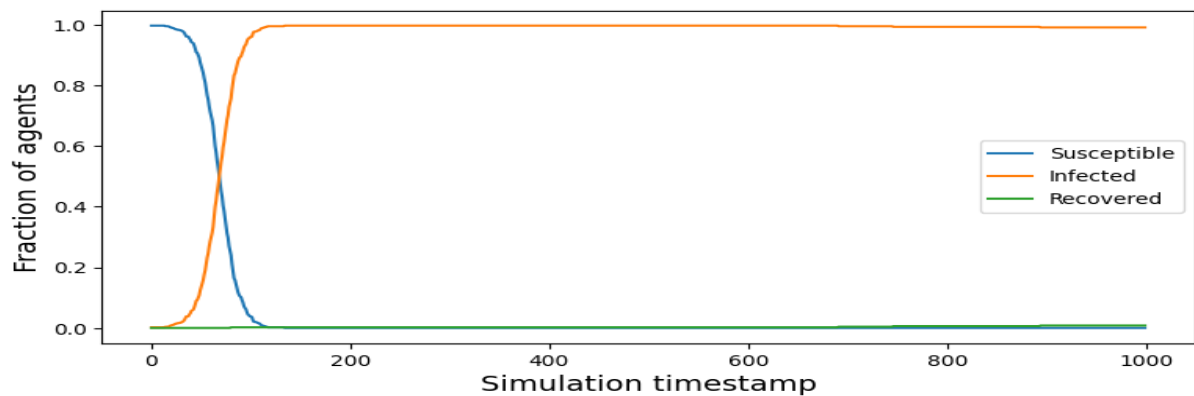
SIR plot for ER graph, $\mu=0.005$, $\gamma=0.01$



SIR plot for ER graph, $\mu=0.05$, $\gamma=0.001$



SIR plot for ER graph, $\mu=0.05$, $\gamma=0.00001$

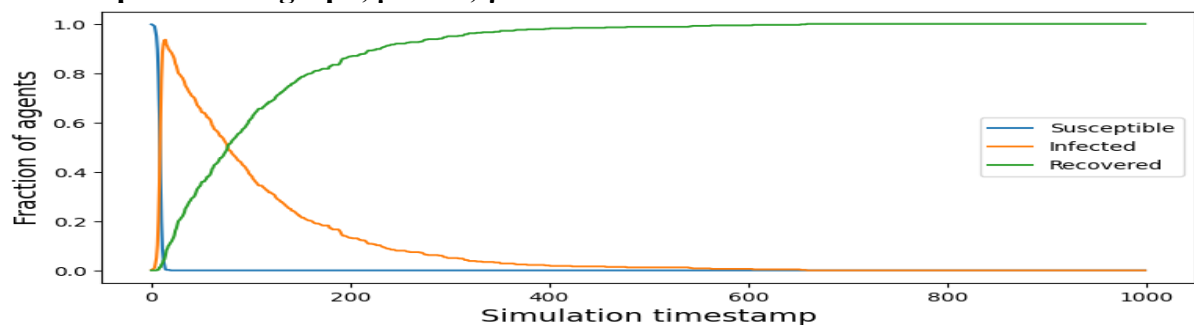


Insights:

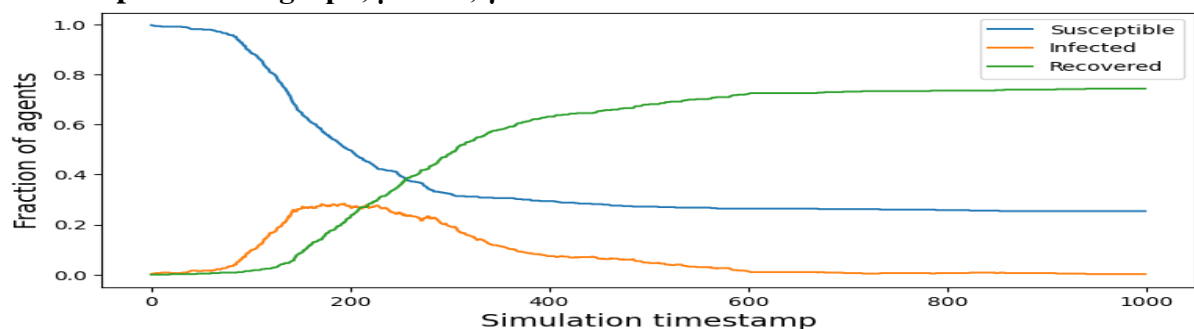
- Higher μ leads to a quicker, higher peak in infections.
- Higher γ causes faster recovery, flattening the infection peak.
- There's a threshold-like behavior for the gamma where infection either dies out or becomes widespread.

Topology Variation

SIR plot for ER graph, $\mu=0.05$, $\gamma=0.01$



SIR plot for BA graph, $\mu=0.05$, $\gamma=0.01$



Observations:

- BA networks show quicker infection due to influential hubs; however it does not lead to quicker recovery.
 - ER shows moderate behaviour where the rise and the fall of the infection is balanced in their own relative scenarios.
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Conclusion

This assignment demonstrated how epidemic models behave on different network structures.

Key takeaways:

- **Transmission (μ) and recovery (γ) rates** significantly affect outcomes.
- **Network topology** plays a major role:
 - BA promotes rapid, widespread infection.
 - WS shows variability based on parameters.
 - ER behaves predictably with random spread.

The models are simple but capture essential behaviours seen in real epidemics. This simulation framework can serve as a basis for exploring more complex scenarios in public health or information spreading.