



Abstract

Human societies can be effectively visualized as community networks, where individuals belong to various overlapping groups. This project focuses on modeling epidemic spread in such overlapping community networks, simulating the dynamics of disease transmission within a population of 200 members. Our analysis, using a custom SIR (Susceptible-Infected-Recovered) model, provides valuable insights into the progression of an epidemic and its impact on a day-by-day basis. We found that the overlapping nature of communities substantially influences disease propagation. Specifically, we observed how the number and size of communities influence the spread of a disease and the rate of recovery. Additionally, we examined the effects of limiting the number of communities on the epidemic. These findings contribute to a deeper understanding of epidemic dynamics in human societies, highlighting the complexity introduced by overlapping communities and the limitations of node-targeted intervention strategies.

Background

Real-world societies can be effectively modeled as complex networks, where individuals (nodes) interact within and across various social groups (communities). These communities often overlap, with people participating in multiple groups. This network structure plays a crucial role in the spread of infectious diseases. Highly mobile individuals, who bridge connections between communities ("hyperactive nodes"), can significantly accelerate disease transmission [1]. We leverage the concept of overlapping community networks, as described in [2].

Our simulations explore disease spread within a population of 200 individuals. We model two community scenarios:

S-1 Large Communities (10 communities of 20 each): This reflects a more open social structure with a moderate degree of overlap.

S-2 Small, Restricted Communities (40 communities of 5 each with a 3-community limit per person): This simulates a scenario with smaller social groups, potentially reflecting restrictions like lockdowns.

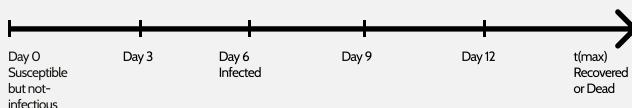
Model

SIR Compartments:

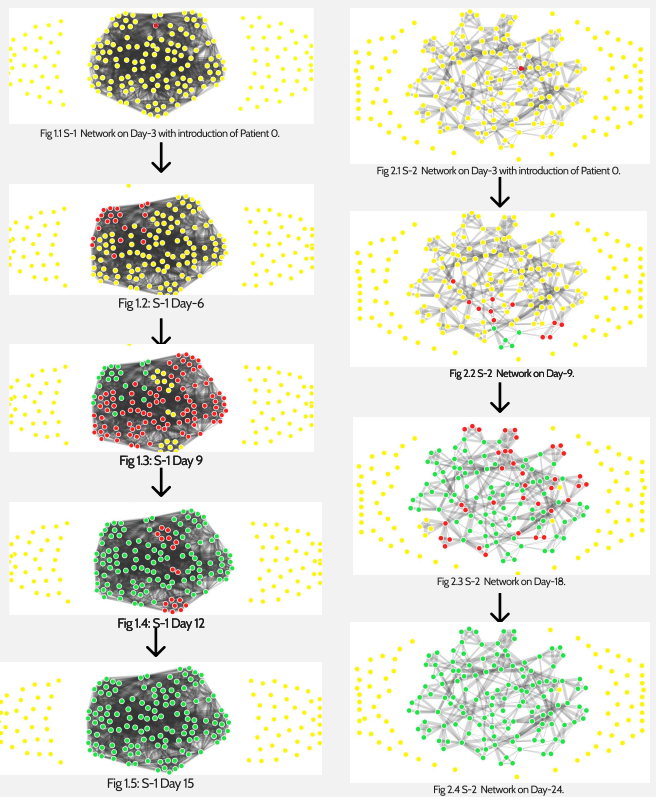
- Susceptible (S): Individuals who can contract the disease.
- Infected (I): Individuals who have the disease and can transmit it to others.
- Recovered (R): Individuals who have recovered from the disease and are immune.

Progression:

- Initially, all individuals are susceptible (S).
- A random individual is chosen as the "patient zero" and transitions to infected (I) on Day 0.
- Between Day 0-3, susceptible individuals connected to patient zero are exposed but not yet infectious.
- On Day 5 or 6, these exposed individuals become infectious (I).
- Infected individuals can transmit the disease to susceptible contacts.
- On Day 9, infected individuals recover or die (R) and gain immunity.



Results



Conclusion and Future Work

Our simulations demonstrated that disease spread rapidly through both community structures with everyone recovering or succumbing within a short timeframe (15-24 days for a population of 200). Interestingly, removing a single hyperactive individual had minimal impact on the outbreak in the large community scenario (10 communities of 20 members). This suggests that the extensive overlap between these large communities creates multiple pathways for disease transmission, rendering targeted interventions against single individuals less effective. However, in the scenario with smaller, more restricted communities (40 communities of 5 members with a 3-community limit), hyperactive agents were likely limited in their ability to bridge connections due to the restricted nature of the communities. Here, future work could involve ranking hyperactive agents (S-1) and adding hyperactive agent (S-2).

References

- [1] Granovetter, M. S. (1973). The strength of weak ties. *American Journal of Sociology*, 78(6), 1360-1380
- [2] Karan, R., & Biswal, B. (2017). A model for evolution of overlapping community networks. *Physica A: Statistical Mechanics and its Applications*, 474, 380-390