Generating, Populating, and Analyzing Ego Networks to Mitigate the Spread of MRSA

Student: Kushagra Singhai
Mentors: Abhijin Adiga, Anil Vullikanti

Computation Epidemiology

Background

**MRSA:** Methicillin-resistant Staphylococcus aureus
- Staph Bacteria resistant to antibiotics
- Studying Epidemiology is crucial, as antibiotics are ineffective

Cascade Graph
- Illustrates spread of certain disease from node to node along directed edges

Contact Network
- Similar to Cascade Graph, except illustrates how two or more nodes may be connected, illustrating possible pathways for transmission.
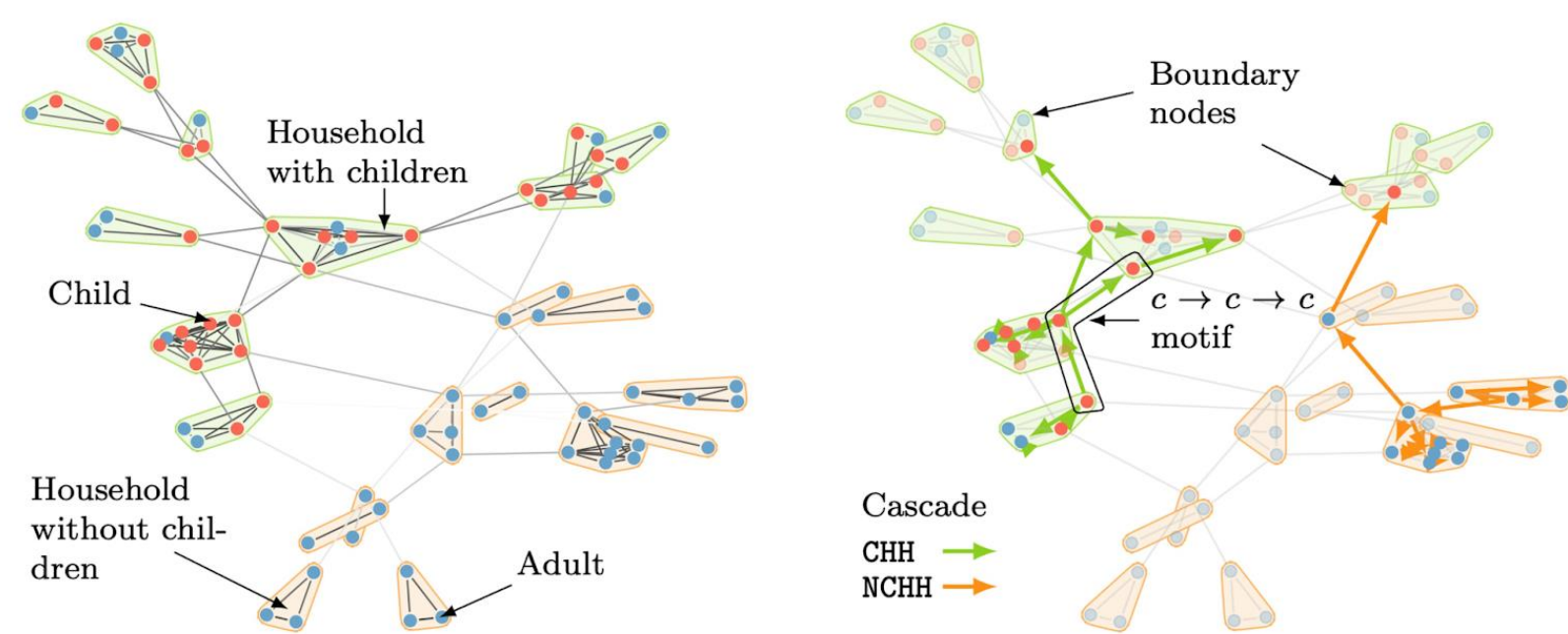
Figure #1: Contact Network, Cascade Graph

By analyzing generated Cascade Graphs + Contact Networks, we can identify recurring patterns that are indicative of MRSA spread.

Properties include: cascade size, duration, secondary infection rates, degree centrality, clustering coefficient, community structures, etc.

Research Question

How can the analysis of the cascade graph and the identification of recurring properties in the cascade and contact network contribute to understanding the significance of these properties in the spread of MRSA and guide the optimization of testing and isolation strategies?

Expected Results

The analysis of the cascade graph is expected to identify recurring properties indicative of MRSA spread dynamics, such as cascade size, duration, and secondary infection rates. The contact network analysis will reveal correlations between cascade properties and network characteristics, such as influential nodes, connectivity patterns, and community structures. These correlations will inform the optimization of testing and isolation strategies, leading to the development of targeted approaches focused on nodes, communities, or network features associated with high MRSA transmission rates. This optimization is expected to result in more effective control measures. Implementing the optimized strategies is anticipated to mitigate the spread of MRSA within the network, reducing the overall number of MRSA infections and potentially containing MRSA outbreaks through targeted identification and isolation of infected individuals.

Methodology

1. Gather data on the cascade graphs, which represent the spread of MRSA within the network, capturing information such as the sequence and timing of infections and the individuals involved.
2. Collect data on the contact network, which represents the interactions and connections between individuals in the population.
3. Analyze the cascade graph to extract relevant properties and characteristics of the MRSA spread.
4. Identify the recurring properties of the Cascade Graph, such as the size of the cascades, the duration of the cascades, the number of secondary infections, or any other properties that may be indicative of the disease spread dynamics.
5. Generate and Analyze Ego Networks to identify properties and measures related to the network structure.

EGO NETWORKS

These networks are, simply put, contact networks generated around one singular node. Using the NetworkX package, we have almost completed generating these for any given individual. Although the real data will contain many more connections, here is the progress on the contact networks that are being generated right now:
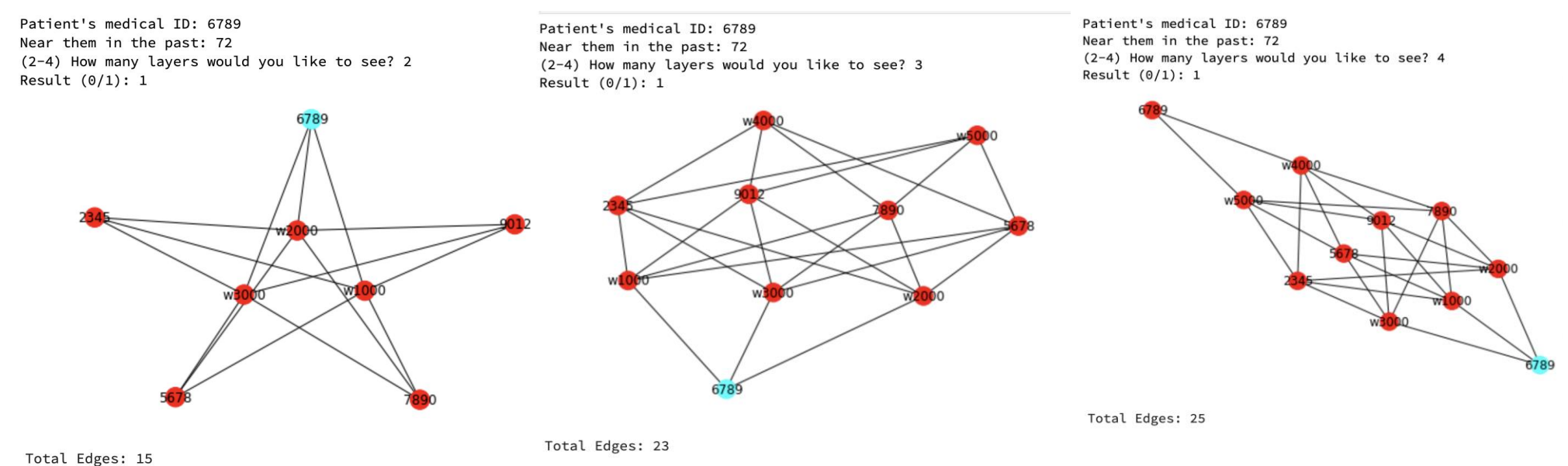
Figure #2: Generated Ego Networks

6. Explore metrics such as degree centrality, clustering coefficient, community structure, or any other network measures that may reveal patterns or correlations with the MRSA cascade properties.
7. Examine the relationship between the properties identified in the cascade graph and the contact network.
8. Determine if there are significant correlations or associations between recurring cascade properties and specific network characteristics.
9. Utilize the insights gained from the correlation analysis to inform the optimization of testing and isolation strategies.
10. Incorporate the recurring properties of the cascade and network into the selection of nodes for testing and isolation, considering factors such as the probability of infection, influential nodes, or communities with high transmission rates.

UNIVERSITY of VIRGINIA

BIOCOMPLEXITY INSTITUTE