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Impact of Social Networks on the Spread of Disease

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Impact of Social Networks on the Spread of Disease

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Abstract

Social mixing among heterogeneous subgroups is critical to understanding the dynamics of disease transmission in populations. Although a unified theory and representation of social mixing has been described mathematically, the epidemiological implications of various mixing patterns are still poorly understood. We present a novel approach to investigate the impact of social mixing networks on the spread of a disease in a population. Individuals are assigned an average contact rate (from a Poisson distribution) and a mixing rate (from a uniform distribution) for within network interactions. As the system evolves, contact networks are constructed from interactions that occur between individuals. We investigate the spread and control, using isolation and/or quarantine, of an SIR (Susceptible-Infected-Recovered) epidemic in a population with various mixing frameworks.

Model Description

In an SIR model, a contact between a susceptible individual and an infected individual can result in the infection of the susceptible individual. At the end of each day, when all contacts have been completed, an individuals status can change to recovered, dead, or isolated if they meet the criteria.

n - total number of people
c - number of contacts each person makes each day
I - number of individuals infected on Day 1
p - exponent for controlling network exclusivity
β - chance of infection after a susceptible-infected contact
γ - chance of recovery
μ - chance of death from the infection
ι - chance of isolation/quarantine
(infected person isolated from the population)

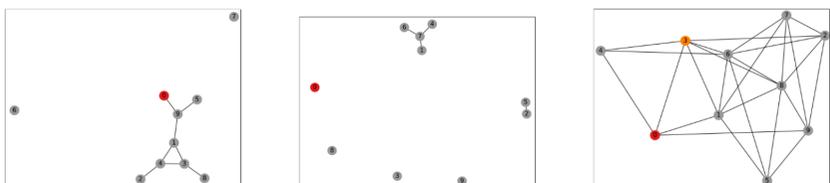## Network Diagrams/Construction

Figure 1: Examples of various network configurations

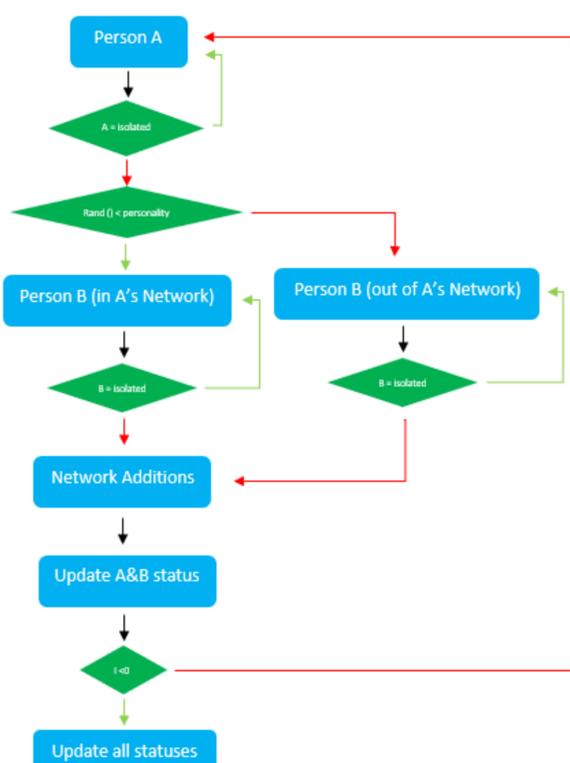Figure 2: Visual representation of an interaction between two people from the population.

Figure 3: Visual representation of a day of interactions.

Number of Initial Infected

In the SIR epidemic model, we varied the initial number of infected individuals (1, 2, 4, 8, 16, 32, 64). These data serve as a basis for the spread of infection through a population that can be compared to containment strategies (isolation) and social networks for SIR epidemic models.
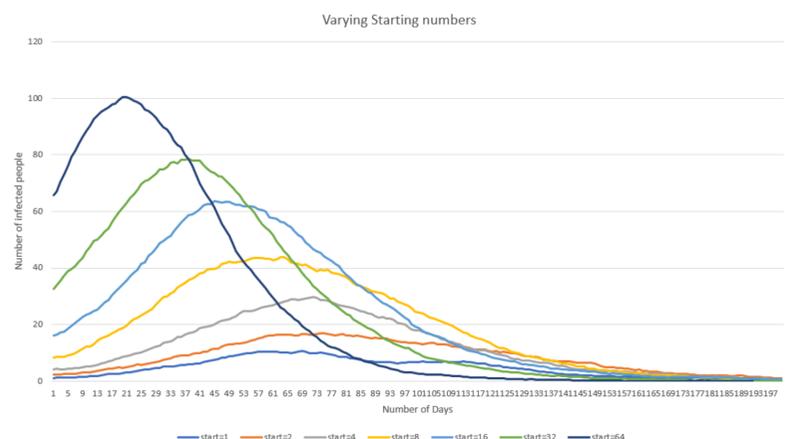

Figure 4: Number of people infected as a function of time where $n = 2000$, $c = 5$, $\beta = .05$, $\gamma = .1$, $\mu = .1$, $\iota = 0$, $p = 1$, and $I = 1, 2, 4, 8, 16, 32, 64$ over 100 trials.

Isolation Levels

In the SIR epidemic model, we varied the percentage of the infected population for isolation/quarantine ($\iota = 0, 0.01, 0.02, 0.04, 0.08$). An individual in isolation/quarantine is not allowed to contact individuals in the population.
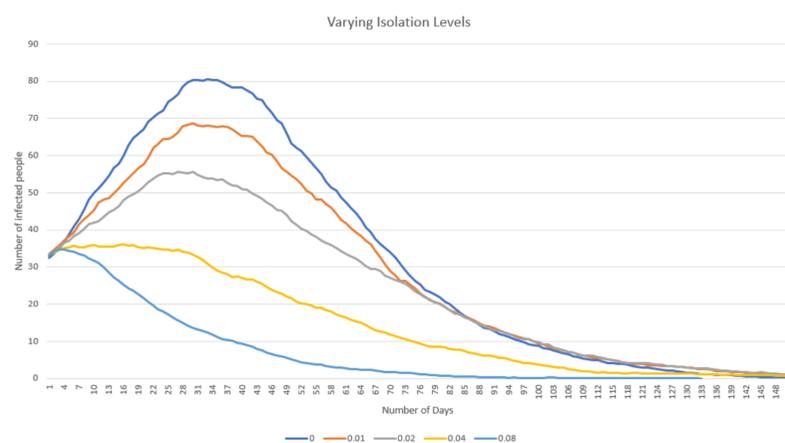

Figure 5: Number of people infected as a function of time where $n = 2000$, $I = 32$, $c = 5$, $p = 1$, $\beta = .05$, $\gamma = .1$, $\mu = .1$, $\iota = 0, 0.01, 0.02, 0.04, 0.08$ over 100 trials.

Network Exclusivity

The epidemic model we used includes a network component where each person has a group of individuals (e.g., friends or family) they are more likely to have contacts with. By varying a value p in a modified distance formula, we are able to prioritize 'nearby' interactions over 'distance' interactions. We let

$$d = 1 - ((x_1 - x_2)^2 + (y_1 - y_2)^2)^p.$$

represent the chance that a person at location (x_1, y_1) will add someone at location (x_2, y_2) to their network.
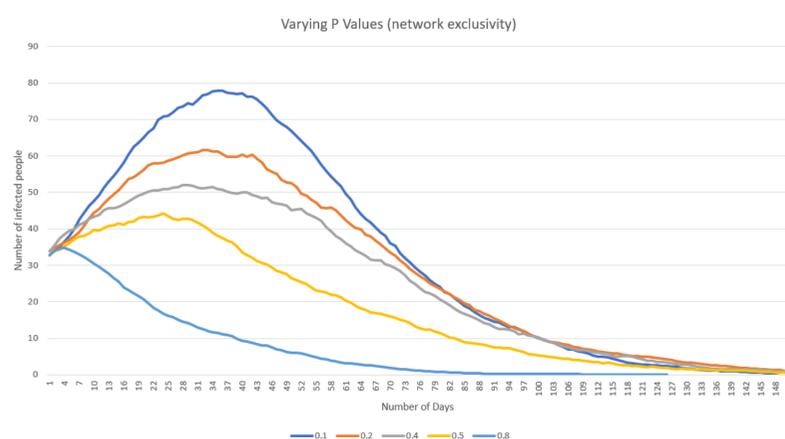

Figure 6: Number of people infected as a function of time where $n = 2000$, $I = 32$, $c = 5$, $\beta = .05$, $\gamma = .1$, $\mu = .1$, $\iota = 0$, and $p = 0.1, 0.2, 0.4, 0.5, 0.8$ over 100 trials.