# Network Dynamics and Learning Report on Homework 3

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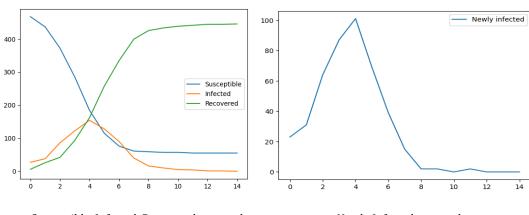
This report uses the SIR model to study the spread of the 2009 H1N1 pandemic in Sweden. It simulates how the disease spreads through networks that mimic real social connections, including the role of superspreaders. The model uses infection and recovery rates based on real data and tests how vaccination affects the spread. The goal is to use these simulations to help design better public health strategies.

### Problem 1

# A) simulate an epidemic

the simulation is run on a 500-node graph with k=6, using  $\beta=0.25$  and  $\rho=0.6$  for 15 weeks. The simulation begins with 10 randomly chosen infected individuals. Each week, the number of newly infected individuals and the total number of Susceptible, Infected, and Recovered people are tracked. The results are iterated 100 times and averaged for convergence. After stabilizing, less than 100 people remain susceptible. The number of infections peaks around weeks 4–5 and declines to zero by week 12. The maximum number of infections occurs when the number of Recovered and Susceptible people intersect. The weekly new infections approach a cap of 100 before decreasing.

Here the results of simulation are reported with plots



Susceptible, Infected, Recovered per week

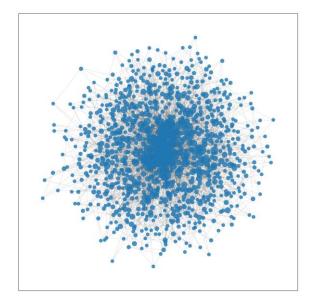
Newly Infected per week

### B) Generate a random graph

a random graph is generated using the preferential attachment model, which models how people with more connections are more likely to form new connections. Starting with a complete graph of k+1 nodes at time t=1, each new node added at t $\geq$  connects to existing nodes in the graph based on their degree. The new node connects to c=k/2 existing nodes, with the probability of connecting to each existing node proportional to that node's degree. This ensures that nodes with more connections are more likely to receive new links. Special care is taken to avoid adding multiple links to the same node. If k is odd, alternating between adding [k/2]and [k/2]links ensures the average degree is still k as the graph grows.

### C) Preferential attachment

we visualize a sample graph created using the preferential attachment algorithm. The resulting graph consists of 900 nodes with an average degree k=6. The algorithm is flexible and can be applied to other examples and iterations to observe how the network evolves as more nodes are added.



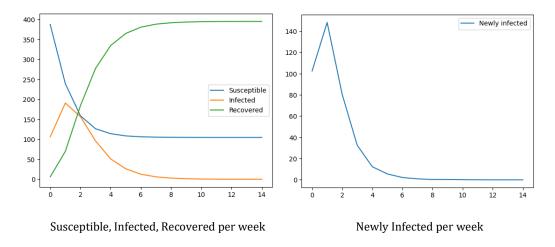
Preferential attachment graph

#### Problem 2

# A) Simulate a pandemic without vaccination and Preferential attachment

In this simulation, a pandemic is modeled on a graph of 500 nodes created using the preferential attachment algorithm, with k=6,  $\beta$ =0.25, and  $\rho$ =0.6, over 15 weeks. The simulation starts with 10 infected individuals. The results show that the number of Recovered individuals stabilizes below 400, while the number of Susceptible individuals remains above 100, near 150, at stabilization. The peak of infections occurs before the Susceptible and Recovered curves intersect. The highest number of newly infected individuals happens in week 2, with 140 infections, likely due to the preferential attachment model, where individuals with more connections spread the infection rapidly in the initial weeks.

Here the results of simulation are reported with plots



#### **Problem 3**

# A) Simulate a pandemic with vaccination and Preferential attachment

In this simulation, vaccination is introduced into the pandemic model. The vaccination rate increases each week, with the percentages defined as follows:

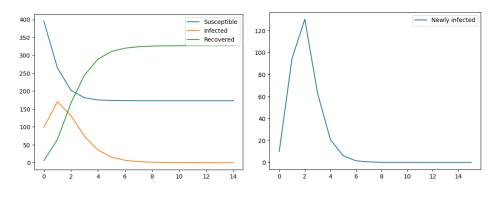
Vacc(t) = [0,5,15,25,35,45,55,60,60,60,60,60,60,60,60]

This means the government vaccinates a certain percentage of the population each week, and vaccinated individuals are no longer susceptible or able to infect others. The

vaccination takes effect immediately in the same week, and people cannot be vaccinated twice.

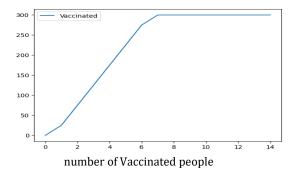
The weekly vaccination numbers are calculated based on the difference between the current and previous week's percentages, and the simulation tracks how vaccination impacts the epidemic spread, reducing the number of susceptible and infected individuals over time.

Here the results of simulation are reported with plots



Susceptible, Infected, Recovered per week

Newly Infected per week



## problem 4

# A) The H1N1 pandemic in Sweden 2009

This section simulates the spread of the H1N1 pandemic in Sweden using a network model to estimate parameters that fit the actual 2009 data. It involves generating a graph representing the population's social connections using the preferential attachment model, which results in a scale-free network where some individuals are more connected than others.

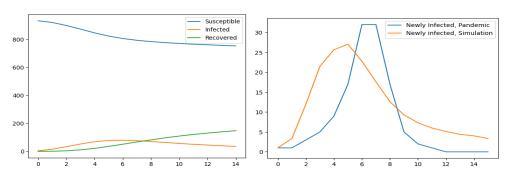
The SIR (Susceptible-Infected-Recovered) model is then used to simulate the disease's spread, considering vaccination over time. The vaccination schedule increases weekly, with vaccinated individuals becoming immune to the disease. The simulation runs for 15 weeks, starting in week 42 of 2009, and is repeated 10 times to ensure reliable results.

To compare the simulation with real data, the number of newly infected individuals each week is recorded, and the Root Mean Square Error (RMSE) is calculated to measure the difference between the simulated and actual data. The model parameters—number of connections (k), infection rate ( $\beta$ ), and recovery rate ( $\rho$ )—are adjusted to minimize the RMSE, thus providing the best estimate of how the disease spread in Sweden.

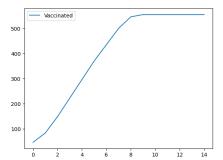
# B) estimate the average degree of k and the disease -spread parameters for the pandemic

The simulation aimed to replicate the 2009 H1N1 pandemic in Sweden. The optimal parameters found were k = 9,  $\beta$  = 0.1, and  $\rho$  = 0.2, with an RMSE of 6.16. The results, illustrate the number of Susceptible, Infected, Recovered, and Vaccinated individuals over time. Vaccination and the social network structure in Sweden significantly reduced the spread, leaving about 750,000 of the 934,000 people still susceptible by the end of the simulation.

Here the results of simulation are reported with plots



Susceptible, Infected, Recovered per week



number of Vaccinated people

Newly Infected per week