

CLASS NAME

Project Report

Your Name

3rd September, 20XX

Abstract

In this project we simulated the spread of the Corona Virus in interpersonal community networks. We considered parameters such as the transferring rate of virus over connections, the recovery and the death rate for the infected individuals, and the susceptible grace period for a newly infected person (the length of time in which a newly infected individual will be diagnosed as Susceptible Patient rather than a certain Infected Patient). We used graph node data structure in our programming to simulate the interpersonal connections and record the statistical outputs during each time interval. We noticed that it's surprisingly easy and quick for a virus to spread in the population as the transferring rate is usually much higher than the death rate or then recovery rate. Thus, we highly recommend keeping social distance and reducing exposure in public with others.

Background

As it's well-known, we are living in a historical moment in human history that we are facing a global epidemic that is threatening the whole society. Governments world-wide had made various trials and experienced countless tribulations in pushing new policies to limit the spread of the Covid-19, the name of the current global epidemic. Thus, we hope to simulate how a virus may spread in a community, and collect the statistics of our simulation to numerically show the severity of an epidemic in different social network models.

There are usually five health statuses in response to the influence of an epidemic virus: Healthy, Recovered, Infected, Susceptible, and Death. We define the healthy status as one has not been infected ever; recovered status as one recovered from infection; susceptible status as one newly infected but not showing typical symptoms (we use a parameter named **suspe_time** to define the length of such "grace period" for one to be diagnosed as "susceptible" before "infected", notice that people in "susceptible status" can still spread virus to others); infected status as one showing obvious symptoms (passed susceptible period); death status as one died from infected status. To simulate the spreading effect, we used **trans_rate** to define the spreading possibility for one to get infected by a connected infected person; **recov_rate** to define the possibility of one getting recovered by infection; **death_rate** to define the possibility of one die by infection. We use a parameter **int_code** to define the number of timesteps we perform the simulation.

Methodology

We use the graph node structure to simulate the relationship among social networks. Such networks are not completely the same as the Tree model since people may not have only one parent node nor a certain limited number of children nodes -- it's much more complicated as social relationships can be "messy" (parents and children nodes are collected as the "connected" nodes). Thus, we borrowed the Tree structure to better understand people's hierarchical relationship structure and use all social connections each one have when analyzing the health status change over a timestep.

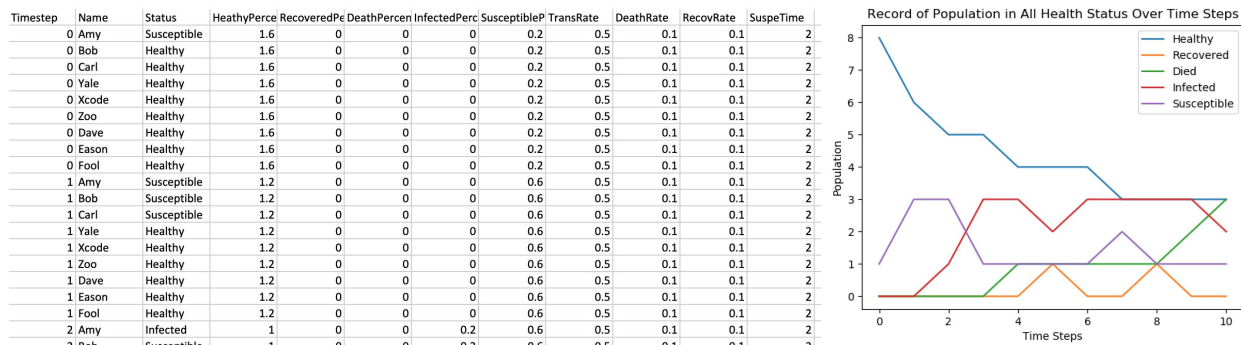
After loading the initial people's health status and the network model, we start the simulation by updating all people's healthy status over each timestep. If a healthy one has N connected neighbors who were infected, he/she has a probability of $(1 - \text{transrate})^N$ for staying healthy and $1 - (1 - \text{transrate})^N$ probability of getting infected. Thus when $N = 0$, he/she is certainly staying healthy to the next timestep.

For someone who is infected, he/she has a probability of **death_rate** and **recov_rate** respectively for dying or recovered from the virus. Of course he/she has a probability of **1 - death_rate - recov_rate** for staying infected. However, if he/she stays infected, notice that he might be in "Susceptible" status. We will reduce the recorded time he/she was in the Susceptible status until he has passed the susceptible time (**suspe_time**) and be classified as the Infected status.

By running **python main.py -[flag] netfile trans_rate recov_rate death_rate suspe_time int_code** where "-[flag]" can be "-s" for simulation mode, or "-i" for interactive mode, user can (in simulation mode) save the statistical results as csv files (shown below in Results section) and the population health status tendency over timesteps as png plot images (shown below in Results section); user can also (in interactive mode) see each person's health status and their overall health status changes as printed in terminal. By running in either mode user will also see the overall statistics over all health statuses (names and percentages of population that result in each health status)

Results

As described above, below shows the statistical data stored as csv files which records each person's health status and the parameters over each timestep. Below shows the plot of population in all health status over time steps as introduced in Methodology section:



Network structure, display of each person's health status over each time step, and overall statistics will be displayed as below after running in interactive mode:

```
=====
[ Amy ] has parents: [ ] , and children: ['Bob', 'Carl']
[ Bob ] has parents: ['Amy'], and children: ['Yale']
[ Carl ] has parents: ['Amy'], and children: [ ]
[ Yale ] has parents: ['Bob'], and children: ['Xcode', 'Zoo']
[Xcode] has parents: ['Yale'], and children: [ ]
[ Zoo ] has parents: ['Yale'], and children: [ ]
[ Dave ] has parents: [ ] , and children: ['Fool', 'Eason']
[Eason] has parents: ['Dave'], and children: [ ]
[ Fool ] has parents: ['Dave'], and children: [ ]

TimeStep: [3]
['Amy', 'Died']
['Bob', 'Infected']
['Carl', 'Healthy']
['Yale', 'Susceptible']
['Xcode', 'Healthy']
['Zoo', 'Healthy']
['Dave', 'Healthy']
['Eason', 'Healthy']
['Fool', 'Healthy']

=====
[ Healthy ] people are [44.44%] of the population; their names are ['Carl', 'Dave', 'Eason', 'Fool']
[ Recovered ] people are [22.22%] of the population; their names are ['Bob', 'Zoo']
[ Died ] people are [33.33%] of the population; their names are ['Amy', 'Yale', 'Xcode']
[ Infected ] people are [ 0.0% ] of the population; their names are [ ]
[ Susceptible ] people are [ 0.0% ] of the population; their names are [ ]
=====
[ Amy ]: Susceptible -> Died -> Died -> Died -> Died -> Died -> Died -> Died -> Died -> Died
[ Bob ]: Healthy -> Susceptible -> Susceptible -> Infected -> Infected -> Recovered -> Susceptible -> Recovered -> Recovered -> Recovered -> Recovered
[ Carl ]: Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy
[ Yale ]: Healthy -> Healthy -> Healthy -> Susceptible -> Susceptible -> Infected -> Infected -> Died -> Died -> Died -> Died
[Xcode]: Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Susceptible -> Susceptible -> Infected -> Infected -> Died
[ Zoo ]: Healthy -> Healthy -> Healthy -> Healthy -> Susceptible -> Susceptible -> Infected -> Infected -> Recovered -> Recovered -> Recovered
[ Dave ]: Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy
[Eason]: Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy
[ Fool ]: Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy -> Healthy
```

Conclusion and Future Work

We successfully simulated the spread of an epidemic virus in a social network. The spreading simulation was probability based in spreading, recovering, and dying. Thus the result may vary over trials in the same network. However, we witnessed the horrible threat it may affect the population. In the future, we can simulate in a larger network and compare the simulation with and without social distancing in the same network so that we can prove the effectiveness of social distancing statistically.