Infectious Disease Simulation
-A Short Report on an Independent Mini-Project-

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Abstract

Computation is crucial in order to simulate an infectious disease. This reports outlines a very basic simulation which should not be used to guide action in the event of a spread. However, such simulations provides the foundation for ones that are used to save lives. This simulation accurately modelled the infection of a singular person with a less accurate modelling of spread amongst a population with the leading cause being the inability to code the recovery of multiple infected individuals simultaneously.

1 Introduction

The goal of this project was to create a some-what realistic model of the spread infectious diseases. This project was proposed in [1] . This simulation should not an cannot be used to model the spread of any contemporary or historic epidemics, pandemics or predict the future spreads . The model employed here is much to simplistic and lacks nuance. Models that can be used to predict such events are done on supercomputers and require large amounts of time to code and compute.

2 Methodology

This simulation employs the use of C++ classes, objects, functions, conditionals, logic statements, loops etc. to emulate the infection, recovery and immunity of 1 person, as well as the spread amongst a large population. A 'Person' class was created and functions were coded to infect, update and return the status of an "person". Similarly, a 'Population' class was created which included function to compute an array of 0s (represented susceptible peoples of a population), infect a random person out of the "population", transfer the disease to nearest and random people and to vaccinate a certain amount of random citizens to test herd immunity via vaccination.

3   Discussion

The simulation of an infection of a singular person was fairly accurate since the duration of infection could be manipulated which simulates the strength of the individual's immune system . The population simulation was also accurate since the nearest neighbours of the infected individual had a probability of being infected and the infected individual could also come into contact with a variable number of random people per day. Also, a certain number of people in the population could be vaccinated which better simulates diseases with an already existing vaccine (e.g. yearly seasonal flu, chicken pox, malaria etc.).

However, the biggest problem with the population simulation is the inability to code recovery time without having the infected individuals recover one at a time. This could potentially be fixed in the future, however, it was not done in this project due to time constraints. Thus, a short recovery time was chosen (2 days) to prevent instant recovery. A longer recovery time was avoided since it is much less accurate as the recovery for other infected individuals would be further delayed. Lastly, the simulation seemed to accurately predict the length of time a spread lasts given the size of the population (i.e. increasing the size of the population leads to a longer time for infections to reach 0).

4   Conclusion

The simulation could be much improved. Recovery time could be varied, simulating the disparity in immune response amongst a population. Also, a death rate could be coded which can be varied to match the level of compromised individuals in a populations (e.g. elderly people, comorbidity etc.). Lastly, a more mathematical approach (outlined in [1]) will lead to a more accurate simulation. The following differential equations are note-worthy:

1. The number S_i of susceptible people at time i decreases by a fraction

$$S_{i+1} = S_i \left(1 - \lambda_i dt\right)$$

where λ_i is the product of the number of infected people and a constant that reflects the number of meetings and the infectiousness of the disease. We write:

$$S_{i+1} = S_i \left(1 - \lambda I_i dt\right)$$

2. The number of infected people similarly increases by $\lambda S_i I_i$, but it also decreases by people recovering (or dying):

$$I_{i+1} = I_i \left(1 + \lambda S_i dt - \gamma dt\right).$$

3. Finally, the number of 'removed' people equals that last term:

$$R_{i+1} = R_i \left(1 + \gamma I_i\right).$$

[1]

This is, thus, not a sufficiently accurate simulation to be used for predictive purposes in the unfortunate event of a pandemic, epidemic of small local spread. However, the code in this project may be used as a foundation in that pursuit.

5   References

[1] PROJECTS FOR SCIENTIFIC PROGRAMMING IN C++ AND OTHER LANGUAGES VICTOR EIJKHOUT 2020 2. (n.d.). [online] Available at: https://web.corral.tacc.utexas.edu/CompEdu/pdf/isp/EijkhoutProgrammingProjects-book.pdf [Accessed 27 Jul. 2022].