

Simulation of the Spread of a Virus Throughout Interacting Populations with Varying Degrees and Methods of Vaccination

This project is designed to expand upon the common agent-based simulation of a virus infecting a very generic population. Factors such as multiple populations, different forms of transportation, and social interactions will be accounted for. Different maps with different types of pseudo-random populations will be created and different types of existing and fictional viruses will be simulated. Once working models are finished, the effects of vaccinating parts of the population can be modeled to determine the most effective methods and minimum percentages of vaccination needed to stop a viruses spread.

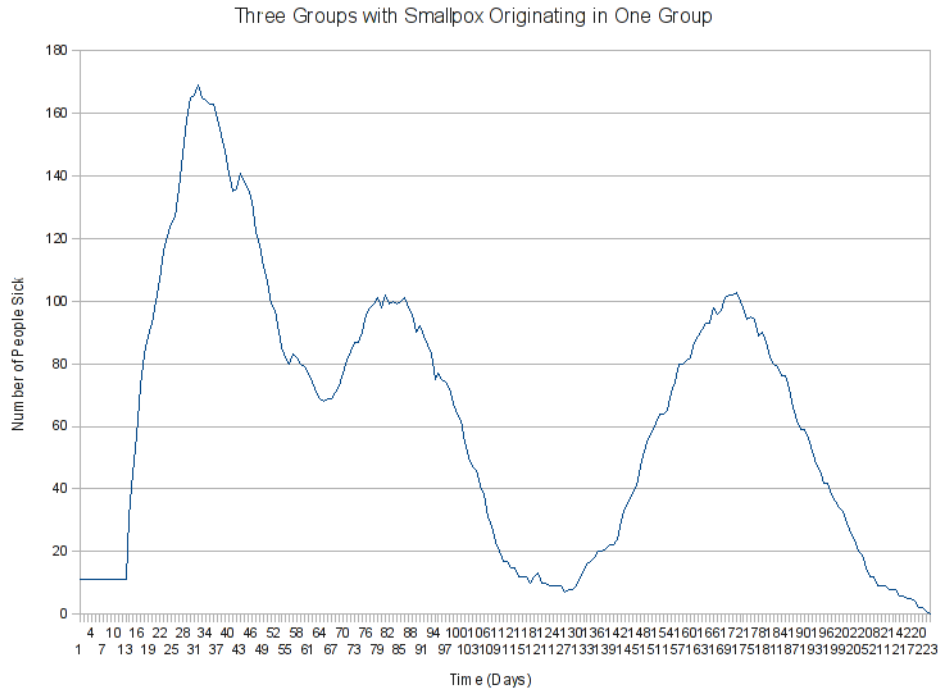
Virus simulation is by no means a new technology or study, and thus material on the subject is plentiful. Using vaccination is also a popular model to simulate, and in one paper by Bret D. Elder, Vanja M. Dukic, and Greg Dwyer the differences in efficiency between trace vaccination and mass vaccination were studied. Other papers describe the mathematics behind various models and the variables used, such as R_0 or P_r for probability of recovery. While much of this research focuses on system dynamics, it still has material covering agent-based modeling. The article on spatial simulation gives great insight into how to approach the modeling of an environment as it factors in locations such as schools, dorms, homes, work places, and hospitals, much like I intend my own simulation to use. The MIT paper compares agent-based mods to differential equation models to determine the advantages and disadvantages of both, and how they can be combined to reduce the inaccuracy inherit in both.

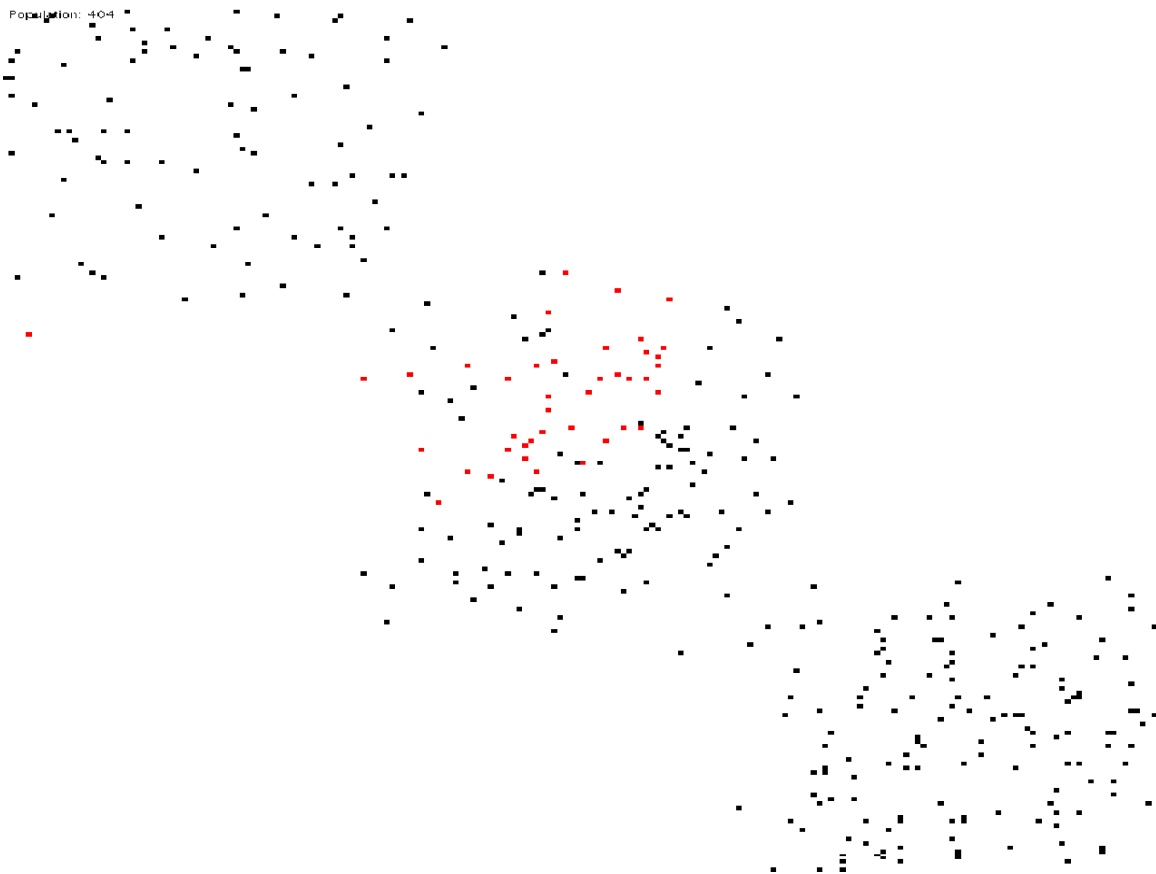
Because this project will be solely agent-based instead of incorporating system dynamics, the scope of the simulation will be limited by the processing power of the computer. There is also a limit to how detailed each agent can be. The ideal simulation would have incorporate the unique nature of each individual, but this is obviously impractical, so there will be classes of people to simulate different things like people who travel, people who work, etc. One important feature that will have to be included is hospitals because of their significant influence on the spread of disease. The variables for vaccination will include effectiveness, chance of causing the infection itself, percentages of the population vaccinated, and perhaps even some form of trace vaccination.

In order to create this simulation, my plan is to start off with a basic agent-based model, showing an extremely simple population with random movement, with basic mass vaccination and virus spread. I will use this as a stepping stone to implement more advanced modeling. Resources I will need are primarily limited to research papers already written and calculated values relating to different viruses. Visuals of my project will include charts showing the frequency of people sick, deaths, people vaccinated, people recovered, etc. as well as maps that show incremental snapshots of the viruses spread. The error analysis will be somewhat limited, but will primarily consist of comparisons to real world epidemics and the results of models by other researchers and scientists. At a minimum, in its final form, my simulation should be able to model small sections of modern real-life populations as well as past populations, such as medieval villages. It should be able to track to an extent the interaction of different populations and how that affects the spread of a virus. Simulating vaccinations by the "trace" method is of a lower priority than mass vaccination, but will still be

programmed to some degree.

This graph show the trend in the number of people sick among three populations with several patient zeros infected with smallpox in only one group. No vaccinations were used. While this graph show the total people sick, the simulation will later be programmed to output the number of people that have been infected at any point, death rates, data from each population separately, etc. The image below the graph shows a frame of the visual representation the spread of the virus in the simulation in real time.





Sources:

- Uncertainty in predictions of disease spread and public health responses to bioterrorism and emerging diseases. Bret D. Elder, Vanja M. Dukic, and Greg Dwyer. *Proc Natl Acad Sci U S A*. 2006 October 17; 103(42): 15693–15697. Published online 2006 October 9. doi: 10.1073/pnas.0600816103.
- Aschwanden, C. 2004. Spatial Simulation Model for Infectious Viral Diseases with Focus on SARS and the Common Flu. In *Proceedings of the Proceedings of the 37th Annual Hawaii international Conference on System Sciences (Hicss'04) - Track 6 - Volume 6* (January 05 - 08, 2004). HICSS. IEEE Computer Society, Washington, DC, 60137.2.
- Rahmad, Hazhir Serman, John, : Comparg - (October 2004). Heterogeneity and Network Structure in the Dynamics of Diffusion: Comparing Agent-Based and Differential Equation Models. MIT Sloan Workg Paper No. 4512-04. Available at SSRN: <http://ssrn.com/abstract=607302>