TJHSST Computer Systems Lab Senior Research Project
Simulation of the Spread of a Virus Throughout Interacting Populations with Varying Degrees and Methods of Vaccination
2008-2009

Jack DeWeese

June 10, 2009

Abstract

This project is designed to expand upon the common agent-based simulation of a virus infecting a very generic population. Factors such as work, school, hospitals, age, and population size are accounted for. Different different types of existing and fictional viruses will be simulated. The effects of vaccinating parts of the population can be modeled to determine the most effective percentages of vaccination needed to best prevent the effects of a virus' spread.

1 Introduction - Elaboration on the problem statement, purpose, and project scope

1.1 Scope of Study

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 theorertically ideal simulation would have to incorporate an actual population, factoring in every detail. Obviously this is not a realistic goal to expect of any simulation. There will be classes of people to simulate different things like people who travel, people who work, etc. Professions also play a large part in how a person is affected by the spread of a virus. A doctor working in a hospital is much more likely to become infected as he helps his patients who are likely there to be treated because of the viral infection. On the other hand someone going to work might not have nearly as much interaction with other people, let alone those who are infected, expecially since people in the workplace environment will likely not show up to work once they begin to show symptoms. In terms of buildings, an important feature that will have to be included is hospitals because of their significant influence on the spread of disease as mentioned before with doctors. Schools are frequently called a "cesspool" for disease, and with good reason. Children are less likely to take the appropriate measures to limit their exposure to viral infection, and thus will quickly spread it among their peers. The variables for vaccination will include effectiveness, chance of causing the infection itself, percentages of the population vaccinated, and some form of trace vaccination.

1.2 Type of research

Because of the nature of this project, it will be for the most part pure applied research, because it will attempt to apply current knowledge of viruses and vaccination to determine efficient methods of vaccination different populations. There is some use-inspired basic research, as viruses that have not been modeled can theoretically be used in this program.

2 Background and review of current literature and research

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. Elderd, 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 R0 or Pr 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 I am not including any significant degree of system dynamics in my simulation, the mathematical models will not be particularly useful and have thus been merely touched upon here, rather than having formulas listed and going in depth on how they work.

I have done a lot of research on how different viruses work in order to figure out how to set the variables for each type of virus. Smallpox for instance has a high rate of infection and can be airborne. It has an incubation period of roughly 12 to 14 days, but can be between 7 and 17. This range can be modeled in my software with dynamic variables and will account for 12 to 14 days being more common by assigning this range a higher probability. During the first 2 to 4 days, symptoms begin, but the infected person is not very contagious. After this a rash begins to appear, and the person become highly infectious - this lasts for about four days. The next five days are characterized by the formation of pustles and a slight drop in the extreme level of contagiousness. Over the following five days the pustles begin to scab over, then for the last six days the scabs fall off leaving scars. After all of the scabs have resolved (fallen off), the person is no longer contagious. Methods will be created to model this change in how contagious a person is, but right now there is only a constant rate of infection.

3 Development

After doing some research into other virus simulation programs, I found Jill Dunham's program which serves as a good base for my own simulation. While I began this quarter working on my original simulation from scratch, I moved to doing research on how other researchers worked with different variables and the differences between dynamic and agent-based modeling. It was during this research that I came upon Mrs. Dunham's model and began learning how the software works. Because of the proximity of this discovery to the end of the quarter, I have not made drastic changes to the program in terms of the code itself, but I continued my research of how to change aspects of the program. The program initially contained a basic flu virus, but I have implemented my own smallpox model and done some tweaking of her pre-done viruses.

3.1 Results

This project is an attempt to determine the most effective methods of vaccinating a population, considering the factors of the type of population and what virus is infecting it. Different percentages of vaccination have been used to see if vaccinating certain percentages (relative to the size) of the population makes a difference and regression models have been created to attempt to create mathematical models of the simulation results.

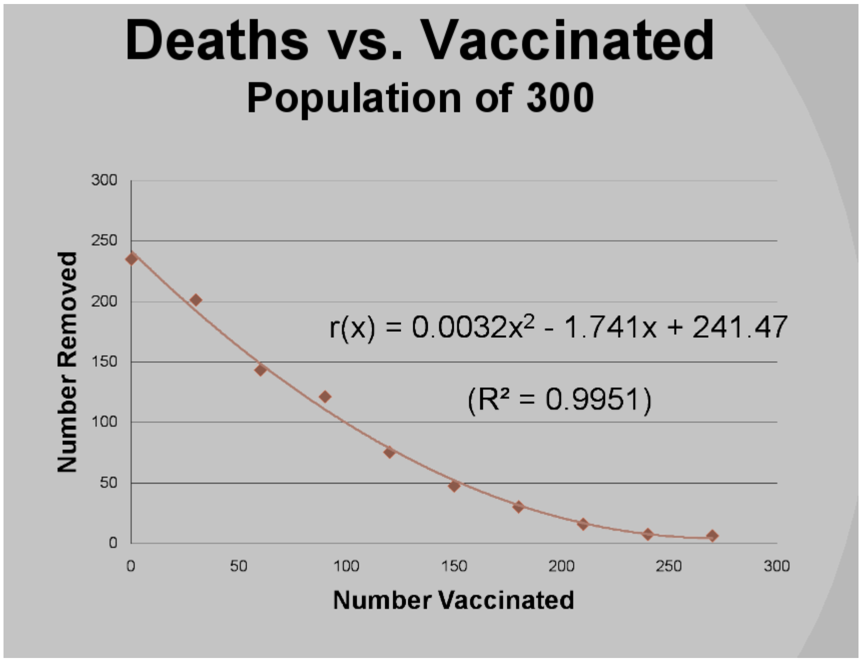
This formula shows the number of people that should be vaccinated in a population of size n with a vaccine, which has a death rate of r_v.

$$x = -\frac{r_v + \beta_1}{2\beta_2}$$

This formula is the regression model for the number of deaths as a function of percentage of the population vaccinated.

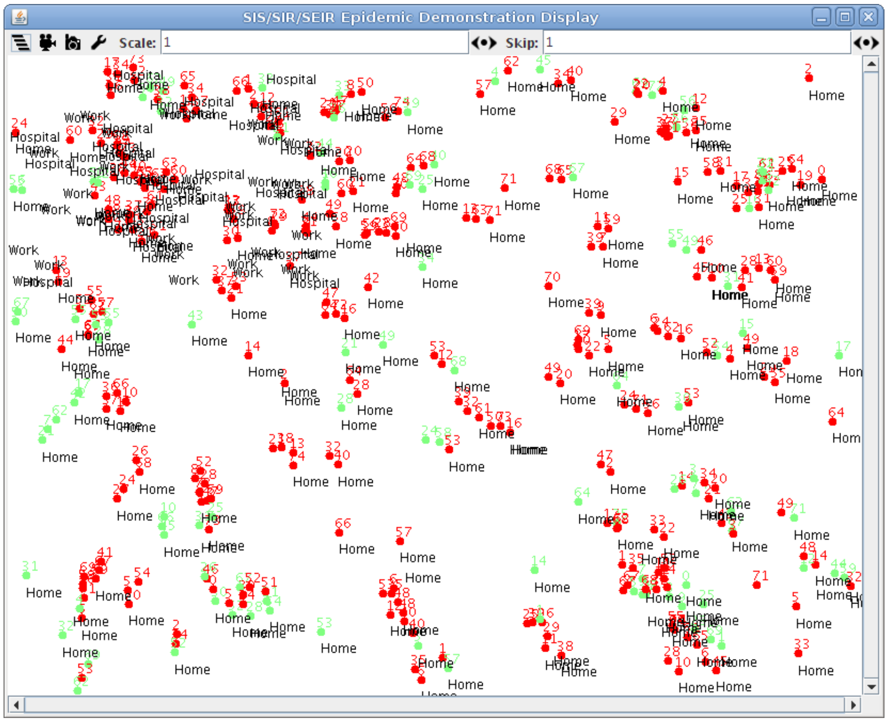
$$r(x) = \beta_0 + \beta_1 x + \beta_2 x^2$$

This graph shows an example of a simulation output for a population of 300 people. The relationship between percentage vaccinated and number of deaths is shown.



To further the regression model, I decided to try making the coefficients of the above equation functions of population size. This makes the mathematical model even more useful as it means simulation runs don't even have to be run to determine these coefficients before calculating the aforementioned coefficients. The set of formulae shown below is the regression model I used. Note that this is also a quadratic regression model, though the 'r' values I calculated for these were not as high as the above regression models, albeit still very good. ('n' is the population size.)

The image below is an example of a visual run of the model I am using. Green represents uninfected, red - infected, black - dead.



$$\{\beta_k(n) = a_k n^2 + b_k n + c_k\}_{k=0}^{2}$$

In the process of programming this simulation, I have learned about the spread of viruses among populations and how to model not only this spread, but to use it to create mathematical models.

4 Conclusion

Expectations for my program included working models of past epidemics and the capability to models possible future epidemics to a fair degree of accuracy, and while this was not accomplished, I did take large steps to achieve this goal. This type of model is especially useful in today's world, where the threat of bio-terror attacks is a real fear, and precautions must be made to react to such an event. The model I have created uses regression to try to best simulate what the effect of increasing the percentage of vaccination will be on a population, and at what point it is no longer useful or even harmful to continue vaccinating. For example if there is a vaccine that has a certain death rate, the model can show at what point the risk of vaccine outweighs the benefits of preventing spread of the virus.

5 References

Centers for Disease Control and Prevention. 2004. Smallpox Disease Overview. http://www.bt.cdc.gov/agent/smallpox/overview/disease-facts.asp

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 Sterman, 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

Dunham, Jill Bigley. An Agent-Based Spatially Explicit Epidemiological Model in MASON. Journal of Artificial Societies and Social Simulation. ISSN 1460-7425. Vol. 9. 2005. ¡http://jasss.soc.surrey.ac.uk/9/1/3.html¿.