TJHSST Computer Systems Lab Senior Research Project

2008-2009

Modeling Virus Transmission on Population Dynamics using Agent Based and Systems Dynamics Modeling

Dheeraj Manjunath

April 2, 2009

Abstract

This goal of this project is to model the transmission dynamics of viruses and their affect on populations based on user input. The project model the effect of virus transmissions on populations for real situations, such as the 1918 Spanish Flu. Since there is ample data about major infections such as the 1918 Spanish Flu, the variables can be modeled using this program [1]. Also, the project combines various types of modeling, Systems Dynamics Modeling and Agent Based Modeling, to create a model fit for use by anyone since little knowledge about computer programming is required to use the model.

Keywords: modeling, agent based, systems dynamics, netlogo, virus

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

1.1 Scope of Study

A very simple approach was taken to design the model; compartmentalize the model and add as many features as possible. The model will represent, as close as possible to real life, normal parameters that can significantly affect populations. The end result of the model will present different classes of people, different infection rates, and different immunities and mutations.

There are two types of modeling used in this paper are Systems Dynamics modeling and Agent based Modeling. Systems Dynamics modeling is the general flow of one variable into another variable and deals exclusively with modeling a general flow. Agent Based modeling shows the individual agents behaving under a given set of instructions.

Systems Dynamics was the primary form of modeling used in this project. The use of Systems Dynamics was particularly advantageous because large amounts of flows can be represented with relatively minimal number of computations, as opposed to Agent Based, in which during every loop, every agent must be processed. In addition, Systems Dynamics is useful to see general trends, thus the model was created to show the effects of virus transmissions on a population. Certain techniques used to implement Agent Based functions were used in this model, although this model is not intended to use agents.

There are specific implemented functions to model a population to a certain degree of accuracy. Among the functions for children and adults include: births, deaths, infections, immunitiy, mutations, and human tendencies.

1.2 Expected results

This model will give the population data for different types of people for a virus in a certain amount of specified time. This data can either be accessed by a plot in the modeling software NetLogo or as a .csv file in Mircosoft Excel.

This project is for both virus transmission modeling and the integration of both Systems Dyanmics and Agent Based Modeling [2]. A research paper written about the integration of these two types of modeling sparked the question of whether they can be effectively combined to create a better model. Thus, the model actually has a dual purpose and the results will help both parts of the research. However, this research paper is not a true representation of Agent Based Modeling since individual agents are not being modeled. The extent of use is to accomplish functions using the Agent Based Modeling which would either be excessively difficult or impossible to do in Systems Dynamics Modeling.

1.3 Type of research

My project is a mix of two areas, use-inspired research and pure applied research. The use-inspired research and the pure applied research both apply, as the goal of the project is to create a usuable model, applied research, and try to integrate systems dynamics with agent based modeling, use-inspired research. The use-inspired aspect is the creation of a model to better help combat global outbreaks of major diseases, such as the Bird Flu(H5N1) virus. The pure applied research aspect is the use of two very different types of modeling to try to optimize the model from different points of view.

2 Background and review of current literature and research

Researchers are currently doing research in this area to try to create a model which can represent a historical virus outbreak, so future outbreaks can be avoided. One research paper discusses creating a model with detailed parameters for infection, susceptibility and transmission in different people in different age categories [1]. The negative aspect is that this model is not universal, and is based off one specific outbreak, but it did influence this virus model to present a general solution.

Another paper discusses the pros and cons of the two types of modeling. The ultimate conclusion was that the integration of the two types of models according to the situation was the best idea[2]. My model also strives to do this.

Significant research is being done on other non-biological effects of viruses.

3 Procedures and Methodology

The breakdown of the project is as such. During the 1st Quarter, the goal was to create the basic framework for the program. Some features added were the adult uninfected and infected popluations, along with birth and death rates (See Fig-1). In the 2nd Quarter, more consideration to age factors was given so children will be more susceptible to catching the infections. Each age group will have distinct death rates, and there will be a simulation of ageing. In the 3rd Quarter, there was research done on whether the effect of human knowledge would impact infection rate. There is a dampening effect to simulate the spread of human concern for the oubreak, so people will protect themselves. Finally, in the 4th Quarter, the model was tested to make sure it was ready and accurate.

The program is created using NetLogo, which has a GUI interface (See Fig-2). It displays the graphs the user defines and can show visually the patterns in the data. There are both advantages and disadvantages to the pattern approach. Since exact data cannot be accurately simulated by Systems Dynamics modeling, the modeling used in this research, there is a lack of detail in data. However, the advantage is that the data trend can easily be seen.

The following system of differential equations are the equations for the Lotka-Volterra model. The Lotka-Volterra equations were used in this model to represent the population. In the model the population of the prey is represented by x and the population of the predator, y.

$$\frac{dx}{dt} = x(\alpha - \beta y)$$

$$\frac{dy}{dt} = y(\gamma - \delta y)$$

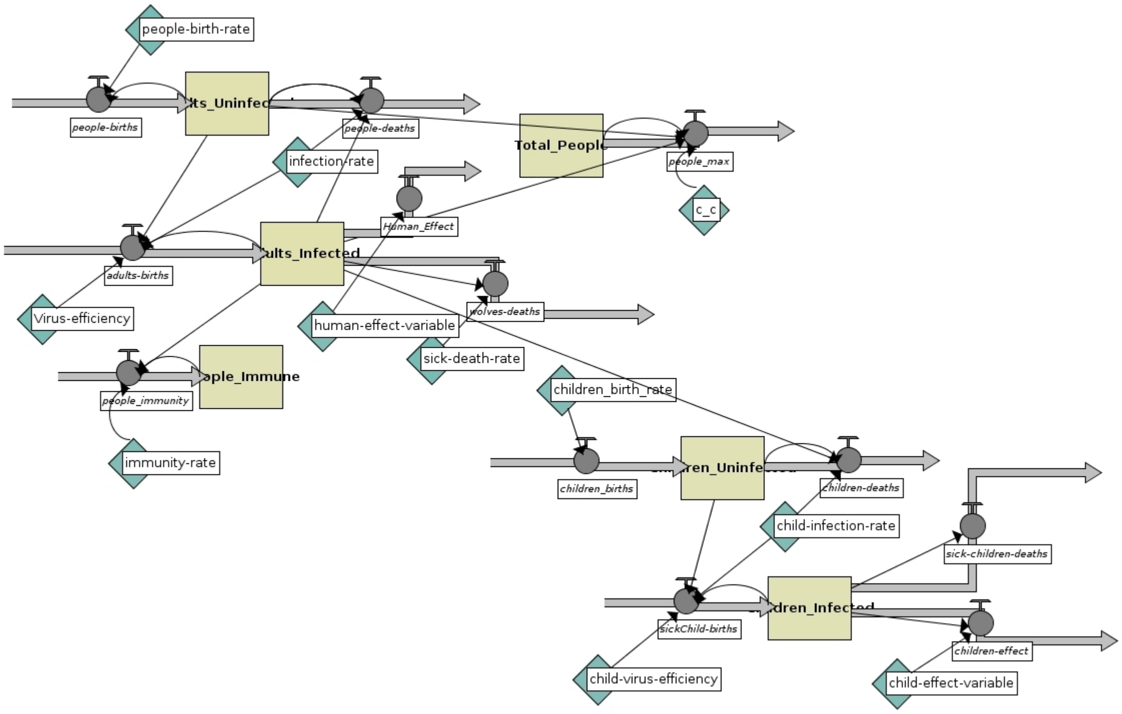
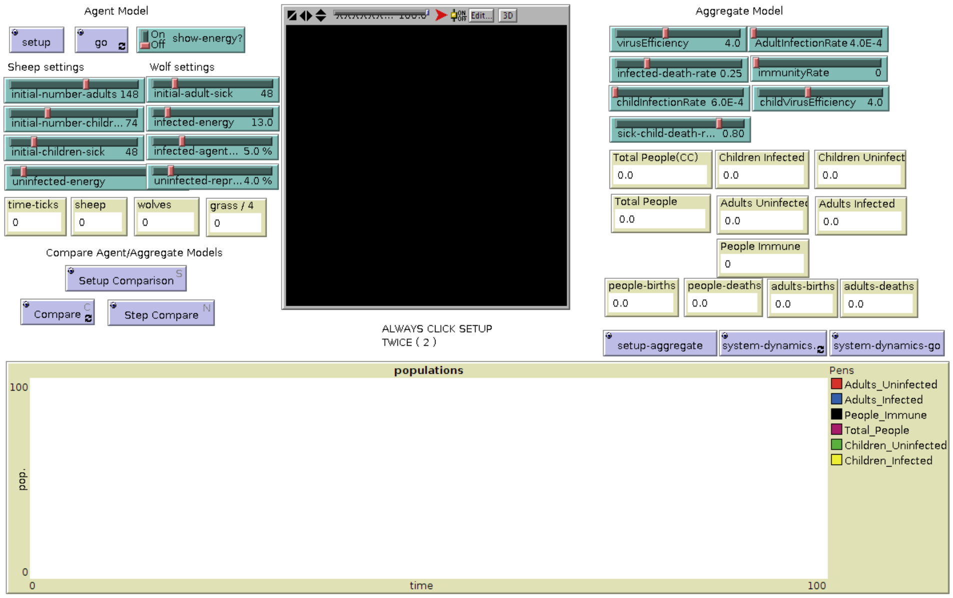


Fig-1

Testing of the program is done as soon as a new part is completed. Since the model is dynamically affected by every new parameter, the testing is an ongoing phase. The final test of the model will include actually modeling a real situation, so the results of the model will be compared against the real situation and see how close the model actually was to predicting a real outbreak. NetLogo includes a built in method called BehaviorSpace, which tracks the values of every variable and outputs it into a csv file in excel. That can be used to plot and test whether the model works.



initial-number-adults 148
initial-number-childr... 74
initial-children-sick 48
uninfected-energy
initial-adult-sick 48
infected-energy 13.0
infected-agent... 5.0 %
uninfected-repr... 4.0 %

time-ticks 0
sheep 0
wolves 0
grass / 4 0

virusEfficiency 4.0
AdultInfectionRate 4.0E-4
infected-death-rate 0.25
immunityRate 0
childInfectionRate 6.0E-4
childVirusEfficiency 4.0
sick-child-death-r... 0.80

Total People(CC) 0.0
Children Infected 0.0
Children Uninfect 0.0
Total People 0.0
Adults Uninfected 0.0
Adults Infected 0.0
People Immune 0
people-births 0.0
people-deaths 0.0
adults-births 0.0
adults-deaths 0.0

Fig-2

The Systems Dynamics flowchart above represents the flow of the model. The methods that have been implemented in the model are: birth rate for adults and children, death rate for adults and children, immunity rate for adults, and carrying capacity for the total population. The next methods to be implemented are the methods stated above for seniors, the susceptibility rate, population density, and aging of the population to adults and seniors, and virus spread timing.

The Maryland Virtual High School for Science and Math has a model on their website dealing with epidemics. The model creates a basic starting point for an epidemic study [4]. Some of these functions will be used to enhance the accuracy of the model.

4 Development and Algorithm

This project was developed by using an existing predator-prey model as a starting point. Uri Wilensky from Northwestern University included a Wolf-Sheep model in the NetLogo program, and that was developed into the virus model. The reason this was possible is because the Lotka-Volterra system of equations was used in both models. This is the basic interaction system which my model, as well as many other models, follow.

The basic model was developed from a model by Uri Wilensky's which utilized a basic Lotka-Volterra model. The features in the model were modified to create a basic human model. Then, the more specific functions were added. The model started out with a simple predator and prey stock, which represents the humans and the virus. The only other function this model contained was predation. Therefore, when this project was started, it contained he human, the virus, and the infection stocks. Some of these functions were not completely suitable for modeling viruses, such as births and deaths, and required modification. After these modifications, multiple other stocks were added, such as immunity, community situations, and the human concern effect.

5 Expected Results

Models are used frequently to predict various situations in life and are used by individuals, companies, organizations and the government. Even though agent based and system dynamics models are used, they are not used often together, so integrating them will offer a different outlook to the model. My primary purpose is to model a realistic situation, so this model will not be specific to any situation, but rather just have the basic necessities for the virus transmission model and the user will choose the others values.

This project is a good fundamental starting point for a virus model and for a modeling project. The students pursuing a virus model next year will be able to add additional features which could not be added due to time constraints. Any number of odd factors could affect virus transmission, so there will be no shortage of features to add.

The results of the population graph should be in a form of harmonic motion once the model experiences initial turbulence. Oscillations are expected and are part of the normal patterns and results[5]. Shown in Fig-3 is the expected oscillation from a "pure" Lotka-Volterra model, retrieved from the website of Leon Kaganovskiy at the University of Michigan-Ann Arbor. A run of the initial virus model created for this project is shown in Fig-4. The model shown in Fig-4 does not have the full features of the complete virus model, but it is a "pure" Lotka-Volterra model. This was used for testing purposes to see whether the model was effective, and after seeing the results, it can be seen that the model is effective.

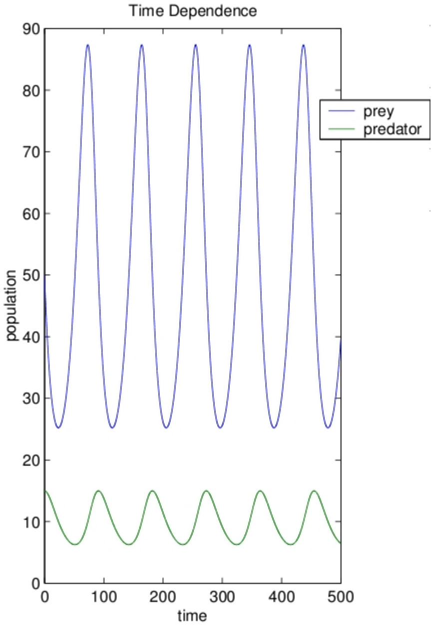

Time Dependence
90
80
70
60
50
40
30
20
10
0
population
0
100
200
300
400
500
time
prey
predator

Fig-3

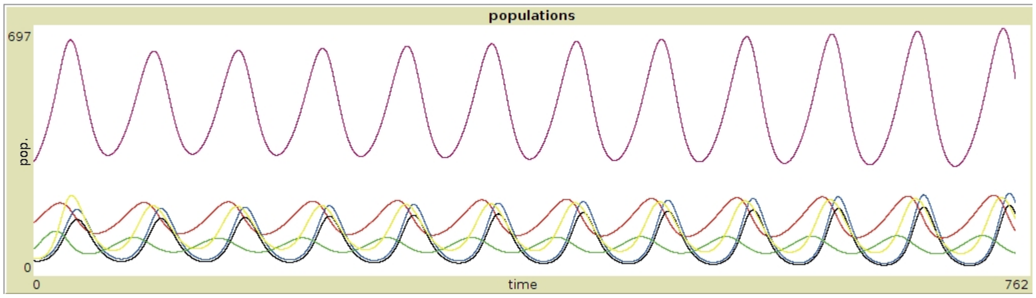

populations
697
pop.
0
0
time
762

Fig-4

References

[1] G. Chowella, C.E. Ammon, N.W. Hengartner, J.M. Hyman Transmission dynamics of the great influenza pandemic of 1918 in Geneva, Switzerland: Assessing the effects of hypothetical interventions

[2] Nadine Schieritz and Andreas Grler. Emergent Structures in Supply Chains A Study Integrating Agent-Based and System Dynamics Modeling

[3] Uri Wilensky. BehaviorSpace Guide NetLogo 4.0.3 User Manual. Northwestern University http://ccl.northwestern.edu/netlogo/docs/behaviorspace.html

[4] MVHS Modeling the Spread of an epidemic http://mvhs1.mbhs.edu/mvhsproj/epidemic/epidemic.html

[5] Leon Kaganovskiy Predator-Prey Models-Generalization of Lotka-Volterra Model University of Michigan-Ann Arbor http://faculty.ncf.edu/lkaganovskiy/LaTeX/talkmylotkaextend.pdf