Modeling an Epidemic in *NetLogo*

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Abstract

Even with today's modern scientific and medical breakthroughs, there exists the threat of a widespread epidemic. Could Avian Flu wreck havoc on the human population like the Spanish Influenza nearly a century ago? By creating a model that uses system dynamics, one may determine how widespread a given epidemic would be by experimenting with variables corresponding to preconceived epidemic and environmental behaviors and characteristics.

Background

If an epidemic were to occur, there would be two types of factors that would affect its duration and severity. There would be the variables corresponding to how a population reacted (in terms of quarantine and the probability of transmission) and characteristics unique to the disease, such as its severity and its genetic make up (which then decides what percentage of the population has a natural immunity.) By experimenting with these values, one can find out how one variable affects the overall behavior of the situation (i.e. a delay in establishing a quarantine would likely prolong the duration of the epidemic and its severity.)

By programming in NetLogo, one can take advantage of a unique programming approach known as System Dynamics. Rather than typing out loops and methods, one simply defines populations ("stocks"), changes between populations ("flows), and variables, all "linked" together to produce a constant flow of populations ever "tick" (the unit of time NetLogo uses.) This simpler approach can be useful in explaining the model to someone not literate in traditional coding languages such as C or Java, and also allows one to easily expand on the model by adding flows on top of an existing model without having to define or change a new variable in multiple loops.

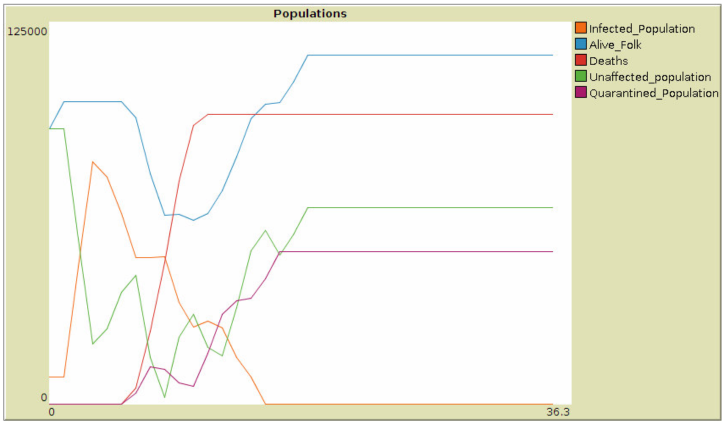

Figure 1. Sample run of an epidemics effect on a population over the course of 35 ticks (with a cure found at 10 ticks)

Preliminary Testing

In scientific journals, parametric and complicated differential epidemic models are frequently published, but no system dynamic model was found. Thus my model must be analyzed without being able to compare it to a vetted model. My model seems to run in a somewhat logical manner, as seen by the snapshot of a 35 tick runtime in Figure 1. Initially a great deal of the population gets sick, but no one dies for the first five ticks, as the program defines duration_of_infection to be 5. On the fifth day, however, people are either quarantined or die. By t=10, a cure is found and gradually the population climbs back to a level similar to its initial level. However, some problems do exist, as some of the population levels are exaggerated, including "Deaths" and the rapid climb of the variable "Alive_Folk" after a cure is found. The problems should be easy to address and once they are fixed the systems dynamics model will be made more complicated and realistic .

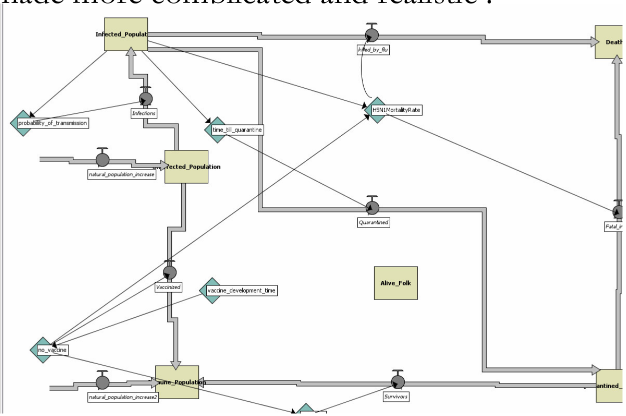

Figure 2. An epidemic model system dynamics diagram