Modeling Influenza Pandemic Response Effectiveness in Canada

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1.0 INTRODUCTION

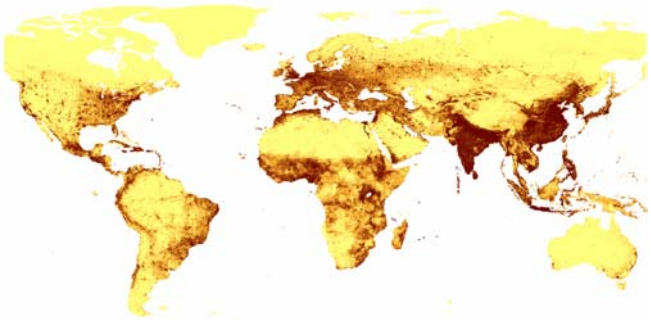
As the risk of a global influenza pandemic increases there is growing response preparedness efforts within Canada. One question that governmental decision makers have in this context is what is the most effective distribution of anti-virals, such as oral oseltamivir, within the population of first responders, health care workers, administrators and the general public in addition to what extent should the anti-virals be used as prophylactics. To provide an answer to this question, we have developed a Canada-wide influenza pandemic simulator and visualization system that allows for the modeling of various patterns of anti-viral distribution and use.

2.0 BACKGROUND

The seminal paper on modeling the effects anti-viral distribution and use in response to an influenza pandemic is that of [Ferguson *et. al.* 2005]. This paper focused on an indigenous outbreak of influenza from within Thailand and its eventual spread to neighboring countries within South East Asia.

We have presently presented a simple agent-based disease simulation model. This presentation represents the continued development of this on-going project.

3.0 ADAPTING TO CANADA



Unlike South East Asia, it is very unlikely that pandemic influenza will spontaneously develop internally. Rather, the entry into Canada of pandemic influenza is likely to occur at either Canada-US border crossings or at one of Canada's international airports. Also, unlike South East Asia, Canada has a different socioeconomic distribution, broader domestic travel routines in addition to having a significantly more geographically distributed population with relatively few major urban centers. These present modeling tasks not faced by [Ferguson *et. al.* 2005].

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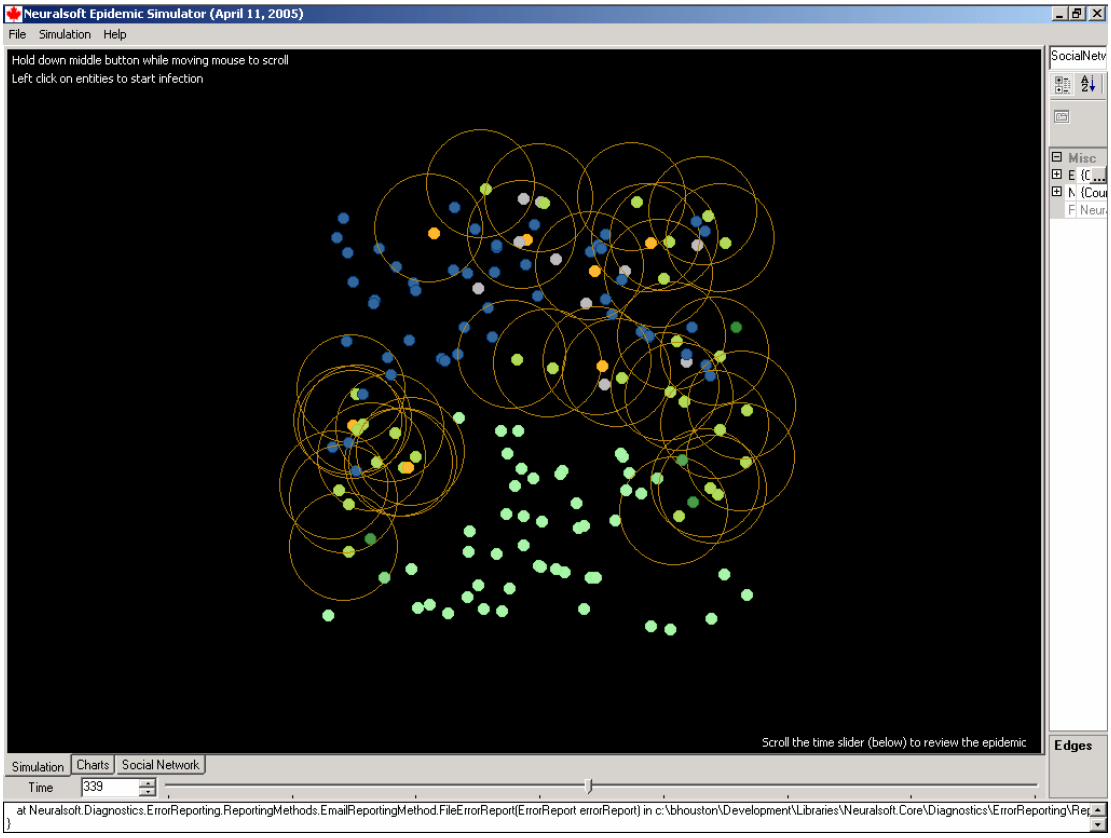
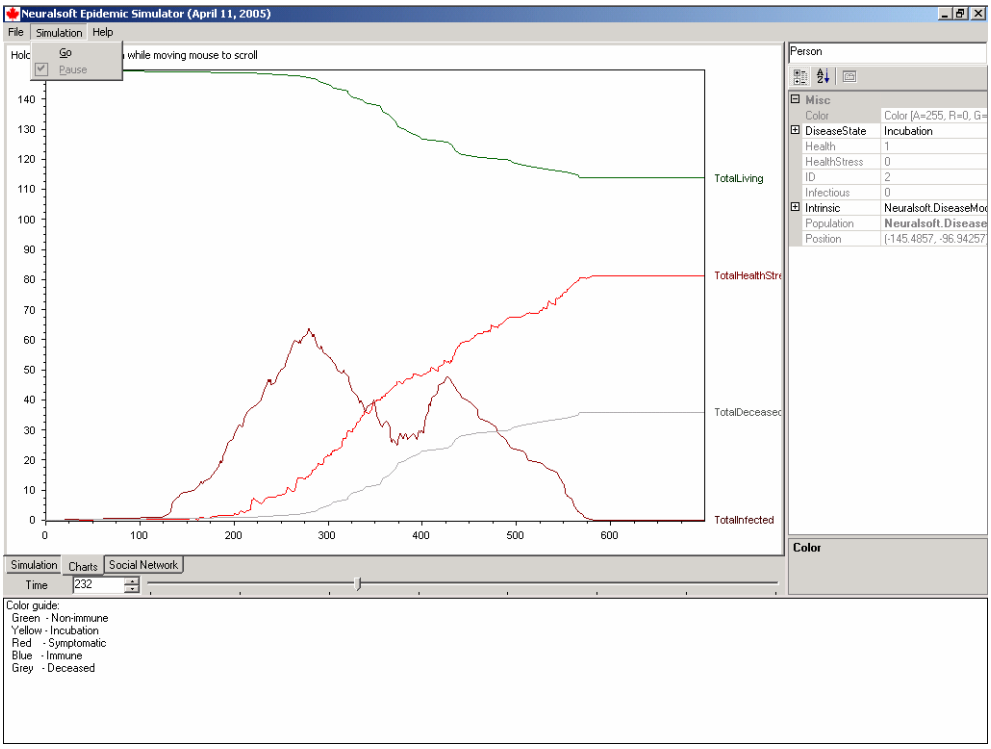
4.0 VISUALIZATION

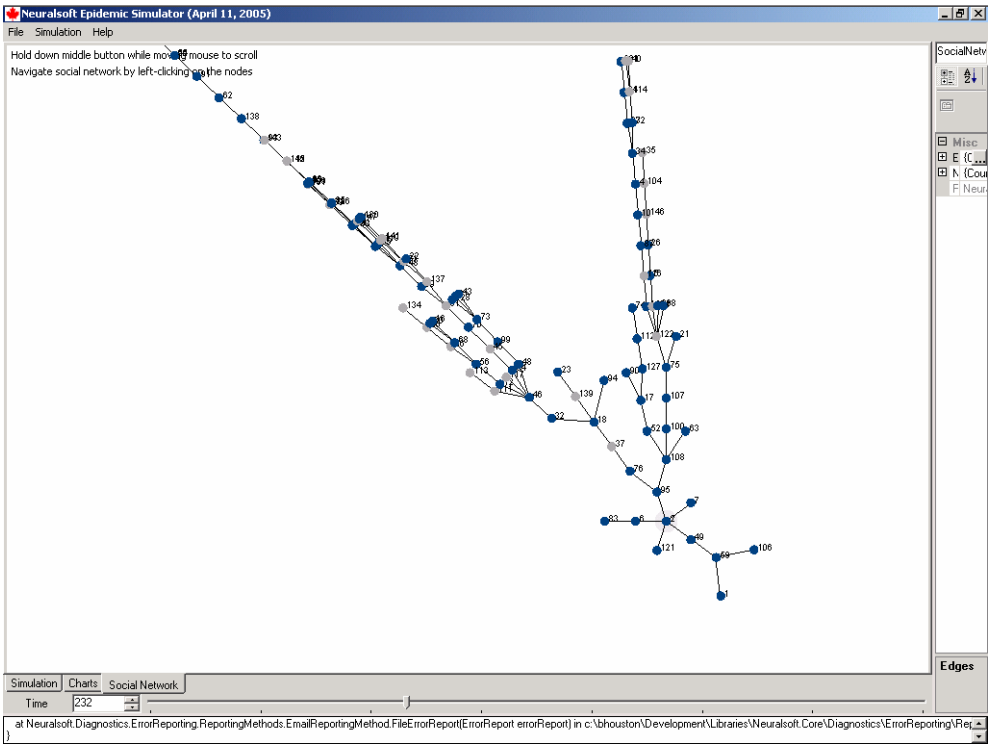
The end result of our simulation work is massive amounts of population, disease and response pattern data which represent the dynamics of the disease spread over time. We have developed a geographically-based visualization system that displays the incremental spread of the disease in tandem with the dynamic response in anti-viral usage and distribution.

Previous work showed a SARS-like disease outbreak on a featureless plane, the outbreak profile and the social network of infection:

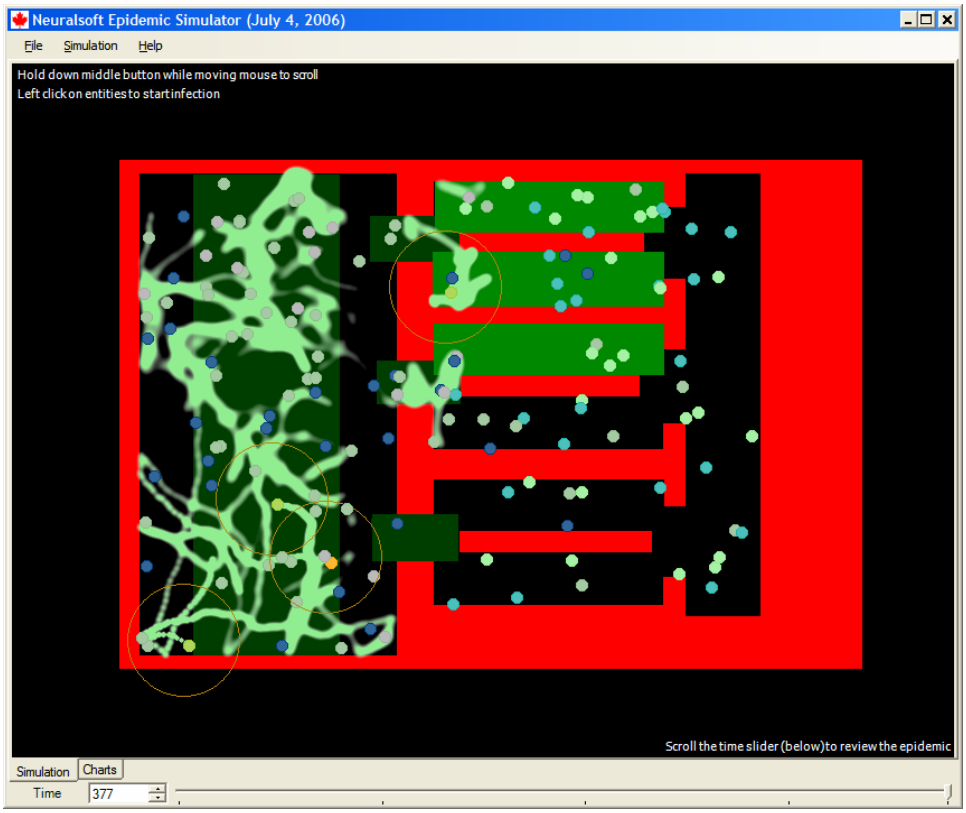




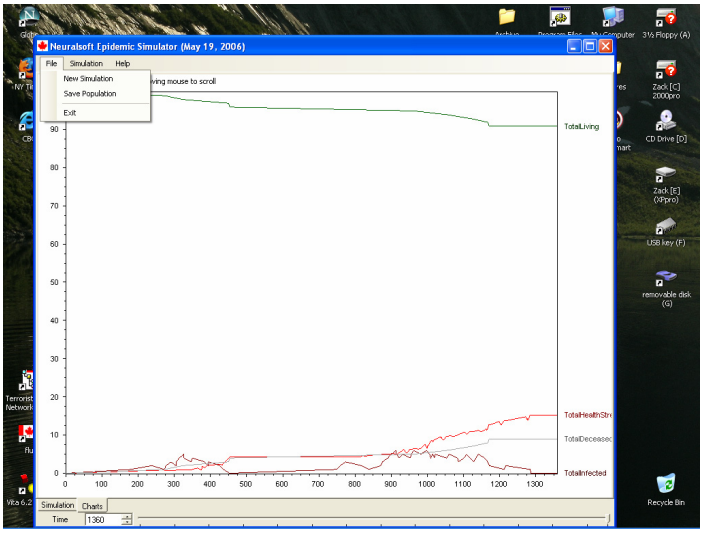
Notice the two-lobed outbreak, similar to SARS in Toronto. Our simulations show that this is a surprisingly frequent finding in the course of generic outbreaks, due to the chaotic nature of events.



The next figure is taken from our current pandemic flu model, in a fictitious hospital floor. Green are susceptible, yellow are infected, recovered are blue and grey are dead. The disease spreads through the air [yellow circles] and through residue on surfaces [green traces].



Following is the course of the disease. Due to the spread of the influenza-like disease by pathogen residue, the social network of who infected whom is less significant.



We have active projects to make this modeling more realistic, modeling two Toronto area hospitals in order to forecast resource allocation needs. However we intend now to use the simpler models to show regional and broader expected results, and to begin to answer practical questions in general, concerning vaccination, antiviral use, effects to be expected from isolation and quarantine, and other questions of immediate use to policy makers; our experience is, the simple stochastic models are of great use in that manner.

5.0 REFERENCE

Ferguson, Neal *et alii* . "Strategies for containing an emerging influenza pandemic in Southeast Asia" *Nature*, 2005. Available online at:
http://www.nature.com/nature/journal/v437/n7056/full/nature04017.html