

# Modeling the Spread of Mutating Pathogens

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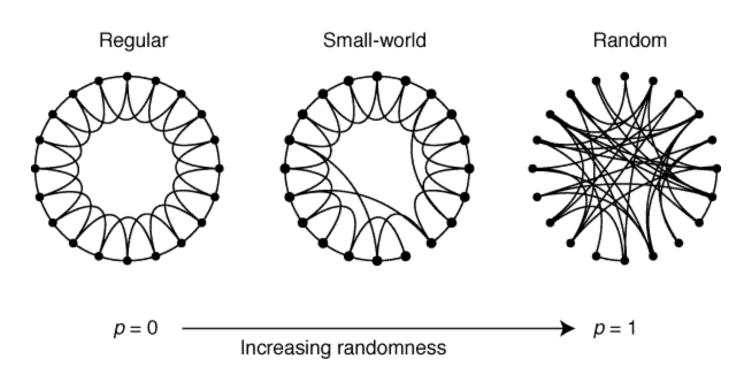
- Model the spread of a mutating pathogen using a small world network (SWN)
- We used a numerical simulation, coded in Matlab, to analyze pathogen dynamics
- Certain conditions cause the number of infected people to follow a damped oscillatory pattern

## Scientific Challenges

- The model must accurately construct a SWN
- The model must account for a large number of possible pathogens
- The effects of cross-immunity can be much more thoroughly followed

#### **Small World Networks**

A means of representing an interconnected population



Connectivity of small world networks [2]

## Glossary of Technical Terms

Bitstring: A string of zeros and ones, by which viruses and their mutations are modeled

Hamming Distance: The number of bits that are different in two viruses R: Number of time steps for which a person is removed, or immune to future infection

SpontProb: The probability of a random virus being introduced into a random node in the SWN

#### References

[1]Shao, Zhi-Gang et al. "Epidemics with Pathogen Mutation on Small-World Networks." Physica A: Statistical Mechanics and its Applications. Volume 363, Issue 2. (2006): 561-566.

[2] Watts, Duncan J. and Steven H. Strogatz. "Collective Dynamics of 'Small-World' Networks." Nature 393. (1998): 440-442.

## Methodology

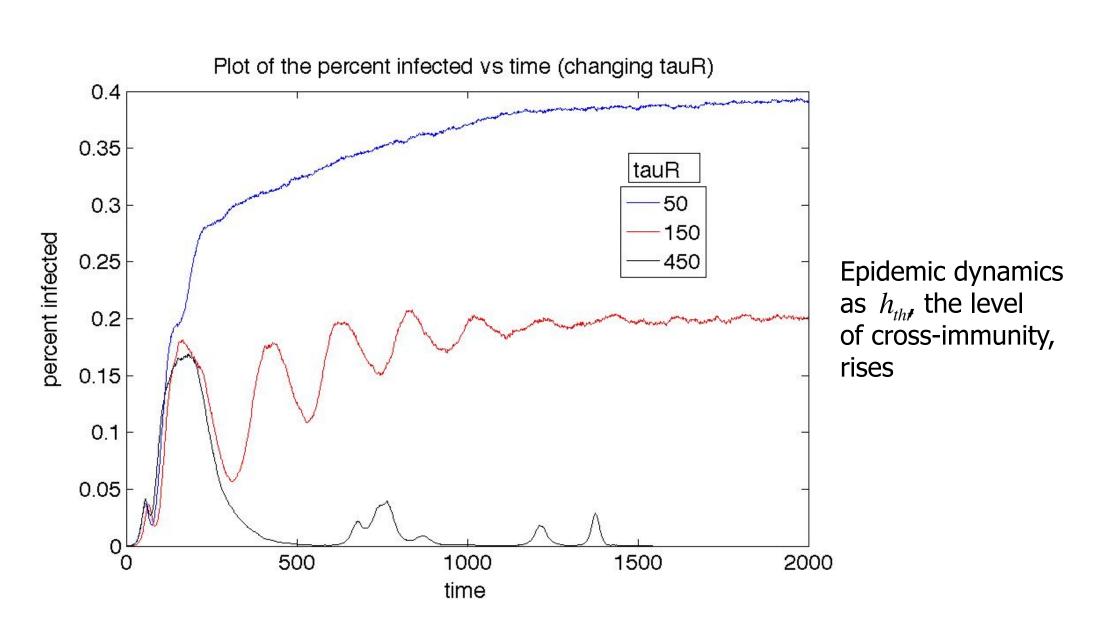
Jeremy Lerner

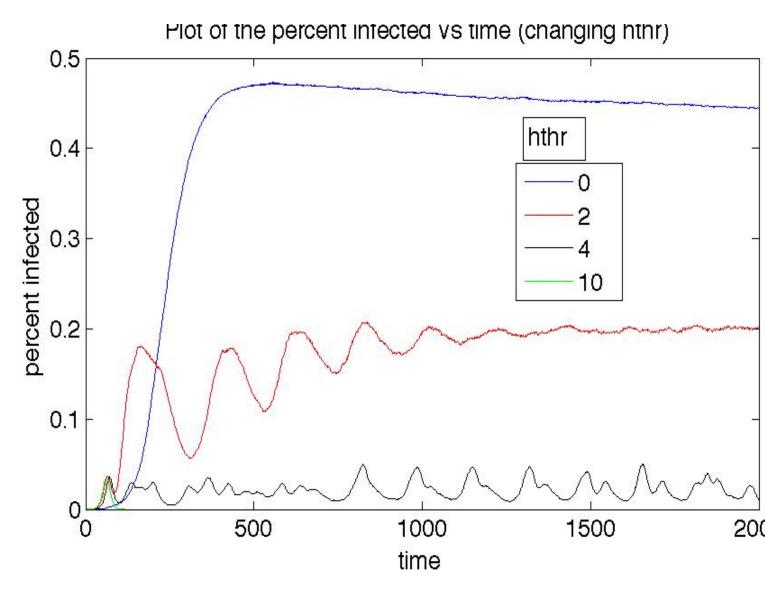
J. Sofia FitzGerald

- 1. The model starts with a single infected node and the virus spreads through the population via connections between nodes.
- 2. Variables that were adjusted in testing were  $h_{thr}$  (the maximum hamming distance for which cross-immunity occurs), population size, and  $\tau_R$  .
- 3. We then augmented our model with the spontaneous probability of adding a virus at any time step

#### Results

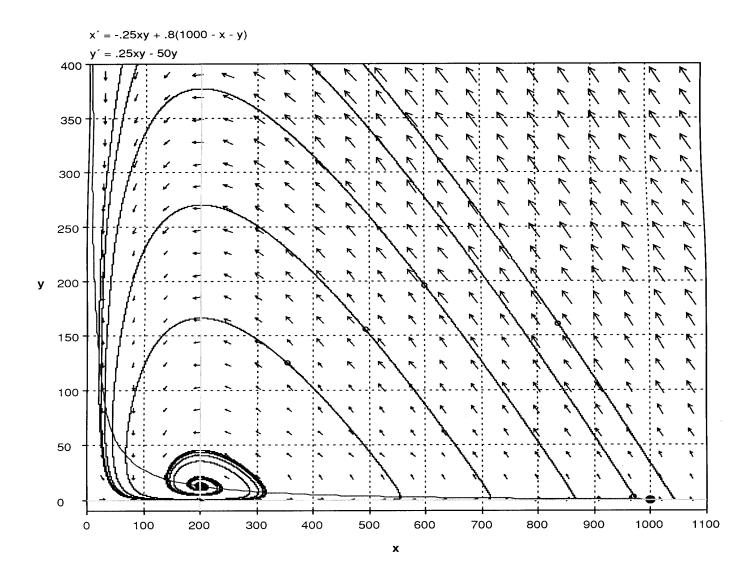
1. The decaying oscillation in the  $h_{thr}$  and  ${\mathcal T}_R$  graphs was found to be characteristic of epidemics with mutating pathogens [1].





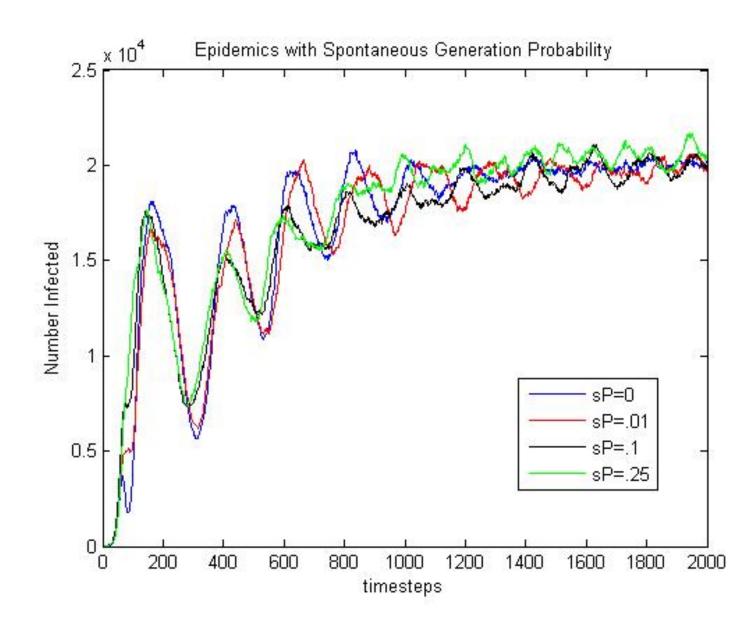
Dynamics as the length of immunity to a virus increases, showing the virus saturates at lower levels and then dies as  $au_R$  grows

2. For small populations, the infection dies off; for larger ones, the number of infected reaches a stable equilibrium.



Phase plane analysis of SIRS system where x is the number of susceptible individuals and y is the number of infected. Population size = 1,000

3. For populations of size 100,000 we found that spontProb produced no significant behavioral changes



Dynamics as the probability of a random virus entering the network increases. Population size= 100,000

### Acknowledgments

This project was mentored by Suz Tolwinski-Ward, whose help is acknowledged with great appreciation.