

# Compartmental Models in the Spread of Influenza A H1N1 Virus



Victor Rusu<sup>1,2</sup> and Shlomo Ta'asan<sup>3</sup>

<sup>1</sup>Bioengineering & Bioinformatics Summer Institute, Dept. of Computational Biology, University of Pittsburgh, 15260

<sup>2</sup>Department of Mathematics, Indiana University, 47405

<sup>3</sup>Department of Mathematical Sciences, Carnegie Mellon University, 15213

## Abstract

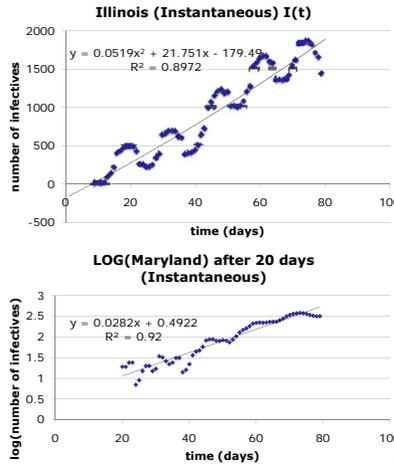
The influenza A H1N1 virus, responsible for the current outbreak of swine flu, is considered particularly dangerous since the swapping of entire RNA segments between viruses and an absence of RNA proofreading enzymes lead to large genetic diversity in the virus population. For many infectious diseases, compartmental models have been good mathematical models. They organize individuals with varying susceptibility or infectivity into different classes, and use ordinary differential equations to model the relationships between these classes. One can then obtain a system of ordinary differential equations which describes the severity of the epidemic. However, there seems to be difficulties in fitting the existing models to the swine flu data. This study focuses on the disagreement between these theoretical models and the number of infected individuals in the fifty states in an attempt to provide insight into improving existing models.

## Method

The goal of my summer research was to determine which behavior swine flu best resembles.

- SEIR-type-model → sum of exponentials solution (difficulty: at least one of the eigenvalues must be negative)
- SEIR-type-model with repeated eigenvalue 0 → polynomial (difficulty: certain restrictive conditions must be satisfied by the rate constants)
- SIR model (difficulty: poor linear fit for  $\alpha$  VS S)
- SIR-type-model with travel between states

$$\frac{dI}{dt} = \begin{bmatrix} \alpha_1 - \sum_{i=1}^{n-1} k_{i1} & k_{12} & \dots & k_{1n} \\ k_{21} & \alpha_2 - \sum_{i=1}^{n-1} k_{i2} & \dots & k_{2n} \\ \dots & \dots & \dots & \dots \\ k_{n1} & k_{n2} & \dots & \alpha_n - \sum_{i=1}^{n-1} k_{in} \end{bmatrix} I$$



## Conclusion

Each of the models that was used to fit the swine flu data was able to characterize some of specific qualities of the data. Each of them also had certain difficulties in fitting to the data. Also interesting are the fluctuations that are associated with the instantaneous data and whether they are intrinsic to the data, noise, or the result of inaccurate data. Questions to be answered by further study:

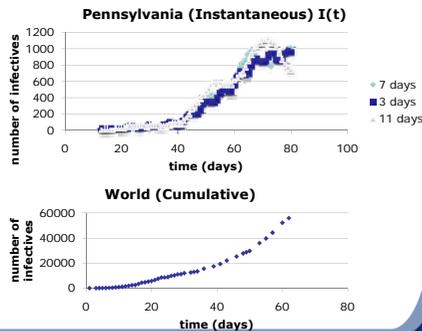
- Why is the behavior of the spread of swine flu different in the early phases than in the later phases?
- Compartmental models have been good models for infectious diseases in the past. Are there better types of models for swine flu (perhaps models that incorporate stochastic processes)?
- Are the fluctuations intrinsic to the data? If so how do they arise?
- Besides state populations and percentage of the population that is urban/rural what other factors should be included in modeling the spread of swine flu?

## Introduction

The SIR Model has been a good model for the spread of infectious diseases in the past.

$$\begin{cases} S + I \xrightarrow{\lambda} I + I \\ I \xrightarrow{\tau} R \end{cases} \quad \begin{cases} \frac{dS}{dt} = -\lambda SI \\ \frac{dI}{dt} = \lambda SI - \tau I \\ \frac{dR}{dt} = \tau I \end{cases} \quad \frac{dI}{dt} = (\lambda S - \tau)I \Rightarrow I(t) = I_0 e^{(\lambda S - \tau)t} = I_0 e^{\alpha t}$$

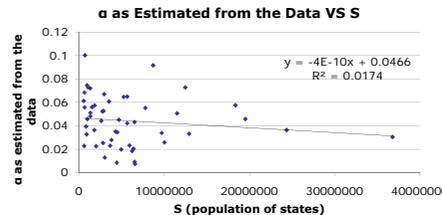
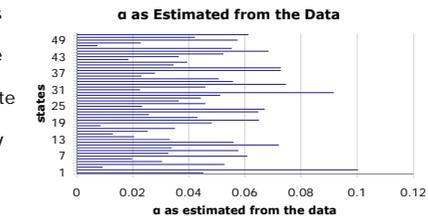
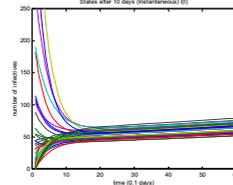
CDC gave the cumulative number of infectives; however, the instantaneous number of infectives (denoted by I(t)) is used in the models. It appears that data processing introduces fluctuations into the data. The world cumulative data from the WHO demonstrates two phase behavior.



## Results

The compartmental models studied were not very good models for the spread of swine flu.

- there is significant variance in the  $\alpha$  distribution
- the linear fits to determine the rate constants  $\lambda$  and  $\tau$  are poor → SIR model for each state independently is not a very good model
- other factors must be considered: such as rural/urban percentage of state's population
- Matlab simulations: fluctuations appear early in a SIR-type model with travel as numerical artifacts



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Department of Computational Biology, University of Pittsburgh

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