

Pandemic Flu Simulation

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Abstract

- Problem
- Previous approaches
- Novelty
- Key findings

Background

Understanding the behavior of the spread of infectious disease, like flu pandemics, is critical for advising and informing policy making. For example, studying behavior of virus transmission and recovery rates allows health professional and policymakers to define how much antiviral medication should be at hand to reduce the likelihood of outbreaks, the importance of vaccination to contain spread, and other measure to curtail an outbreak. Furthermore, being able to communicate the results of an infectious disease outbreak is very important.

There are a number of models which have been used to describe pandemic viruses (e.g., flu, COVID-19, ebola, etc.). SIR (susceptible-infected-recovered) and SEIR (susceptible-exposed-infected-recovered) are two deterministic models that have been used to describe pandemic flu and other viruses with success. Metapopulation stochastic models are, as the name implies, a stochastic alternative that have also successfully described the spreading behavior of infectious diseases. Each has its advantages and disadvantages, which will be discussed later in this paper.

Literature Review

Many researchers studying the spread of infectious disease explicitly cite the 1918 influenza outbreak (Berkessel et al. 2021; Germann et al. 2006; Johnson and Mueller 2002) as a motivating factor for their work. In the case of Johnson and Mueller (2002), the objective was to review previous records and data to verify morbidity of that pandemic, and the authors made the observation that each time the statistics are review, the total deaths from the pandemic seem to increase. In the 1920s, the record was approximately 21.5 million deaths; in 1991, this was updated to 24.7-39.3 million; Johnson and Mueller (2002) estimated the death toll is on the order of 50 million but the authors do not make this claim definitively. Instead, they allow for speculation on higher records in future estimates because there are many places affected by the 1918 influenza for which we do not have any data.

Clearly, the capacity for large-scale damage from pandemic infectious disease outbreaks is a very real threat. Hence, understanding how these things spread and what impact different mitigation strategies have on the rate of spread and severity of illness is critical.

Early research on modeling infectious diseases goes back to 1980 Soviet Russia. Much of that work is relatively inaccessible due to the fact that it is written in Russian, but other European and American scientists from the era have referenced that work (Longini, Fine, and Thacker 1986). These early models partitioned populations into a number of sub-groups, and described the change in size of each group and movement of individuals between groups using differential equations. Today, these are referred to as SIR, SEIR, and other derivatives.

Initial reactions to these deterministic models was skeptical, and multiple reasons can be cited. First, Russian scientists were applying these models to Russian cities to model the interaction between individuals within and between cities. But, many of the areas studied are relatively

far from each other and relatively isolated, hence the applicability of these models on a global scale was not considered robust (Longini, Fine, and Thacker 1986). Furthermore, for the time, these models and the algorithms required to use them were computationally expensive. Longini, Fine, and Thacker (1986) note the impracticality of applying these models, stating that over 90% of time spent analyzing infectious disease spread is dedicated to running the algorithms themselves.

Today, high-performance computing is readily available, so the application of deterministic differential equation models is straight-forward, and stochastic simulation and other simulation techniques have become popular.

Colizza et al. (2007), Cooper et al. (2006), Ferguson et al. (2005), Germann et al. (2006), Tan et al. (2021) all used some stochastic process to model the spread of influenza or other infectious disease as well as the impact of mitigation strategies. Colizza et al. (2007) found that large-scale application of prophylaxis antiviral agents could successfully contain a pandemic H5N1 influenza given a viral reproduction ratio of 1.9 or lower. Cooper et al. (2006) found that only significant air travel restrictions could delay the spread of pandemic influenza, but not contain an epidemic altogether. Germann et al. (2006) agreed with the previously stated positions and also found that rapid and preferential vaccination of children could contain an outbreak when the reproduction ratio of influenza is at or below 1.9.

Furthermore, some have explored the impact of geographic variables such as altitude on incidence rates and severity of illness (Arias-Reyes et al. 2021; Stephens, Chernyavskiy, and Bruns 2021). It was found that above 1000 meters above sea level, incidence rates and severity for infectious disease decline.

The purpose of this paper will be to simulate pandemic flu spread and identify critical thresholds for covariates such as altitude and solar radiation in minimizing the risk of a severe outbreak.

- Overview of major flu pandemics (e.g., 1918, 2009 H1N1).
- Transmission dynamics and public health impact.
- Role of environmental and demographic factors in flu spread.
- Impact of altitude on viral transmission and host susceptibility.
- Studies linking high-altitude regions to delayed or reduced flu spread.
- Obesity as a risk factor for flu severity and transmission.
- How models account for population-level obesity rates.
- Influence of UV radiation on virus viability and immune response.
- Seasonal patterns and their incorporation into predictive models.

Modeling

As previously mentioned, there are three common approaches to modeling this type of system: SIR, SEIR, and metapopulation models. We will begin by discussing the SIR model because it is relatively simple, yet also flexible, and it will establish a good foundation from which to discuss subsequent techniques.

The SIR model categorizes a population into three groups: susceptible, infected, and recovered. The rate of change of each of these groups is defined using differential equations, and we can account for mortality and birth rates in their definitions.

$$\begin{aligned}\frac{dS}{dt} &= \delta - \frac{\beta \times S \times I}{N} - \mu \times S \\ \frac{dI}{dt} &= \frac{\beta \times S \times I}{N} - (\gamma + \mu) \times I \\ \frac{dR}{dt} &= \gamma \times I - \mu \times R\end{aligned}$$

Here, S , I , R stand for the susceptible, infected, and recovered groups respectively. The population is denoted by N , and the rates of transmission, recovery, mortality, and birth are denoted by β , γ , μ , and δ .

The outbreak status is described by the reproduction ratio, which is the ratio between the transmission rate and recovery rates. When $\beta/\gamma > 1$, more people are becoming infected than are recovering, hence the system is in a state of outbreak. And, supposing that there is some percentage of the population that is already vaccinated (i.e., already in the recovered group), this ratio becomes $(\beta \times S(0))/(\gamma \times N)$, where $S(0)$ is the number of people in the susceptible group at time $t = 0$.

These facts make it easy to define different transmission, recovery, and vaccination population and rate targets to avoid a pandemic outbreak. Hence, the SIR is a simple model, but very effective at communicating clear actionable results to policy makers and authority figures.

The SEIR model is an extension of the SIR model, and it categorizes a population into four groups: susceptible, exposed, infected, and recovered. Mathematically, it is very similar to the SIR model, with an additional differential equation dedicated to the exposed group. For brevity, see others' work to describe this model. Additionally, there are more extensions to this model that are not described for brevity.

The metapopulation stochastic model relies on randomness to model the spread of infectious diseases.

- Strengths and limitations in modeling flu pandemics.
- Case studies using SIR models for H1N1, SARS, or seasonal influenza.
- Use of stochastic vs. deterministic approaches.

Method

- Data sources: WHO, CDC, climate databases, demographic surveys.
- Statistical and computational techniques for integrating covariates.
- Challenges in parameter estimation and model validation.
- Results: data visualization and tabulation, and implications.

Discussion

Future Work

- Underexplored covariates or regions.
- Need for interdisciplinary models combining epidemiology, climatology, and public health.
- Potential of machine learning to enhance traditional SIR frameworks.

Conclusions

- Summary of key findings.
- Implications for pandemic preparedness and policy.
- Call for more nuanced, data-rich modeling approaches.

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