

Pandemic Flu Simulation

Nathan Kurtz-Enko

Table of contents

Abstract	1
Background	2
History	2
Modeling	2
Covariates	3
Altitude	3
Obesity	4
Solar Radiation	4
Method	4
Discussion	4
Future Work	4
Conclusions	4
References	5

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 the spread of virus, such as the flu, COVID-19, and others, which have reached pandemic status. 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 behavior of infectious disease spread. Each has its pros and cons, which will be discussed later in this paper.

History

- State the purpose of the review: to explore how SIR-based models incorporate covariates such as altitude, obesity, and solar radiation.
- 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.

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 communicate 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.

Covariates

Altitude

- Impact of altitude on viral transmission and host susceptibility.
- Studies linking high-altitude regions to delayed or reduced flu spread.

Obesity

- Obesity as a risk factor for flu severity and transmission.
- How models account for population-level obesity rates.

Solar Radiation

- Influence of UV radiation on virus viability and immune response.
- Seasonal patterns and their incorporation into predictive models.

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.

References