Mathematical modelling of spread of diseases

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Abstract

This study constructs mathematical models to analyze the spread of infectious diseases, focusing on the 1968 Hong Kong flu pandemic. Beginning with a Susceptible-Infected (SI) framework, the model evolves into a Susceptible-Infected-Recovered (SIR) system incorporating recovery dynamics. Key parameters such as the transmission rate β, recovery rate γ, and basic reproduction number R_0 are derived and analyzed. Analytical solutions and equilibrium stability criteria confirm that epidemics occur when $R_0 > 1$. Applied to the Hong Kong flu ($R_0 = 1.5$), the model aligns with historical outbreak data. Simplifying assumptions include a constant population and homogeneous mixing.

Introduction

Mathematical models simplify disease dynamics by categorizing populations into compartments (e.g., susceptible, infected). This study examines the 1968 Hong Kong flu pandemic, which affected a constant population of $N = 3.1$ million (Hong Kong, 1961). We assume no births, deaths, or immunity loss. The progression from a basic SI model to an SIR framework with recovery dynamics is detailed, alongside derivations of critical thresholds for epidemic emergence. Key references to historical data and epidemiological parameters are included.

Model Formulation and Analysis

Basic SI model

In real life, each virus and individual has their own properties of infectiousness and immunity, but simplifying assumptions can be made for the ease of modelling. The starting population will be denoted by $N = 3.1$ million [1], which is Hong Kong's population in 1961 (previous to the 1968's pandemic). This population number is a constant due to the assumption is made that no one will be born or die during the pandemic.
It is also assumed there are only two types of individuals in a set population: the susceptible (who are not infected but could become infected) and the

infected (who stay infected). The number of each group is denoted by S and I respectively. This document will be focusing on the Hong Kong flu, which was highly infectious via direct contact. There is a fixed probability that if a susceptible person came into contact with an infected person, the latter will transmit the virus to the former. For the purpose of this study, everyone has the same contact per unit of time, and that the population has no separated areas.

We let $S(t)$ and $I(t)$ be functions of time, which will be measured in days that define the susceptible population and infected. In this simple model, the rate at which new infections occur is $\beta I(t)S(t)$ with β being a positive constant. When a new infection occurs, the infected individual moves from the susceptible class to the infected class. Thus, the first differential equation is formulated:

$$\frac{dS}{dt} = \frac{-\beta SI}{N}. \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N}. \tag{2}$$

There is a minus sign because the people who were susceptible will later be infected, hence leads to a decrease in susceptible number. On the other hand, the infected population can be described with the following differential equation, which is positive as it will only increase due to the assumption: the people who are infected stay infected.

The proportionality constant, β, is the average number of disease-spreading contacts between a susceptible and an infected per unit of time. Since the number of infected people over time are more interesting than the susceptible, substituting $S(t) = N - I(t)$ into (2) to obtain

$$\frac{dI}{dt} = \frac{\beta I(t)[N - I(t)]}{N}.$$

The solution to the above equation is

$$I(t) = \frac{Ne^{c_1 N+\beta t}}{e^{c_1 N+\beta t} + 1} \tag{3}$$

where the constant c_1 can be expressed in terms of $I(0)$.

Naturally and intuitively, the expression on the right-hand side of (3) increases as $t \longrightarrow \infty$ and with enough time, the number of infected $I(t)$ will be equal to the population number N.

SRI model with recovery

Discarding the notion that an infected person can't recover, the next step is to introduce necessary function and constant that describe the recovery process. Define γ as the probability that a person recovers (stop being infectious) during a time period Δt. Clearly with the newest addition, the infected population will decrease (recover) over time by a factor of γI which gives rise to the equation

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I. \tag{4}$$

The recovery period is assumed to be exponentially distributed with the probability $e^{-\gamma t}$ and the average time equal to $\frac{1}{\gamma}$ [5]. The flu of 1968 is assumed to have an infectious period of 2 days [2] and thus, $\gamma = \frac{1}{2}$.

Normalised SRI model

Once someone is infected with the Hong Kong flu and they recover they can't be infected again, therefore it is safe to assume that the recovered population is immune. The population equation now becomes $S(t) + I(t) + R(t) = N$ with the derivatives $dS(t)/dt + dI(t)/dt + dR(t)/dt = 0$. The recovery process can now then be extracted as $dR(t)/dt = -dS(t)/dt - dR(t)/dt$ which can be further simplified to

$$\frac{dR}{dt} = \gamma I \tag{5}$$

The current model can be more conveniently described by using the proportions of susceptible and infected in the population instead of the whole. That is, to introduce the new variables

$$\begin{aligned} s(t) &= \frac{S(t)}{N} \\ i(t) &= \frac{I(t)}{N} \\ r(t) &= \frac{R(t)}{N}. \end{aligned}$$

Let $\tau = \gamma t$ be a time variable which translates the unit time period of 1 day to 2 days. Combine the new time variable with the proportions obtained above to arrive at a new system

$$\begin{aligned} \frac{ds}{d\tau} &= -\frac{\beta}{\gamma} si \\ \frac{di}{d\tau} &= \frac{\beta}{\gamma} si - i \\ \frac{dr}{d\tau} &= i. \end{aligned}$$

Let $R_0 = \frac{\beta}{\gamma}$, it is the reproduction number (also called basic reproduction ratio) of a virus. This ratio dictates the average number of people who will contract the disease from an infected person where the entire population is susceptible or the contagiousness of the disease [3].

Equilibrium and Epidemic Threshold

In this model, the equilibrium state is considered to be when the entire population is still susceptible and there are no infected individuals. Let α

be the deviation from the equilibrium. At the equilibrium, the fraction of susceptible people in the total population is $s(t) = 1$ and the fraction of infected is $i(t) = 0$. Thus, near the equilibrium $s(t) = 1 - \alpha$ and $i(t) = \alpha$, for α very small. Removing the quadratic terms from the system of equations to get a linear one that approximates the solutions near this equilibrium

$$\begin{aligned}
\frac{ds}{d\tau} &= -\frac{\beta}{\gamma}\alpha \\
\frac{di}{d\tau} &= \frac{\beta}{\gamma}\alpha - \alpha \\
\frac{dr}{d\tau} &= \alpha.
\end{aligned}$$

The deviation is infinitesimally close to 0 so all the differentials go to 0.

By definition, an epidemic will break out if there are more people getting infected than recovering which correspond to the following condition

$$\frac{di}{d\tau} = \frac{\beta}{\gamma}\alpha - \alpha > 0.$$

Since $\gamma I(t)$ is positive, the preceding inequality can be determined by the factor R_0, specifically, $R_0 > \beta/\gamma$. Due to the fact that $S(t)$ can only decrease through time, the value of $S(t)$ at time $t = 0$ is the maximum value of the function which leads to

$$\begin{aligned}
&(\frac{\beta}{\gamma} - 1)\alpha \\
&R_0 - 1 > 0 \\
&R_0 > 1
\end{aligned}$$

Being the necessary condition for the occurrence of an epidemic in our model.
In the case of the Hong Kong flu, it had $R_0 = 1.5$ [4], meaning that there was indeed a flu outbreak in 1968.

Conclusion

This study develops SI and SIR models to analyze disease spread, deriving analytical solutions and stability criteria. The reproduction number R_0 determines outbreak potential: $R_0 > 1$ triggers exponential growth. Applied to the Hong Kong flu ($R_0 = 1.5$), the model aligns with empirical observations. Future extensions could relax assumptions (e.g., births/deaths, spatial heterogeneity).

References

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