Mathematical Methods *through* Dance

The SIR Model of Infectious Disease



Kinesthetic Expressions of the Beauty and Utility of Math

Scene 1. The SIR model of infectious disease epidemics

Epidemics have plagued humankind for thousands of years. However, it is only over the last 100 years that mathematical models have been developed to study the spread of infectious disease. These models have provided insight into the conditions that lead to epidemics, and measures that can be taken to stop the spread of disease.

Modeling the rate of infection and recovery

The SIR model divides the total population into *susceptible* individuals, *infectious* individuals, and *recovered* individuals.¹ Susceptible, Infectious, Recovered. SIR.

The model predicts how the number of infected individuals in a population increases with time. The rate of infection is proportional to the probability that a susceptible individual encounters an infectious individual

rate of infection =
$$b \times #$$
 susceptible $\times #$ infected

where *b* is the number of infectious contacts per day made by an infected individual (and \times is the multiplication sign).

Ignoring mortality, the SIR model assumes the rate of recovery is proportional to the number of infected individuals

rate of recovery =
$$k \times \#$$
 infected

where *k* is the recovery rate and $\frac{1}{k}$ is the average number of days required to recover from the illness (see Figure 1).

Rates of infection and recovery define the Reproduction Number R₀

When does an infectious disease lead to an epidemic and when can it be controlled. The SIR model provides an answer to that question. If the rate of infection is greater than the rate of recovery, an epidemic will occur. When the rate of recovery is greater than the rate of infection, and epidemic can be avoided. These factors are captured in a single parameter known as the *reproduction number*, \mathcal{R}_0 , defined

$$\mathcal{R}_0 = b \frac{1}{k} = #$$
 contacts per day × infectious period in days

When $\mathcal{R}_0 > 1$, the rate of infection exceeds the rate of recovery and an epidemic occurs (see Figure 1).

The *susceptible phrase* expresses the openness and vulnerability of the individual lacking infection or immunity to disease. Contact between a susceptible and infected individual is expressed through expansion, the outreach to others, and contraction, internalizing the infection. The *infected phrase* expresses the fear and anxiety resulting from the abrupt transition from wellness to illness. The *recoved phrase* pulls elements from the previous phrases to embody the comfort and relief of recovery and the return to openness. In this scene, the reproduction number \mathcal{R}_0 is less than one and the epidemic is avoided.

¹ Originally developed to study the 1666 plague and 1865 cholera epidemics in London. WO Kermack and AG McKendrick, "A Contribution to the Mathematical Theory of Epidemics," *Proc. Roy. Soc. Lond. A* **115**, 700-721 (1927).



Figure 1: SIR model of time evolution of six epidemics from influenza (1918). In the case of influenza (1918) the infection extends to the majority of individuals $(\mathcal{R}_0 > 1)$. Initially, the population is composed of susceptible individuals $\mathbf{s}(t)$ (blue). An infected individual is introduced. As the infection spreads, the number of infected individuals $\mathbf{i}(t)$ grows (red). After some recovery time, the number of recovered individuals $\mathbf{r}(t)$ grows (green). Note that at the end of the epidemic, most individuals in the society have contracted the disease.

Scene 2. Reproduction number and onset of an epidemic

Let's explore the predictions of the SIR model for a number of infectious diseases that have occurred over the past 100 years.

A hundred years of epidemics

The table below lists data for infectious diseases relevant to the SIR model starting with the influenza epidemic of 1918 and reaching the 2019 coronavirus (Covid-19) epidemic.

Epidemic model parameters			
disease	<i>b</i> (per day)	$\mathcal{R}_0 = \frac{b}{k}$	mortality= \mathcal{M}_0
influenza (1918)	1	2.4 - 4.4	10%
Hong Kong flu(1968)	1/2	1.2 - 3.6	0.5%
SARS (2003)	1/12	0.5	11%
coronavirus (2019)	1/2	2.2 (initial US)	3.4%

A typical number of daily infectious contacts per day in the absence of *social distancing* is two ($b = \frac{1}{2}$ per day). Exceptions are higher values for the influenza epidemic of 1918, which impacted large confined populations, and SARS, for which early isolation measures were effective.



Figure 2: SIR model of the time evolution of the coronavirus epidemic with three different values of the reproduction number ranging from $R_0 = 1/2$ (controlled) to $R_0 = 2$ (epidemic). A long recovery time and lack of social distancing result in epidemic conditions.

Epidemics then and now

In the current coronavirus epidemic, countries implementing effective social distancing protocols, along with quarantine and contact tracing, lowered the reproduction number below one, turning back the epidemic. The lack of effective social distancing led to reproduction numbers $R_0 > 1$ and an epidemic spread of coronavirus in the US.

An initial population of susceptible individuals is shown in *black and white. Fog* covers a single cell representing the first infected individual. *Sepia* expresses the contact between an infectious and susceptible individual before the onset of infection and fog. *Color and clarity* are used to express the state of recovery. In this scene, the reproduction number \mathcal{R}_0 is one with an equal rate of infection and recovery.

Scene 3. Impact of social networks on the evolution of disease

The SIR model assumes the chance of encountering any individual in the population is equally likely. However, our social organizations are based on clusters of individuals that we see frequently, such as family members and work colleagues, and those we see rarely, such as distant relatives or strangers. The details of the *social network* have an impact on the spread of disease.

Exponential and power-law growth

Consider the following data from the World Health Organization (WHO) representing coronavirus related mortality in China during the early days of the epidemic. The data show rapid growth in the number of coronavirus related deaths over a 25 day period (see Figure 3). The SIR model predicts *exponential growth* of infectious disease in time. It turns out the data in Figure 3 does not show exponential growth. It is best described as a *power-law growth*.

Six degrees of separation and small world networks

The network of social contacts assumed by the SIR model fails to reflect the diverse structure underlying social networks. In contrast, *small-world networks* can give rise to power-law growth reflected in the initial spread of the coronavirus epidemic of 2019.



Grouping individuals into pods can limit the spread of disease and prevent epidemics. The hyperconnection of individuals created by frequent and distant travel facilitated the coronavirus pandemic. Limiting travel and forming pods can prevent the onset of a pandemic (see Figure 4).

Within the population there are small communities, expressed by four quadrants. Each community harbors an infected individual. Over time the infection spreads to reach every individual. The kaleidoscopic vision expresses the overwhelming feeling of disorientation and confusion at the onset of an epidemic. In this scene, the reproduction number \mathcal{R}_0 is greater than one. The rate of infection is greater than the rate of recovery, leading to the onset of the epidemic.



Figure 3: The growing number of deaths $\dagger(t)$ attributed to coronavirus in the early phase of the epidemic in China.

Figure 4: A social network of 114 individuals (red dots) forming 7 clusters. The distance between dots represents social distance.(Left) All clusters are connected and every individual is linked to every other individual. (Right) Clusters are disconnected and there is no longer connectivity between all individuals.