**Introduction**

One of the fundamental questions in epidemiological studies is that of the long-term behavior of a disease. That is, whether the disease will die out naturally, persist at endemic levels, or infect the entire population until herd immunity is achieved. A key tool for investigating these questions as they pertain to flu-like diseases, which result in immunity or death for infected populations, is the Susceptible, Infected, Removed (SIR) Model.

SIR Models use a system of differential equations to track the changes in a population of size N over time as they move from the non-immune compartment Susceptible (S), to Infected (I), and either die or develop immunity and are Removed (R). Under certain assumptions, this system of differential equations can be linearized into a transition matrix ***A*** where the entries of ***A*** represent the probability of movement from one compartment to another. The spectral radius of ***A*** represents the long-term behavior of the system and is termed *R0*, the basic reproduction number (O. Diekmann 2009).

*R0* is biologically understood to represent the number of secondary infections that an index case infective will cause over the course of their infectious period in a population with no previous immunity. It can be expected that *R0* > 1 will result in complete infection of a population, where *R0* < 1 will result in the disease naturally clearing from the population (J.M. Heffernan 2005).

This paper will demonstrate the usage of eigenvalues to determine *R0* from real-world COVID-19 data in a simple SIR model, then expand to discuss the methodology in more complex, multi-compartmented models.

**Assumptions**

The simplest SIR Models rely on several assumptions (Jones 2007):

1. An unchanging population size N with no births or underlying death rate.
2. Constant effective contact and removal rates (β and γ, respectively).
3. A well-mixed population, implying that an infected individual has an equal chance of contacting and infecting any susceptible individual.

More complex models account for these assumptions and will be addressed later.

**The Model**

The following three ordinary differential equations form the simple SIR Model:

The constant β represents the number of new infections an infected individual generates per unit time (usually daily), and γ represents the probability that and infected individual is removed from compartment I (either through recovery or death).

We are interested in the behavior of this system at the equilibrium points , which results in two solutions. The first, R = N, implies that the infection has passed through the entire population already. The second, known as the disease-free equilibrium, is when S = N and I = 0. This solution defines the system before any individual has been infected and is the equilibrium point of interest in calculating *R0*. By making the additional assumption that S ≈ N near the initial conditions and focusing our assessment solely on the transition of susceptible individuals to infected individuals, we are able to linearize the ordinary differential equations into the form:

We can then represent the system with the state-change matrix:

In epidemiology, the basic reproduction number R0 is a measure of the number of subsequent infections caused by a single infected individual in a population without prior immunity. R0 represents the tendency of an outbreak to infect a population, where a disease with R0 < 1 will naturally die out and a disease with R0 > 1 will tend towards infecting the entire susceptible population (O. Diekmann 2009).