Case Study 1: SIR Models

Session 1:

There are 3 components to consider:

1. Susceptible $S(t)$ - *those who can get the disease*
2. Infectious $I(t)$ - *those who have the disease*
3. Recovered $R(t)$ - *those who had the disease and no longer do*

People in these catagories move from one another via the routine:

$$S \xrightarrow{\beta I} I \xrightarrow{\gamma} R$$

To model this we use the **Law of Mass Action** i.e. the idea that **the rate of change is proportional to the product of reactants involved in the equation**.

For example we have:

$$A + B \xrightarrow{k} C$$
$$\frac{d[A]}{dt} = -k\,[A]\,[B]$$

In our context we thus have the equations:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$
$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$
$$\frac{dR}{dt} = \gamma I \tag{3}$$

Here β is the infection rate (per time, per infective), γ is the rate at which the infected are removed.

Note that:

$$S(0) = S_0$$
$$I(0) = I_0$$
$$R(0) = 0$$

We have several assumptions inherent to our basic model:

A1 No natural births or deaths,

A2 No spatial effects,

A3 System is well mixed,

A4 Infection and "fixing" (i.e. whatever process causes someone to no longer be infected) occur instantaneously,

We can add equations (1) - (3) to see that $S + I + R = S_0 + I_0 := N$, where N is a constant which is the total population.

Also note that (3) is able to be decoupled.

We note now that

$$\frac{dI}{dt} = \beta (S - \rho) I \tag{4}$$

where $\rho = \gamma/\beta$. We now define an **epidemic** which describes the situation if, at $t = 0$

$$\frac{dI}{dt} > 0.$$

We let $R_0 = S_0/\rho = \beta S_0/\gamma$ be the **basic reproduction number**; we have then that if $R_0 > 1$, an epidemic will occur.

Epidemics only occur if $S_0 > \rho$ at $t = 0$.

To recap:

1. βS_0 is the rate at which an infected person produces infections in a population of S_0 people susceptible to the disease.
2. $1/\gamma$ is the time someone is infectious.
3. An infected person will produce $\beta S_0 \times 1/\gamma$ new infected people.

Session 2:

Nondimensionalisation might be useful in order to better highlight important constants, and also puts the model into a framework in order to better focus on the size of variables.

For population models we tend to use N as the scaling variable i.e. $\hat{S} := S/N, \hat{I} := I/N$. We then have:

$$\frac{N}{[t]}\frac{d\hat{S}}{d\hat{t}} = -\beta N^2 \hat{S}\hat{I}$$
$$\frac{N}{[t]}\frac{d\hat{I}}{d\hat{t}} = \beta N^2 \hat{S}\hat{I} - \gamma N \hat{I}$$

In our case we might define:

1. $S \to [S]\hat{S}$
2. $I \to [I]\hat{I}$
3. $t \to [t]\hat{t}$

Where "hatted" variables have been scaled by the bracketed variables, i.e. $\hat{S} := S/[S]$.

where $t = [t]\hat{t}$. We might then scale $[t] = 1/\gamma$ e.g:

$$\frac{d\hat{S}}{d\hat{t}} = -\beta N \hat{S}\hat{I}\gamma$$
$$\frac{d\hat{I}}{d\hat{t}} = \beta \frac{N}{\gamma}\hat{S}\hat{I} - \hat{I}$$

Here t has been scaled by the timescale of recovery, whereas if we had chosen $[t] = 1/\beta N$ it would represent the timescale of infection,

$$\frac{d\hat{S}}{d\hat{t}} = -\hat{S}\hat{I} \tag{5}$$
$$\frac{d\hat{I}}{d\hat{t}} = \hat{S}\hat{I} - \mu\hat{I} \tag{6}$$

where $\mu := \frac{\gamma}{\beta N}$

Further Exploration

- Include a vaccination rate which kicks in at time T, and is a function of the amount dead, infected, and susceptible etc