MA 138 – Calculus 2 with Life Science Applications
A Model for Epidemics
(Section 11.5.5)

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- Mathematical models are used throughout epidemiology. They are used both to predict the future growth of emerging disease outbreaks like Ebola and vaccination strategies to eliminate or control diseases like measles.
- We introduce the most basic mathematical models of infectious disease epidemics and endemics. These models form the basis of the necessarily more detailed models currently used by world health organizations, both to predict the future spread of a disease and to develop strategies for containment and eradication.
- In a simpler two-state model for a given disease we could divide the population into two classes; individuals who have the disease and individuals who do not have it. In that model after recovering from the disease, an individual is immediately returned to the population that does not have the disease, which means that they can immediately catch the disease again.

Kermack and McKendrick SIRS model

- For many diseases like measles, however, after a person recovers their immune system adapts to the disease, which makes them immune to it for some period of time (though this immunity can also be lost).
- To model the progression of such a disease we will use a model that was created by **Kermack** and **McKendrick** (1927, 1932, 1933).
- We will divide the population, say of N individuals, into three classes:
  - **susceptible individuals** who do not have the disease, but who could catch it. We denote this number with $S(t)$;
  - **infected individuals** who currently have (and can also transmit) the disease. We denote this number with $I(t)$;
  - **recovered individuals** who had the disease but who have since recovered from it, and are now immune to the disease. We denote this number with $R(t)$.

- Individuals start off in the susceptible class (S). After contact with an infected individual, they too may become infected (I). An individual will remain infected until their immune system fights off the disease. Then they enter the recovered class (R). After some time, an individual's immunity to the disease may wear off, returning them to the susceptible class.
- We can diagram these transitions using chemical reaction notation

$$S \longrightarrow I \longrightarrow R \longrightarrow S$$

  This kind of model is known as an **SIRS model**.
- We assume that the population under study is well mixed so that every person has equal probability of coming into contact with every other person. This is a major approximation.

Word Equations

Let's model the movements of individuals between the three classes, starting with word equations:

$$\left\{\begin{array}{c}\text{Rate of change of} \\ \text{no. susceptibles}\end{array}\right\} = -\left\{\begin{array}{c}\text{Rate at which} \\ \text{susceptibles} \\ \text{are infected}\end{array}\right\} + \left\{\begin{array}{c}\text{Rate at which} \\ \text{recovered individuals} \\ \text{lose immunity}\end{array}\right\}$$

$$\left\{\begin{array}{c}\text{Rate of change of} \\ \text{no. infected}\end{array}\right\} = \left\{\begin{array}{c}\text{Rate at which} \\ \text{susceptibles} \\ \text{are infected}\end{array}\right\} - \left\{\begin{array}{c}\text{Rate at which} \\ \text{infected individuals} \\ \text{recover}\end{array}\right\}$$

$$\left\{\begin{array}{c}\text{Rate of change of} \\ \text{no. recovered}\end{array}\right\} = \left\{\begin{array}{c}\text{Rate at which} \\ \text{infected individuals} \\ \text{recover}\end{array}\right\} - \left\{\begin{array}{c}\text{Rate at which} \\ \text{recovered individuals} \\ \text{lose immunity}\end{array}\right\}$$

Key Assumption

The key assumption in the model is that the *incidence of the disease*, that is the rate at which susceptibles are infected, is an increasing function of both S and I, say $\lambda(I)S$.

The function $\lambda(I)$ is called the *force of infection* and it is defined to be the probability density of a given susceptible contracting the disease in unit time.

We have $\lambda(I) \propto b\frac{I}{N}$, where b denotes the number of other individuals that a single individual comes in contact with in one unit of time.

This key assumption goes under the name of the *law of mass action*.

The SIRS Model

Putting all these ingredients together, we derive the following system of differential equations to model the spread of the disease through the population:

$$\begin{cases} \dfrac{dS}{dt} &= -\dfrac{kb}{N}SI + aR \\ \dfrac{dI}{dt} &= \dfrac{kb}{N}SI - cI \\ \dfrac{dR}{dt} &= cI - aR \end{cases}$$

Here k denotes the **transmission rate**; c denotes the **recovery rate**; and a denotes the **rate of immunity loss**.

Closed Population

Our model consists of three separate differential equations for the three dependent variables, S, I, and R. However , we have assumed that all of the individuals must belong in exactly one of the three classes. This assumption means that: $S(t) + I(t) + R(t) = N$.

In other words, we assume that the modeling time scale is short compared to the lifetime of its hosts, so that we can neglect birth and death. Since $S + I + R$ is a conserved quantity, it does not change with time.

We can check that this $S + I + R$ really is constant by using the differential equation system:

$$\begin{aligned}\frac{d}{dt}(S + I + R) &= \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\ &= \left(-\frac{kb}{N} SI + aR \right) + \left(\frac{kb}{N} SI - cI \right) + \left(cI - aR \right) = 0\end{aligned}$$

Simplified System of Differential Equations

In other words, if we know S and I at any point in time, we can always calculate R from $R(t) = N - S(t) - I(t)$.

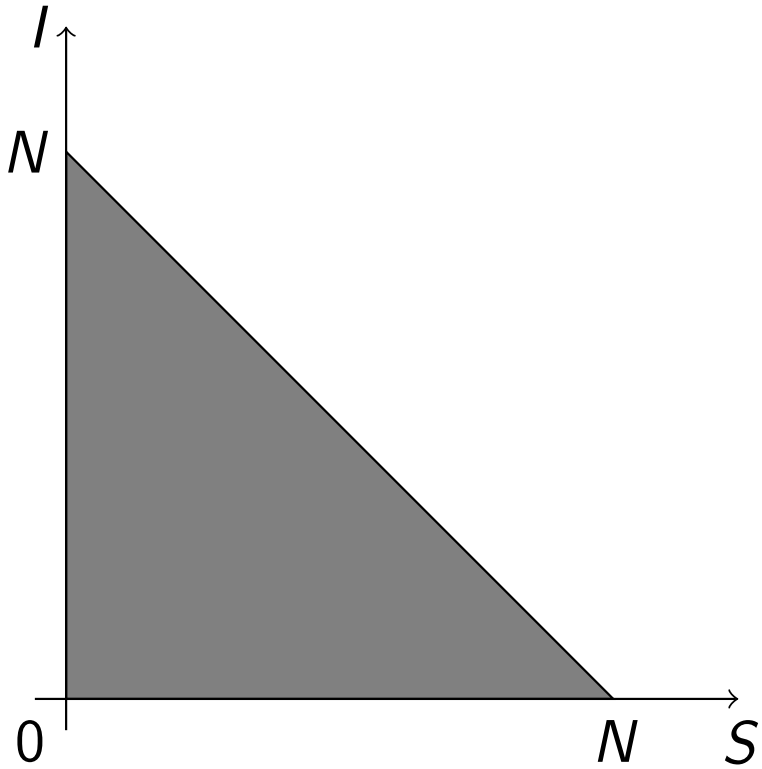
We can use this equation to eliminate R from the model. We obtain a simplified system of non linear differential equations that we can discuss with the techniques learned in Section 11.3:

$$\begin{cases} \dfrac{dS}{dt} &= -\dfrac{kb}{N}SI + a(N - S - I) \\ \dfrac{dI}{dt} &= \dfrac{kb}{N}SI - cI \end{cases}$$

Domain

Since S, I, and R all represent numbers of individuals, all three quantities must be non-negative, meaning that

$$S \geq 0, \quad I \geq 0, \quad \text{and} \quad N - S - I \geq 0 \quad \textit{or} \quad S + I \leq N$$



The picture to the left shows the domain of the differential equation system

Equilibria Analysis: Two Potential Equilibria

To analyze this model we identify its equilibria, that is, we look for values $(\widehat{S}, \widehat{I})$ that satisfy the equations

$$\begin{cases} -\dfrac{kb}{N}SI + a(N - S - I) &= 0 \\ \left(\dfrac{kb}{N}S - c\right)I &= 0 \end{cases}$$

In our initial analysis of the equations we will assume that all of the constants in our model (N, a, b, c, and k) are positive. Starting with the second equation we obtain that either $\widehat{I} = 0$ or $\widehat{S} = \dfrac{c}{kb}N$. If we substitute either of these two values in the first equation we then obtain after a few calculations the following two possible equilibrium points

$$(\widehat{S}_1, \widehat{I}_1) = (N, 0) \qquad \text{and} \qquad (\widehat{S}_2, \widehat{I}_2) = \left(\frac{c}{kb}N, \frac{aN}{a+c}\left(1 - \frac{c}{kb}\right)\right).$$

The first equilibrium point $(\widehat{S}_1, \widehat{I}_1) = (N, 0)$ always lies in the domain of the differential equation system because the inequalities

$$\widehat{S}_1 \geq 0,\ \widehat{I}_1 \geq 0 \text{ and } \widehat{S}_1 + \widehat{I}_1 \leq N$$

are certainly satisfied.

For the other equilibrium point $(\widehat{S}_2, \widehat{I}_2) = \left(\frac{c}{kb} N, \frac{aN}{a+c}(1 - \frac{c}{kb}) \right)$, we certainly have $\widehat{S}_2 \geq 0$ because $c, k, b, N > 0$. However a necessary and sufficient condition for the other inequalities

$$\widehat{I}_2 \geq 0 \text{ and } \widehat{S}_2 + \widehat{I}_2 \leq N$$

to be satisfied is that $\boxed{c \leq kb}$. In fact is easy to check that

$$N - \widehat{S}_2 - \widehat{I}_2 = \frac{Nc}{(a+c)} \left(1 - \frac{c}{kb} \right).$$

Jacobi Matrix

If $\mathbf{f}(S,I) = \begin{bmatrix} f_1(S,I) \\ f_2(S,I) \end{bmatrix} = \begin{bmatrix} -\frac{kb}{N}SI + a(N-S-I) \\ \frac{kb}{N}SI - cI \end{bmatrix}$ denotes the vector-valued function that correspond to out simplified SIRS model, then the Jacobi matrix that we need to analyze at the two possible equilibria is

$$D\mathbf{f}(S,I) = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial I} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial I} \end{bmatrix} = \begin{bmatrix} -\frac{kb}{N}I - a & -\frac{kb}{N}S - a \\ \frac{kb}{N}I & \frac{kb}{N}S - c \end{bmatrix}.$$

Only One Equilibrium Point $(\widehat{S}_1, \widehat{I}_1)$ with $c > kb$

The Jacobi matrix evaluated at the equilibrium $(N, 0)$ is an upper triangular matrix, namely

$$D\mathbf{f}(N,0) = \begin{bmatrix} -a & -kb-a \\ 0 & kb-c \end{bmatrix}$$

so the eigenvalues may be read off from the diagonal entries:

$$\lambda_1 = -a \quad \text{and} \quad \lambda_2 = kb - c.$$

As we discussed earlier, if $c > kb$ there is only one equilibrium, at $(\widehat{S}_1, \widehat{I}_1) = (N, 0)$, and this equilibrium is a stable node because both eigenvalues are real and negative. All solutions converge to $(\widehat{S}_1, \widehat{I}_1) = (N, 0)$ as $t \to +\infty$. At this equilibrium also $\widehat{R}_1 = 0$.

In other words, **the disease disappears from the population.**

Second Equilibrium Point $(\widehat{S}_2, \widehat{I}_2)$ with $c < kb$

If $c < kb$, then the equilibrium $(\widehat{S}_1, \widehat{I}_1) = (N, 0)$ is a saddle point, and therefore unstable. However, a second equilibrium occurs in this case! The Jacobi matrix evaluated at this equilibrium $(\widehat{S}_2, \widehat{I}_2)$ is

$$D\mathbf{f}\left(\frac{c}{kb}N, \frac{aN}{a+c}\left(1-\frac{c}{kb}\right)\right) = \begin{bmatrix} -a\dfrac{(kb+a)}{a+c} & -(a+c) \\ a\dfrac{(kb-c)}{a+c} & 0 \end{bmatrix}$$

Note that the trace of this Jacobi matrix is clearly negative and its determinant is equal to $a(kb-c) > 0$. This means that that the second equilibrium point is stable (i.e., either a stable node or a stable spiral). All solutions converge to the stable equilibrium point with $\widehat{S}_2$ and $\widehat{I}_2$ both non-zero. That is, the disease becomes **endemic**. It neither dies out nor infects everyone, but remains present in the population at a stable level.

The Basic Reproductive Number, R_0

We can interpret the conditions $c > kb$ or $c < kb$ that we encountered as follows. Suppose that we start with a population made up almost entirely of susceptibles, with a very small number of infected individuals, that is, $S \approx N$. Then we deduce that:

$$\frac{dI}{dt} = \frac{kb}{N} SI - cI \approx (kb - c)I.$$

So the infected population, I, will grow or decay exponentially; growing if $c < kb$, and decaying if $c > kb$.

A common way that epidemiologists write this condition is to define a new constant, R_0, called the **basic reproductive number** and defined by:

$$R_0 = \frac{kb}{c}.$$

The disease spreads if $R_0 > 1$, and dies out if $R_0 < 1$.