Mathematical models are used to study a wide variety of natural processes. Models vary widely in complexity, from one equation to page-long systems. In the case of mathematical epidemiology, there are several simple models that form the basis for the more complex models that are used to study specific diseases. The focus of this paper is the behaviour of one simple model and three more complex related models.

The basic compartmental model for epidemics was developed by W.O. Kermack and A.G. McKendrick in 1927. This model separates the total population (of constant size N) into three classes. The first, $S(t)$, is the susceptible class, which denotes the number of people who have not been infected at time t . The second, $I(t)$, is the infective class, which denotes the number of people who are infected and contagious at time t . The third, $R(t)$, is the removed class, which denotes the number of people who cannot become infected or spread infection because they have recovered from the disease and have developed immunity.

The model is formulated using three differential equations that describe the flow into and out of each class, or compartment. This only makes sense in a population large enough that the size of each compartment can be considered differentiable by time, so we will assume that we are dealing with such a population. Called the SIR model, it is

$$S' = -\beta SI$$

(1)

$$I' = \beta SI - \alpha I$$
$$R' = \alpha I.$$

The model is based on the following assumptions:

(i)   An average member of the population makes contact sufficient to transmit infection with βN others per unit time.

(ii)   Infectives leave the infective class at rate αI per unit time.

(iii)   The total population is a constant size.

(iv)   There is no entry into or departure from the population.

Assumption (iii), it should be noted, implies that $N = S + I + R$. This means that R is determined once S and I are known. Therefore, we can simply focus on S and I , along with their initial conditions

$$S(0) = S_o, \qquad I(0) = I_o$$

while conducting our analysis.

The question we would like this model to answer is whether a disease will die out or result in an epidemic. Therefore, a quantity with a threshold value (which determines whether there is an epidemic or not) would be useful. Fortunately, such a quantity can be found in the basic reproduction number.

The basic reproduction number, or $\mathcal{R}_o$, is the number of secondary infections caused by a introducing one infective into a wholly susceptible population. If $\mathcal{R}_o < 1$, the disease dies out immediately and there is no epidemic, but if $\mathcal{R}_o > 1$, an epidemic occurs. According to the assumptions above, an infective makes βN contacts per unit time and the mean infective period is $\frac{1}{\alpha}$.

Therefore, $\mathcal{R}_o = \frac{\beta N}{\alpha}$.

The disease dies out when $I = 0$, and there is no epidemic if $I' < 0$ for all t. $I' < 0$ when $\beta S - \alpha < 0$, or equivalently, $S < \frac{\alpha}{\beta}$. Inspection of (1) shows that $S' < 0$ for all t, and thus, whether there is an epidemic or not, eventually $S < \frac{\alpha}{\beta}$. This means the disease will always die out eventually, even if an epidemic occurs initially. It also implies that there will be no epidemic if $S_o < \frac{\alpha}{\beta}$, or $\frac{\beta S_o}{\alpha} < 1$. Since $S_o < N$, if $\mathcal{R}_o < 1$, there will be no epidemic.

A more complicated model than (1) could include natural births and deaths. In this case, the disease being modelled is presumed to be an endemic one – that is, the disease being modelled is assumed to persist in the population for a significantly longer period than one modelled using the basic SIR model.

For simplicity, the birth and death rates are set equal to each other, allowing this model to also have a constant population size, N. The SIR model with natural births and deaths is

$$S' = \mu N - \beta SI - \mu S, \qquad S(0) = S_o$$

(2)

$$I' = \beta SI - (\alpha + \mu)I, \qquad I(0) = I_o$$
$$R' = \alpha I - \mu R, \qquad R(0) = 0.$$

While assumption (iv), above, no longer holds, the first three assumptions continue to apply to (2). For this model,

$$\mathcal{R}_o = \frac{\beta N}{\alpha + \mu}.$$

PROOF WHEN R < 1

We would like to show that I' decreases monotonically to zero when $\mathcal{R}_o < 1$ for (2) as well as (1). $I' < 0$ when $\beta S - \alpha - \mu < 0$. If $\mathcal{R}_o < 1$, then $\beta N < \alpha + \mu$. Since $\beta > 0$ and $S \leq N$, by assumptions (i) and (iii), respectively, this implies that $\beta S < \alpha + \mu$. This is equivalent to $\beta S - \alpha - \mu < 0$, which implies that indeed $I' < 0$.
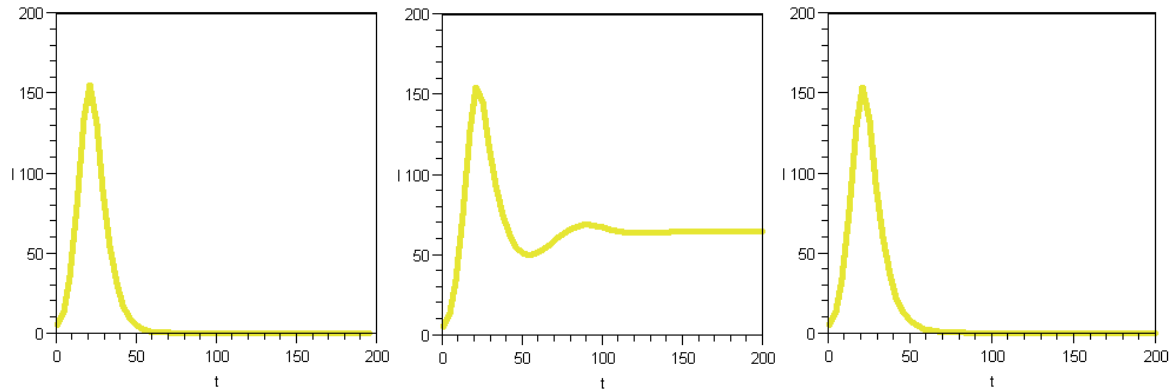
When $\mathcal{R}_o > 1$, the situation is more complicated. In this case, and for all the following models, a proof is not attempted. Instead, the behaviour of the system is investigated numerically. Figure 1a shows the number of infectives predicted by (1) when $\mathcal{R}_o = 2$. The disease eventually dies out when $I = 0$. On the other hand, the disease modeled by (2) does not die out, and after some initial oscillations, approaches a positive limit, as shown by figure 1b. However, figure 1c shows that as $\mu \to 0$, its behaviour begins to approach that of (1).

Another possible extension of the basic SIR model is to include disease deaths in the model. This model would be used for a potentially fatal epidemic disease. In this case, a fraction, $0 \leq f < 1$, of those removed from the infective class develop immunity, while the remainder die from the disease. This model is

$$S' = -\beta SI, \qquad S(0) = S_o$$

(3)

$$I' = \beta SI - \alpha I, \qquad I(0) = I_o$$
$$R' = \alpha f I, \qquad R(0) = 0$$

and neither assumption (iii) nor (iv) applies, though (i) and (ii) still do. Since N is no longer constant, an equation for it is required. That equation is

$$N' = -(1 - f)I, \qquad N(0) = N_o = S_o + I_o$$

and $N = S + I + R$, as before. This means that the fourth quantity is determined once three are known. Because of this, it is possible to use S , I , and N in the analysis and to leave out R . The equation for $\mathcal{R}_o$ is

$$\mathcal{R}_o = \frac{\beta N_o}{\alpha}.$$
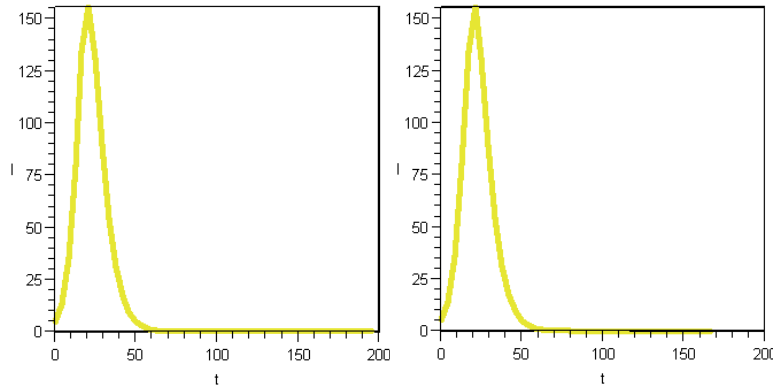
As can be seen from figure 2, the behaviour of (1) and (3) are identical when $\mathcal{R}_o > 1$. Because neither S nor I rely on N , this is to be expected. The disease deaths are not changing the rate of flow from I , they are simply redirecting a fraction of that flow.

The final model that will be analyzed is one that includes both natural births and deaths and disease deaths. This corresponds to a potentially fatal endemic disease, and the model contains elements from all three of the models already analyzed. The model is
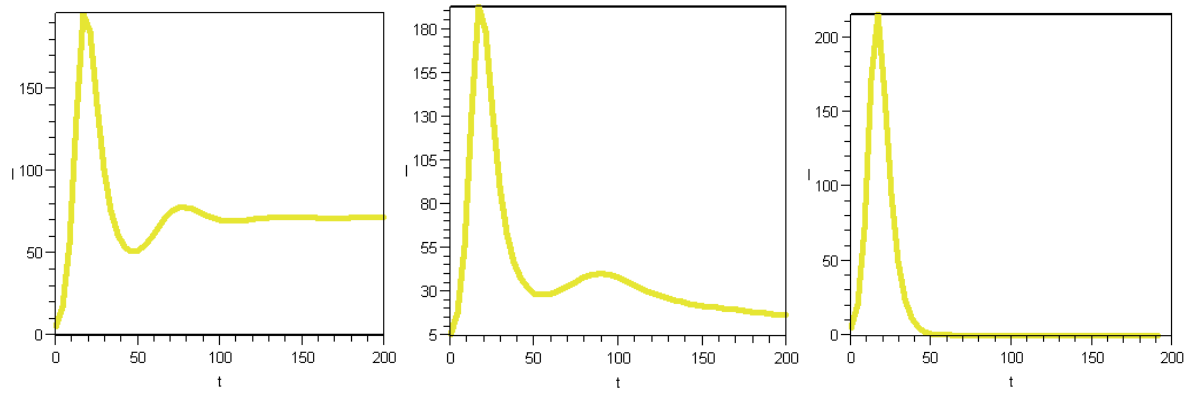
$$S' = \mu N - \beta S I - \mu S, \qquad S(0) = S_o$$

(4)

$$I' = \beta S I - (\alpha + \mu)I, \qquad I(0) = I_o$$
$$R' = \alpha f I - \mu R, \qquad R(0) = 0 .$$

and, again, the equation for N is

$$N' = -(1 - f)I, \qquad N(0) = N_o = S_o + I_o .$$

Once again, $N = S + I + R$ and only S , I , and N will be used in the analysis.

For this model, because S depends on N – the birthrate depends on population size – disease deaths have an effect on the behaviour of the disease. As shown in figure 3b, this effect is significant. In fact,