

## Modeling the spread of diseases

Most likely you have heard about the “swine flu” striking the world right now. As of today there are about 2,000 worldwide confirmed cases, about 350 here in the US.

Through history epidemics of infectious diseases have devastated large numbers of humans. Most recently, in 2003, SARS (severe acute respiratory syndrome) spread quickly and killed about 700 people. In the US, the CDC (Center for Disease Control) reports that about half million people have died from AIDS in the years from 2002 to 2006.

There is no single model that can apply to all diseases. We will construct an elementary model of a disease that satisfies some basic conditions. The first is that we consider that the population that it is affected is constant: we ignore new births and immigration. More complex models could account for that, but this assumption is quite reasonable. For example, this could apply to a break of chickenpox at an elementary school.

¶ 1. Give examples of diseases where this condition of “constant population” is appropriate.

¶ 2. Give examples of diseases where this condition of “constant population” is not very appropriate.

We will also assume that the disease transmits by direct constant between individuals in the population.

¶ 3. Do you know of any examples where this “infection by direct contact” is not true?

And we will also assume that the population under study mixes homogeneously: all members of the population interact to one another to the same degree, so that all uninfected individuals face the same level of exposure to the disease by those already infected.

¶ 4. Is the “homogeneous mixing” assumption a reasonable one for

- (a) a break of chickenpox at an elementary school?
- (b) an outbreak of chicken pox in all the elementary schools in the US?
- (c) for the swine flu?

¶ 5. What other examples can you think of where this “homogeneous mixing” assumption is reasonable? unreasonable?

To formulate our model, at each time  $t$  we divide the population  $N$  into three categories:

- $S(t)$  the susceptible class: those who may catch the disease, but are not currently infected.
- $I(t)$  those that are infected with the disease and are currently contagious.
- $R(t)$  the removed class: those that cannot get the disease nor transmit it, because the either have recovered permanently, became immune, or have died.

¶ 6. Explain which, at any time  $t$ , the following holds:

$$S(t) + I(t) + R(t) = N$$

¶ 7. Suppose that you are using this to model an outbreak of flu in your high school. How would you expect the sizes of each of the populations to change from the moment that it occur until it subsides? If you were to plot the graphs of  $S(t)$ ,  $I(t)$  and  $R(t)$  as a function of time  $t$ , how do you think their graphs would look like?

Tracking the size of the infective class  $I(t)$  gives the clearest indication of the course of a typical disease. For an epidemic to occur, the size of the infected class  $I(t)$  must increase with  $t$ . A large increase in a single time step means a rapidly spreading outbreak, while a small increase means a more gradual spread. Thus the magnitude of change  $\Delta I = I(t + 1) - I(t)$  gives an indication of the virulence of the disease. We expect that  $I(t)$  increases as more and more individuals become infected. But with time, individuals will recover and  $I(t)$  will start to decrease in size. The change  $\Delta I = I(t + 1) - I(t)$  would be  $\leq 0$ , and the graph of  $I(t)$  turns down.

### SIR Model

In this basic model, members of the population progress through the three classes in order: susceptibles remain disease-free or become infected, infectives go thru an infectious period until they are cured and removed permanently, and these will never contract the disease again. The scheme is:

$$S \longrightarrow I \longrightarrow R$$

To actually model the disease, we need to specify how the susceptible move into the infective class, and how these move into the removed class. The disease spreads when a susceptible come into contact with an infective class. Because of our “homogeneous mixing” assumption, a reasonable measure of the number of encounters between susceptible and infective at time  $t$  is just the product  $S(t)I(t)$ . However, not every encounter between a susceptible individual and an infective one will result in the healthy individual contracting the disease. We will the introduce a parameter  $A$ , the transmission coefficient, which will measure the likelihood that a contact between a susceptible and an infective will result in a new infection. Because the number of susceptibles  $S(t)$  will decrease as suscepibles became infected, we expect that

$$S(t + 1) = S(t) - A \cdot S(t) \cdot I(t)$$

¶ 8. The transmission coefficient represents the probability that an encounter between a susceptible individual and an infective one results in the first individual becoming infective. You have two diseases, one with  $A = 0.02$  and another with  $A = 0.05$ . If the diseases are equal otherwise, which one will spread faster?

Next we model how  $I(t)$  changes in one time step to  $I(t + 1)$ . The infective class grows by the addition of the newly infected, which is  $AS(t)I(t)$ , but at the same time, some infectives will have moved into the removed class because they recovered or died, so  $I(t)$  will decrease by certain amount which will be added to the removed class. The amount of transition from the I class to the R class at time  $t$  is proportional to the number of infectives at that time, and the proportion constant  $B$  is the removal rate. It measures the average number of time steps that an infective individual spends in the infective state.

¶ 9. In modeling an outbreak of flu we may assume that it takes about 7 days to recover, so  $B = 1/7$  and measuring the different sized on a daily basis, but  $B = 1/14$  if we measure the sized twice a day.

This considerations lead to the equation

$$I(t + 1) = I(t) + A \cdot S(t) \cdot I(t) - B \cdot I(t)$$

Finally, all infected individuals that recover move into the removed class R, so

$$R(t + 1) = R(t) + B \cdot I(t)$$

To understand the behavior of the size of the different groups of the population and the disease, we will examine this model with the TI-84.

- (a) We set the calculator in sequence mode by pressing

$\boxed{\text{MODE}} \downarrow \downarrow \downarrow \rightarrow \rightarrow \rightarrow \boxed{\text{ENTER}}$

Then exit the setup mode with  $\boxed{2\text{ND}} \boxed{\text{QUIT}}$

- (b) Press  $\boxed{2\text{ND}} \boxed{\text{ZOOM}}$  and select the appropriate display Time or uv

- (c) Press  $\boxed{\text{Y=}}$ . If the graph style is not '·', press  $\leftarrow \leftarrow \boxed{\text{ENTER}}$  until '·' is displayed, and the press  $\leftarrow \leftarrow$

- (d) Enter nMin=1

- (e) Define the sequence u(n) This will be the susceptible class. We use the formula

$$u(n) = u(n - 1) - A * u(n - 1) * v(n - 1)$$

The left side of the formula is already written. To write the right side you press:

$\boxed{2\text{ND}} \boxed{7} \left( \boxed{\text{X,T,}\theta,n} - \boxed{1} \right) - \boxed{\text{ALPHA}} \boxed{A} \boxed{2\text{ND}} \boxed{7} \left( \boxed{\text{X,T,}\theta,n} - \boxed{1} \right) \boxed{2\text{ND}} \boxed{8} \left( \boxed{\text{X,T,}\theta,n} - \boxed{1} \right) \boxed{\text{ENTER}}$

- (f) The number u(nMin) will given in the main program, and it represents the initial number of susceptible individuals.

- (g) Similarly, enter the expression for the sequence v(n) which represents the number of infectives at time n:

$$v(n) = v(n - 1) + A * u(n - 1) * v(n - 1) - B * v(n - 1)$$

- (h) The number v(nMin) will be given in the program, and is the number of infectives at the beginning of the outbreak.

- (i) Enter the expression for the sequence w(n) which represents the number of removed at time n:

$$w(n) = w(n - 1) + B * v(n - 1)$$

Next we write the program that will allow us to view the graphs of the S, I and R populations as functions of time, and to see how those graphs depend on the parameters A and B.

To write nMax you press  $\boxed{\text{VAR}} \boxed{1} \leftarrow \boxed{5}$

To write u(nMin) you press  $\boxed{\text{VAR}} \boxed{1} \leftarrow \boxed{1}$  and similarly for v(nMin) and w(nMin)

To write u(nMax) you press  $\boxed{2\text{ND}} \boxed{7} \left( \boxed{\text{VAR}} \boxed{1} \leftarrow \boxed{5} \right)$

PROGRAM: SIR

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:Input 'SUSCEPT=', u(nMin)
:Input 'INFECTD=', v(nMin)
:Input 'REMOVED=', w(nMin)
:Input 'A=', A
:Input 'B=', B
:Input 'nMax=', nMax
:0>Xmin
:nMax>Xmax
:0>Ymin
:u(nMin)+v(nMin)+w(nMin)>Ymax
:DispGraph
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You can view the table of values of the different sequences  $u(n)$ ,  $v(n)$  and  $w(n)$  by pressing  $\boxed{2ND}$   $\boxed{GRAPH}$

¶ 10. To analyze the SIR model and gain some insight into the parameters of the model we write the equations in the form

$$\begin{aligned}\Delta S &= S(t+1) - S(t) = -AS(t)I(t) \\ \Delta I &= I(t+1) - I(t) = AS(t)I(t) - BI(t) \\ \Delta R &= R(t+1) - R(t) = BI(t)\end{aligned}$$

An epidemic occurs if  $\Delta I > 0$  for some time: the group of infective grows in size at that time. If  $\Delta I \leq 0$ , then the size of the infective class does not increase, and no wider outbreak of illness takes place. So the first step to understand the spread of the disease is to understand the sign of  $\Delta I$ . For this we write

$$\Delta I = AS(t)I(t) - BI(t) = (AS(t) - B)I(t)$$

We see immediately that if  $I(t) = 0$ , then  $\Delta I = 0$ . This is not surprising because if the population is disease free (there are no infectives), it will remain that way.

Suppose then that  $I(t) > 0$  at some time. Then  $\Delta I$  will be  $< 0$ ,  $= 0$ , or  $> 0$  according to whether  $AS(t) - B$  is  $> 0$ ,  $= 0$ , or  $< 0$ . Since  $A > 0$ , we have that

- If  $S(t) > B/A$ , then  $\Delta I > 0$
- If  $S(t) = B/A$ , then  $\Delta I = 0$
- If  $S(t) < B/A$ , then  $\Delta I < 0$

We always have that  $\Delta S \leq 0$ , so  $S(t)$  can never increase. This means that if  $S(0) < B/A$ , then  $S(t) < B/A$  for all times. That is, if the size of susceptibles  $S(0)$  is below  $B/A$ , then  $\Delta I < 0$ , and the disease decreases in the population. On the other hand, if  $S(0) > B/A$ , then the number of infectives will grow and an epidemic results.

The ratio  $B/A$  is thus important to understanding the spread of a disease. It is a threshold value which is called the **relative removal rate** of the disease.

¶ 11. Write  $r_0 = A/BS(0)$ . This number is called the **basic reproduction number**. Verify that  $r_0 > 1$  if and only if  $\Delta I > 0$ .

This number  $r_0$  contains the same information as the basic reproductive ratio, but is absolute and easier to understand. Write

$$r_0 = (AS(0)) \left( \frac{1}{B} \right)$$

then  $AS(0)$  represents the number of new cases arising from one infective per unit time, and  $\frac{1}{B}$  represents the average duration of the infection.

¶ 12. One infective is introduced in a population of 500 susceptible individuals. The data indicates that the likelihood that a healthy individual becomes infected from a contact with one infective is 0.1%, and that, once becoming ill, it takes 10 days to recover, during which period the infective is contagious.

- What are  $A$  and  $B$ ?
- What is the relative removal rate'?
- What is the basic reproduction number  $r_0$ ?
- Will there be an epidemic?