

MODELLING PROJECT

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MODELLING EPIDEMICS

PROBLEM:

In a given population, we would like to assess how a group of individuals with a given communicable infection, spread the disease to a population able to catch it over a period of time t . We will be dealing with a model that is without vital dynamics, since the transitions are from one class, to the second class, and to the third class. This is known as the Kermack - McKendrick model (1927).

VARIABLES:

$S(t)$ = Number of Susceptibles

$I(t)$ = Number of Infectives

$R(t)$ = Number of Removed Class

R_0 = Basic reproduction rate of the infection (ie. number of secondary infections produced by one primary infection).

a = Removal rate of the infection (a constant > 0)

r = The infection rate (a constant > 0)

$\rho = a/s$
 a/r

explain ✓ see next page

$R(\infty) = \text{limit as } t \rightarrow \infty \text{ of } R(t)$

$S(\infty) = \text{limit as } t \rightarrow \infty \text{ of } S(t)$

$I(\infty) = \text{limit as } t \rightarrow \infty \text{ of } I(t)$

N = the total size of the population, and is a constant.

ASSUMPTIONS:

1. This is a disease directly transmitted which, after recovery, confers immunity. (This includes deaths.)
2. There are three distinct classes:
 - a) Susceptibles - who can catch the disease
 - b) Infectives - those who have the disease and can transmit it
 - c) Removed class - those who have been infected, but cannot transmit the disease for some reason. (e.g. immune or isolated until recovered).
4. The progress of individuals is described by: (a model without vital dynamics)

$$S \rightarrow I \rightarrow R.$$

3. Gain in the infected class, $I(t)$ is at a rate proportional to the number of infectives and susceptibles. Since those who can catch the disease or

already have it are the only variables that can alter $I(t)$.

$$\rightarrow rSI \quad r > 0, \text{ is a constant}$$

uses the
"incompleteness
principle"

4. The rate of removal of the infectives to the removed class is proportional to the number of infectives. Since the removed class can only contain infectives, they must come from this class.

$$\rightarrow aI \quad a > 0, \text{ is a constant}$$

5. The incubation period will be considered short enough to be ignored. That is, a susceptible who contracts the disease is infective ^{ed} right away.
6. All three classes are uniformly mixed, so every pair of individuals has equal probability of coming into contact with each other.
7. Only dealing with non-negative solutions for S , I , and R . Obviously, a negative population is of no use.
8. Initial conditions:

$$S(0) = S_0 > 0$$

$$I(0) = I_0 > 0$$

$$R(0) = 0$$

Since we have non-negative solutions, the above must be greater than or equal to zero.

PROBLEM:

So based on our assumptions, we can come up with three equations for S, I, and R with respect to time.

$$\frac{dS}{dt} = -rSI \quad (1)$$

$$\frac{dI}{dt} = rSI - aI \quad (2)$$

$$\frac{dR}{dt} = aI \quad (3)$$

- $r > 0$, is the infection rate

- $a > 0$, is the removal rate of infection

(This is known as the Kermack - McKendrick model).

From the above 3 equations:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \quad (4)$$

error!

Therefore, (integrate)

$$S(t) + I(t) + R(t) = N \quad (5) \quad (N > 0, \text{ is the total population})$$

Since N is the upper limit (can not exceed the population), we can determine that S , I , and R are all bounded above by N . So given r , a , S_0 , and I_0 ,

we need to determine if the infection will spread or not. If it does, how does it develop with respect to time and when it will start to decline.

From (2),

$$\left. \frac{dI}{dt} \right|_{(t=0)} = I_0(rS_0 - a), \quad \begin{matrix} > 0, \text{ if } S_0 > a/r \\ < 0, \text{ if } S_0 < a/r \end{matrix}$$

But since, $\frac{dS}{dt} = -rSI \leq 0$, then $S \leq S_0$ and $S_0 < a/r$. *why?*

Therefore, *when* $S_0 < a/r$.

$$\frac{dI}{dt} = I(rS - a) \leq 0 \quad \text{for all } t \geq 0 \quad (6)$$

In this case, $I_0 > I(t)$ and $I(\infty) = 0$, which means the infection will eventually die out with no epidemic occurring. But if $S_0 > a/r$, $I(t)$ initially increases and an epidemic will occur. (ie. $I(t) > I_0$)

Thus we have a **Threshold Phenomenon**, and this threshold value is a/r .

The initial population of susceptibles must exceed this value if the disease is to spread and an epidemic to occur. Subsequently, if

$S_0 > a/r$, an epidemic **will** occur

$S_0 < a/r$, an epidemic **will not** occur

Since $\rho = \frac{a}{r}$, is the relative removal rate, then the reciprocal, $\sigma = \frac{r}{a}$, is the

*2 cases!
not explained
very well*

infection's contact rate and

$$R_0 = \frac{rS_0}{a} \quad (7)$$

is the reproduction rate of the infection.

If $R_0 > 1$, then an epidemic occurs. That is, more than one secondary infection is produced from one primary infection. From equations (1) and (2),

$$\begin{aligned} \frac{dI}{dS} &= \frac{dI/dt}{dS/dt} \\ &= \frac{-(rS - a)I}{rSI} \end{aligned}$$

$$= -1 + \frac{a}{rS}$$

$$= -1 + \frac{\rho}{S}$$

$$dI = \left(-1 + \frac{\rho}{S}\right)dS$$

$$\int dI = \int \left(-1 + \frac{\rho}{S}\right)dS$$

$$I = -S + \rho \ln(S) + C$$

$$I(0) = C - S_0 + \rho \ln(S_0) = I_0$$

$$C = I_0 + S_0 - \rho \ln(S_0)$$

$$\therefore I = \rho \ln(S) - S + I_0 + S_0 - \rho \ln(S_0) \quad (8)$$

explain terminology

(***refer to figure1, because (8) gives the (I,S) phase plane trajectories)

Furthermore, if this epidemic exists, we will need to know how severe it will be. From equation(6), the maximum I , (I_{max}) occurs at $S = \rho$ where

$\frac{dI}{dt} = 0$. So if we substitute $S = \rho$ (from equation (6)) into equation (8) then,

$$\begin{aligned} I_{max} &= \rho \ln(\rho) - \rho + I_0 + S_0 - \rho \ln(S_0) \\ &= I_0 + (S_0 - \rho) + \rho \ln(\rho/S_0) \end{aligned}$$

Recall: $I_0 + S_0 + R(0) = N$ ($R(0) = 0$)

$$\therefore I_{max} = N - \rho + \rho \ln(\rho/S_0) \quad (9)$$

Where I_{max} is the maximum number of infectives possible.

So for any initial values I_0 and $S_0 > \rho$, $I(t)$ increases from I_0 and an epidemic begins.

Note: It may not be a severe epidemic, if I_0 is close to I_{max} .

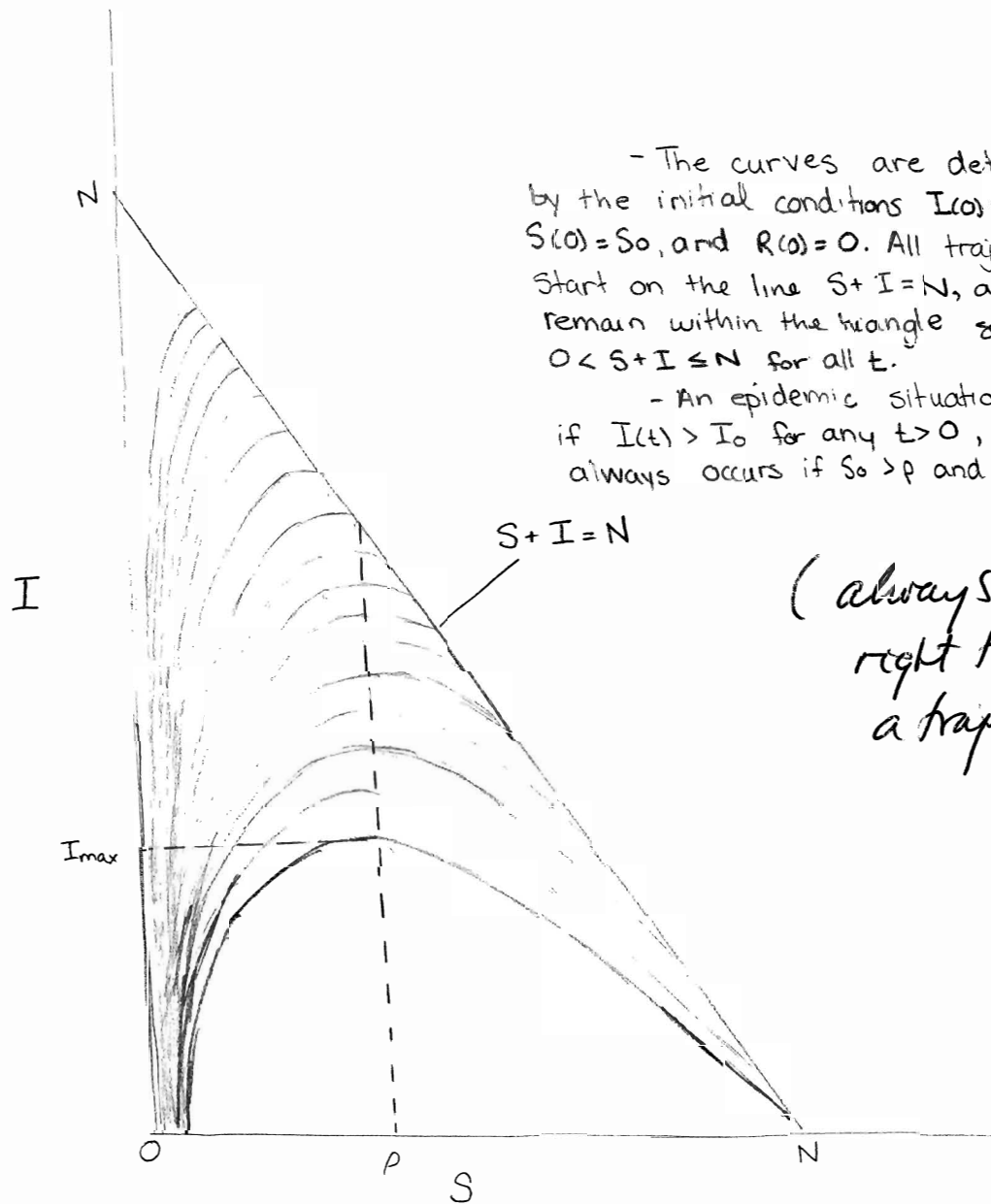
From equations (1) and (3), we can see $S(t)$ decreases since $\frac{dS}{dt} < 0$ for

$S \neq 0$, and $I \neq 0$.

$$\frac{dS}{dR} = \frac{dS/dt}{dR/dt}$$

Figure 1

(S, I) Phase-Plane



- The curves are determined by the initial conditions $I(0) = I_0$, $S(0) = S_0$, and $R(0) = 0$. All trajectories start on the line $S + I = N$, and remain within the triangle since $0 < S + I \leq N$ for all t .

- An epidemic situation exists if $I(t) > I_0$ for any $t > 0$, which always occurs if $S_0 > p$ and $I_0 > 0$.

(always move right to left on a trajectory).

$$= \frac{-rS}{a}$$

$$= \frac{-S}{\rho}$$

what is k?

$$\frac{\rho k}{S} dS = -dR$$

$$\int \frac{\rho}{S} dS = -\int dR$$

$$\rho \ln(S) = -R + K$$

$$\ln(S) = \frac{-R}{\rho} + \frac{K}{\rho}$$

(K, K* are constants > 0)

$$S = K^* e^{\frac{-R}{\rho}}$$

$$S(0) = S_0 = K^*$$

$$\therefore S = S_0 e^{\frac{-R}{\rho}}$$

when
t=0
S=S₀
R=R(0)=0

and since S is bounded by N,

$$0 < S(\infty) \leq N$$

so,

$$S > S_0 e^{\frac{-R}{\rho}}$$

$$S \geq S_0 e^{\frac{-N}{\rho}}$$

? explain

From figure 1, you can see,

$$0 < S(\infty) < \rho$$

and if, $I(\infty) = 0$, this implies (from (5)) that

$$R(\infty) = N - S(\infty)$$

$$\therefore S(\infty) = Soe^{\frac{-R(\infty)}{\rho}}$$

$$\therefore S(\infty) = Soe^{\frac{-(N - S(\infty))}{\rho}} \quad (\text{a positive solution})$$

Therefore, the total number of susceptibles who can catch the disease during the epidemic is,

$$I_{Total} = Io + So - S(\infty) \quad (9)$$

What this implies, is that the disease dies out from a lack of infectives and not from a lack of susceptibles since,

$$I(t) \rightarrow 0, \text{ and } S(t) \rightarrow S(\infty)$$

The relative rate, ρ varies with the community, and so determines whether an epidemic may occur in one community and not another. So if the removal rate, a of infectives is low and the number of susceptibles, r is high, then an epidemic is likely to occur because So will likely be greater than ρ .

But it is difficult to determine how many new infectives there are each day, since only those that are removed, $R(t)$, can be counted. This is why we

need to know the number removed, $\frac{dR}{dt}$, as a function of time.

$$\frac{dR}{dt} = aI = a(N - R - S)$$

$$\frac{dR}{dt} = a(N - R - Soe^{\frac{-R}{\rho}}) \quad (10)$$

This can be solved, if a , r , So , and N are known by computing the solution numerically. If not all the parameters are known, a best-fit procedure must be carried out. If the epidemic is not large, we can assume R/ρ is small, so $R/\rho < 1$. Equation (10) is then approximated by Kermack and McKendrick. The approximation is done using Taylor's Expansion about zero. The expansion is applied to $Soe^{\frac{-R}{\rho}}$. After expanding we get,

$$So - \frac{SoR}{\rho} + \frac{SoR^2}{2\rho^2} - \dots$$

Only need the first 3 terms, because R is small, so the other terms will be insignificant.

and substituting the expansion into equation (10) we get,

$$\frac{dR}{dt} = a \left[N - So + \left(\frac{So}{\rho} - 1 \right) R - \frac{SoR^2}{2\rho^2} \right] \quad (11)$$

Applying the quadratic equation,

$$R = \frac{\left(1 - \frac{So}{\rho}\right) \pm \sqrt{\left(\frac{So}{\rho}\right)^2 - 4\left(\frac{So}{2\rho^2}\right)(N - So)}}{\frac{So}{\rho^2}}$$

Only want positive values, so take

$$R = \frac{\left(1 - \frac{So}{\rho}\right) + \sqrt{\left(\frac{So}{\rho}\right)^2 - 4\left(\frac{So}{2\rho^2}\right)(N - So)}}{\frac{So}{\rho^2}} \quad (12)$$

And $-4\left(\frac{So}{2\rho^2}\right)(N - So)$ must be greater than zero.

After some simplification, we will approximately have,

$$\frac{dR}{dt} = \frac{a\alpha^2\rho^2}{2So} \operatorname{sech}^2\left(\frac{at\alpha}{2} - \phi\right) \quad (13)$$

and

$$R(t) = \frac{\rho^2}{So} \left[\left(\frac{So}{\rho} - 1 \right) + \alpha \tanh\left(\frac{at\alpha}{2} - \phi\right) \right]$$

$$\alpha = \left[\left(\frac{So}{\rho} - 1 \right)^2 + \frac{2So(N - So)}{\rho^2} \right]^{1/2} \quad \phi = \frac{\tanh^{-1}\left(\frac{So}{\rho} - 1\right)}{\alpha} \quad (14)$$

*** Can only be used for a small epidemic

If R/ρ is not small, then we must differentiate equation (10) to determine $R(t)$ and no approximations can be used.

EXAMPLES:

1. The Bombay Plague Epidemic (1905-1906)

(Not a severe epidemic relative to population size.)

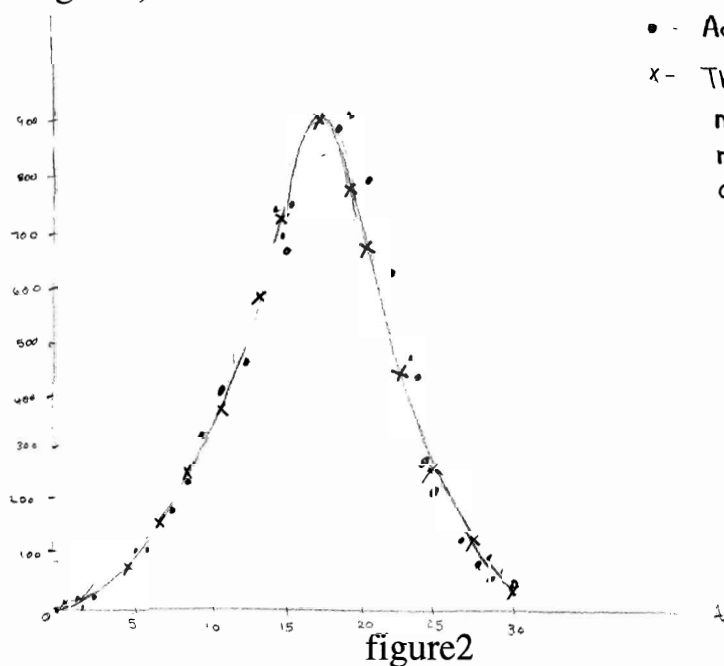
This epidemic lasted for almost a year, and since most of the victims who got the disease died, the number removed per week approximately equals the number of deaths per week.

It was assumed that the epidemic was not severe relative to the population size so we can apply the equation (13) and compare it with the actual data.

Therefore, after the Kermack and McKendrick model was applied,

$$\frac{dR}{dt} = 890 \sec h^2(0.2t - 3.4) \quad (14)$$

(see figure2)



- - Actual Data
- x- Theory from a small epidemic model using (13) and the number of deaths is approximately $\frac{dR}{dt}$, given by (14)

2. Influenza Epidemic in a Boarding School - Severe Epidemic

An influenza epidemic occurred in an English Boarding School in 1978. There were 763 boys and of these boys, 512 were confined to bed during the epidemic. It is suspected that one infected boy initiated the epidemic, so $R_0 > 1$ since more than one boy was infected with the disease.

$I(t)$ can be determined directly from the data, since when a boy was infected, he was put to bed. From the data, we have,

$$N = 763$$

$$r = 2.8 \times 10^{-3} / \text{day}$$

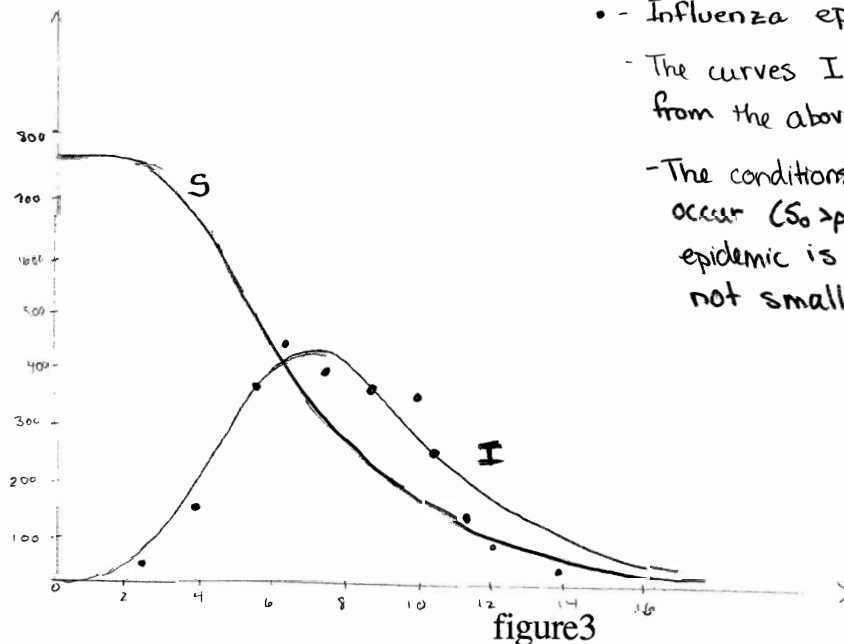
$$S_0 = 762$$

$$\rho = 202$$

$$I_0 = 1$$

$$R/\rho \gg 1, \text{ so epidemic is severe}$$

(see figure3)



- - Influenza epidemic data
- The curves I and S were obtained from the above data
- The conditions for an epidemic to occur ($S_0 > \rho$) is satisfied and the epidemic is severe since R/ρ is not small.

IMPROVEMENTS:

1. Since we assumed the disease was of a short duration, $S(t)$ did not include birth and death terms. So if a disease is not of short duration, then mortality due to natural causes should be included in the equation for the infectives and the removed class.
2. An incubation period could have also been included. When a susceptible has become infected, they are often not infectious yet. For example, measles has an eight to thirteen day latent period, while AIDS can have a period anywhere from a few months to years after catching the virus. This is known as a delay effect, $E(t)$, where the susceptible remains for a given length of time before moving into the ineffective class. (This gives rise to an oscillatory behavior.)
3. Age is also often a crucial factor in disease susceptibility and infectiousness. So the models would not only depend on time t , but on age a , as well. Therefore, we would be dealing with equations that have independent variables (t, a) .
5. Models where the susceptible class is renewed (by recovery or loss of immunity), could also be used. Here, we would need to assume that

good.

infected

this takes place at a rate proportional to the population in the renewed class. so equations (1) and (3) would need to be modified to take this into account. (ie. Add to (1) and subtract from(3).)

4. Overall, modifications which can be incorporated into epidemic models really depend on the disease. So the basic model of Kendrick - McKernick should be modified to the disease you want to model.

Epidemic models can be of great importance to predict an outcome, but they generally must go through several versions before they can be used with any degree of confidence. Therefore great care must be exercised before practical use is made of any epidemic models. However, even simple models should ask important questions to the possible means of control of the disease or epidemic. As far back as 1760, a mathematical model was used to assess the practical advantages of a vaccination control program. Here the effect of a cow-pox inoculation on the spread of smallpox and child mortality was modeled by Bernoulli. Subsequently, models can be extremely useful in giving reasoned estimates for the level of vaccination for the control of directly transmitted diseases. One of these models is the one developed by Kermack and McKendrick (1927). This is a very basic model which is able to be

modified with the different diseases involved.

Unfortunately, epidemics are still occurring, even with the advancement of modern medicine. Probably the most well-known, recent epidemic is AIDS, which can be modeled with modifications to the above model. This model is a lot more complicated since the incubation period is so unpredictable and the possibility of new viral strains appearing makes modelling this disease quite involved. The rate at which this epidemic is being spread is very alarming and it is considered to be the most serious epidemic since the Black Death in the fourteenth century. Hopefully, a cure or vaccination can be found before it can be termed the worst epidemic in history.

REFERENCES

Edelstein-Keshet, Leah, *Mathematical Models in Biology*. New York: Random House, 1988.

James, D.J.G., ed. *Studies in Mathematical Modelling*. New York: John Wiley and Sons, 1981.

Jones, D.S. and Sleeman, B.D., *Differential Equations and Mathematical Biology*. London: George Allen and Unwin, 1983.

Murray, J.D., *Mathematical Biology*. New York: Springer-Verlag, 1989.