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Model of an Epidemic

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An epidemic is the spread of an infectious disease through a community that affects a significant proportion of the population. Initially, the number of individuals having the disease increases. The epidemic may begin when a certain number of infected individuals enter the community. This could result, for example, from new people moving to the community or old residents returning from a trip.

The basis problem discussed in this paper is to describe the spread of an infection within a population. To do this, certain assumptions are required to describe the characteristics of the disease and the mixing of the population. From these assumptions a mathematical model is formulated. The model is analyzed, and the results of the analysis (hopefully) interpreted in epidemiological terms and thereby insight is gained into the nature of the phenomenon.

The following is a sequence of three increasingly complicated mathematical models for the development of an epidemic. The first model is so simple as to be almost entirely unrealistic; however, its shortcomings suggest how it can be improved. The second model, which results from modifying the first model, is considerably better, but still leads to unacceptable results. The third model is likewise an outgrowth of the previous models. Although still imperfect, the third model manifests a property which was not built into the formulation explicitly, but which is in fact observable in an actual epidemic of a contagious disease.

Before looking at specific models, we will make a number of assumptions which will be common to all models.

1) The disease is transmitted by contact between an infected individual and a susceptible individual. ✓

2) Initially, everyone in the population is susceptible to the disease; that is, no one is immune. ✓

3) There is no latent period for the disease, hence the disease is transmitted instantaneously upon contact. ✓

4) All susceptible individuals are equally susceptible and all infected individuals are equally infectious. ✓

5) After the disease is introduced into the population, the total population remains fixed. This means that no births or migration occurs, and all deaths are taken into account. This is reasonable for populations with moderate birth and death rates and for diseases of relatively short duration. ✓

6) The population is homogeneous and uniformly mixing. This means that everyone is the same and is equally likely to come into contact with any other member of of the population. ✓

Other assumptions will be added and explained as we work through each model.

A Trivial Model:

Consider a population which is essentially infinite in size. Initially everyone in the population is susceptable to a contagious disease, with the exception of a small number of individuals who are already infected.

Let the independent variable be time, t, and also let:

$I(t)$ = number of infected individuals at time t

B = average number of contacts by an infected individual, per unit time, with a susceptible individual who becomes infected.

To find the number of infected individuals at time $t+\Delta t$ in terms of the number of infected individuals at time t, sum the number of infectives at time t, $I(t)$, plus the number of new infectives who contract the disease in the time interval t to $t+\Delta t$.

$$I(t+\Delta t) = I(t) + BI(t)\Delta t$$

Rearranging, we get:

$$\frac{I(t+\Delta t) - I(t)}{\Delta t} = BI(t)$$

If we let $\Delta t \to 0$, this gives

$$\frac{dI(t)}{dt} = BI(t) \qquad \checkmark$$

This equation is essentially the Mathusian Law It tells us that the instantaneous infection rate is directly proportional to the number of infectibles. Also, from

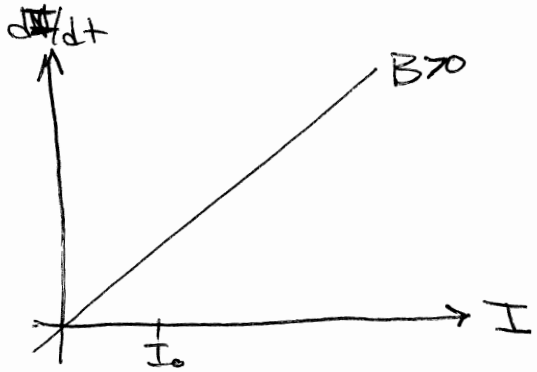
$$\frac{1}{I}\frac{dI}{dt} = B$$

we see that the relative instantaneous infection rate of the population is constant.

B

$$\frac{dI}{dt} = BI = f(I)$$

The right hand side of the equation does not involve t explicitly (the d.e. is autonomous) therefore we can do phase plane analysis.



From this we expect the number of infectibles to grow without bound.

Solve the differential equation:

$$\frac{dI}{dt} = BI$$

separating variables

$$\frac{dI}{I} = B\,dt$$

and integrating

$$\ln I = Bt + C$$
$$I = e^{Bt+C}$$
$$I = e^{C} e^{Bt}$$
$$I = De^{Bt}$$

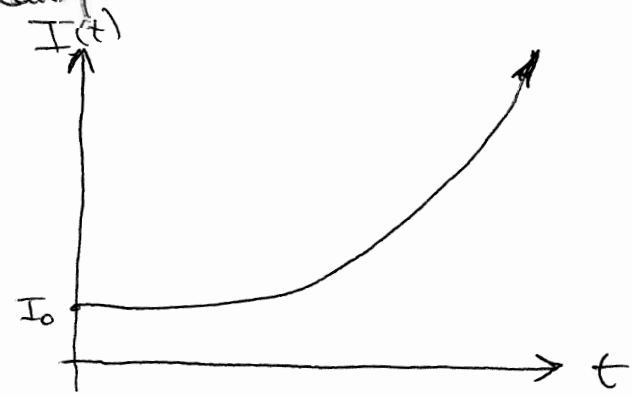
at $t=0$, $I=I_0$
therefore

$$I_0 = De^{B0}$$
$$I_0 = D$$

the equation can be rewritten as

$$I = I_0 e^{Bt}$$

Graphically:



✓

The basic defect of the model is easily seen from the graph above. As time passes, the number of infectibles grows without bound. The reason for this comes from the ipitial premise that the population at risk of catching the disease is infinite in size. A more realistic model will take into account that there are only a finite number of susceptible individuals.

A Simple Model:

To overcome the problem encountered in the previous model, it is assumed that, at all times, the total population consists of N individuals. N is a constant. Everyone in the population is either susceptible to the disease or else infected with the disease.

For this model let:

$I(t)$ = number of infected individuals at time t

$S(t)$ = number of susceptible individuals at time t

β = average number of contacts by an infected individual, per unit time, per susceptible, with a susceptible individual who becomes infected.

Note: by comparing the definitions of B and β we see that $B = \beta S(t)$. Although B was treated as a constant in the first model, it now varies with the number of susceptibles.

The total population size never entered into the derivation of the equation for the number of infectives in the first model. Therefore, by replacing B with $\beta S(t)$ we get

$$\frac{dI(t)}{dt} = \beta S(t) I(t)$$

Since the total population size is always N, and since all individuals are either susceptible or infected,

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

To get the differential equation for the number of susceptibles, differentiate the above equation with respect to time and substitute the equation for $I(t)$ to get

$$\frac{dS(t)}{dt} = -\beta S(t) I(t)$$

$S(t)$ can be eliminated using $S(t) = N - I(t)$ in the differential equation for $I(t)$

$$\frac{dI(t)}{dt} = \beta I(t)[N - I(t)]$$

This is basically the logistic equation

Without solving the d.e. we know that:

i) The number of infectives can never be negative (in the real world). It can be 0 but then there is no epidemic. Therefore, $I(t)$ must be > 0 for all t. Likewise the number of infectives can never exceed N. If it equals N, then everyone is infected and the epidemic is over. Therefore, $I(t) < N$ during the epidemic. From this we can see that the right side of the equation

$$\frac{dI(t)}{dt} = \beta I(t)[N - I(t)]$$

is never zero or negative. Therefore dI/dt is always positive ✓

noted later

2) Differentiating to get the second derivative:

$$\frac{d^2I}{dt^2} = \beta \frac{dI}{dt}(N-I) - \beta I \frac{dI}{dt}$$

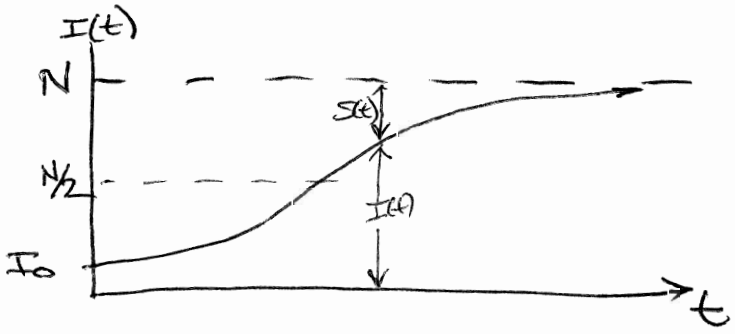
$$= \beta \frac{dI}{dt}(N-2I)$$

Since $\beta \frac{dI}{dt} > 0$, the sign of $\frac{d^2I}{dt^2}$ depends entirely on $N-2I$

ie: when $I < N/2$, the graph is concave up
when $I > N/2$, the graph is concave down
$\therefore$ when $I = N/2$ and $\frac{d^2I}{dt^2} = 0$, the graph has an inflection point.

From the above, we see that, in a large population with a small initial number of infectives, at first the epidemic grows essentially exponentially. Then, as fewer susceptibles are available, the rate of growth decreases, but the epidemic does not end until everyone in the population has contracted the disease.

A typical sol'n as a fcn of time is the following:



(The equation is essentially the same as the logistic equation for population growth)

could use this observation to shorten discussion.

Solving the differential equation:

$$\frac{dI(t)}{dt} = \beta I(t)[N - I(t)]$$

Separating variables

$$\frac{dI}{I(N-I)} = \beta\, dt$$

and integrating we get:

$$\int_0^t \frac{dI}{I(N-I)} = \int_0^t \beta\, t$$

using partial fractions

$$\frac{1}{I(N-I)} = \frac{A}{I} + \frac{B}{N-I}$$

$$1 = A(N-I) + BI$$

$$1 = AN + (B-A)I = 1 \quad \Rightarrow \quad AN = 1$$

$$A = 1/N$$

$$(B-A)I = 0$$

$$\therefore B = 1/N$$

$$\therefore \frac{1}{NI} + \frac{1}{N(N-I)} = \frac{1}{I(N-I)}$$

initial time chosen as $t=0$

$$\frac{1}{N}\int_{0}^{t}\frac{dI}{I}+\frac{1}{N}\int_{0}^{t}\frac{dI}{N-I}=\beta t$$

$$\left\{\frac{1}{N}\ln I(t)\Big|_{0}^{t}-\ln[N-I(t)]\Big|_{0}^{t}\right\}=\beta t$$

$$\ln I(t)-\ln I(0)-\ln[N-I(t)]+\ln[N-I(0)]=\beta N t$$

$$\ln\frac{I(t)[N-I(0)]}{I(0)[N-I(t)]}=\beta N t$$

$$\frac{I(t)[N-I(0)]}{I(0)[N-I(t)]}=e^{\beta N t}$$

$$I(t)[N-I(0)]=I(0)e^{\beta N t}[N-I(t)]$$

$$I(t)[N-I(0)+I(0)e^{\beta N t}]=NI(0)e^{\beta N t}$$

$$I(t)=\frac{NI(0)e^{\beta N t}}{N-I(0)+I(0)e^{\beta N t}}$$

✓

Although the analytic form of $I(t)$ is known and a similar expression for $S(t)$ follows immediately from the fact that $S(t) = N - I(t)$, in practice one is less often interested in the graph of these than what is called the "epidemic curve", $W(t)$.

This curve shows the rate at which new cases of infection are appearing. It is considered a good measure of the strain placed on healthcare resources at time t (it measures new cases that show up at the doctor's office or a hospital) $W(t)$ is just another notation for dI/dt. The formula can be obtained by differentiating the equation for $I(t)$ or by substituting the ~~equation~~ expression for $I(t)$ into the equation for dI/dt.

$$W(t) = \frac{dI}{dt} = \frac{\beta N^2 I(0) e^{\beta N t}[N - I(0) + I(0)e^{\beta N t}] - N I(0) e^{\beta N t}(\beta N I(0) e^{\beta N t})}{[N - I(0) + I(0)e^{\beta N t}]^2}$$

$$= \frac{\beta N^2 I(0) e^{\beta N t}[N - I(0)]}{[N - I(0) + I(0)e^{\beta N t}]^2}$$ ✓

to analyze set $a = \frac{\beta N^2}{I(0)}$ and $b = \frac{[N - I(0)]}{I(0)}$ a should be βN^2 only

$$\therefore \quad W(t) = \frac{dI}{dt} = \frac{abe^{\beta N t}}{(b + e^{\beta N t})^2}$$

Taking the derrivative of $W(t)$:

$$W(t) = \frac{abe^{\beta N t}}{(b+e^{\beta N t})^2}$$

$$\frac{dW(t)}{dt} = \frac{\beta N abe^{\beta N t}(b+e^{\beta N t})^2 - 2abe^{\beta N t}(b+e^{\beta N t})(\beta N e^{\beta N t})}{(b+e^{\beta N t})^4}$$

$$= \beta N abe^{\beta N t}(b+e^{\beta N t})\underbrace{\left[(b+e^{\beta N t}) - 2e^{\beta N t}\right]}_{\left[b-e^{\beta N t}\right]}$$

- everything is positive so $[b-e^{\beta N t}]$ determines the sign of dW/dt.

$$b - e^{\beta N t} = 0$$
$$\beta N t = \ln b$$
$$t = \frac{\ln b}{\beta N}$$

$\therefore$ $W(t)$ has its maximum at $t = \frac{\ln b}{\beta N}$

Also, using l'Hopitals Rule we see that as $t \to \infty$

$$\frac{abe^{\beta N t}}{(b+e^{\beta N t})^2} = \frac{\infty}{\infty} \qquad \frac{\beta N abe^{\beta N t}}{2(b+e^{\beta N t})\beta N e^{\beta N t}} = \frac{ab}{2(b+e^{\beta N t})} = \frac{ab}{\infty} = 0$$

which says that eventually the epidemic will end (as it should).

To show $W(t)$ is symmetric about its maximum at $t = \frac{\ln b}{\beta N}$ let

$$T = t - \frac{\ln b}{\beta N}$$

$$t = T + \frac{\ln b}{\beta N}$$

$$\beta N t = \beta N T + \ln b$$

$$W(T) = \frac{abe^{\beta NT + \ln b}}{(b + e^{\beta NT + \ln b})^2} = \frac{ab^2 e^{\beta NT}}{(b + be^{\beta NT})^2}$$

$$= \frac{ae^{\beta NT}}{(1 + e^{\beta NT})^2}$$

again, how is this from the above? please please draw a diagram!

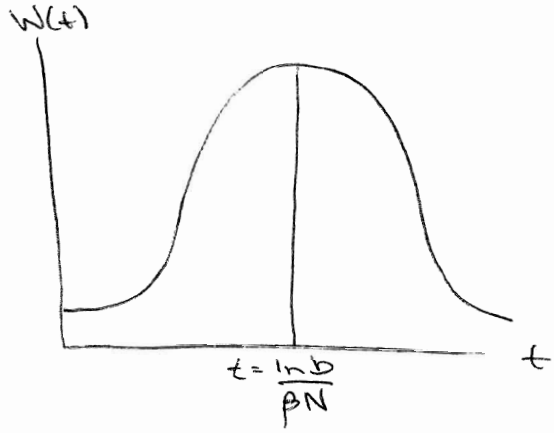
$$W(-T) = \frac{ae^{-\beta NT}}{(1 + e^{-\beta NT})^2} \quad \frac{e^{2\beta NT}}{e^{2\beta NT}}$$

$$= \frac{ae^{\beta NT}}{(e^{\beta NT} + 1)^2}$$

$$= W(T)$$

$\therefore$ $W(t)$ is symmetric about $t = \frac{\ln b}{\beta N}$. ✓

Typically this function looks like



how do we know this? experimental evidence?

This second model is considerably better than the first, but still has one unrealistic aspect. Notice that whenever an epidemic gets started, everyone in the population ultimately contracts the disease. The reason for this can be traced to the fact that infectives remain infected forever. A more realistic model must take into account that for most diseases infectives either recover or else they die.

good

General Epidemic Model:

In order to overcome the problem encountered in the previous model, it is assumed that infectives are removed from circulation at a rate which is proportional to the current number of infectives. Since for many diseases a natural immunity occurs, it is further assumed that former infectives enter a new class which is not susceptible to the disease.

Note: By introducing a class of removed individuals it is not necessary to state precisely the severity of the disease which is being modeled. The removals may be recovered and immune, they may be quarantined and thus out of circulation or they may be dead. All that is necessary is that the disease not be available to any individual more than once.

funny wording!

For this model let:

$I(t)$ = number of infected individuals at time t

$S(t)$ = number of susceptible individuals at time t

β = average number of contacts by an infected individual, per unit time, per susceptible, with a susceptible individual who becomes infected

and let:

$R(t)$ = number of individuals removed at time t

γ = average rate of removal of infectives from circulation per unit time, per infective in the population.

Since the new class of individuals, the removals, in no way interacts with the susceptibles, the equation for susceptibles is the same as that of the second model:

$$\frac{dS(t)}{dt} = -\beta S(t) I(t)$$ ✓

The differential equation previously developed for the number of infectives must be modified to take into account the removals. It is the number of infectives minus the number of removals.

$$\frac{dI(t)}{dt} = \beta S(t) I(t) - \gamma I(t)$$ ✓

The ~~equation~~ for the removals is, from above ✓

$$\frac{dR(t)}{dt} = \gamma I(t)$$

ie: the rate of change of removals is directly proportional to the number of infectives

Since all individuals in the population are either susceptible, infected or removed, it follows that since the population is constant in size

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

By differentiating the above expression with respect to time, we get

$$\frac{d(S+I+R)}{dt} = 0$$

which says that the sum of the three governing equations must sum to zero (which they do).

Also, the expression guarantees that once the size of any two classes is known, the size of the third can be found by simple arithmetic.

Before we do anything with this model, we should define initial conditions. Assume at time $t=0$ there are no removed individuals, a very small number, I_0, of infectives and the remainder of the population, S_0, is susceptible.

ie at $t=0$, $\quad S(0) = S_0 = N - I_0$
$I(0) = I_0 << N$
$R(0) = 0$

Before solving any equations, it is informative to examine the differential equations.

Can anything be said about the relative size of S & ρ?

$$\text{ie} \quad \frac{dI(t)}{dt} = \beta S(t) I(t) - \gamma I(t)$$

$$= I(t)[\beta S(t) - \gamma]$$
$$\beta I(t)[S(t) - \rho]$$

$\rho = \gamma/\beta$

Since $I(t) \geq 0$, the sign of dI/dt is determined by $[S(t) - \rho]$

$$\therefore \quad \frac{dI(t)}{dt} > 0 \quad \text{if and only if} \quad S(t) > \rho$$

Since susceptibles become infected and no new susceptibles are made if $S(0) < \rho$ then $S(t) < \rho$ for all $t > 0$ and $dI/dt < 0$ for all future time. This means that if the initial number

of susceptibles is smaller than some critical number, ρ, there will not be an epidemic (a large, one-time outbreak of the disease). Or, viewed in another way, the relative removal rate must be sufficiently small to allow the disease to spread. This is known as the Threshold Theorem.

Also, from $\frac{dI}{dt} = \beta I[S-\rho]$ we can conclude that the number of infectives reaches a maximum when $S(t)=\rho$, since $I(t)$ is positive and S is nonincreasing.

Some insight into the progress of an epidemic can be seen by examining the trajectories in the S-I plane, the phase plane of the equations for dS/dt and dI/dt.

The differential equation of the trajectory is (dividing dI/dt by dS/dt):

$$\frac{dI}{dS} = \frac{\beta SI - \gamma I}{-\beta SI} = -1 + \rho/S \qquad 1/\rho = \gamma/\beta$$

integrating gives

$$I = -S + \rho \ln S + K \qquad (K\text{- constant of integratic}$$

Using initial conditions, $I = I(0)$

$$S = S(0) = N - I$$
$$R = R(0) = 0$$
$$\therefore N = I + S$$

we get

$$K = N - \rho \ln S_0$$

Which results in

$$I = N - S + \rho \ln(S/S_0)$$

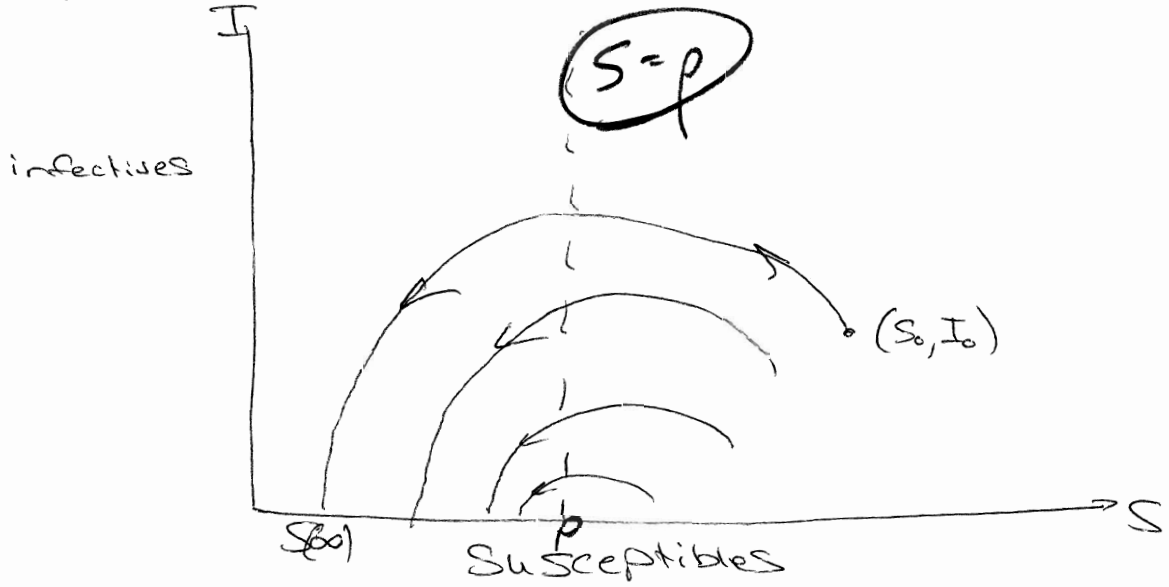
Now from this we see that:

$I \to -\infty$ as $S \to 0$ ✓
and $I = I_0 > 0$ when $S = S_0$

Hence there exists at least one point, say $S(\infty)$ when $I = 0$.
(from dI/dt and dS/dt, we see that $I = 0$ is an equilibrium point)

What this means is that, once an epidemic begins, it is not necessary that everyone in the population become infected! The epidemic may run its course before the population of susceptibles has been exhausted. (This was not so in the previous model). Or, another way, the spread of the disease does not stop for lack of a susceptible population. ✓

Typical trajectories in the S-I plane are.



We see that as t increases, the pt (S,I) moves along the trajectory with S decreasing, and I decreases if $S(0) < \rho$. On the other hand, if $S(0) > \rho$, then initially I increases reaching a peak when $S = \rho$ (I_{max}) and then decreases to zero. Clearly the parameter ρ is a vital parameter. It is called the threshold value, since an epidemic occurs only if the initial number of susceptibles, $S(0)$ is greater than this value.

Another way to show that once an epidemic has started, not all members of the population will become infected is by the following

Assume $S_0 > \rho$
let $S_0 = \rho + v$ where $v \ll \rho$
also assume $I(0)$ is small

} these may not be compatible

now, from $I = N - S + \rho \ln(S/S_0)$
as $t \to \infty$

$$0 = N - S(\infty) + \rho \ln(S(\infty)/S_0)$$

and $N \approx S(0)$ ($I(0)$ small)

Thus
$$0 = S(0) - S(\infty) + \rho \ln\left[\frac{S(0) - (S(0) - S(\infty))}{S(0)}\right]$$

$$= S(0) - S(\infty) + \rho \ln\left[1 - (1 - S(\infty)/S(0))\right]$$

$$= S(0) - S(\infty) + \rho\left\{\left(1 - \frac{S(\infty)}{S(0)}\right) - \frac{1}{2}\left(1 - \frac{S(\infty)}{S(0)}\right)^2 \cdots\right\}$$

ie
$$0 = (S_0 - S(\infty))\left[1 - \rho/S_0 - (\rho/2S_0^2)(S(0) - S(\infty))\right]$$

Thus
$$S(0) - S(\infty) = \frac{2S(0)^2}{\rho}(1 - \rho/S(0))$$

$$= 2S(0)(S(0)/\rho - 1)$$

$$= 2(\rho + v)(\rho + v - \rho)/\rho \quad \text{since } S(0) = \rho + v$$

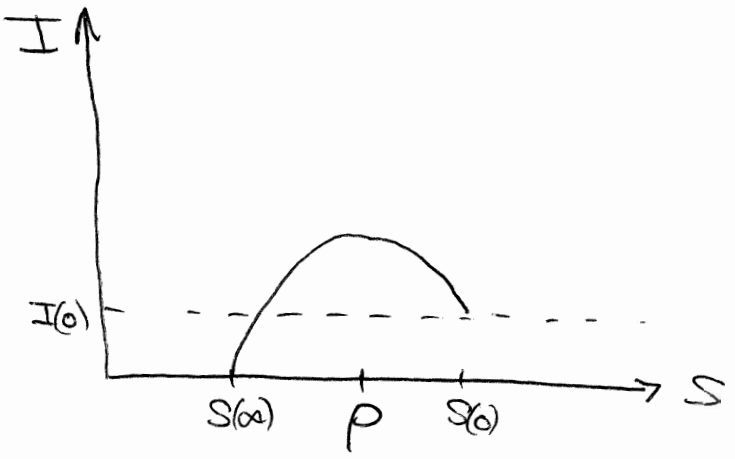
$$= 2\frac{v}{\rho}(\rho + v)$$

$$\approx 2\frac{v}{\rho}\rho \quad \text{since } v \ll \rho$$

ie
$$S(0) - S(\infty) \approx 2v$$

This says that if $S(0) > \rho$ and $S(0) - \rho$ is small compared to ρ, then the number of individuals who ultimately contract the disease is approximately $2(S(0) - \rho)$

Graphically:



The above shows that, once an epidemic has started, not everyone in the population must become infected.

Call $W = N - S(\infty)$ the extent of the epidemic: it is the total number of individuals infected. A formula for W can be obtained from:

$$I = N - S + \rho \ln\left(S/S(0)\right)$$

$$I + S - N = \rho \ln\left(S/S(0)\right)$$

let $t \to \infty$

$\therefore\ I(\infty) = 0$

$$S(\infty) - N = \rho \ln\left(\frac{S(\infty)}{S(0)}\right)$$

let $W = N - S(\infty)$

$$\therefore\ -W = \rho \ln\left(\frac{N-W}{S(0)}\right)$$

multiplying both sides by β/γ and exponentiating, we get

$$e^{(-\beta/\gamma)W} = \frac{N-W}{S(0)}$$

$$N - S(0)e^{(-\beta/\gamma)W} - W = 0$$

If β an γ are >0 it is impossible to find an explicit solution for W in terms of β, γ and N. The best we can do is solve it numerically. This is a reasonable thing to do using Newton's Method.

from above we know that I is at its maximum when $S(t) = \rho$.

$\therefore$ from

$$I = N - S + \rho \ln\left(S/S(0)\right)$$

Substitute $S = \rho$

$$I = N - \rho + \rho \ln\left(\rho/S(0)\right)$$

$$I_{(max)} = N + \rho\left[\ln\left(\rho/S(0)\right) - 1\right]$$

therefore this is the formula for the maximum number of infectives

Cases of the disease are usually counted as victims who seek medical attention. This is also the time at which individuals are removed from active circulation. Therefore, to compare the predicted results of this model with actual data we must determine dR/dt as a function of time, t.

First, make use of the relation $S+I+R=N$ in the equation dR/dt:

$$\frac{dR}{dt} = \gamma I(t) = \gamma[N - R(t) - S(t)]$$

Now we can determine S as a function of R from

$$\frac{dS}{dR} = \frac{dS/dt}{dR/dt} = \frac{-\beta SI}{\gamma I} = -\frac{S}{\rho}$$

Separating and integrating:

$$\int \frac{dS}{S} = -\frac{1}{\rho}\int dR$$

$$\ln S = -\frac{R}{\rho} + D$$

$$S = Ke^{-R/\rho}$$

at $t=0$, $S = S_0$, $R_0 = 0$

$$S_0 = Ke^0$$

$$S_0 = K$$

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

Therefore, substituting into the equation, we get

$$\frac{dR}{dt} \simeq r\left[N - R - S_0\left(1 - R/\rho + R^2/2\rho^2\right)\right]$$

$$\frac{dR}{dt} = r\left[N - S_0 + \left(S_0/\rho - 1\right)R - S_0 R^2/2\rho^2\right]$$

Separating variables and integrating leads to:

$$R(t) = \frac{\rho^2}{S_0}\left[\frac{S_0}{\rho} - 1 + \alpha \tanh\left(\frac{\alpha r t}{2} - \phi\right)\right]$$

Where $\alpha = \sqrt{\left(\frac{S_0}{\rho} - 1\right)^2 + 2\frac{S_0 I_0}{\rho^2}}$

$$\phi = \tanh^{-1}\left[\left(\frac{S_0}{\rho} - 1\right)/\alpha\right]$$

Note: Developing this solution is straightforward, (complete the square and make a hyperbolic trigonometric substitution.), but does involve a considerable amount of rather messy algebra.

As with the second model, we are really more interested in knowing the shape of the predicted epidemic curve, $N(t)$, than the cumulative number of removals, $R(t)$.

Now, substituting into dR/dt, we get:

$$\frac{dR}{dt} = r(N - R - S_0 e^{-R/P})$$

Note that $R(t)$ is the only one of the dependent variables which appears in this equation. Although it is possible to solve this differential equation exactly, the methods are rather complicated. We therefore, seek an approximate solution.

The difficulty in solving the equation results from the presence of the exponential term. We can replace the exponential by a polynomial. To do this we expand the exponential in a Taylor series about the point $R(0) = 0$:

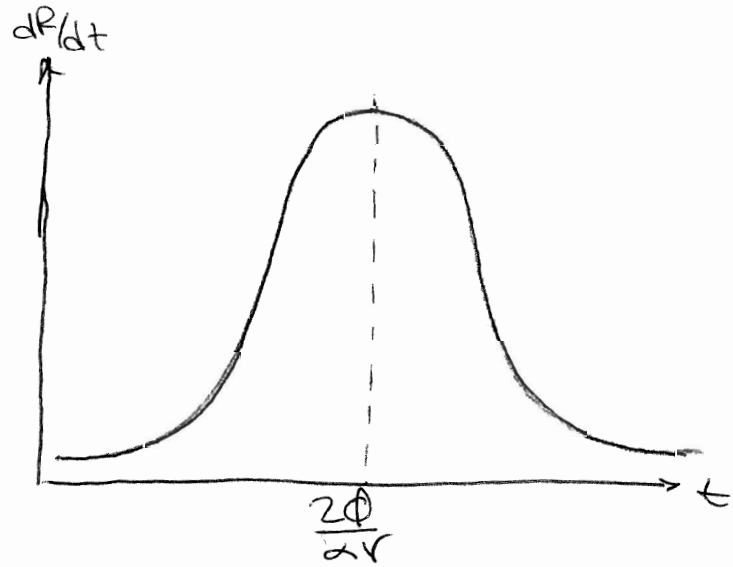
$$e^{-R/P} = 1 - \frac{R}{P} + \frac{1}{2}\left(\frac{R}{P}\right)^2 - \frac{1}{6}\left(\frac{R}{P}\right)^3 + \cdots$$

By truncating the series after the first few terms, a fairly easily solved, separable differential equation will result. If only the terms up to the linear one are kept, the solution results in nonsense. On the other hand, if terms up to the cubic one are kept, the integration is very hard. Therefore, to balance realism with solvability, we will keep the terms up to the quadratic one.

Since $\frac{d}{dx}(\tanh x) = \operatorname{sech}^2 x$, we see that

$$W(t) = \frac{dR(t)}{dt} = \frac{\rho^2 \alpha^2 V}{2S_0} \operatorname{sech}^2\left(\frac{\alpha V t}{2} - \phi\right)$$

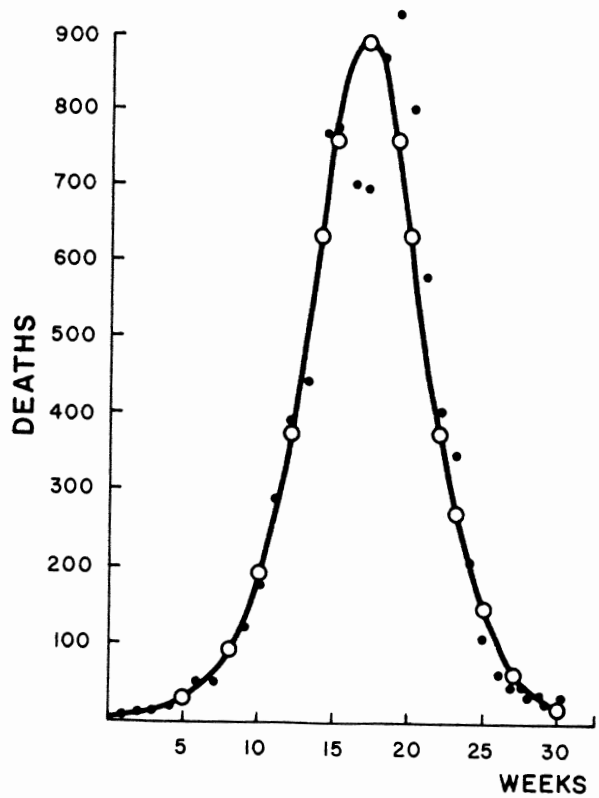
This expression describes a function which rises to a single maximum at time $t = 2\phi/\alpha V$ and then falls away symmetrically. This is very similar to the result for the epidemic curve in the second model, however, in this model not all susceptibles need to be infected.



Predicted rate of removals.

Kermack and McKendrick used this model to describe an actual epidemic, a plague in Bombay in 1905-06. The graph below shows deaths per week against time in weeks. Since almost all cases terminate fatally, the number of deaths per week is approximately dR/dt. They took parameter values so that:

$$\frac{dR}{dt} = 890 \operatorname{sech}^2(.2t - 3.4)$$



The curve does a pretty good job of approximating the epidemic.

The third model is a much better model than the previous two. We see that there is a threshold value in which the initial susceptible population must exceed for there to be an epidemic (the relative removal rate must be sufficiently small to allow the infection to spread). We see that some individuals will escape the disease altogether, and in particular, the spread of disease does not stop for lack of a susceptible population. It illustrates very well the common observation that in many actual epidemics the number of new cases reported each day climbs to a peak value and then dies away again.

good

Before finishing, I will mention some of the limitations of this model. The constants β and r often vary with time. Also, the recovered individuals may, after a time, lose their immunity and reenter the susceptible state.

Looking at the assumptions, we could develop a model in which there is a latent period for the disease. This means that a person could be infected but cannot, yet, transmit the disease. Also, if the disease does not spread quickly, the population may not remain fixed.

Other factors might be that the disease is age dependent or perhaps the disease is trying to be controlled through vaccination.

The models looked at here were deterministic. One could look at a stochastic model where the chance factors involved in the spread of an epidemic are no longer ignored.

There are countless ways of modifying the model to explain different conditions and different diseases. However, even simple models like the ones examined here can give us the kind of insight needed to study more complicated situations.

References:

① Paul Waltman, Deterministic Threshold Models in the Theory of Epidemics. Lecture Notes in Biomathematics, Vol. 1. New York: Springer-Verlag (1974).

② Walter J. Meyer, Concepts of Mathematical Modeling. McGraw-Hill, Inc. New York. (1984).

③ C. Frauenthal, Mathematical Modeling in Epidemiology. Springer-Verlag. New York. (1980).

④ Daniel P. Maki, Maynard Thompson, Mathematical Models and Applications. Prentice-Hall, Inc. USA. (1973).

⑤ Norman T. J. Bailey, The Mathematical Theory of Epidemics. Charles Griffin and Company Ltd. London. (1957).

⑥ David N. Burghes, Modelling with Differential Equations. Ellis Horwood series in mathematics and its applications. Ellis Horwood. Chichester. (1981).

⑦ Derrick and Grossman, Introduction to differential equations with boundary value problems. Third Ed. West Publishing Company (1987).