

#FlattenTheCurve

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Abstract

In this paper we adapt a common model used in Economics to study the diffusion of innovations to model the transmission of a virus. Emphasis is placed on the evolution of the number of new infections and the cumulative total number of infections over time and how they might be influenced by different policies. Although the model is very simple it does yield some useful implications for public policy.

1. Introduction

The purpose of this paper is to give you some insight into a simple model of the way in which a virus might spread within a population. The model set out below is a slight modification of one which is used widely in economics and marketing to study the diffusion of new innovations and the take-up of new consumer durables.¹ An advantage of using a simple model is that it is relatively easy to show some of the concepts and methods we use when we develop models of the time path of a variable of interest to us. While the model is very simple it does yield some useful insights into public policy to deal with an epidemic.

We begin by setting out some simple assumptions about the very abstract world in which we will develop our model.

¹ Early examples of models of the diffusion of an invention and which were developed along similar lines as that presented here include Bain (1962), Griliches (1957), Mansfield (1961) and Roos (1934).

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1.1 Some assumptions and notation

We assume that there is a given population of a particular size and that in each period one member of the population meets only one other member of the population. We assume that the (given) population is homogeneous in the sense that all possible pairs of members of the population have an equal chance of meeting. We are assuming that meetings occur at random and that the only way the virus can spread is by close contact between people.

Let:

Y_t be the total number of people in the population who are infected with the virus by the end of the current period – note that they might have been infected at any date in the past as this is the cumulative sum of all past new infections. Many of the graphs we see on TV these days show how the number infected has risen since the first cases were reported for that country. In this simple model we assume that any infected people will continue to spread the infection until the end of the epidemic, i.e. they never recover or die.

Y_{t-1} be the total number of people in the population who are infected with the virus at the beginning of the current period (i.e. the total or ‘cumulative’ number who were infected by the end of the previous period).

$dY = Y_t - Y_{t-1}$ is the number of people newly infected in any period, i.e. the difference between the total number infected at the end of the period and the total number infected at the beginning of the period.

K is the total number of people in the population who would be infected if the epidemic were allowed to run its course over a number of periods with no health or public policy intervention.² For future reference we note that, given our definitions and that Y will be rising over time it must be the case for any period that $Y_{t-1} \leq Y_t \leq K$. For now, we will assume that K is equal to the total size of the population. This, taken together with our other assumptions means that, in the absence of policy intervention, every member of the population will sooner or later become infected. (We will drop this assumption later).

$(K - Y_{t-1})$ is therefore the number of people in the population who are not infected by the virus at the beginning of the current period.

and let β (beta) measure how likely it is that the virus will be transmitted when someone who is infected with the virus meets someone who does not already have the virus.³ As we have come to know the chance of an infected person passing on

² Another way to think of K is that it is the total number of the population who, just prior to the introduction of the virus into the population, are ‘susceptible’ to infection.

³ So, $0 < \beta < 1$.

the COVID-19 virus to someone who is not yet infected depends upon the physical closeness of the two people when they meet, amongst other things. For the moment we assume there is no restriction on how close people may get when they meet. We will assume that the probability that a person who is infected will pass on the virus to the person they meet (β) is a constant over time and is the same for all infected members of the population.

2. Developing a model of the spread of a virus

An important feature of any model of an epidemic is what it has to say about how the number of infected people rises over time. We will write the change in the number infected between the beginning and the end of any period as $dY = Y_t - Y_{t-1}$. Many of the tables and graphs we see on TV these days show the figures for the number of new cases (the number of newly infected people) over a 24-hour period.

The key to building a model of the spread of a virus amongst a population is to recognise that the only meetings that can result in a spread of the virus is where someone who is infected meets someone who is not infected. If someone who already has the virus meets someone else who already has the virus this cannot result in an increase in the number of people who are infected with the virus. Likewise, if someone who is not infected meets someone else who is not infected this also cannot result in a spread of the virus. So, our model must be built on a foundation that recognises that a rise in the number infected can only occur when someone who is infected meets someone who is not infected.

We will develop the model of the transmission of the virus in a series of steps.⁴ We will begin by asking, given our assumptions, what is the probability that a person who is not yet infected, will become infected in the current period.

2.1 The Hazard Rate⁵

An important concept related to any diffusion or contagion process and especially a process involving the spread of a virus is that of the Hazard Rate. A Hazard Rate is defined as the probability of an event occurring in the current period, given that it has not yet occurred. In our model it is the probability that a person who is not yet infected, will become infected in the current period.

Given the definitions of Y and K and our assumption that people meet at random, the Hazard Rate will be the number of people newly infected in any period (this is

⁴ The model set out below is very similar to that set out by Mansfield (1961) in his study of the diffusion of new techniques of production amongst firms in the USA.

⁵ Peter Bernstein (1996, p 13) has pointed out that the word Hazard comes from *al zahr*, the Arabic word for dice. His book is very interesting and very readable. It was a New York Times bestseller.

$(Y_t - Y_{t-1})$ divided by the number who are not infected at the start of the current period (this is $(K - Y_{t-1})$) so that the Hazard Rate is:

$$(Y_t - Y_{t-1}) / (K - Y_{t-1}) \quad (1)$$

The next step is to ask what might determine how the Hazard Rate will vary over time? It is plausible to think that the probability that a person who is not yet infected will become infected in the current period is proportional to the proportion of the population who are carrying the virus at any time.⁶ However, we also need to recognise that not all interactions between an infected person and an uninfected person will result in the transmission of the virus.⁷ Earlier we defined β to be the likelihood that transmission will occur in the event of a meeting between an infected person and an uninfected person, so we need to include this in our model.⁸ Given all this the Hazard Rate will vary over time according to

$$(Y_t - Y_{t-1}) / (K - Y_{t-1}) = \beta(Y_{t-1}/K) \quad (2)$$

Since Y_{t-1}/K is rising over the whole course of the epidemic this tells us that the Hazard Rate is also rising over the whole course of the epidemic. This is not surprising because over time Y rises while K is constant and so the probability that someone not yet infected will meet someone who is already infected will be steadily rising over time.

2.2 *The number newly infected in each period*

An important aspect of any model of an epidemic (important not least because it informs us about the likely growth in the demand for hospital beds, medical equipment such as ventilators etc) is what it tells us about how the number newly infected varies over time.

⁶ To keep things simple, I will assume that the Hazard Rate varies 1 for 1 with Y_{t-1}/K . We could drop this assumption but it will not make any significant difference to our conclusions.

⁷ In other words we need to recognise that a meeting may not always result in the transmission of the virus (people may be maintaining a 'social distance', wearing masks, practicing hand hygiene etc) and must take this into account. We do this by including in the model a measure of the likelihood that the virus will be transmitted when someone who is infected with the virus meets someone who does not already have the virus, and this is given to us by β .

⁸ In economic models of the diffusion of new methods of production β is rarely taken to be a constant. Instead it is made a function of expected profitability amongst other things. Griliches (1957) and Mansfield (1961) are good examples of this.

Rearrangement of equation (2) indicates that the increase in the number infected (i.e. the number of newly infected people in any period e.g. a 24-hour period), will be⁹

$$dY = Y_t - Y_{t-1} = \beta Y_{t-1}((K - Y_{t-1})/K) = \beta Y_{t-1}(1 - (Y_{t-1}/K)) \quad (3)$$

which is to say that the size of the increase in the number infected in any period (dY), given β and K , depends upon two things: (i) the total number infected at the start of the period (this is Y_{t-1}), and (ii) the number not yet infected at the start of the period (this is $K - Y_{t-1}$).¹⁰

To explain the evolution over time of the increase in the number infected in any period (dY) it is convenient to work with the following expression which is a simple manipulation of the first term on the RHS of equation (3) above:¹¹

$$dY = Y_t - Y_{t-1} = (\beta/K)Y_{t-1}(K - Y_{t-1}) \quad (4)$$

Since β and K are assumed to be constant it is clear that to understand variations in dY over time we only need to explain the variations in $Y_{t-1}(K - Y_{t-1})$ over time.

It is a ‘mathematical’ property of the equations in (3) and (4) above, that dY – which is the number of newly infected persons each period – will be positive unless $Y_{t-1} = 0$ or $Y_{t-1} = K$. In other words, for the whole course of the epidemic from the time the virus is first introduced up until the time when the whole population is infected the number newly infected in every period will be positive. Notice in passing that this implies that the total number infected (Y) must continually rise over time. Now, before the virus is introduced dY will be zero and we note that once the whole population is infected i.e. $K = Y_{t-1}$, then again dY will equal zero. So we can say that once a virus is introduced it must be the case that over time dY (the number newly infected each day) rises above zero, reaches a peak and then starts to fall and keeps falling until it equals zero again. It is important to note that it is dY which rises *and falls* NOT the level of Y . Since dY is always positive¹² the level of Y will always be rising, albeit rising at different rates depending on the value of $Y_{t-1}(K - Y_{t-1})$.

⁹ In the literature on the diffusion of innovations the equation for the spread or ‘take-up’ of the new product or production process is often written as the last term on the RHS of equation (3).

¹⁰ Alternatively we can say that the size of the increase in the number infected in any period, given β and K , depends upon two things: (i) the total number infected at the start of the period (this is Y_{t-1}), and (ii) the proportion of the population not yet infected at the start of the period (this is $(K - Y_{t-1})/K$).

¹¹ Model builders will often see if there are different ways their key equations can be written as some ways of expressing the relationship (i.e. some equations) may be more open to intuitive explanation than others and/or easier to code.

¹² Except for the beginning and end points where $Y_{t-1} = 0$ and $K - Y_{t-1} = 0$.

An intuitive explanation for the behaviour of dY over time goes something like this: imagine that Y_{t-1} is very low relative to $K - Y_{t-1}$ (i.e. we must be in the early stages of the epidemic, perhaps very soon after the virus has been introduced into the population) there will be a very low probability that anyone who is not infected will meet someone who is infected and so dY will be small. However, as Y_{t-1} rises the number newly infected will rise. This is because as Y_{t-1} rises the total number infected at the beginning of any period rises relative to the number uninfected at the beginning of any period, i.e. $K - Y_{t-1}$ which will be falling as Y_{t-1} rises. However after some point (as we will see below this point is where $Y_{t-1} = K - Y_{t-1}$ (i.e. when $Y_{t-1} = 1/2K$)) the probability that someone who is infected will meet someone who is already infected is greater than the probability that someone who is infected will meet someone who is not infected and so even though Y_{t-1} continues to rise, the number newly infected (dY) will become smaller and smaller each period after the peak value of dY has been reached.

In the previous paragraph it was asserted that the probability that someone who is infected will meet someone who is not infected will be greatest when $Y_{t-1} = K - Y_{t-1}$, in other words when $Y_{t-1} = 1/2K$. This is because all values of Y_{t-1} which are below or above $1/2K$ will generate a smaller value of the product $Y_{t-1}(K - Y_{t-1})$ than when Y_{t-1} is exactly equal to $1/2K$. This makes sense since if the number who are already infected is small, the virus spreads slowly, while if the number of people not yet infected is small, the virus will also spread slowly. We expect the number of new infections (dY) to be highest when the number who are already infected and the number not yet infected are both large. I think the proposition that the growth in the number infected will be greatest when $Y_{t-1} = 1/2K$ is intuitively obvious – especially given the point made in the previous sentence – but a numerical experiment might make it clear. Imagine that $K = 100$. Now let's calculate $Y_{t-1}(K - Y_{t-1})$ for a range of values of Y_{t-1} . If Y_{t-1} equals 10 the value of $Y_{t-1}(K - Y_{t-1})$ will be 900. If Y_{t-1} equals 25 then $Y_{t-1}(K - Y_{t-1})$ will be 1875. If Y_{t-1} equals 50 then $Y_{t-1}(K - Y_{t-1})$ will be 2500. If

Y_{t-1} equals 75 then $Y_{t-1}(K - Y_{t-1})$ will be 1875 and if Y_{t-1} equals 90 then $Y_{t-1}(K - Y_{t-1})$ will be 900. Notice that the maximum value occurs when $Y_{t-1} = 50$, in other words when $Y_{t-1} = 1/2K$. Notice also that it is a feature of this model that the levels of $Y_{t-1}(K - Y_{t-1})$ and thus dY for any given value of Y_{t-1} are symmetric either side of the value where $Y_{t-1} = 1/2K$. That is to say, if we move a certain number of periods either side of the period where $Y = 1/2K$, the value of dY will be the same.¹³

We have seen that given the probability of transmission β , the rate of spread at any given point in time is proportional to the number of the population already infected multiplied by the number of the population not already infected. A graph of the behaviour of dY over time for given values of K and β is set out in Figure 1.

¹³ It is this symmetry property that sometimes leads researchers to use this distribution as an approximation to a normal distribution.

[FIGURE 1 NEAR HERE]

Notice that, consistent with our earlier discussion, the curve is symmetric either side of the peak. We will come back to this shortly.

2.3 *An aside on the value of R*

In News bulletins and in Press Conferences we often hear reference to a measure called ‘R’. It is usually mentioned in the context of a statement that people’s behaviour and policy settings should be such that (hopefully) R will be below 1. Now R is defined as the number of new infections (dY) in any period (say, period t) relative to the number of new infections in the previous period (period t-1). So, we can write

$$R = dY_t/dY_{t-1} \quad (5)$$

Given what we have covered in the previous sections of this paper we are in a position to make two comments on R. First, it is obvious that if dY_t is smaller than dY_{t-1} then the growth in dY (and in Y) is slowing. So it is easy to understand why R might be used as a policy indicator and why it is of concern if R is greater than 1.¹⁴ Second, we know both from equations (3) and (4) and from an inspection of Figure 1 that before the peak value of dY is reached R will be rising as dY_t/dY_{t-1} will be greater than 1 while after dY reaches its peak value R will be falling as dY_t/dY_{t-1} will be less than 1.

2.4 *The evolution of the total number infected (Y) over time*

Thus far our focus has been on how Y is changing over time (i.e. dY). We now ask the following question: given the model set out above, what will happen to the total or cumulative number infected (Y) over time? It is possible to approach this by a mathematical technique known as ‘integral calculus’. However, given that we have already explored the features of both the equations and the graph of dY for our model it is quite straight-forward to infer what must be happening over time to the total number infected (Y) over time from our knowledge of the behaviour of dY over time.

When we looked at the behaviour of dY over time we noted that: (i) except at the upper and lower boundaries (when it will equal zero) the value of dY will always be positive, implying that between the two boundaries Y will always be rising; (ii) half-way through the process the value of dY will be a maximum, and; (iii) before we reach that point dY will be rising and after that point dY will be falling. Taken together (ii) and (iii) imply that up until the ‘mid-point’ where $Y = 1/2K$, the total number of people infected (Y) will be rising at a steadily increasing rate while after the mid-point it will be rising at a steadily decreasing rate. A curve or function that behaves this way is called a “Logistic Curve” or “Logistic Function”.

¹⁴ Ideally, we want R to not only be below 1 but to be close to if not equal to zero.

A Logistic Curve for given values of β and K is depicted in the graph below. Notice that the behaviour of Y after it reaches the mid-point where $Y = 1/2K$ (i.e. after the point of inflection¹⁵) is a mirror image of the behaviour of Y before it reaches the mid-point (i.e. before the point of inflection). This is because of the symmetry in the behaviour of dY discussed above.

[FIGURE 2 NEAR HERE]

3. Flattening the curve

In examining any model of an epidemic, it is important to ask the following question: What determines the maximum or peak number of new infections – i.e. what determines and what will be the value for dY – when it is at its maximum?^{16,17}

Now, we have seen above that the maximum value of dY will occur when $Y_{t-1} = 1/2K$. This means that we can now ask: if $Y_{t-1} = 1/2K$ what will be the value of dY ? To answer this, we substitute $Y_{t-1} = 1/2K$ into any of the equations for dY given above and solve for the value of dY that results (let's call this dY_{\max}). If we do this, we find:

$$dY_{\max} = \beta(1/4)K \quad (5)$$

which is to say that the curve for dY – the number of people newly infected in each period – will be taller (higher) or flatter (lower) depending on the values of β and K . In other words, a fall in one or both of β and K will “flatten the curve”.

3.1 Flattening the curve by changing the value of β

Introducing policies such as social distancing (it is really ‘physical distancing’), hand washing, respiratory hygiene and mandating the wearing of face masks in

¹⁵ The point of inflection of a curve is the point on a curve at which the sign of the curvature (i.e. the concavity) changes. The curve in Figure 2 goes from being convex to being concave. The curve in Figure 1 is concave throughout.

¹⁶ This is the height of the curve in Figure 1 when it is at its maximum.

¹⁷ We are working with a ‘discrete time’ model. If we were to express equation (1) in continuous time it would be written as (say) $dY/dt = (\beta/K)Y_t(K - Y_t)$ which can be written as $dY/dt = \beta Y_t - (\beta/K)Y_t^2$. Again, I am taking advantage of the fact that both β and K are constants to simplify the algebra – see footnote 11 above. We know that when dY/dt is a maximum it will be (momentarily) constant, in other words when dY/dt is a maximum $d(dY/dt)/dt$ will be zero. Differentiating our expression for dY/dt with respect to time we find that $(dY/dt)/dt = \beta - 2(\beta/K)Y_t$. Setting that equal to zero we find that dY/dt will be a maximum when $Y_t = 1/2K$. If we now substitute that result into our equation for dY/dt we will be able to find an expression for the highest value of dY/dt will reach during the course of the epidemic. It will be equal to $dY_{\max} = \beta 1/4K$, which is the same as our ‘intuitive’ result for the discrete time model.

public will lower the value of β and will make the curve flatter, in the sense that at any date the value of dY will be smaller for a lower β than for a higher β . Although taken alone these policies do not alter the chance that an infected person will ‘meet’ a person who is not yet infected, they do reduce the chance that the virus will be transmitted in the event that someone who has the infection meets someone who does not have the infection. If the policies succeed in doing this, then they will lower the maximum value that dY will adopt – see equation (5) above. Figure 3 below shows the time path of dY for two values of β one where $\beta = 0.5$ and the other where $\beta = 0.2$.¹⁸ However, unless the policy somehow influences the value of K the total number of people in the population who will ultimately be infected will be the same in the two scenarios. We can see this in Figure 4 below which shows how the total number infected (Y) rises in the two scenarios depicted in Figure 3. We see that in both scenarios the end state involves everyone becoming infected. But note that this doesn’t mean that public policy designed to reduce β alone is not worthwhile as by lowering the number of new cases that arise in each period it reduces the demand and especially the peak demand on health services (such as ventilators) in each period and this may be judged desirable especially in the early period of the epidemic while resources required to provide adequate medical treatment only slowly become available.¹⁹

[FIGURE 3 NEAR HERE]

[FIGURE 4 NEAR HERE]

3.2 *Flattening the curve by changing the value of K*

We have seen that policies such as social distancing, hand washing, respiratory hygiene etc do “flatten the curve”. However, we also noted that these policies by themselves do not alter the probability that an infected person will meet someone who is not infected. Instead they simply act to reduce the risk of the transmission of the virus, should a meeting take place. In the absence of policies that alter the size of K , all that we are doing is slowing down the time it takes for everyone sooner or later to be infected. If we want to reduce the total number of people who will be infected, we need to reduce K . For this reason, we need to add to policies of social distancing, hand washing etc other policies which are designed to reduce the chance that someone who is infected will meet someone who is not infected. One way is to ensure that those who are infected have a very much reduced chance of meeting anyone who is not infected by enforcing ‘stay at home’ and quarantine rules or isolating anyone who is infected in hospital wards. Widespread testing, including testing at random, would assist identifying people who are

¹⁸ The value of K is the same in both cases. So, the reason why the two curves differ is a result of change β alone.

¹⁹ When TV news items deal with the UK, we often see on the TV screen signs stating that people should stay at home in order to “save the NHS”. The NHS is the British National Health Service.

infected and who will then have their mobility restricted. Another way to reduce the chance that someone who is infected will meet someone who is not infected is to reduce the mobility of people who are not yet infected by insisting that *they* also stay at home and keep meetings with ‘outsiders’ to as few as possible. A third way to reduce transmission is to use travel bans to restrict both international travel and domestic travel across national, state or regional boundaries and to isolate any travellers from the community for a period of time.

A graph showing the effect on dY – the number of new infections in any period – of changing K (given β) is given in Figure 5. We see that a fall in K will ‘flatten’ the curve - this is not surprising given equation (5) above.²⁰

[FIGURE 5 NEAR HERE]

Figure 6 below shows how the fall in K will alter the evolution of the total number infected (Y) over time. Not surprisingly, given the curves for dY depicted in Figure 5, the lower curve in the Figure (where $K = 500$ compared with $K = 1000$) involves a smaller number of people infected when the epidemic has run its course.

[FIGURE 6 NEAR HERE]

4. Final Remarks

Our simple model has shown us one important thing when it comes to public policy to deal with an epidemic and that is that we should introduce both sets of policies, i.e. those aimed at reducing β and those aimed at reducing K and not rely on one alone. While our model has made some totally unrealistic assumptions (the virus is only transmitted when people meet face-to-face, people who are infected neither recover or die²¹), it does seem to be capturing some essential and policy-relevant features of an epidemic.²²

²⁰ We can also infer this by looking at equation (5) above.

²¹ Our model of the spread of an epidemic is related to the “SI model” which identifies two mutually exclusive elements of the population: the Infectious (I, this is our Y) and those susceptible to infection (S, this is our $(K - Y)$) and focuses on how those two groups interact. See the video by Julia Collins and Nadia Abdelal titled “The Spread of Disease – Maths Delivers” <https://www.youtube.com/watch?v=buZjhRAAKH4> for an explanation of the SI model and the effect of relaxing various assumptions, eg allowing for recoveries and fatalities and the introduction of a vaccine. You might also be interested in the video “Oxford Mathematician explains SIR Disease model for COVID-19 (Coronavirus)” <https://www.youtube.com/watch?v=NKMHhm2Zbkw> which also modifies the SI model to allow for some people to recover from the disease.

²² Nicholas Taleb and his co-authors has some interesting remarks about the need to capture non-linear aspects of the spread of an epidemic. You might be interested in Taleb (2010) on fat-tailed distributions. It is a very stimulating read and will be of interest to anyone studying finance as well as economics.

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Figure 1 Graph of the evolution of dY over time.²³

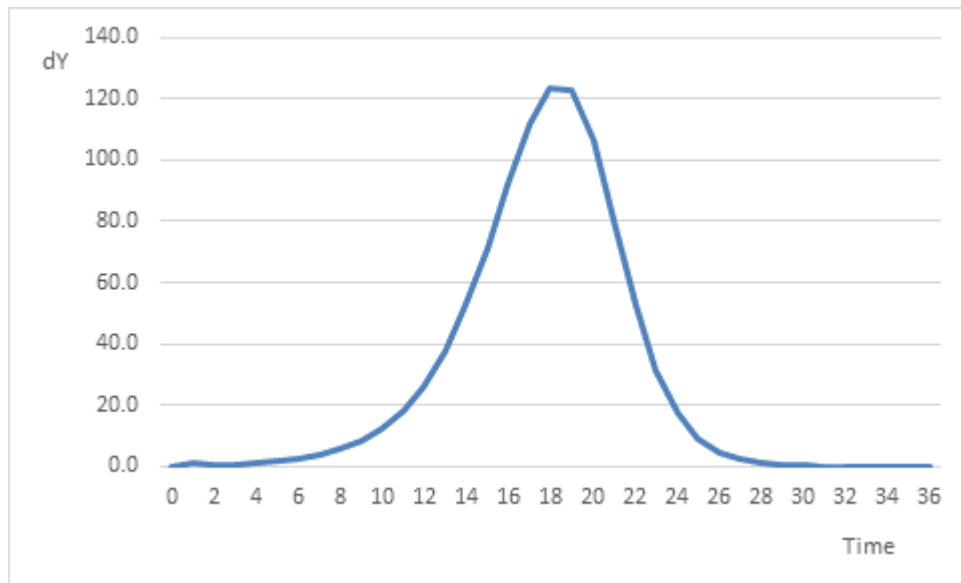
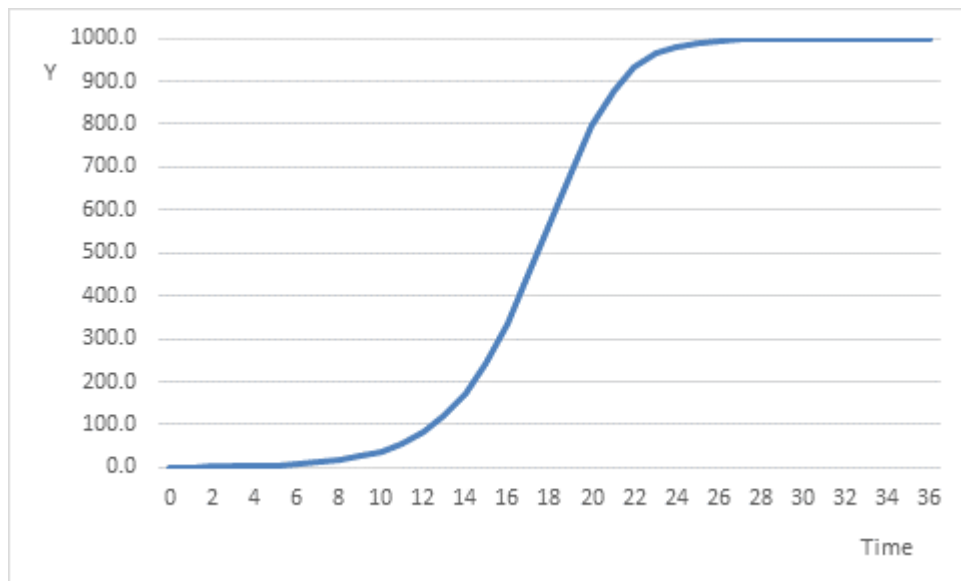


Figure 2 Graph of the evolution of Y over time.²⁴



²³ For given values of K and β the results of the simulation of the behaviour of dY over time will be the same whether we use equation (4) or either variant of equation (3). I have generated Figure 1 using Excel with K set at 1000 and β set at 0.5. I have commenced the simulation assuming that no one is infected in period 0 and that 1 person becomes infected in period 1. I have then simulated the implied time path for dY using the equations $dY = \beta Y_{t-1}(1 - (Y_{t-1}/K))$ and $Y_t = Y_{t-1} + dY$.

²⁴ I have generated Figure 2 using Excel with K set at 1000 and β set at 0.5. Again, I have commenced the simulation assuming that no one is infected in period 0 and that 1 person becomes infected in period 1. I have then simulated the implied time path for Y using the equation $Y_t = Y_{t-1} + dY$.

Figure 3 The effect on the time path of dY of a change in the value of β from 0.5 to 0.2 with K unchanged.²⁵

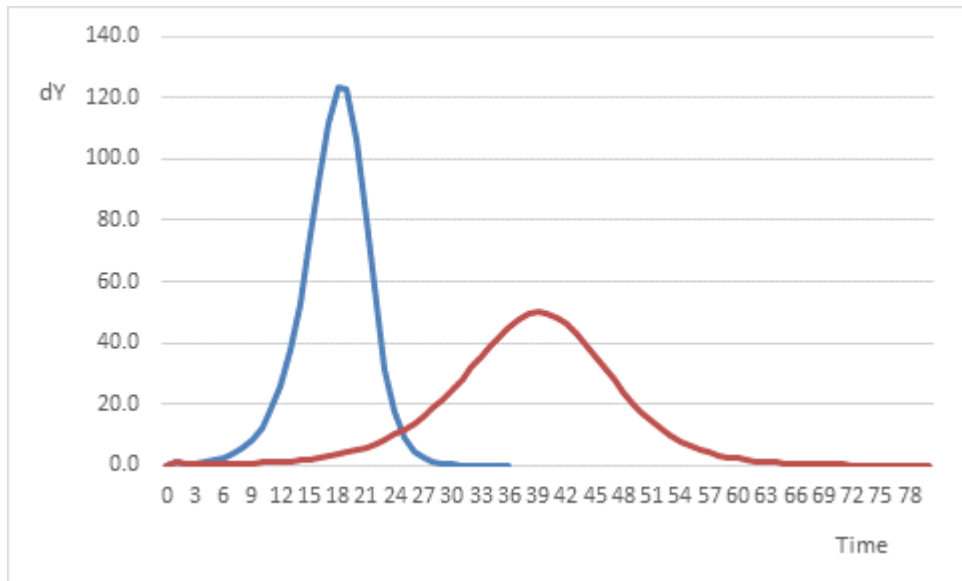
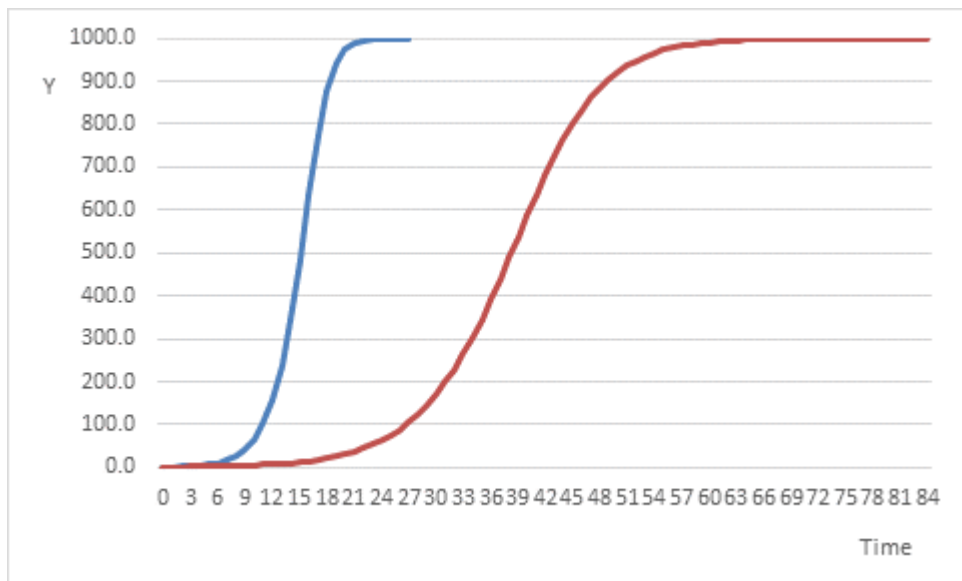


Figure 4 The effect on the time path of Y of a change in the value of β from 0.5 to 0.2 with K unchanged.²⁶



²⁵ I have assumed that $K = 1000$ and that β is 0.5 (blue curve – this is actually the same curve as in Figure 1) and 0.2 (red curve).

²⁶ As with Figure 3 I have assumed that $K = 1000$ and that β is 0.5 (this value of β gives the blue curve – this is actually the same curve as in Figure 2) and 0.2 (this value of β gives the red curve).

Figure 5 The effect on dY of a change in the value of K with β unchanged.²⁷

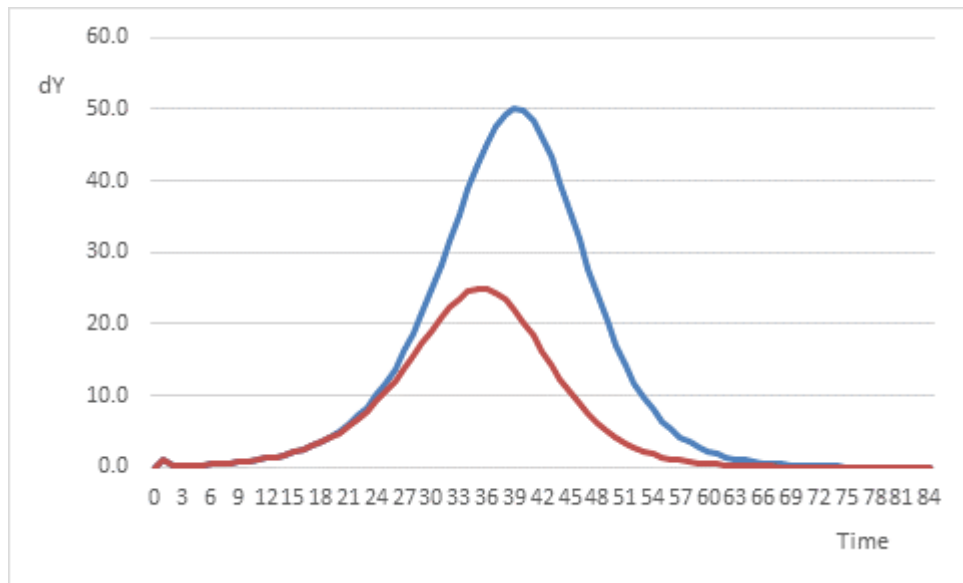
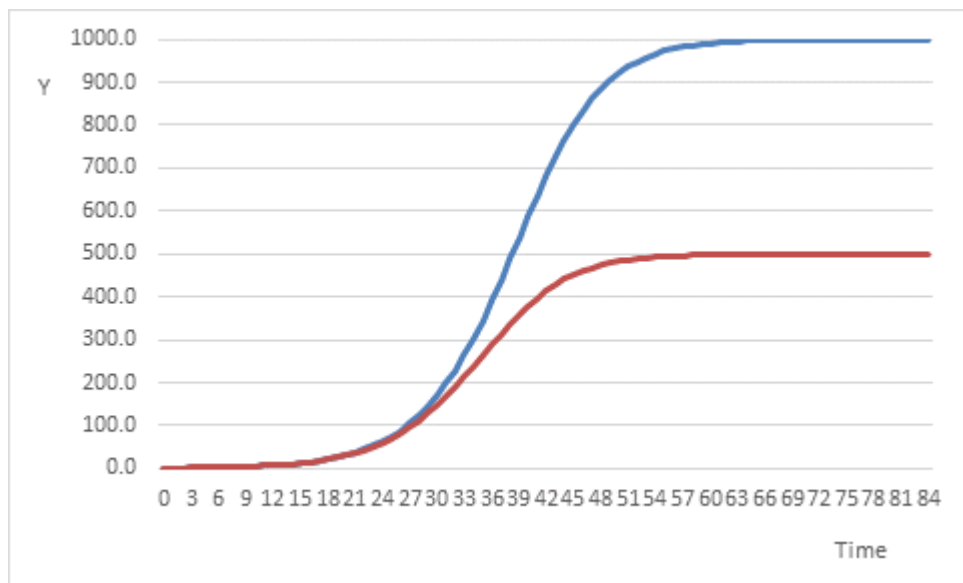


Figure 6 The effect on the time path of Y of a change in the value of K from 1000 to 500 with β unchanged.²⁸



²⁷ I have assumed that β is 0.5 and is unchanged while K changes from 1000 (blue curve) to 500 (red curve).

²⁸ As with Figure 5 I have assumed that β is 0.5 and is unchanged while K changes from 1000 (blue curve) to 500 (red curve).