

Part 1: Growth modelling

Darren Wilkinson

darrenjw.github.io

Exponential models

Discrete time, deterministic dynamics

In the early stages of an epidemic, most people are susceptible to the disease, so in a random interaction between an infectious person and another person, that other person is very likely to be susceptible. In that case we shall assume that each infectious person infects s susceptibles per day, for some parameter s related to how infectious the disease is (and lots of other things, such as population density, behaviour, etc.), and that they then cease to be infectious.

If we start with x_0 infectious individuals on day 0, we will have $x_1 = x_0 \times s$ on day 1, $x_2 = x_1 \times s$ on day 2, etc.

Time course as a stream

The relationship between x_t and x_{t-1} (for *any* t) gives us a way to compute x_t (for some *specific* t) from x_0 , either recursively or iteratively.

Some Scala code

```
val x0 = 3; val s = 2
val xs = Stream.iterate(x0)(xt => xt*s)

xs.take(5).toList
// res0: List[Int] = List(3, 6, 12, 24, 48)
```

Continuous approximation to population size

Of course, there is no reason to assume that the “average” number of people infected each day is an integer, so to model the “expected” size of the infected population, we must switch to Doubles.

```
val x0 = 2.0; val s = 1.5
val xs = Stream.iterate(x0)(xt => xt*s)

xs.take(4).toList
// res2: List[Double] = List(2.0, 3.0, 4.5, 6.75)
```

This just confirms the closed-form solution of this model:

$$x_t = x_0 s^t.$$

Plot using *EvilPlot*

```
import com.cibo.evilplot._
import com.cibo.evilplot.plot._
import com.cibo.evilplot.plot.aesthetics.DefaultTheme._
import com.cibo.evilplot.numeric.Point

val points = xs.zipWithIndex
  .map{case (xt, t) => Point(t, xt)}
  .take(25).toList
val plt = ScatterPlot(points)
  .xAxis().yAxis()
  .frame()
  .xLabel("t").yLabel("x(t)")
  .render()

displayPlot(plt)  // display in a window on the console
```

Plot of x_t against t

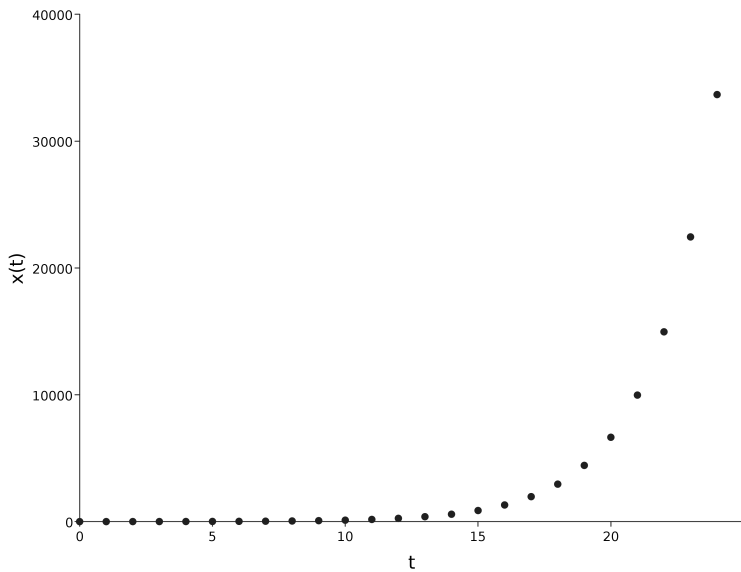


Figure 1:

Geometric growth, exponential growth, and logarithms

The number of infected people in this model is said to follow a *geometric sequence*. So the growth in such a sequence should probably be referred to as *geometric growth*. However, this is just the discrete time version of *exponential growth*. The growth is said to be exponential because it can be described by an exponential curve. Since *logarithms* are the inverse of exponential functions, the logarithm of values in a geometric series have *arithmetic* or *linear* growth.

This is why people often use a logarithmic y -axis on epidemic plots. Transforming our recurrence $x_t = sx_{t-1}$ gives

$$\log x_t = \log s + \log x_{t-1}.$$

Similarly, transforming the solution $x_t = x_0 s^t$ gives

$$\log x_t = \log x_0 + t \log s.$$

The slope of the line is the log of the growth rate.

Continuous time, and stochastic infections

Continuous time

Rather than modelling one day at a time, it is sometimes better to think about events playing out in continuous time. This leads to a linear *differential equation* whose solution is the *exponential function*.

Discrete stochastic updates

Alternatively, we can stick with discrete time, but insist on an integer number of infected individuals at each time. The best way to do this is by assuming that the number of individuals infected at each time is a discrete random quantity, described by a *binomial* or *Poisson* distribution.

Continuous time and discrete stochastic updates

In fact, it is often better still to have a continuous time model with discrete stochastic infection events, where the time between infections is described by a continuous random quantity such as an *exponential distribution*.

Logistic models

Logistic growth

Exponential growth models capture the behaviour of the early part of an epidemic quite well, but an obvious limitation is that they continue to grow very quickly, so before long they will be predicting more people infected than there are people on Earth.

A simple extension is to suppose that the population size is fixed, and that the number of susceptibles is just the number not currently infected. We then suppose that the number of new infections relates to the number of susceptibles in an intuitive way.

At time t the number infected is x_t , so the number of susceptibles is $P - x_t$, where P is the population size. We now assume that r is the propensity for any infectious individual to infect any susceptible, so the number of infections from each infectious individual is $r \times (P - x_t)$ (so approximately $s = rP$), and the total number infected at the next time point will be $x_t \times r \times (P - x_t)$. In other words,

$$x_{t+1} = rx_t(P - x_t).$$

This is the so-called *logistic map*.

Logistic map

```
val x0 = 2.0; val r = 2.0e-7; val P = 1.0e7  
val xs = Stream.iterate(x0)(xt => r*xt*(P-xt))
```

```
xs.take(4).toList  
// res5: List[Double] = List(  
//    2.0,  
//    3.9999992,  
//    7.999995200001278,  
//    15.999977600017914  
// )
```

So for an appropriate choice of r , the early behaviour of this epidemic is very similar to that of the exponential growth model. The differences kick in later in the epidemic.

Plot

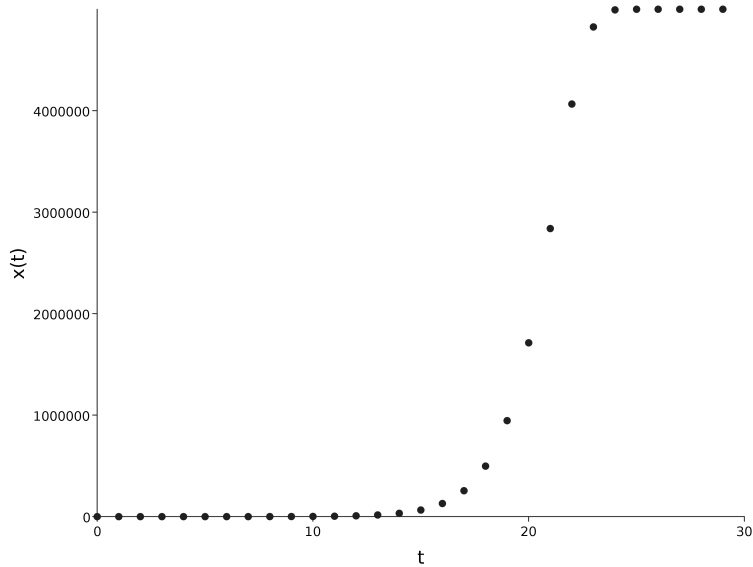


Figure 2:

Log Plot

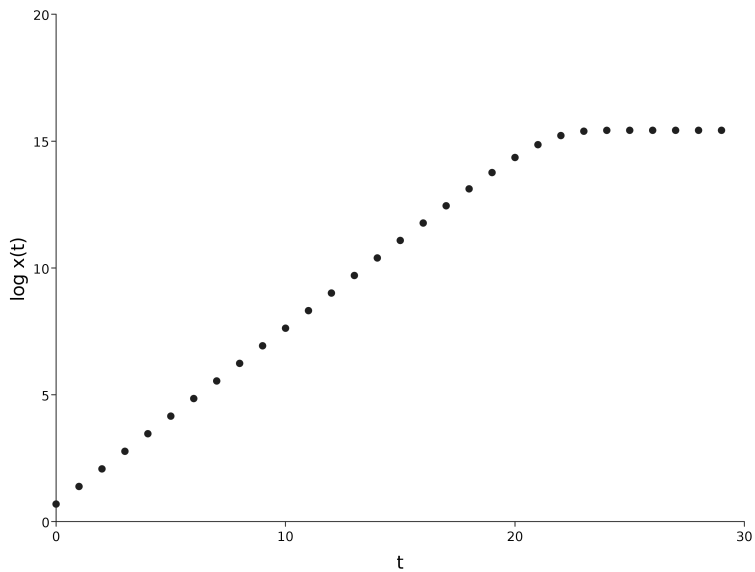


Figure 3:

Logistic growth model

One possibly undesirable feature of this model is that it assumes at after one day (or other time unit) that all infectious individuals cease to be infectious and immediately become susceptible again. A simple variation on this is to assume that individuals remain infectious, leading to the relation

$$x_{t+1} = x_t + rx_t(P - x_t).$$

But in fact, we can re-write this as

$$x_{t+1} = rx_t \left(P + \frac{1}{r} - x_t \right),$$

which is the same as the logistic map, but with the population size differing by $1/r$.

A convenient property of *this* parameterisation of *logistic growth* is that it tends to a limit, often known as the *carrying capacity*, of P .

Limitations

Limitations of simple growth models

The logistic growth model corrects an important problem with the pure exponential growth model (unboundedness), and is still sometimes used in practice by epidemiologists, in some situations, due to its relative simplicity.

However, it still has very serious limitations. It is not realistic to assume either that infectious individuals remain so forever, or that they immediately return to full susceptibility. But to model this, we need a model containing multiple different classes of individuals. These are often known as *compartmental models*.