Exact solution for a nonlinear SI epidemiological model

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Abstract

A simple nonlinear Susceptible-Infective (SI) epidemiological model is constructed, illustrating the formulation of a compartmental model. Using very elementary techniques such as taught in an introductory differential equations course, an exact solution is obtained. The conclusions are general enough that they give students a good feel for epidemiological models.

1 Introduction

When teaching quantitative methods in the context of ordinary differential equations, it is hard to give examples of models that are at the same time amenable to analysis and realistic. Indeed, the methods taught to students work mainly with linear equations, whereas models are frequently nonlinear. The model presented here is a real epidemiological model, despite its simplicity. It contains the basic elements that are in all deterministic epidemic models: a nonlinear incidence, and susceptible and infective classes. After a transformation of the system, one of the equations is shown to be a Bernoulli equation. Thus an explicit solution is found. Studying this solution, a threshold is characterized that distinguishes between the disease becoming extinct or endemic in the population. This threshold is the *basic reproduction number* $\mathcal{R}_0$, a key concept in epidemiology. Thus, this provides an interesting example to present after having explained integrating factors and Bernoulli equations.

2 Formulation of the model

We consider a closed population, and are going to model the spread of an infectious disease in this population. We suppose that individuals in the population can be in one of two states: *susceptible*, if they have not yet contracted the disease, and *infective*, if they have contracted the disease and are spreading it. This defines two compartments, and the object of the modelling is to describes how the population in each of the compartments evolves.

Let $S(t)$ and $I(t)$ be the numbers of susceptibles and infectives in the population at time t, respectively. Thus, at time t, the total population is

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

In order to formulate the model, we must make hypotheses about the different populations and their interactions.

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We suppose that susceptible individuals

- are born at a rate d proportional to the total population N,
- die at a rate d proportional to the susceptible population S.

Note that since we assume that all newborns are susceptibles, we are not taking into account any *vertical transmission* of the disease, where the mother can infect a newborn.

We suppose that infectives

- die at the rate d, proportional to the infective population I,
- never recover from the disease.

We do not consider any disease specific mortality. The above assumptions describe diseases with very short or inexistent periods of incubation, and such that once infected, an individual remains infective for his whole life. Examples of diseases that have these type of characteristics are diseases caused by bacteria such as *staphylococcus aureus*, *streptococcus pyogenes*, *chlamydia pneumoniae* or *neisseria gonorrhoeae*.

When an infective meets a susceptible, disease transmission might occur. The function $f(S, I)$ of S and I that describes this process is called the *incidence* function. Incidence is defined as the number of new cases per unit time, so f is a *rate*. It consists of two components:

- a count of the number of contacts taking place,
- and a description of the probability that such a contact results in the transmission of the disease.

Finding an incidence function that adequately describes the contact process is a difficult task; see, e.g., [4]. One popular incidence function is the *mass action* incidence, which takes the form

$$f(S, I) = \beta SI$$

The parameter β is the disease transmission coefficient. The modelling assumption is that every infective can meet every susceptible (note the analogy to gas dynamics or chemistry, where it is assumed the every atom/molecule is likely to interact with every other). In a large enough population, this is unrealistic (for humans or animals), and another incidence function used is the *proportional* incidence. It takes the form

$$f(S, I) = \beta \frac{SI}{N}$$

The meaning of this incidence function is that each infective can meet only a proportion of the susceptibles.

Taking all these hypotheses into account, and choosing a proportional incidence function, the model has the flow diagram shown in Figure 1. To obtain a system from this flow diagram, we write that, for a given compartment (S or I), incoming arrows correspond to positive rates, outgoing arrows are negative rates. Thus the equations describing the evolution of the numbers of susceptibles and infectives take the following form, where $' = d/dt$,

$$S' = \underbrace{dN}_{\text{birth}} - \underbrace{\beta \frac{SI}{N}}_{\text{infection}} - \underbrace{dS}_{\text{death}} \tag{1a}$$

$$I' = \underbrace{\beta \frac{SI}{N}}_{\text{infection}} - \underbrace{dI}_{\text{death}} - \underbrace{\gamma I}_{\text{recovery}} \tag{1b}$$

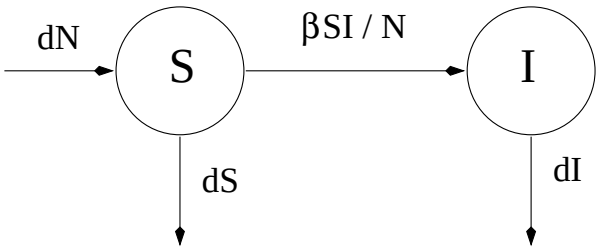

Figure 1: Flow diagram of the model, showing the rates of movement of individuals into, out of and between the different compartments.

We consider the initial value problem consisting of this system together with initial conditions $S(0) = S_0 \geq 0$ and $I(0) = I_0 \geq 0$.

A model such as (1) is called an SI model, for susceptible-infective. If we supposed that infectives recover (and thus became susceptible again), the model would have to incorporate another flow (from I to S), and we would speak of an SIS model. Note that the analysis that follows would also be valid in the case of an SIS model. More elaborate models are built when other classes are considered; for example, SEI models incorporate a class of individuals, called exposed individuals, who have contracted the disease but are not yet spreading the disease. Note finally that the model can be used to describe a situation where "birth" and "death" correspond to an individual entering and leaving a risk group, respectively. Readers interested by more details about mathematical models in epidemiology can refer to, e.g., [2, 3].

3 Some analysis

System (1) is a nonlinear system. In principle, we would analyze it using qualitative techniques. Here, however, an exact solution can be found.

The total population is constant

First, we show that the total population is constant. Indeed,

$$\begin{aligned} N' &= S' + I' \\ &= dN - \beta\frac{SI}{N} - dS + \beta\frac{SI}{N} - dI \\ &= dN - d(S + I) \\ &= 0 \end{aligned}$$

Therefore, have, for all t, $N(t) \equiv N_0 := S_0 + I_0$.

Working in proportions

Now consider the proportions $s(t)$ and $i(t)$ of susceptibles and infectives in the total population at time t, respectively:

$$s = \frac{S}{N} \qquad i = \frac{I}{N}$$

Note that $s + i = (S + I)/N = 1$. Taking the time derivative of i gives

$$i' = \frac{I'N - IN'}{N^2} = \frac{I'}{N} - \frac{iN'}{N}$$

Since $N' = 0$,

$$i' = \frac{I'}{N}$$

Substituting the right hand side of (1b) into this equation gives

$$i' = \beta\frac{SI}{N^2} - d\frac{I}{N} = \beta si - di$$

Now, since $s + i = 1$, we can substitute $s = 1 - i$ into this last equation, giving $i' = \beta(1 - i)i - di$. Thus the system *in proportion* is given by

$$s = 1 - i \tag{2a}$$
$$i' = \beta(1 - i)i - di \tag{2b}$$

Since N is constant, solutions of (1) can be deduced directly from solutions of (2). From now on, we study (2).

The equation for i is a Bernoulli equation

Rewrite equation (2b) as

$$i' - (\beta - d)i = -\beta i^2 \tag{3}$$

This is a Bernoulli equation. So we let $u = i^{-1}$, giving $u' = -i^{-2}i'$, or, equivalently, $i^{-2}i' = -u'$. Multiplying both sides of (3) by i^{-2}, substituting for u and u' gives the linear differential equation

$$-u' - (\beta - d)u = -\beta$$

so that finally, we consider the linear differential equation

$$u' + (\beta - d)u = \beta \tag{4}$$

Solving the associated linear equation (4)

Equation (4) is a linear equation of the form

$$x' + P(t)x = Q(t)$$

with $P(t) = \beta - d$ and $Q(t) = \beta$. An integrating factor is then given by

$$\mu(t) = \exp\left(\int P(t)dt\right) = e^{(\beta-d)t}$$

Multiplying both sides of (4) by $\mu(t)$, it follows that

$$(\mu(t)u)' = \beta e^{(\beta-d)t}$$

Integrating both sides,

$$\mu(t)u = \frac{\beta}{\beta - d} e^{(\beta-d)t} + C$$

for $C \in \mathbb{R}$, and so

$$u = \frac{\beta}{\beta - d} + Ce^{-(\beta-d)t}$$

Here, it is easier to find the value of C before writing the solution in terms of i. The initial condition $i_0 = I_0/N$ is $u(0) = 1/i_0$. Thus

$$u(0) = \frac{1}{i_0} = \frac{\beta}{\beta - d} + C$$

which implies that

$$C = \frac{\beta - d - i_0\beta}{i_0(\beta - d)}$$

So the solution to the linear equation (4) is given by

$$\begin{aligned} u &= \frac{i_0\beta + (\beta - d - i_0\beta)e^{-(\beta-d)t}}{i_0(\beta - d)} \\ &= \frac{i_0\beta(1 - e^{-(\beta-d)t}) + (\beta - d)e^{-(\beta-d)t}}{i_0(\beta - d)} \end{aligned}$$

and the solution to (3) is

$$i(t) = \frac{i_0(\beta - d)}{i_0\beta(1 - e^{-(\beta-d)t}) + (\beta - d)e^{-(\beta-d)t}}$$

4 The basic reproduction number

Summing up, the solution to (2) is given by

$$s(t) = 1 - \frac{i_0(\beta - d)}{i_0\beta(1 - e^{-(\beta-d)t}) + (\beta - d)e^{-(\beta-d)t}} \tag{5}$$

and

$$i(t) = \frac{i_0(\beta - d)}{i_0\beta(1 - e^{-(\beta-d)t}) + (\beta - d)e^{-(\beta-d)t}} \tag{6}$$

Observing (5) or (6), we see that there are two cases:

- If $\beta - d < 0$, then $\lim_{t\to\infty} e^{-(\beta-d)t} = +\infty$, so $\lim_{t\to\infty} s(t) = 1$ and $\lim_{t\to\infty} i(t) = 0$.
- If $\beta - d > 0$, then $\lim_{t\to\infty} e^{-(\beta-d)t} = 0$, so $\lim_{t\to\infty} s(t) = 1 - (\beta - d)/\beta$ and $\lim_{t\to\infty} i(t) = (\beta - d)/\beta$.

We can reformulate this conclusion using a quantity of fundamental importance in epidemiology, the *basic reproduction number*, which is usually denoted $\mathcal{R}_0$. Let

$$\mathcal{R}_0 = \frac{\beta}{d}$$

Then we have the following equivalences,

$$\mathcal{R}_0 < 1 \Leftrightarrow \beta - d \leq 0$$
$$\mathcal{R}_0 > 1 \Leftrightarrow \beta - d > 0$$

Also,

$$\frac{\beta - d}{\beta} = 1 - \frac{1}{\mathcal{R}_0}$$

Thus, we have proved the following theorem.

Theorem 1. *For system* (1)*, we have the following alternative:*

- *If* $\mathcal{R}_0 < 1$*, then* $\lim_{t\to\infty} s(t) = 1$ *and* $\lim_{t\to\infty} i(t) = 0$*, the disease becomes extinct.*
- *If* $\mathcal{R}_0 > 1$*, then* $\lim_{t\to\infty} s(t) = 1/\mathcal{R}_0$ *and* $\lim_{t\to\infty} i(t) = 1 - 1/\mathcal{R}_0$*, the disease becomes endemic.*

$\mathcal{R}_0$ thus determines whether the disease establishes itself in the population or not, and the aim of disease control policies is to reduce $\mathcal{R}_0$ to a value less than 1. In words, $\mathcal{R}_0$ is the average number of secondary infections produced when an infective individual enters a totally susceptible population [1]. Remark that in the case of our model, $1/d$ is the average time spent in the I class (before death), and β is the probability of disease transmission.

In the case where $\mathcal{R}_0 > 1$, we can remark that the larger $\mathcal{R}_0$, the higher the proportion of infectives in the population, as shown in Figure 2. Thus, further from being a threshold of disease invasion, $\mathcal{R}_0$ is also an indicator of the infectiousness of the disease. $\mathcal{R}_0$ can be estimated from disease data; see, e.g.,

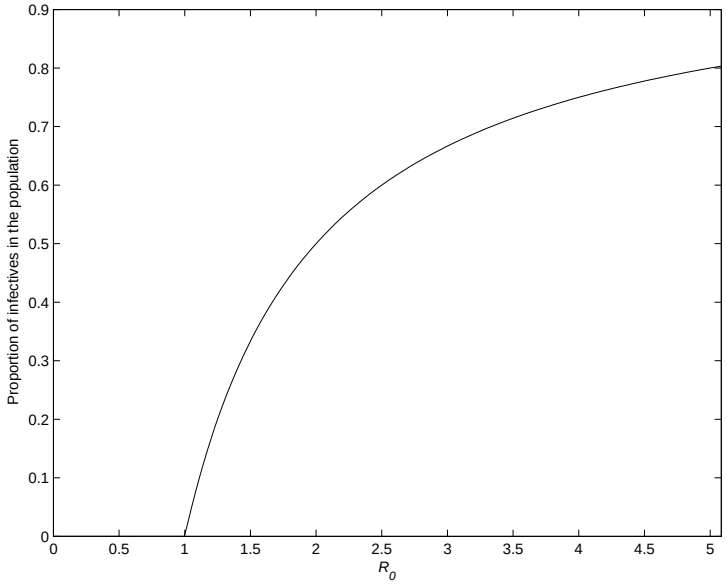

Figure 2: Proportion of infectives in the population as a function of $\mathcal{R}_0$.

[1, 2]. Note that the value of $\mathcal{R}_0$ can vary a lot for the same disease, depending on the population. For example, in the case of measles, values of $\mathcal{R}_0$ were estimated between 5 (Kansas, USA, 1918-1921) and 18 (England and Wales, 1950-1968) [1].

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