1 Abstract

The SIR pandemic model suffers from an unrealistic assumption: The rate of removal from the infectious class of individuals is assumed to be proportional to the number of infectious individuals. This means that a change in the rate of infection is simultaneous with an equal change in the rate of removal. A more realistic assumption is that an individual is removed at a certain time interval after having been infected. A simple modified SIR model is proposed which implements this delay, resulting in a single delay differential equation which comprises the model. A solution to this equation which is applicable to a pandemic is of the form $A + BL(t)$ where $L(t)$ is a logistic function, and $A$ and $B$ are constants. While the classical SIR model is often an oversimplification of pandemic behavior, it is instructive in that many of the fundamental dynamics and descriptors of pandemics are clearly and simply defined. The logistic model is generally used descriptively, dealing as it does with only the susceptible and infected classes and the rate of transfer between them. The present model presents a full but modified SIR model with a simpler logistic solution which is more realistic and equally instructive.

2 Introduction

In the following, subscripted variables of the form $t_x$ will represent a particular time, $T_x$ will represent a particular time interval and $f_x$ will represent the associated frequency: (i.e. $T_xf_x = 1$)

The SIR model consists of three classes or compartments[1, 2]:
S(t) - The fraction of the population which has never been infected, and is therefore susceptible to infection.

I(t) - The fraction of the population which is "infectious" - members of this compartment have been infected, but have not yet become immune (or died), and are capable of passing the infection on to any susceptible person that they come in contact with.

R(t) - The fraction of the population which has been removed from the susceptible and infectious compartments. These are individuals who have either become immune or have died from the disease. Removal is irreversible.

It is assumed that birth and death rates have an insignificant effect on the total population, which will be assumed constant. There are two assumptions made in the classical SIR model concerning the rates of transfer between compartments. The first assumption is that the fractional rate of transfer of individuals from the susceptible class to the infected class \( v(t) \) is given by:

\[
v(t) = f_c S(t) I(t)
\]

where \( f_c \) is the average frequency of potentially infectious contacts experienced by an individual member of the population. A potentially infectious contact is one which, if the contacting pair consists of a susceptible and an infectious individual, the susceptible individual will certainly become infected. The second assumption is that the probability of an infectious individual moving from the infectious class to the removed class in time \( dt \) is \( f_r dt \) where \( f_r \) is a constant. This probability is thus independent of the time since infection. The rate of removal is then proportional to the fraction of infectious individuals divided by the average infectious period \( T_r = 1/f_r \). The SIR model is then:

\[
S'(t) = -f_c S(t) I(t)
\]
\[
I'(t) = f_c S(t) I(t) - f_r I(t)
\]
\[
R'(t) = f_r I(t)
\]

3 A Modified SIR model

A problem with the SIR model is that, via the \( f_r I(t) \) term in the expression for \( I'(t) \), a spike in the infection rate results in an immediate spike in the recovery rate, which is
unrealistic. This results from the unrealistic assumption that the probability of removal during a particular time interval is independent of the time since infection. In the present model, it is assumed that an individual spends a fixed amount of time $T_r$ in the infectious compartment. A spike in the infection rate will result in an equal spike in the recovery rate at time $T_r$ later, assuming no deaths have occurred in the interim. In other words, the rate of removal at time $t$ is equal to the rate of infection at time $t - T_r$.

To model this situation, it is useful to define $n(t)$, the cumulative number of individuals who have ever been infected ($n(t) = I(t) + R(t)$). The fractional populations may then be written as:

$$
S(t) = 1 - n(t)
$$

$$
I(t) = n(t) - n(t - T_r)
$$

$$
R(t) = n(t - T_r)
$$

The rate of infection is again assumed to be:

$$
v = n'(t) = f_c S(t) I(t)
$$

The model is then described by a single delay differential equation:

$$
n'(t) = f_c S(t) I(t) = f_c [1 - n(t)] [n(t) - n(t - T_r)]
$$

the solution to which will allow the $S$, $I$, and $R$ functions to be found. This equation involves two "pandemic parameters" which describe the dynamics of the pandemic, $f_c$ and $T_r$. A pandemic model will usually assume as an initial condition that $n(-\infty) = n_m$ which is constant and often set to zero unless studying an outbreak in a partially immune population. There will also be a constant of integration $t_h$ which specifies the "center" of the pandemic. As shown below, the main equation (3.1) then has the following logistic solution:

$$
n(t) = n_m + \frac{n_p - n_m}{1 + e^{-f_e (t - t_h)}}
$$

where the phenomenological parameters $n_p$ and $f_e$ are functions of the pandemic parameters $f_c$ and $T_r$ and initial condition $n_m$. (Phenomenological parameters may be obtained by
fitting the logistic solution to measured pandemic data.) \( n_p = n(\infty) \) is the fraction that have ever been infected at infinite time (disease-free equilibrium). \( t_h \) is the “half way point”: The time at which \( n(t) = (n_p + n_m)/2 \) and it is an initial condition. \( t_h \) is also the inflection point of \( n(t) \) and so specifies the peak rate of infection.

Note that the standard SIR model can be recovered from this model by assuming that \( T_r \) is so small that the following approximation may be made:

\[
n' (t - T_r) \approx \frac{n(t) - n(t - T_r)}{f_r} = f_r I(t)
\]

4 Expression for \( f_e \) in terms of \( f_c \) and \( T_r \)

\( f_e \) can be found by considering the situation near time plus or minus infinity. As \( t \to -\infty \), \( e^{f_e(t - t_h)} \) is small, and the main equation \( 3.1 \) to first order is:

\[
n'(t) \to f_c [1 - n_m] [n(t) - n(t - T_r)]
\]

which can be solved:

\[
n(t) \to n_m + (n_p - n_m) e^{f_e(t - t_h)}
\]

where \( f_e \) obeys:

\[
f_e = f_c (1 - n_m) (1 - e^{-f_e T_r})
\]

and has the following solution:

\[
f_e T_r = R_m + W(0, -R_m e^{-R_m})
\]

where \( R_m = f_c T_r (1 - n_m) = R_0 (1 - n_m) \), \( R_0 = f_c T_r \) being the basic reproduction number\(^2\) and \( W[j, z] \) is the \( j \)th Lambert W function, also known as the product log function. \( j \) has been set to zero, since only for \( j = 0 \) will \( f_e \) be real and finite.
5 Expression for $n_p$ in terms of $f_c$ and $T_r$

A similar analysis at near infinite time yields:

$$n(t) \rightarrow n_p - (n_p - n_m) e^{-f_a(t-t_h)}$$

From the symmetry of the logistic function, it can be seen that $f_a = f_e$ and, assuming $f_e$ is positive and finite, it will obey:

$$f_e T_r = -R_p - W(-1, -R_p e^{-R_p})$$

where $R_p = R_0(1 - n_p)$. It follows that:

$$n_p - n_m = \frac{f_e}{f_c}$$ (5.5)

The model equations 3.2 along with Equations 4.4 and 5.5, now express $n(t)$ as a function of parameters $f_c$ and $T_r$, and initial conditions $n_m$ and $t_h$. Note that the pandemic parameters $f_c$ and $T_r$ may in turn be expressed in terms of phenomenological parameters $f_e$ and $n_p$ and initial condition $n_m$ by:

$$f_c = \frac{f_e}{n_p - n_m}$$ (5.6)

$$T_r = (1/f_e) \ln \left( \frac{1-n_m}{1-n_p} \right)$$ (5.7)

6 Proof of solution

Supressing the time dependencies, and defining $n_p = n(t - T_r)$, the derivative of the logistic solution given in Eq. 3.2 is:

$$n' = f_c(n-n_m)(n_p-n)$$

The logistic solution will be a solution to the pandemic model if it can be shown that the above derivative is equal to the derivative given in the model equations 3.1, 4.4, and 5.5.
so that:

\[(n - n_m) (n_p - n) = (1 - n) (n - n_r)\]  \hspace{1cm} (6.8)

Define:

\[\epsilon = e^{-f_e (t-t_h)}\]

Solving Eq 3.2 for \(\epsilon\) yields

\[\epsilon = \frac{n_p - n}{n - n_m}\] \hspace{1cm} (6.9)

Define \(\epsilon_r = e^{f_e T_r}\). Using Equations 4.3 and 5.5 it follows that:

\[\epsilon_r = \frac{1 - n_m}{1 - n_p}\] \hspace{1cm} (6.10)

From Eq. 3.2 it follows that:

\[n(t - T_r) = n_r = n_m + \frac{n_p - n_m}{1 + \epsilon_r \epsilon}\] \hspace{1cm} (6.11)

With \(\epsilon\), \(\epsilon_r\), and \(n_r\) now expressed in terms of \(n\), \(n_p\) and \(n_m\) by equations 6.9, 6.10 and 6.11, simple substitution and algebraic manipulation will demonstrate that Eq. 6.8 is in fact true.

7 Bibliography

References

[1] Kermack, W. O.; McKendrick, A. G. (1927). "A Contribution to the Mathematical Theory of Epidemics". Proceedings of the Royal Society A. 115 (772): 700721. Bibcode:1927RSPSA.115..700K. doi:10.1098/rspa.1927.0118.
[2] Herbert W. Hethcote, "The Mathematics of Infectious Diseases", SIAM Review, Vol. 42, No. 4. (Dec., 2000), pp. 599-653. https://www.maths.usyd.edu.au/u/marym/populations/hethcote.pdf