EPIDEMIOLOGY: MATHEMATICAL MODELLING AND PUBLIC HEALTH

Abstract. In this report we aim to review the derivation and applications of the SIR model. In the first section we look at some relevant background information from the field of epidemiology. We then proceed to examine the assumptions necessary for the development of the model, and derive a system of three coupled non-linear ordinary differential equations from them. In the results section, we discuss some consequences of the model in the context of public health and present some examples of it in action. We also consider the practical aspects of this model and give some possible generalisations or alternatives to it.

1. Introduction

According to [1], epidemiology is the science that studies the patterns, causes, and effects of health and disease conditions in defined populations. Mathematical models can be used to predict the consequences of the presence of infectious diseases in the population. Applications include the prediction of the likely outcome of an epidemic and the effectiveness of a vaccination program. Epidemiologists use information about the disease and the population in which it is present to develop better means of control and prevention in order to obtain the best outcomes for public health.

The theory of disease was developed during the 1800s, due to the scientific experiments performed by van Leeuwenhoek (existence of micro-organisms), Henle (establishing a causative relationship between microbes and disease), Koch (rejecting the previous theory of spontaneous generation and suggesting four postulates relating micro-organisms and disease), and Pasteur (the concept of vaccination).

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With the discovery of the way in which infections are transmitted, it became possible to model this mechanism mathematically. According to [3], the first contributors to modern mathematical epidemiology were Enko in 1873 (using a discrete time model for measles epidemics), and R.A. Ross, W.H Hamer, A.G. McKendrick and W.O. Kermack, who laid the foundations of the idea of compartmental models in epidemiology in the early 20th century. Particularly notable was Ross' work on malaria: he demonstrated that mosquitoes transmitted malaria to humans, and suggested that malaria could be controlled by reducing mosquito populations, which led to huge advancements in the control and prevention of the disease.

The SIR (or Susceptible-Infectious-Removed) model, developed by McKendrick and Kermack in the early 1900s, used the idea of dividing the population into *compartments* that represent their health status. It was suggested to explain the patterns by which patient numbers varied during epidemics, for example, the bubonic plague (London 1665-1666 and Bombay 1906) and cholera (London in 1865).

Many other models for disease transmission have since been suggested, such as the SIS model (Susceptible-Infectious-Susceptible), MSIR model (SIR with an additional compartment for maternally derived immunity), SEIR model (SIR with an additional compartment for an *exposed* state - infected but not infectious), SIRS model and SEIS model (both with an additional Susceptible compartment).

2. The Mathematical Model

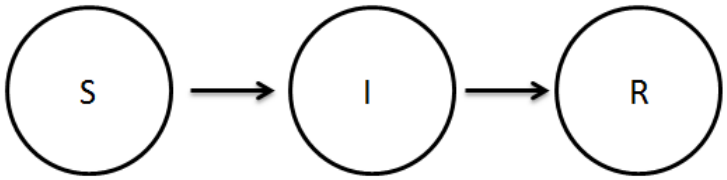
2.1. **Assumptions** The SIR model is a compartmental model that divides the population into three categories: Susceptible (have not yet been infected but not immune), Infectious (have been infected and are capable of transmitting the infection to others) and Removed (have already been infected but neither infectious nor infected presently and assumed to have lifelong immunity). It is assumed that upon becoming infected, the individual is immediately capable of infecting others (that is, there is zero latent period), and is infectious for the duration of their time in the Infectious category, although this is not true for all infectious diseases. For example, this assumption would be more reasonable when modelling an outbreak of the common cold (latent period of a couple of days) than an outbreak of chicken pox (latent period of a couple of weeks).

We assume that the population is large and closed (that is, it remains at a constant size). Although it is unrealistic, it is assumed that there are no births or deaths in the population, and that nobody arrives or leaves due to immigration.

Mass action mixing is assumed: that is, that the rate of encounters between susceptible and infected individuals is proportional to the product of the population sizes. We also assume that the members of the population in each compartment are distributed homogeneously in space (they do not mix more frequently in smaller groups) so that every individual is equally likely to contact any other individual in a certain time period. This is not a reasonable assumption as people are more likely to have contact with family members, friends, colleagues etc. than with strangers. Additionally, infected individuals are more likely to isolate themselves from the rest of the population (for example, staying home instead of going to work or school when sick) so they will contact fewer people. However, in this report we will retain the assumption of mass action mixing in order to simplify the mathematical model.

It is assumed that the disease transmission rate and recovery rate are constants. We assume that the age, social class, gender, etc. of individuals has no effect on the transmission of the disease, although this is not realistic.

2.2. **Derivation of the SIR Model** The movement between compartments is shown in this diagram:



We have the following word equation:

{**rate of change in susceptible population**} =

-{ **rate at which susceptible individuals are infected** }

This is due to the assumption of mass action mixing. If we denote the rate of transmission of the disease by β then this word equation implies the following mathematical equation:

$$\frac{dS}{dt} = -\beta SI$$

Now, considering the I compartment:

{**rate of change in infectious population**} =

{ **rate at which susceptible individuals are infected** } -

{ **rate at which infected individuals recover** }

Once again we have used mass action mixing. Let us denote the rate of recovery by γ. We obtain the mathematical equation

$$\frac{dI}{dt} = \beta SI - \gamma I$$

Finally, we consider the R compartment:

{**rate of change in removed population**} =

{ **rate at which infected individuals recover** }

Hence, the mathematical equation:

$$\frac{dR}{dt} = \gamma I$$

Combining the three equations gives the SIR model:

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Note that since $S + I + R = n$, the population size, it is not necessary to use all three equations, since any one can be derived from the other two. (The change in population $\frac{dn}{dt} = 0$ as we assumed that the population size remains constant, so, for example, $\frac{dR}{dt} = \frac{dn}{dt} - \frac{dS}{dt} - \frac{dI}{dt} = 0 + \beta SI - \beta SI + \gamma I = \gamma I$ as above).

3. Results and Discussion

3.1. **Theorems** Although we do not have an exact solution for this system of differential equations, it is possible to determine some information about the behaviour of the three compartments. In the theorems below, we follow the ideas presented in [2].

Theorem 1. *Long term limits exist, that is,* $S(\infty), R(\infty), I(\infty) < \infty$.

Proof. We have $\frac{dS}{dt} \leq 0$ since $S, I, \beta \geq 0$. Now, $0 \leq S(t) \leq S(0) \leq n$ so $S(\infty) = \lim_{t\to\infty}$ exists.

Similarly, $\frac{dR}{dt} \geq 0$ as $\gamma, I \geq 0$. We have $0 \leq R(0) \leq R(t) \leq n$ and so $R(\infty) = \lim_{t\to\infty}$ exists.

Finally, $I(\infty) = \lim_{t\to\infty} = n - S(\infty) - R(\infty)$ exists. □

Theorem 2. *The epidemic always ends:* $I(\infty) = 0$.

This is saying that in the long term, the disease always dies out, regardless of the initial conditions.

Proof. Suppose, by way of obtaining a contradiction, that $I(\infty) \neq 0$. This implies that for sufficiently large t, we have $\frac{dR}{dt} > \frac{1}{2}\gamma I(\infty) > 0$, so $R(\infty) = \infty$, contradicting the previous theorem. □

One of the most important results involving the SIR model is the Epidemic Threshold Theorem, which dictates whether an infectious disease will cause an epidemic or not. Suppose that each individual in the Infectious compartment has k contacts per unit time, a number which is independent of the population size n. The proportion $\frac{kS}{n}$ of them are going to be in the Susceptible compartment. Let τ be the transmissibility of the infectious disease (the proportion of susceptible contacts who will become infected). Then $\frac{k\tau S}{n}$ of the susceptible individuals contacted by the infectious individual will themselves become infectious. We therefore have $\beta = \frac{b}{n}$, where $b = k\tau$.

Now, define the effective reproductive number $R_e = \frac{S(0)}{n}\frac{b}{\gamma}$. The following theorem shows that R_e is the threshold value that determines whether an outbreak of an infectious disease will result in an epidemic.

Theorem 3. *If $R_e \leq 1$ then $I(t)$ decreases monotonically to 0 as $t \to \infty$. If $R_e > 1$ then $I(t)$ increases, reaches a maximum and then decreases to 0 as $t \to \infty$.*

In the first case, the disease quickly dies out, having only infected a small number of people. In the second case, there is an epidemic.

Proof. We have $\frac{dI}{dt} = (\beta S - \gamma)I \leq (\beta S(0) - \gamma)I = \gamma(R_e - 1)I \leq 0$ for $R_e \leq 1$. Since $I(\infty) = 0$, we know $I(t)$ decreases monotonically to 0 as $t \to \infty$.

When $R_e > 1$, we have $\frac{dI}{dt}(0) = \gamma(R_e - 1)I(0) > 0$. So I is increasing at 0. Also, $I(t)$ has exactly one non-zero critical point, which must be a maximum. Since $I(\infty) = 0$, I must behave as described in the second case. □

Theorem 4. *The maximum number of infected individuals, I_{max}, is given by $I(0) + S(0) - \frac{\gamma}{\beta} log(S(0)) - \frac{\gamma}{\beta} + \frac{\gamma}{\beta} log(\frac{\gamma}{\beta})$.*

Proof. We have

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

Dividing the first equation by the second gives the ODE

$$\frac{dS}{dI} = \frac{-\beta SI}{\beta SI - \gamma I}$$

This is separable:

$$\frac{\beta S - \gamma}{\beta S} dS = -dI$$

So

$$-I - S + \frac{\gamma}{\beta} log(S(t)) = I(0) + S(0) - \frac{\gamma}{\beta} log(S(0))$$

I_{max} occurs when $\frac{dI}{dt}$, that is, when $S = \frac{\gamma}{\beta}$. Using the above equation, we obtain

$I_{max} + \frac{\gamma}{\beta} - \frac{\gamma}{\beta} log(\frac{\gamma}{\beta}) = I(0) + S(0) - \frac{\gamma}{\beta} log(S(0))$, which, after rearranging, gives the required value for I_{max}. □

Theorem 5. *The limiting number of susceptible individuals satisfies*

$$S(\infty) \geq S(0)e^{-\frac{b}{\gamma}} > 0$$

Proof. We have

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dR}{dt} = \gamma I$$

Dividing the first equation by the second gives

$$\frac{dS}{dR} = \frac{-\beta IS}{\gamma I} = \frac{-\beta S}{\gamma}$$

This is a separable ODE:

$$\frac{1}{S} dS = \frac{-\beta}{\gamma} dR$$

So

$$S(t) = S(0)e^{-\beta(R(t)-R(0))/\gamma}$$

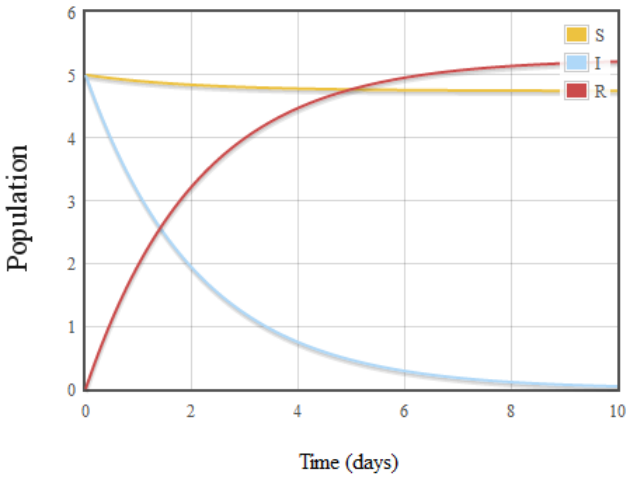
Since $0 \leq R(t) - R(0) \leq n$, we have $S(t) \geq S(0)e^{\frac{\beta n}{\gamma}}$, giving the required result.

□

3.2. **Examples** The following example demonstrates the outcomes of an outbreak of an infectious disease for R_e values above and below 1.

Consider a population of $n = 10$ individuals, 5 of which are infected with a certain disease. Using the program in [4], we graph the sizes of the three compartments over time.

When $\beta = 0.05, \gamma = 0.5$, we have $R_e = 0.5$.

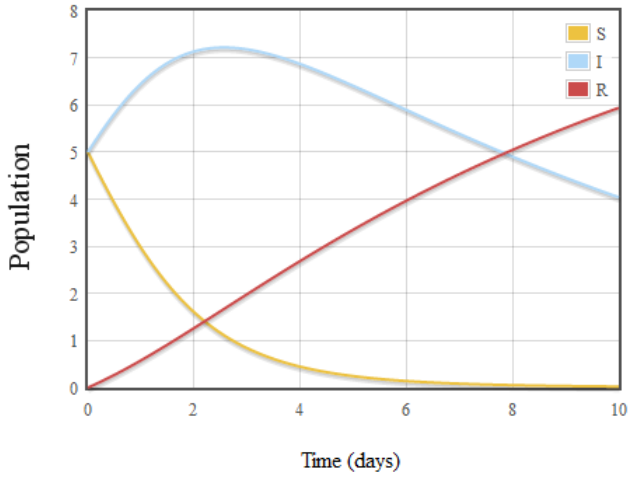


This is as expected - since $R_e < 1$, we predict that the disease would die out. This makes sense - β, the rate of transmission, is very low, and γ, the rate of recovery, is quite high, so few people would catch the disease, and when they did, they would recover fairly easily.

When $\beta = 0.9, \gamma = 0.1$, we have $R_e = 45$.

This is also as expected - since $R_e > 1$, there is an epidemic. The number of infected individuals increases to a maximum then slowly decreases to 0. This makes sense since the rate of transmission, β, is very high, while the rate of recovery, γ, is fairly low. So intuitively, many people would be infected, and it would be difficult for them to recover.

Vaccination is means of controlling the outbreak of disease by removing individuals from the susceptible class without being infected. The phenomenon of herd immunity means that it is possible to prevent an epidemic while only vaccinating a fraction of those who are susceptible.



To prevent an epidemic occurring, it is required that $R_e \leq 1$. Let p be the proportion of susceptible individuals who are vaccinated (assuming the vaccination is 100% effective). So the initial size of the susceptible class is now $(1-p)S(0)$. To prevent an epidemic, we need $(1-p)S(0)\frac{\beta}{\gamma} \leq 1$. This occurs when $p \geq 1 - \frac{1}{R_e}$.

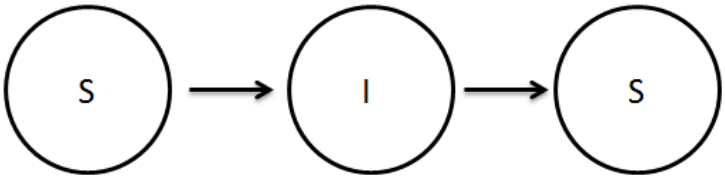
For example: if $R_e = 2$ for some disease, then half of the susceptible population needs to be vaccinated to prevent an epidemic. However, if $R_e = 4$ then 75% of the susceptible population needs to be vaccinated.

3.3. **Practicality and Improvements** Although the SIR model is a useful tool for predicting the severity of an outbreak of infectious disease, it is not entirely realistic as it was based on many assumptions that are generally not true. For example, it was assumed that the latent period of the infectious disease was zero, whereas most diseases have some latent period. Hence, it is more practical to use this model with diseases with a short latent period (such as influenza) than diseases with a longer latent period.

Additionally, as discussed earlier, mass action mixing is not a realistic assumption, since particular individuals encounter each other more frequently, and different people have different numbers of contacts per time period.

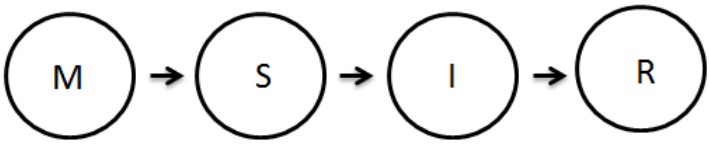
It is reasonable to assume constant population size for a short-lived outbreak such as influenza, but for longer outbreaks, it may be desirable to include births and deaths in the model.

There are many models similar to the SIR model. The most appropriate model to use depends on the infectious disease which is being investigated. One example is the SIS model:



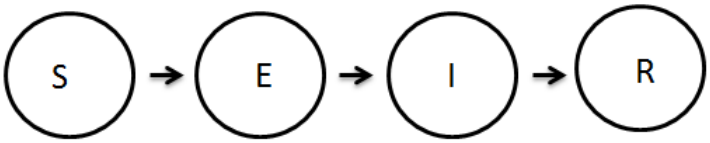
In this model, it is not assumed that immunity to the disease is conferred upon recovery, hence, upon recovery, individuals are once again susceptible.

Some improvements upon the SIR model involve the use of additional compartments. An example is the MSIR model based on the following compartmental diagram:



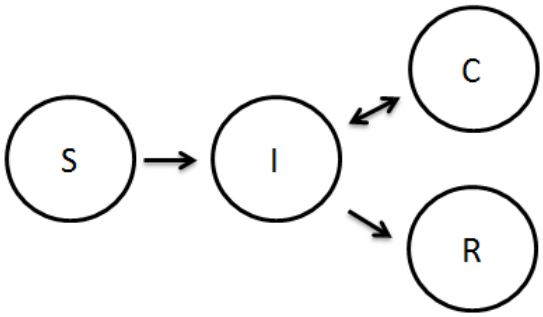
Here, M stands for *maternally derived immunity*. In this model, babies are not susceptible for some period after birth due to the presence of maternal antibodies.

In order to alleviate the scientific inaccuracy present due to the assumption of zero latent period, epidemiologists may use the SEIR model in the following diagram:



E stands for *exposed*. Individuals in this compartment have been infected but are not yet infectious.

Another model involves a *carrier* (C) state, in which an individual is not completely recovered and may still be infectious. Although carriers do not suffer symptoms of the disease, they could still move back into the infectious compartment:



4. Conclusion

The SIR model, despite being based on some assumptions that are not realistic, is still a reasonably good model of a short-lived outbreak of infectious disease in a large population.

References

[1] Wikipedia, (2015): *Epidemiology*, viewed 9/25/15, https://en.wikipedia.org/wiki/Epidemiology

[2] Howard Weiss., 2013 *The SIR Model and the Foundations of Public Health.* Publicaci electrnica de divulgaci del Departament de Matemtiques de la Universitat Autnoma de Barcelona.

[3] Brauer, F., Castillo-Chavez, C., 2001, *Mathematical Models in Population Biology and Epidemiology*, Springer Science Business Media.

[4] Hans Nesse. *Global Health - SIR Model (with vaccine)*, viewed 9/25/15, http://www.public.asu.edu/ hnesse/classes/sirv.html