The SIR Model: An analysis and use case of the SIR model

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Abstract

In this report, we analyse and evaluate the SIR model, its properties and dynamics.

Introduction

In epidemiology, a very useful model that has been the building block of most other epidemiological models is the *SIR* model [3]. This model and the ones that are based on the SIR model, can be used to increase understanding of the manifestation and especially the spreading of infectious diseases. Getting a better understanding of infectious diseases and how they spread can help to improve control or maybe even eliminate the spreading of an infectious disease [2]. In the SIR model, we assume that individuals in a population are either Susceptible, Infectious or Recovered . This report will analyze different types of SIR models. Firstly, we will look into the SIR model with a closed population without any demography (birth/death rate). Then we will evaluate the SIR model with demography and see how the dynamics change compared to the model without demography.

The SIR model without demography

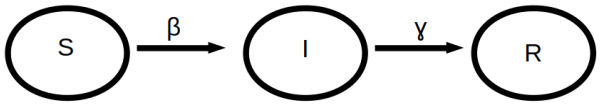
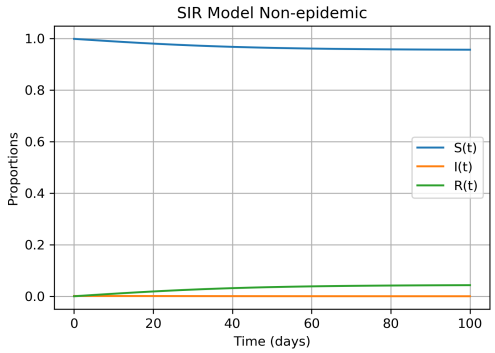


Figure 1: SIR model

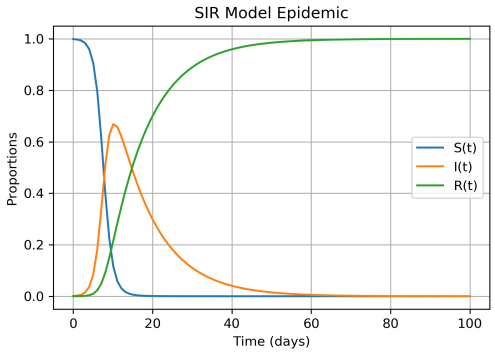
The SIR model starts within these three groups in a closed population as we can see in figure 1. At every timestep t, based on the rate of transmission β and the rate of recovery γ, the dynamics of these groups change. Since this is a simple model, we assume this is a closed population, because we are looking into the infection on the short term (100 days). The model results in the following equations.

$$\frac{dS}{dt} = -\beta SI \qquad (1) \qquad \frac{dI}{dt} = \beta SI - \gamma I \qquad (2) \qquad \frac{dR}{dt} = \gamma I \qquad (3)$$

From these equations, we can deduce what situations lead to an epidemic and what situations do not. For an infection to become an epidemic the growth of the infected group has to be larger than zero ($\frac{dI}{dt} > 0$). If we integrate the equation for $\frac{dI}{dt}$ we find that $I(t+i) = I(t) + (t+i)(\beta S(t)I(t) - \gamma I(t))$. I increases by the rate $\frac{dI}{dt}$. $\frac{dI}{dt} > 0$ holds when $I > 0$ or $S > \frac{\gamma}{\beta}$. We call $\frac{\gamma}{\beta}$ the relative removal rate. The inverse of the relative removal rate is called the basic reproductive ratio R_0: the average number of secondary cases arising from an average primary case in an entirely susceptible population [2]. $R_0 = 1$ means that every person that gets infected infects, on average, another person. We can use this parameter to find when an infection will cause an epidemic breakout or when it will cause the infection to die out. If we look at Figure 2, we can see that for an R_0 of 1. the spreading of the disease will stagnate and for an R_0 of 10 the disease will cause an epidemic.



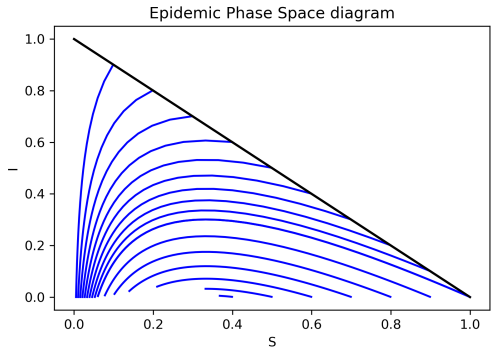
(a) The time-evolution for a non-epidemic state. Here $\beta = 1$ and $\gamma = 1$, thus $R_0 = 1$



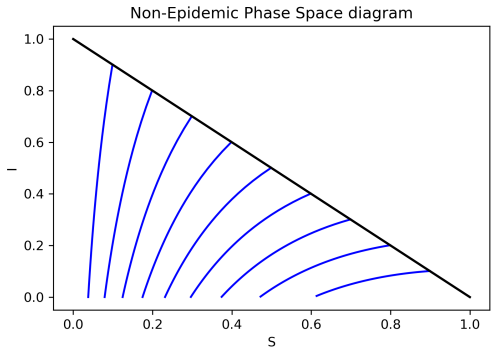
(b) The time-evolution for an epidemic state. Here $\beta = 1$ and $\gamma = \frac{1}{10}$, thus $R_0 = 10$

Figure 2: SIR models for states of a non-epidemic (a) and an epidemic (b)

There will be an epidemic when the reproductive rate exceeds 1. This is when $\frac{\beta}{\gamma} > 1$, and hence the number of infected people will increase more than the number of recovered people. Now it would be interesting to see where the infection peaks, how many susceptible individuals we would have at this peak and how the number of initial susceptibles or infected influence the dynamics of the infection. For this, we can take a look at the phase space diagram, where we plot the number of Infected (I) versus the number of Susceptibles (S) from initial state to end state for $R_0 > 1$ and $R_0 \leq 1$.



(a) Phase Space Diagram for an epidemic breakout. An epidemic breakout occurs when $R_0 > 1$ ($\beta = 3$, $\gamma = 1$)



(b) Phase Space Diagram for a non-epidemic state. An infectious disease will not breakout when $R_0 \leq 1$ ($\beta = 1$, $\gamma = 1$)

Figure 3: Phase Space diagrams for states of an epidemic (a) and a non-epidemic (b) state

For the epidemic ($R_0 > 1$) in Figure 3a, we can see that the number of infectious individuals starts to decline when the number of susceptibles is around 0.3. Note that the number of Susceptibles (S) influences the growth or decline of the number of Infectious (I) because $\beta S < \gamma$, because the number of susceptibles becomes smallerover time. For the non-epidemic ($R_0 \leq 1$) in Figure 3b we see that the number of infectious individuals dies out quite fast.

Let's look at a use case based on some historical data from an English Boarding School where there was an influenza outbreak [1].

Day	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Number	3	8	28	75	221	291	255	235	190	125	70	28	12	5

Table 1: The number of infectious individuals per day on an English boarding school [1].

Now we can fit a model to the initial state ($S = 762, I = 1, R = 0$) by using a simple least squares method. In Figure 4 we can find that for $\beta = 0.0204$ and $\gamma = 0.418$, we get an approximation of the historical data curve.

Preventing an epidemic could be done in two ways: (1) Reducing the number of susceptibles (S) and/or (2) reducing the transmission rate (β), because to make $\frac{dI}{dt} < 0$ we have to make $\beta S < \gamma$. Now the transmission rate can be reduced by, in the case of the school, to motivating students to wash their hands. If that does not help, the number of susceptibles can also be decreased by immunization. If these two factors get reduced enough in such manner that $\beta S < \gamma$, and epidemic could be prevented.

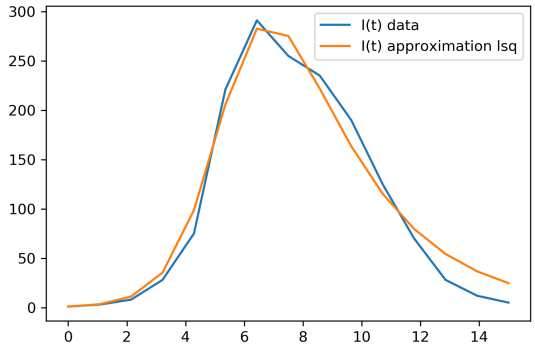


Figure 4: The time-evolution of the real historical data plotted with our least squares approximation

The SIR model with demography

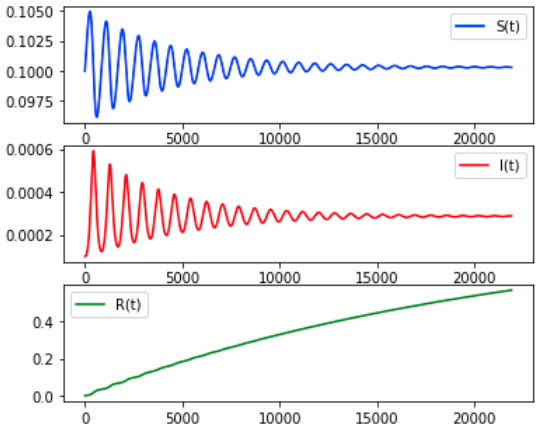
The earlier model without demography did not take into account the birth and death rate of individuals. To explore an infectious disease in the long-term and the endemic dynamics of the disease. In order to do this, we at the term μ, which stands for the rate at which individuals suffer a natural mortality [2]. This influences the dynamics of all three groups since dying a natural death or a baby being born would in all three cases S, I and R leads to a different group size.

$$\frac{dS}{dt} = \mu - \beta SI - \mu S \tag{4}$$

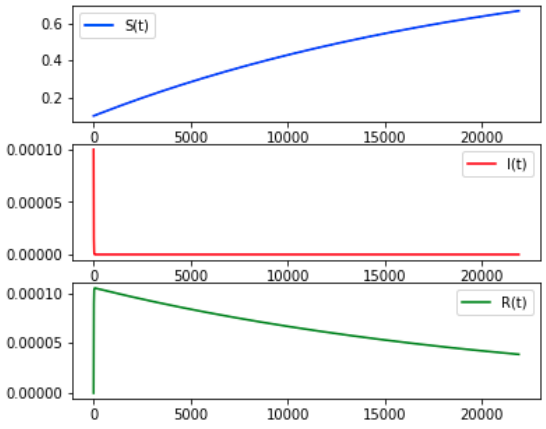
$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I \tag{5}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{6}$$

Note that in this model, the population remains constant since $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$. The time that is spent infectious is $\frac{1}{\gamma+\mu}$. This means that the average number of new infections per infected individual $R_0 = \frac{\beta}{\gamma+\mu}$. The endemic state will only occur if $\frac{\beta}{\gamma+\mu} > 1$. If we apply $R_0 > 1$ and $R_0 \leq 1$ we observe that when $R_0 \leq 1$ we reach a disease-free state, as we see in Figure 5b and 6b, the infection dies out almost immediately. In the endemic state, we observe oscillatory behavior as shown in Figure **??**. The system wil eventually equilibriate over time.

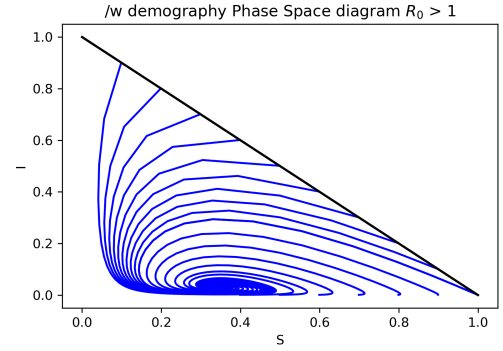


(a) Time-evolution graph for an endemic state. An endemic state will occur when $R_0 > 1$ ($\beta = 520$ per year, $\gamma = \frac{1}{7}$) In the top graph is the amount of susceptible individuals, in the middle the infectious, and the bottom graph shows the recovered individuals. The x-axis displays the time in days.

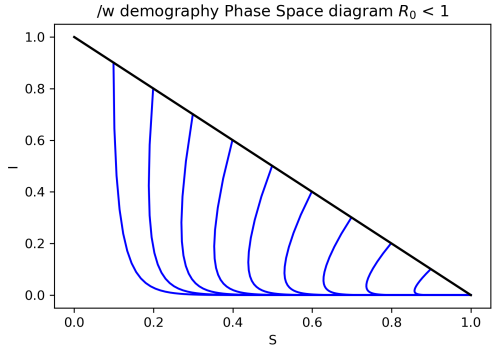


(b) Time-evolution graph for a disease-free state. An infectious disease will die out when $R_0 \leq 1$ ($\beta = 0.0715$, $\gamma = \frac{1}{3}$ and $\frac{1}{\mu} = 60$) In the top graph is the amount of susceptible individuals, in the middle the infectious, and the bottom graph shows the recovered individuals. The x-axis displays the time in days.

Figure 5: Time-evolution diagrams for states of an epidemic (a) and a non-epidemic (b) state



(a) Phase Space Diagram for an endemic state. An endemic state will occur when $R_0 > 1$ ($\beta = 1$, $\gamma = \frac{1}{3}$)



(b) Phase Space Diagram for a disease-free state. An infectious disease will die out when $R_0 \leq 1$ ($\beta = \frac{1}{6}$, $\gamma = \frac{1}{3}$)

Figure 6: Phase Space diagrams for states of an epidemic (a) and a non-epidemic (b) state

References

[1] Anon. "Influenza in a boarding school". In: *British Medical Journal* 1:587 ().

[2] Matt J Keeling and Pejman Rohani. *Modeling infectious diseases in humans and animals*. Princeton University Press, 2011.

[3] William Ogilvy Kermack and Anderson G McKendrick. “A contribution to the mathematical theory of epidemics”. In: *Proceedings of the royal society of london. Series A, Containing papers of a mathematical and physical character* 115.772 (1927), pp. 700–721.