# Modeling epidemics with differential equations

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Abstract. The well known SIR models have been around for many years. Under some suitable assumptions, the models provide information about when does the epidemic occur and when it doesn't. The models can incorporate the birth, death, and immunization and analyze the outcome mathematically. In this project we studied several SIR models including birth, death and immunization. We also studied the bifurcation analysis associated with the disease free and epidemic equilibrium.

## 1. Introduction

Based on some mathematical assumptions, it is known that epidemics can be modeled mathematically in order to study the severity and prevention mechanism. This model (SIR) is used in epidemiology to compute the number of susceptible, infected, and recovered people in a population at any time. It can be used to explain the change in the number of people needing medical attention during an epidemic. The whole population is divided into three classes, $S$, the number of susceptible, $I$, the number of infected and $R$, the number of recovered during an epidemic. This model assumes that the total population remains the same with closed demography meaning that there is no birth and no natural death. Any disease related death, however, can be included in $R$. We study the basic SIR model with some reasonable assumptions. Then we include herd immunity, birth and death into the model. The constant vaccination at birth is also considered . The ultimate goal is to model the issue of saturated susceptible population, the time delay of infected to become infectious, the stability of equilibrium solutions and associated bifurcation.

**Definition 1.** *Susceptible individuals are individuals that have never been infected and they are able to catch the disease. Once they have it, moving into the infected compartment. Infected individuals can spread the disease to susceptible individuals. Recovered individuals in the recovered compartment are assumed to be immune for life.*

Let $S(t)$ be the number of susceptible individuals $I(t)$ be the number of infected individuals and let $R(t)$ be the number of recovered individuals at time $t$ respectively. It is also assumed that $S + I + R = N$. Also we normalize this sum by dividing each of the variables by $N$. We still denote the new variables by the same letters $S, I$ and $R$.

## 2. The SIR Models

SIR models have been around for many years, for example [3, 5, 4, 2, 6] and the references there in. The first one was introduced and published in 1927, in "Contribution to the Mathematical Theory of Epidemics", written by William Kermack and Anderson McKendrick. They introduced the important compartments, which make up the SIR model, S- susceptible, I - infected and R - recovered. They searched for a mathematical answer as to when the epidemic would terminate and observed that, in general whenever the population of susceptible individuals falls below a threshold value, which depends on several parameters, the epidemic terminates.

### 2.1. **The Basis Model.**

The population is fixed so $S + I + R = 1$. The disease spreads through the interaction of susceptible and infected. We assume that only a fraction of this interaction causes the disease to pass from an individual ( $I$) to a susceptible individual ($S$.) So the rate of change of $S$ is proportional to the product of $S$ and $I$. We assume that the individuals recover at a rate of $\beta$ so the period of infection is $\frac{1}{\beta}$ days. The only way a person can leave the susceptible group is to become infected. The only way a person can leave the infected group is to become recovered. Once a person is recovered, the person is no longer susceptible and is immune. Age, sex, race and social status do not affect the probability of a person being affected. There is no inherited immunity at this time. The people of the population mix homogeneously. Based on the above assumptions the differential

equations governing the disease can be modeled as

$$\begin{aligned} \frac{dS}{dt} &= -\alpha SI \\ \frac{dI}{dt} &= \alpha SI - \beta I \\ \frac{dR}{dt} &= \beta I \end{aligned} \tag{1}$$

**Remark.** Since the total population is assumed to be constant, the third equation can be derived from the first two. Basically we study the first two in detail.

It turns out that the epidemic occurs if $\frac{dI}{dt} > 0$, it doesn't if $\frac{dI}{dt} < 0$. So for the epidemic to occur we have to have $\alpha S > \beta$ implying $S > \frac{\beta}{\alpha}$. For the epidemic to terminate the rate of change of $I$ has to be negative, this implies that

$$S < \frac{\beta}{\alpha}.$$

The phase portrait Figure 1 shows this too.

FIGURE 1. The Phase Portrait of SIR model

**Definition 2** (Basic Reproductive Number)**.** *The basic reproductive number $R_0$(the average number of persons infected by one case in a totally susceptible population in absence of interventions aimed at controlling the infection). Since $S = 1$ initially, the ratio $\frac{\alpha S}{\beta} = \frac{\alpha}{\beta} = R_0$.*

This is one of the most important parameters in the SIR modeling of any epidemic. $R_0$ is especially important in this case as it will inform one as to when an epidemic is in progress. So if $R_0 > 1$ an epidemic will occur and if $R_0 < 1$ there will be no epidemic. The values of $R_0$ are known for various diseases. For example for Swine flu, it is reported to be $1.3 - 1.6$ in [1]

The first two equations can be solved for $I$ and $S$ as in [3] The variation of $I$ versus $S$ can be seen from the figure provided Figure 2.

The solutions of $I$ vs. $S$ can be written as, [3].

$$I(S) = -S + \frac{1}{R_0} \ln S + 1. \tag{2}$$

The graphs of this equation 2.6 are shown for different values of $R_0$. The system of equations can be solved for several values of the parameters.

FIGURE 2. The graphs of $I$ vs. $S$, for different values of $R_0$

The typical solutions of the above equations are shown in Figure3, using Matlab.

FIGURE 3. The general solutions over time

2.2. **Herd Immunity.** For this portion of the model we use $p$ to be the proportion of susceptible population that is immunized before the outbreak of an epidemic and assume the above mentioned conditions, new equations governing the disease can be written as.

$$\begin{aligned} S' &= \alpha(1-p)SI \\ I' &= \alpha(1-p)SI - \beta I \end{aligned} \tag{3}$$

An outbreak of the epidemic mathematically means that

$$\begin{aligned} I' > 0 &\Rightarrow \alpha(1-p)SI - \beta I > 0 \\ &\Rightarrow \alpha(1-p)S > \beta \\ &\Rightarrow (\alpha/\beta)(1-p)S > 1 \\ &\Rightarrow R_0 > \frac{1}{1-p} \end{aligned}$$

*Note.* The value of $R_0$ is apprx. 1.6 for Swine flu [1]. The above inequalities says that at least 38% need to be immunized in order to contain the disease.

2.3. **SIR with birth and death.** As a modification to the SIR model we introduce birth and death. We assume that all death is natural. The variable $m$ is used to represent a constant rate of birth and death. The basic reproduction number is now given by $R_0 = \frac{\alpha}{\beta+m}$.The new equations with the consideration of birth and death are:

FIGURE 4. The possible solution curves for a particular disease

$$\frac{dS}{dt} = m - \alpha I - mS \tag{4}$$

$$\frac{dI}{dt} = \alpha IS - (m + \beta)I$$

The system of equations have two equilibrium solutions.
The **disease free equilibrium**,

$$(S_1, I_1) = (1, 0)$$

and the **epidemic equilibrium,**

$$(S_2, I_2) = \left(\frac{\beta + m}{\alpha}, \frac{m}{\alpha}(R_0 - 1)\right).$$

The eigenvalues of the Jacobian matrix reveal the stability of these equilibrium solutions. The Jacobian matrices are computed as

$$J|_{(S_1,I_1)} = \begin{pmatrix} -m & -\alpha \\ 0 & \alpha - \beta - m \end{pmatrix}$$

$$J|_{(S_2,I_2)} = \begin{pmatrix} -m - (R_0 - 1)m & \frac{-\alpha}{R_0} \\ (R_0 - 1)m & 0 \end{pmatrix}$$

The eigenvalues of $J|_{(S_1,I_1)}$ are $-m$ and $\alpha - \beta - m$. They are both negative if $\alpha - \beta - m < 0 \Rightarrow R_0 < 1$. In this case the eigenvalues of the Jacobian $J|_{(S_2,I_2)}$ are both negative. So the disease free equilibrium is locally stable and the epidemic equilibrium is unstable. Likewise if $R_0 > 1$, the eigenvalues of $J|_{(S_1,I_1)}$ are of opposite sign and that of $J|_{(S_2,I_2)}$ are both negative. So the epidemic equilibrium is locally stable and the disease free equilibrium is unstable. Authors [4] have mentioned that these locally stable equilibrium are global as well. The value of $R_0 = 1$, thus provides the **bifurcation point** for the system.

2.4. **Constant Vaccination at Birth.** For this particular model we introduce certain assumptions that involve a constant vaccination for the newly born, which will enter our population. A proportion $p$ of the new born population has the constant vaccination, while others will enter the population susceptible to infection. We still assume that the population is constant.

$$\frac{dS}{dt} = (1 - p)m - (\alpha I + m)s$$

The number of infected is still represented as:

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

It has two equilibrium solutions. The **disease free equilibrium**,

$$(S_1, I_1) = (1-p, 0),$$

and the **epidemic equilibrium**,

$$(S_2, I_2) = \left( \frac{\beta + m}{\alpha}, \ \frac{mR_0(1-p) - m}{\alpha} \right).$$

The Jacobian at these equilibrium solutions are computed to be

$$J|_{(S_1,I_1)} = \begin{pmatrix} -m & -\alpha(1-p) \\ 0 & -\beta - m + \alpha(1-p) \end{pmatrix}$$

$$J|_{(S_2,I_2)} = \begin{pmatrix} -R_0 m(1-p) - 2m & -\beta - m \\ R_0 m(1-p) - m & 0. \end{pmatrix}$$

It can be seen from the eigenvalues of these matrices that if $R_0(1-p) < 1$, the disease free equilibrium is stable while the epidemic equilibrium is unstable. If $R_0(1-p) > 1$, then the disease free equilibrium is unstable and the epidemic equilibrium is stable. It follows that when $R_0(1-p) = 1$, the bifurcation occurs. This value of $p$ as in [1] is called a **critical vaccination**. So the critical vaccination, denoted by $p_c$, as in [1], is given by $p_c = 1 - \frac{1}{R_0}$

*Example.* The value of $R_0$ for Measles is known to be $16 - 18$. So the critical vaccination for this epidemic turns out to be 94.4%. If the new born are vaccinated at a rate higher than 94.5%, then the population will move towards the disease free equilibrium.

2.5. **Saturated Susceptible population.** In the case that the birth and death rate are not constant. There are specific assumptions that must be taken into account. These assumptions are that susceptible individuals, $S(t)$, are born at a rate $M(S, I, R)$, which is a function of the densities of the susceptible, infected, and recovered hosts. Susceptibles are infected at a given rate given by the product of the densities of susceptible and infected hosts.

$$\frac{dS}{dt} = RS - \frac{RS^2}{K} - \alpha SI$$

The number of infected is still represented as:

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

When both host types are well mixed and encounters are random, it is known as mass action kinetics derived from chemical kinetics. Infected hosts recover at a rate $\beta$. Susceptible and recovered host die at a rate $m$, which describes the natural death rate due to causes unrelated to the infection. Infected host die at a rate $m$, which includes both natural death and disease induced death. It has two equilibrium solutions. The **disease free equilibrium**,

$$E_0 = (N, 0) = (1, 0)$$
$$\left(\frac{m+\beta}{\alpha}\right)$$

and the **epidemic equilibrium**,

$$E_1 = (S^*, I^*)$$
$$(mS^* + \beta)(R_0 - 1)$$

where $R_0 = \frac{\alpha}{m+\beta}$,is the reproduction number which denotes the number of individuals infected by a single infected individual placed in a totally susceptible population. The Jacobian at these equilibrium solutions are computed to be

$$J|_{(S_1,I_1),(0,0)} = \begin{pmatrix} r & 0 \\ 0 & -\beta - m \end{pmatrix}$$

$$J|_{(S_2,I_2),(K,0)} = \begin{pmatrix} -r & -\alpha K - m \\ 0 & -\beta + \alpha K - m. \end{pmatrix}$$

where $R_0 = \frac{\alpha}{m+\beta}$,is the reproduction number which denotes the number of individuals infected by a single infected individual placed in a totally susceptible population.

2.6. **Delay.** The delay SIR Epidemic Model makes the assumption that the people in the susceptible group are infectious and carry the disease but only after a certain period of time are they infected.

$$S'(t) = RS(t)(1 - \frac{S(t)}{K} - \frac{\beta S(t)I(t-T)}{1+\sigma S(t)} = 1.$$

$$I'(t) = \frac{\beta S(t) I(t-T)}{1+\sigma S(t)} - \alpha I(t) - \alpha I(t) = 0.$$

For this project the two equilibrium solutions have been set to 0 and 1 to see if there is an epidemic or a disease free occurence. We are able to disipher between the two by finding the infection free equilibrium $E_0 = (0,0), E_1 = (k,0)$.

$$E_+ = (S^*, I^*) = (\frac{\alpha+\alpha}{\beta-\sigma(\alpha+\alpha)}, \frac{rS^{*2}}{k(\alpha+\alpha)}(R_0-1)$$

In conclusion, we see that over a certain period the population is susceptible and infectious, but not everyone is infected at one specific time period. It takes a cetain period of time for infection to circulate throughout a population.

## 3. Conclusion

In conclusion, we reviewed, analyzed, and discussed the continuous SIR epidemic model. Various parameters were discussed such as the act of the SIR model incorporating birth and death, herd immunity, constant vaccination, critical vaccination, saturation, long-term, as well as delay. It was concluded that the model relies on critical values such as $\alpha$, being our transmission rate, $\beta$, being recovery rate, $R_0$, our basic reproduction number, determining epidemic status in population, p(portion of population vaccinated), k(capacity of population), m(birth and death rate), $\sigma$(saturation rate), and r(growth rate). The model relies on these vital parameters because they all play a part in determining epidemic status in population, in other words, whether or not there will be an epidemic in a society and therefore, determining the precaution measures to be made. The SIR model has proven to be a reliable mathematical tool for examining epidemiology in a population.

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