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# Suspectable - Infected - Recovered (SIR) MODEL

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**Computational Dynamics 2023**

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June 24, 2023

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## 1 Abstract

In the realm of epidemic modeling, the Susceptible-Infected-Recovered (SIR) model stands as a prominent framework for understanding the spread and progression of infectious diseases within a population. Since its inception, the SIR model has played a crucial role in predicting and controlling outbreaks, guiding public health interventions, and informing policy decisions. This paper aims to provide a comprehensive overview of the SIR model, its historical background, and its significant contributions to epidemiology. Furthermore, I'll find exact solutions to the model, obtain numerical solutions, using a range of numerical methods, and try to interpret the findings.

## 2 Introduction

The SIR model traces its roots back to the pioneering work of Kermack and McKendrick in the early 20th century. In their seminal paper published in 1927, Kermack and McKendrick introduced a set of differential equations that quantified the dynamics of infectious diseases, giving birth to what is now known as the SIR model.

Since its inception, the SIR model has undergone extensive refinement and enhancement, fueling its widespread adoption across diverse domains. The model has been extensively applied to study and combat several high-profile outbreaks, including the Spanish flu, polio, measles, HIV/AIDS, and, most recently, the ongoing COVID-19 pandemic. Its versatility and adaptability have allowed researchers to gain critical insights into disease transmission, estimate key epidemiological parameters, assess the impact of various control strategies, and predict the course of epidemics under different scenarios.

### 3 The SIR model

#### 3.1 Variables, and constants

Firstly I'll present and explain the variables.

$S(t)$  - number of Susceptible individuals at time  $t$   
 $I(t)$  - number of Infected individuals at time  $t$   
 $R(t)$  - number of Recovered individuals at time  $t$

At time 0 we will have a specific  $S_0$  - the number of individuals susceptible to be infected at time 0 and  $I_0$  - the number of individuals infected by the disease at time 0 .

If we have a set population size  $N$  then at any time  $t$  we will obviously have

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

$N$  is set. Due to simplicity, I am ignoring births, deaths, migration, which obviously occur in nature. More complex variations of the SIR model take into consideration these parameters.

In the following Equation I am using some constants, which I'll now explain.

- $r$  is the infection rate, which denotes the average amount of people an individual has contact with in one day. Not all these contacts are with susceptible individuals. If we assume a homogeneous mixing of the population, the fraction of these contacts that are with susceptibles is  $S(t)/N$ . Thus, on average, each infected individual generates  $r * S(t)/N$  new infected individuals per day.
- $\gamma$  is the recovery rate. For example, if the average duration of infection is four days, then, on average, one-fourth of the currently infected population recovers each day.

#### 3.2 The Equations

With the abovementioned notation I'll now present the SIR model equations.

$$\begin{aligned} S'(t) &= \frac{-r * S(t) * I(t)}{N} \\ I'(t) &= \frac{r * S(t) * I(t)}{N} - \gamma * I(t) \\ R'(t) &= \gamma * I(t) \end{aligned}$$

- **The Susceptible Equation.** How many people are susceptible at a given time  $t$ ? As mentioned, when introducing the  $r$  constant, each infected individual generates on average  $r * S(t)/N$  new infected individuals per day. Hence, in order to obtain the number suspected number of infected individuals, we need to multiply that by  $I(t)$ .

- **The Recovered Equation.** Assuming we have a fixed recovery rate  $r$ , its fairly easy to see that the rate of change in the recovered part of of the population is dependant on  $\gamma$  and  $I(t)$ .
- **The Infectuous Equation.** Upon reflection it is easy to notice that  $S'(t) + I'(t) + R'(t) = 0$ . And so it follows that  $I'(t) = -S'(t) - R'(t)$ .

### 3.3 Solutions

Lets start of with the Infected equation. To do that, I'll begin with dividing (2)/(1).

$$\frac{\frac{dI}{dt}}{\frac{dS}{dt}} = \frac{\frac{rSI}{N} - \gamma I}{\frac{-rSI}{N}} = -1 + \frac{N\gamma}{rS}$$

$$\frac{dI}{dS} = -1 + \frac{N\gamma}{rS}$$

Integrating by variables:

$$\int dI = \int (-1 + \frac{N\gamma}{rS}) dS$$

$$I(t) = -S(t) + \frac{N\gamma}{r} \log S + C$$

Adding initial values:

$$I_0 = S_0 + \frac{N\gamma}{r} \log S_0 + C$$

$$C = I_0 + S_0 - \frac{N\gamma}{r} \log S_0$$

Therefore:

$$I(t) = -S(t) + \frac{N\gamma}{r} \log S + I_0 + S_0 - \frac{N\gamma}{r} \log S_0$$

Now for the Susceptible equation, I'll devide off (1)/(3)

$$\frac{\frac{dS}{dt}}{\frac{dR}{dt}} = \frac{-rSI}{N\gamma I}$$

$$\frac{dS}{dR} = -\frac{rS}{N\gamma}$$

$$\int (\frac{1}{S} dS) = \int (\frac{-rR}{N\gamma}) + C$$

$$\log S = \frac{-r}{N\gamma} R + C$$

$$S(t) = C * e^{\frac{-rR}{N\gamma}}$$

$$S(0) = S_0 = C * 1$$

Therefore, we get:

$$S(t) = S_0 * e^{\frac{-rR}{N\gamma}}$$

where:

$S(0) = S_0$  is the initial number of susceptible individuals,

$I(0) = I_0$  is the initial number of infected individuals.

In order to arrive at the recipe for number of recovered individuals, we should first recall the fact that for any given time  $t$ , the total number of people is equal to  $N$  (we neglect the troublesome issue of mortality). In other words:

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

$$R(t) = N - S(t) - I(t)$$

Hence:

$$R(t) = N - (-S(t) \frac{N\gamma}{r} \log S + I_0 + S_0 - \frac{N\gamma}{r} \log S_0 - S(t)) - (S_0 * e^{\frac{-rR}{N\gamma}}) = N - (\frac{N\gamma}{r} \log S + I_0 + S_0 - \frac{N\gamma}{r} \log S_0 - S(t))$$

## 4 Numerical methods

### 4.1 Euler method

Current implementation of this method in python can be viewed in file attached to mail.

### 4.2 Improved Euler method

Yet to be implemented.

### 4.3 Runge-Kutte method

Yet to be implemented.

## 5 Summary

In conclusion, this paper provided an introduction to the SIR model, its historical background, and its significance in epidemiology. I explored the core equations of the SIR model, which describe the dynamics of susceptible, infected, and recovered individuals within a population during an epidemic. Additionally, I presented the general solutions to the SIR model equations.

The SIR model has proven to be a valuable tool for understanding and controlling the spread of infectious diseases. One interesting avenue for study is the impact of heterogeneity within the population, such as variations in susceptibility and infectiousness. Understanding how individual-level characteristics influence the spread and control of diseases can help refine intervention strategies and improve our ability to predict and manage epidemics.

In addition to its direct applications in infectious disease epidemiology, the SIR model has transcended its original scope and found utility in studying a wide range of dynamic systems. The fundamental principles underlying the SIR model have been employed to explore social contagion, information diffusion, behavioral changes, rumor spreading, and even the dynamics of innovation diffusion in social networks. This too, would lead to interesting insights.

## 6 References

<https://royalsocietypublishing.org/doi/epdf/10.1098/rspa.1927.0118> [https://en.wikipedia.org/wiki/Compartmental\\_models\\_in\\_epidemiology](https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology) <https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model>  
<https://www.youtube.com/watch?v=sk-7cJmQGnk>