Epidemiology model (SIR model)

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29th January, 2024

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Epidemiological models



 The Epidemiological models are mathematical models used to better understand and predict how diseases spread and affect populations

The SIR Model: A Basic Framework



The model divides the population into three categories:

- (S): Susceptible People: Individuals capable of becoming infected but not yet being infected.
- (I): Infected People: These are individuals who have been infected and are capable of infecting susceptible individuals.
- (R): Recovered People: These are people who have been recovered from the infection.

SIR Model



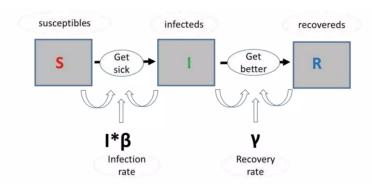


Figure: kermack & mckendrick, 1927

Mathematical Representation of the SIR Model



Ordinary differential equations (ODEs) to describe the changes in the number of individuals in each catagory:

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta IS}{N} \\ \frac{dI}{dt} &= \frac{\beta IS}{N} - \gamma I, \\ \frac{dR}{dt} &= \gamma I \end{aligned}$$

Parameters of SIR model



S: Suspected group

1: Infected group

R: Recovered group

 β : Transmission rate or mixing rate of population

 γ : Recovery rate (depends on medical facilities, medicine)

Assumptions of SIR model



- ► Closed System: Ignoring birth and deaths S(t) + I(t) + R(t) = N
- Reinfection is not considered
- All individuals have the same chances of getting infected.
- the population is considered to be well mixed

4th order Runge-Kutta method



$$k_1 = f_s(t_i, I_i, S_i) = -\frac{\beta S_i I_i}{N}$$

$$I_1 = f_I(t_i, I_i, S_i) = \frac{\beta S_i I_i}{N} - \gamma I_i$$

$$m_1 = f_R(t_i, I_i) = \gamma I_i$$

$$k_2 = -\frac{\beta \left(S_i + \frac{hk_1}{2}\right) \left(I_i + \frac{hl_1}{2}\right)}{N}$$

$$l_2 = \frac{\beta \left(S_i + \frac{hk_1}{2}\right) \left(I_i + \frac{hl_1}{2}\right)}{N} - \gamma \left(I_i + \frac{hl_1}{2}\right)$$

$$m_2 = \gamma \left(I_i + \frac{hl_1}{2}\right)$$



$$k_3 = -\frac{\beta \left(S_i + \frac{hk_2}{2}\right) \left(I_i + \frac{hl_2}{2}\right)}{N}$$

$$l_3 = \frac{\beta \left(S_i + \frac{hk_2}{2}\right) \left(I_i + \frac{hl_2}{2}\right)}{N} - \gamma \left(I_i + \frac{hl_2}{2}\right)$$

$$m_3 = \gamma \left(I_i + \frac{hl_2}{2}\right)$$

$$k_{4} = -\frac{\beta (S_{i} + hk_{3}) (I_{i} + hI_{3})}{N}$$

$$l_{4} = \frac{\beta (S_{i} + hk_{3}) (I_{i} + hI_{3})}{N} - \gamma (I_{i} + hI_{3})$$

$$m_{4} = \gamma (I_{i} + hI_{3})$$



▶ Thus, the numerical solution for the SIR Model :

$$S_{i+1} = S_i + \frac{1}{6}h(k_1 + 2k_2 + 2k_3 + k_4)$$

$$I_{i+1} = I_i + \frac{1}{6}h(I_1 + 2I_2 + 2I_3 + I_4)$$

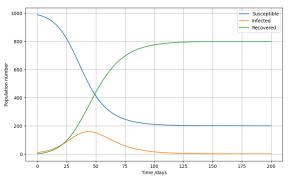
$$R_{i+1} = R_i + \frac{1}{6}h(m_1 + 2m_2 + 2m_3 + m_4)$$

where h is stepsizes

Modeling Covid 19 with SIR



for population number N=1000, $\emph{I}_0=10$, $\emph{R}_0=0$ and $\beta=0.2$, $\gamma=0.1 \emph{days}^{-1}$ for the period of 200 days



As we can see, the transformation between the categories is similar to what is seen from the ordinary differential equations.

Basic Reproduction number R_0



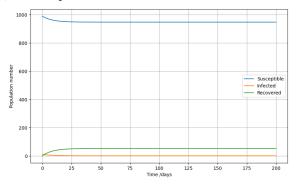
- The ratio β/γ is often used to calculate the basic reproduction number
- which represents the average number of secondary infections produced by a typical case of an infection in a population where everyone is susceptible.

If a disease has an $R_0 = 3$ for example, so on average, a person who has this sickness will pass it on to three other people.

$$R_0 = \begin{cases} > 1, & \text{the disease will spread in the population} \\ < 1, & \text{the disease will decay out in the long run.} \end{cases}$$

Plotting for different values of β and γ

Let's consider the case where we have great medical care systems boosting recovery rate of infected individuals γ , let $\gamma=0.6$ and $\beta=0.5$, where $R_0=0.8$

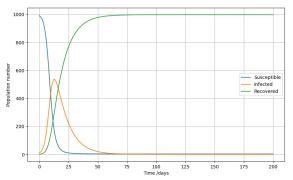


because the recovery rate is dominant over transmission rate, the disease will decay out soon.

Plotting for different values of β and γ



Lets consider a case where there is no serious lockdowns or social distancing rules applied, $\beta=0.6$ and $\gamma=0.1$ where $R_0=6$

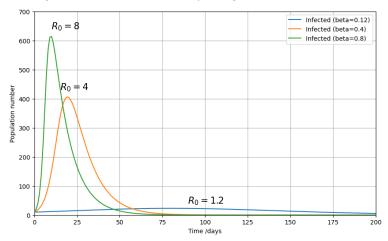


As higher peak for infected individuals can be seen as the contact rate increases.

Plotting for different values of β and γ



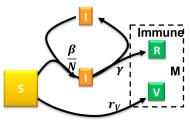
• Plotting for different values of β by fixing $\gamma = 0.1$



SIRV Model



▶ The Susceptible-Infected-Recovered-Vaccinated model is an extended SIR model that accounts for vaccination of the susceptible population.



Mathematical Representation of SIRV model



$$\frac{dS}{dt} = -\frac{\beta(t)IS}{N} - v(t)S$$

$$\frac{dI}{dt} = \frac{\beta(t)IS}{N} - \gamma(t)I$$

$$\frac{dR}{dt} = \gamma(t)I$$

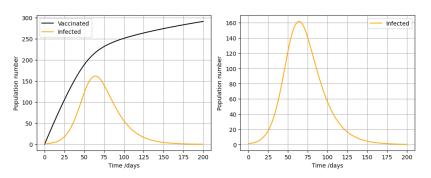
$$\frac{dV}{dt} = v(t)S$$

where ν is called vaccination rate, and V is the vaccinated group of population

plotting for SIRV model



In the case of low vaccination rate v = 0.0045

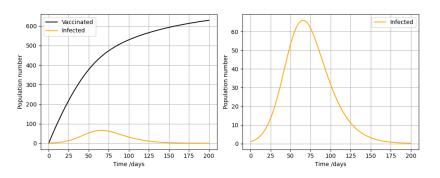


for a lower vaccination rate, more people get infected, around 164.

plotting for SIRV model



▶ In the case of higher vaccination rate v = 0.01



for a higher vaccination rate, number of infected people decreases to around 66.

