

Modeling the spread of COVID'19

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April 10, 2021

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Introduction

- COVID-19 is the infectious disease caused by the severe acute respiratory syndrome novel coronavirus (SARS-CoV-2)
- SARS-CoV-2 was first isolated and named on February 11, 2020
- Most people infected with the COVID-19 virus experience mild to moderate respiratory illness. Older people, and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease, and cancer are more likely to develop serious illness.

Introduction

- On March 14, 2020, the number of confirmed cases in India was just 12. In just 120 days, the number of total infections reached nearly 9,30,000. Merely 60 days later, the number of cases was nearly 50,00,000.
- The spread of infectious diseases is a classic example of exponential growth. The increase in infected population is proportional to its current size of the infected population. Each infected person becomes the source of infection.

Mathematical Modeling of SIR

Firstly, we identify the independent and dependent variables. The independent variable is time t , measured in days.

The set of dependent variables counts people in each of the groups, each as a function of time:

- $S(t)$ - Susceptible population
- $I(t)$ - Infected population
- $R(t)$ - Recovered (removed) population

Mathematical Modeling of SIR

Assumptions of the SIR model are -

- The total population doesn't change except during the death of the population.
- A homogeneous mixing of the population is assumed
- No skipping from S to R and no recovery term from I to S , No one joins the Susceptible group
- All individuals in the population have the same probability to contract the disease
- Homogeneous mixing of the population : Contacts of an individual with the rest of the population also follows a uniform distribution
- Incubation period is short enough and is assumed to be negligible

Mathematical Modeling of SIR

- Susceptible population gets infected at a rate proportional to the size of susceptible population (S) and infected population (I) (proportionality constant $\beta > 0$).
- Infected people die at a rate proportional to I (proportionality constant $\gamma > 0$).
- Recovered individuals are assumed to be immunized to the disease.

Mathematical Modeling of SIR

Schematic diagram for SIR Model



Mathematical Modeling of SIR

The governing equations of the SIR model are -

$$\frac{dS(t)}{dt} = -\beta SI$$

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

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

Here β is the interaction rate and γ is the recovery rate

Mathematical Modeling of SIR

Another way of interpreting the model can be that the total population remains unchanged i.e.

$$\begin{aligned}\frac{d(S + I + R)}{dt} &= \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\ &= -\beta SI + \beta SI - \gamma I + \gamma I \\ &= 0\end{aligned}$$

Integrating both sides give us

$$S + I + R = N$$

here N is the total population.

Instead of the actual population, we can also use the ratios of S , I and R with respect to the total population to plot on a scale of 0 to 1.

Graphing the SIR model in MATLAB

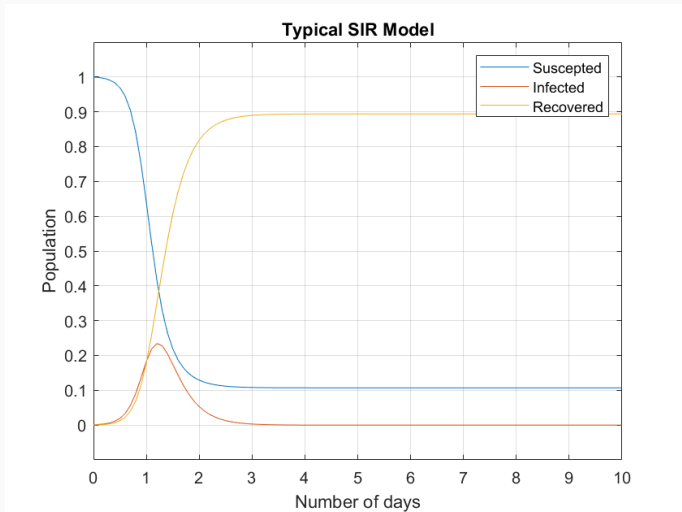


Figure 1: Typical SIR Model

Graphing the SIR model in MATLAB

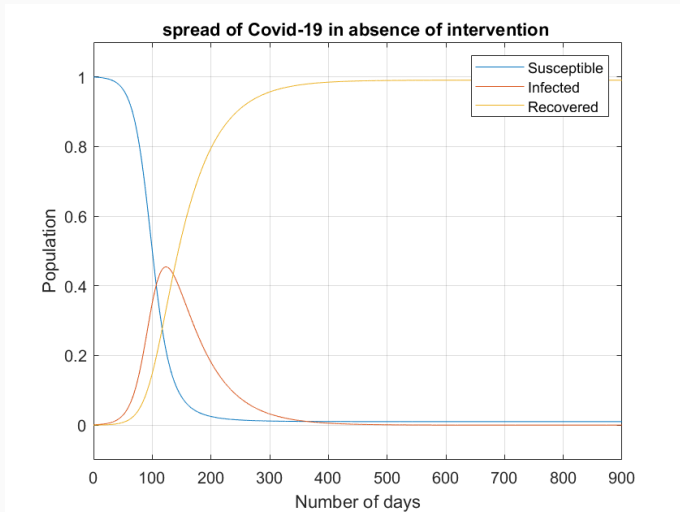


Figure 2: Spread of COVID-19 in absence of intervention

Mathematical Modeling of SIR

Figure 1 depicts the spread of a new disease in a completely susceptible population, considering $S_0 \approx 1$ and $I_0, R_0 \ll 1$. The exponential growth from the second differential equation with these approximations become:

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

whose approximate solution is

$$I(t) = e^{(\beta - \gamma)t}$$

Mathematical Modeling of SIR

If $\beta < \gamma$ the infectious population will decrease, since each infected individual passes the disease to less than 1 person on average. But if

$$\beta > \gamma$$

the number of infected people will double over each time interval of length

$$t_d = \frac{\ln(2)}{(\beta - \gamma)}$$

which is known as the doubling time. This exponential growth will eventually slow as the susceptible population S decreases. The peak is reached in the infectious population when $I'(t) = 0$, i.e. when $\beta S = \gamma$

Equilibrium Points

Since $S + I + R = N$, $R(t_0)$ can be determined by the values of $S(t_0)$ and $I(t_0)$ at any given time t_0 .

For convenience, we can convert this 3-D system to 2-D.

$$\frac{dS(t)}{dt} = -\beta SI = f(S, I)$$

$$\frac{dI(t)}{dt} = \beta SI - \gamma I = g(S, I)$$

At the equilibrium points, $f(S^*, I^*) = g(S^*, I^*) = 0$

On solving the equations, we get the equilibrium point for the system $(S^*, I^*) = (S, 0)$

Stability Analysis

Now to check the stability of the equilibrium points, we find the Jacobian matrix of $f(S, I)$ and $g(S, I)$

$$\begin{aligned}\mathbb{J} &= \begin{bmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} \end{bmatrix} \\ &= \begin{bmatrix} -\beta I & -\beta S \\ \beta I & \beta S - \gamma \end{bmatrix} \\ \mathbb{J}_{S^*, I^*} &= \begin{bmatrix} 0 & -\beta S \\ 0 & \beta S - \gamma \end{bmatrix}\end{aligned}$$

Eigenvalues of this matrix are $\lambda_1 = 0, \lambda_2 = \beta S - \gamma$
and eigen vectors are:

$$v_1 = \begin{bmatrix} 1 \\ 0 \end{bmatrix}, v_2 = \begin{bmatrix} 1 \\ \frac{\gamma}{\beta S} - 1 \end{bmatrix}$$

$$\Rightarrow \begin{bmatrix} S - S^* \\ I - I^* \end{bmatrix} = c_1 \begin{bmatrix} 1 \\ 0 \end{bmatrix} e^{0t} + c_2 \begin{bmatrix} 1 \\ \frac{\gamma}{\beta S} - 1 \end{bmatrix} e^{(\beta S - \gamma)t} \text{ --- (1)}$$

Let us consider the disease free equilibrium point:

$S = N, I = 0, R = 0$. We can see from equation (1) that this point is stable only if:

$$\beta N - \gamma \leq 0$$

$$\Rightarrow N \leq \frac{\gamma}{\beta}$$

$$\Rightarrow N \leq \frac{1}{\frac{\beta}{\gamma}}$$

$\frac{\beta}{\gamma}$ is known as the Reproduction Number and is denoted by R_0 .

If

$$R_0 \leq \frac{1}{N}$$

the equilibrium is stable and the epidemic won't spread.

If

$$R_0 \geq \frac{1}{N}$$

the equilibrium is unstable and the epidemic will spread further.

With the basic SIR model, we consider that the infection rate β is constant in time. The public and government can implement techniques which decreases the infection rate. On 24 March 2020, Prime Minister Narendra Modi ordered a nationwide lockdown for 21 days. The extensive use of masks and sanitizer also decreases the rate of infection to some extent.

With COVID-19, a threatened population may change its behavior in an effort to reduce the rate of contact and slow or halt a disease's spread. This is the goal of the current widespread school and work closures, stay-at-home directives, and other restrictive social distancing measures. The medical literature refers to such phenomena as non-pharmaceutical interventions.

Intervention

Let the fraction of contact prevention through such intervention is $q(t)$. This can be included in the differential equations as -

$$\frac{dS(t)}{dt} = -(1 - q(t))\beta SI$$

$$\frac{dI(t)}{dt} = (1 - q(t))\beta SI - \gamma I$$

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

Quite clearly, if there is no intervention, $q(t) = 0$ i.e. there is no change in effective β . The ideal case of identifying and isolating each infected person would result in $q(t) = 1$.

Increasing the value of $q(t)$ slows the rate of exponential growth. Although the pandemic takes longer to reach equilibrium, the peak it attains is lower. This allows the existing healthcare infrastructure to not be overburdened. This is commonly called “flattening the curve.”

Intervention Plot

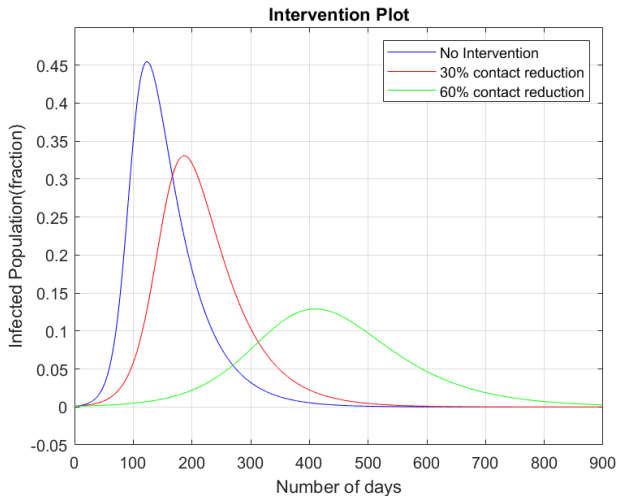


Figure 3: Flattening the curve through contact reduction

The flattening of the curve can be adversely affected if the public and governments stop their intervention measures i.e. $q(t) = 0$. It is tough to fully eliminate a virus on a worldwide scale. The epidemic will re-emerge if the fraction of susceptible population is higher than $\frac{1}{R_0}$. The following plot depicts an example of this scenario for COVID-19.

Exit Strategy plot

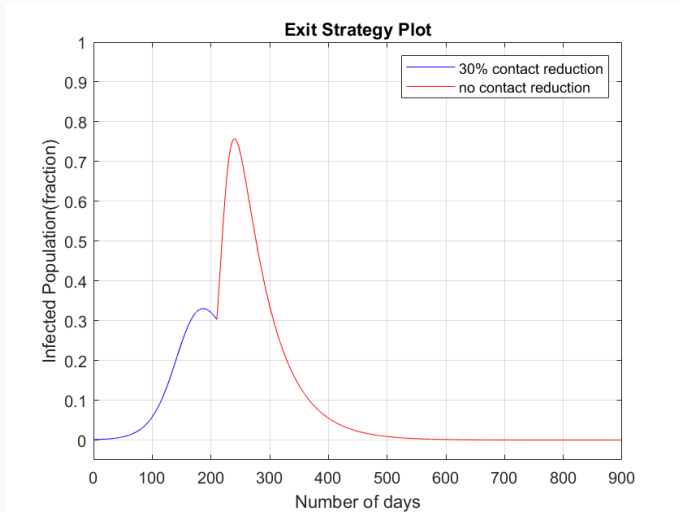


Figure 4: Scenario with a second outbreak after interventions are lifted

Implementing SIR model for different states

To estimate the values of β and γ , we analyzed the data of 90 days starting from March 14.

$$\hat{\beta} = \frac{S_{i+1} - S_i}{S_i I_i dt}$$

$$\hat{\gamma} = \frac{R_{i+1} - R_i}{I_i dt}$$

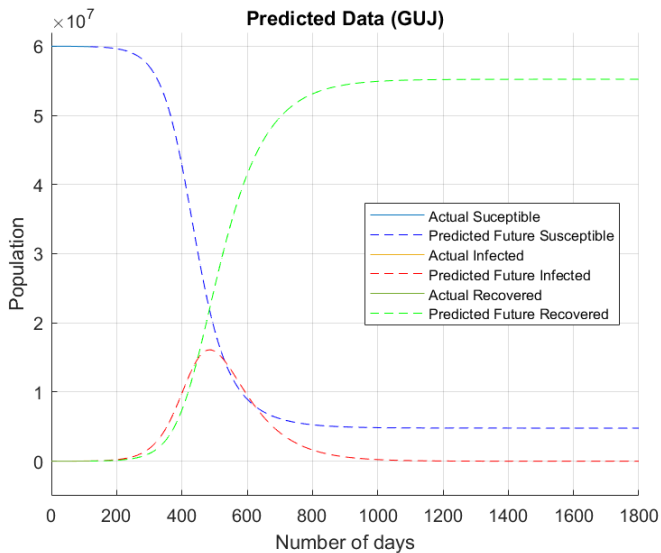


Figure 5: Predicting outbreak in Gujarat using SIR model

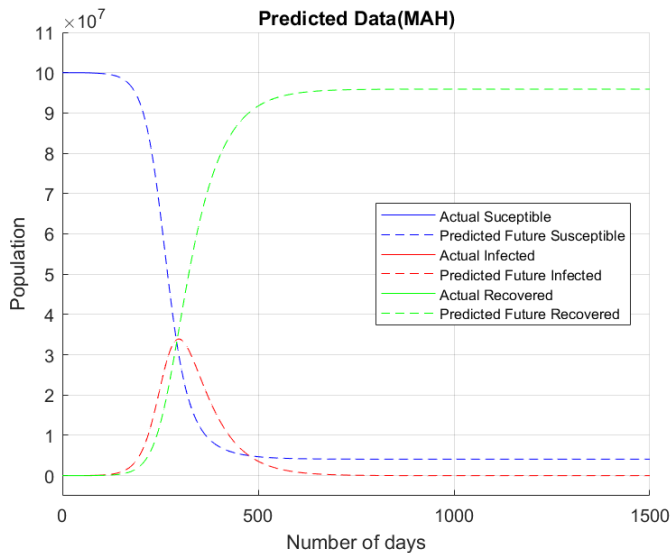


Figure 6: Predicting outbreak in Maharashtra using SIR model

Limitations

- The SIR model is a very basic model and does not take into account many other factors. Hence many extensions of the SIR model exist like SIR model with vaccination, SIR model with mutation, SIER model, SIEARD model etc.
- We have assumed that everyone in the population is equally likely to catch the disease which is not possible in real world scenario some people are more susceptible to the disease than others to the disease
- We are not considering incubation period for COVID-19 which can span from 5-6 days to 14 days. Considering this period would alter the analysis and outcome of the epidemic

Mankind is pretty much brought together in an enormous exertion to drive away the spread of COVID-19. For the time being, this exertion appears to be important to keep the illness from totally overpowering medical services frameworks. Intervention can decrease the measure of epidemiological overshoot, yet even this impact is somewhat restricted. For the 1918 influenza pandemic, retrospection uncover just an exceptionally frail relationship between intervention and spread of infections, thus the loss of life.

In any case, the general terms of this article remain constant for any epidemic or pandemic. While we can't totally keep away from the far-running outcomes of this COVID-19 episode, numerical demonstrating will help us realize what's in store and how to plan for and handle it.

- Code for the MATLAB plot
- Research paper- Modeling the spread of COVID'19- by David I. Ketcheson