Applying the basic SIR model to understand the outbreak of COVID-19

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Abstract. This paper applies the basic compartmental SIR model to explain the transmission dynamics of an pandemic like COVID-19. COVID-19 has created an alarming situation for the whole human kind. Researchers around the world are trying to demystify the prevailed global health emergency and come up with some effective solution. We attempt to implement the basic SIR model to show the spread of the disease. Further, we compared the level of spread of the disease on basis of basic reproduction number. Basic reproduction number is very important measure in order to quantify the proliferation of an infectious illness over the time. One of main assumptions of the model is a recovered person generates immunity towards the disease. Then we have suggested the ways to control the outbreak and normalise the prevailing situation.

Keywords: SIR model, COVID-19, pandemic, basic reproduction model.

1 Introduction

An SIR model is a mathematical model that finds the projected number of people affected with a infectious disease[1]. The simplest SIR model is based on Kermack−McKendrick theory[14] that predicts the number and distribution of cases of an infectious disease as it is transmitted through a closed population over time. The model divides the population into three components. Each component is supposed to have the similar characteristics [2,11].

- Susceptible: The Group of people who are prone to catch the infection. Some of them may be patient when the infection happens.
- Infectious: The group of infectious represents the infected people. They can pass the disease to susceptible people and can be recovered in a specific period.
- Recovered: Recovered people get immunity so that they are not susceptible to the same illness anymore. Figure 1 shows how the number of people in each group can change over time.
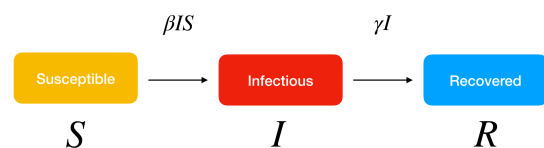

Figure 1: Relationship among S, I and R groups[3]

SIR model may be used to find the basic reproduction number, R_0. It may be termed as the average number of secondary cases produced by a single infection in a completely susceptible population[4]. Smaller the value of R_0, lesser time period it requires to wipe out the outbreak.

The epidemic may be termed as pandemic if an outbreak of the disease that occurs over a wide geographic area and affects an exceptionally high proportion of the population[6].

2 Description of model

The Kermack−McKendrick model is an SIR model for the number of people infected with a infectious disease in a closed population over time. It was proposed to explain the rapid decrease and increase in the number of infected patients observed in epidemics such as the plague and cholera etc. It also assumes a completely homogeneous population with no age, spatial, or social structure[2]. This model uses a system of three nonlinear ordinary differential equations. These assumptions lead us to a set of three ordinary differential equations[5,12,15] for $S(t)$, $I(t)$, and $R(t)$:

$$\frac{dS}{dt} = -\beta S(t)I(t) \tag{1}$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t) \tag{2}$$

$$\frac{dR}{dt} = \gamma I(t) \tag{3}$$

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{4}$$

$$S(t) + I(t) + R(t) = N = constant \tag{5}$$

Here, $S(t)$, $I(t)$ and $R(t)$ correspond to the number of people in each of three compartments; susceptible, infectious and recovered. Sum of number of individuals in all three compartments is constant, i.e. population size (N), at any point of time. It is not considered to have the effect of the natural death or birth rate because the model assumes the outstanding period of the disease is much shorter than the lifetime of the human. We assume that there no new deaths due to some other factors. So the population size does not change and the duration of infection is same as length of the disease. We use two important parameters, β (transmission rate) and γ(recovery rate). When we can estimate the two parameter values, we may have many useful information. If the D is the average days to recover from the disease, it is derived from γ.

$$D = \frac{1}{\gamma} \tag{6}$$

Also, we can estimate the nature of the disease in terms of the power of infection, R_0.

$$R_0 = \frac{\beta}{\gamma} \tag{7}$$

If R_0 is high, the proliferation of pandemic is also higher. The number is also used to estimate the herd immune threshold (HIT). If the basic reproduction number multiplied by the percentage of non-immune people (susceptible) is equal to 1, it indicates the balanced state. The number of infectious people is constant. We consider the proportion of immune people is p, the stable state can be formulated as follows[3].

$$R_0(1 - p) = 1 \rightarrow 1 - p = \frac{1}{R_0} \rightarrow p_c = 1 - \frac{1}{R_0} \tag{8}$$

Therefore, p_c is the HIT to stop the spread of the infectious disease. We can stop the outbreak by vaccinating the population to increase herd immunity[5].

3 Implementation of SIR model

For simplicity, we assume initially(assuming population remains constant), total population(N) is 1. Initial state for infectious category(I_0) is the fraction of total population which is infectious at time T_0. Initial state for susceptible population(S_0) is the remaining population(N-I_0) assuming that no person has been vaccinated. It is also assumed that there is no recovered person in the beginning[7]. When the pandemic starts spreading, number of new infections is proportional to the infection population and susceptible population. Here, number of people newly infected may be taken as $\beta * S * I$ and the count of new recoveries as $\gamma * I$[7]. In simple terms, we may update three compartments of the population(equations (1), (2) and (3) rewritten), over the time, as -

$$S(t + 1) = S(t) - NewI(t) \tag{9}$$

$$I(t + 1) = I(t) + NewI(t) - NewR(t) \tag{10}$$

$$R(t + 1) = R(t) + NewR(t) \tag{11}$$

If the count of newly infected people is greater than that of newly recovered people over the time, the infection may turn into an epidemic. It implies that the rate of transmission is more than rate of recovery. So for a disease to be categorised as epidemic, R_0 must be greater than 1. If R_0 is less than 1, then the epidemic may die out soon[7].

Now we analyze the spread of the illness for different values of basic reproduction number(R_0). It is too early to say more about the R_0, in current scenario, when most of countries are struggling to deal with this disease. As per Forbes Report [8] R_0 for COVID-19 is estimated to be between 2.2 to 5.7. First we present a scenario where R_0 is 5 and Initial state of infectious
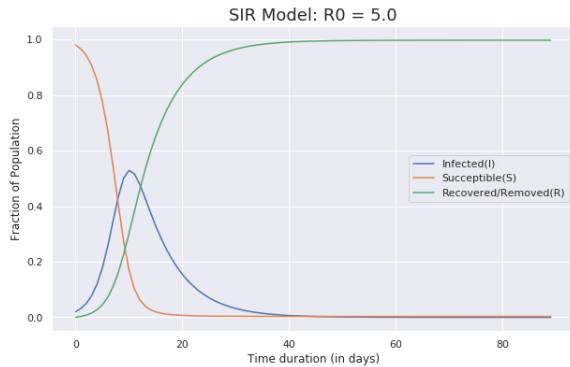
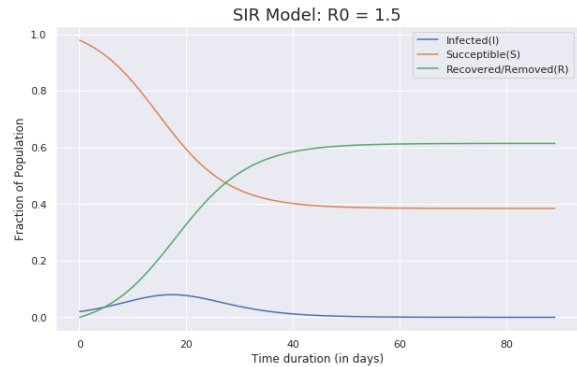**Figure 2:** Maximum Infectious population at a time :52.43% Total Infected population :99.69%

Figure 4: Maximum Infectious population at a time :7.99% Total Infected population :61.5%

population is 2% in Python. We use β=0.75 and γ=0.15 to obtain the desired R_0 of 5.0

The value of R_0 may be reduced by decreasing β or increasing γ. Keeping γ same and reducing β to 0.45, we adjust R_0 to 3. We may easily observe(Fig. 3) that peak infection population gets reduced from around 50% to around 30%. There is delay in peak of infection, infection peaked at around 13th day when R_0=5, whereas it took around 18 days to reach peak of infection when R_0 is reduced to 3.
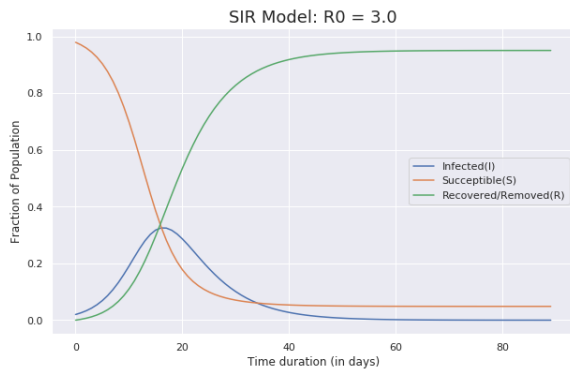

Figure 3: Maximum Infectious population at a time :32.53% Total Infected population :95.14%

Now we set γ=0.3 and β=0.45 to get R_0 = 1.5. We may easily observe(Fig. 4) that peak level of infectious population is only 7.99% that is much lower than the previous case. Infection peaks around 18th day. Only around 62% of the total population is infected.

It may be easily observed that, by decreasing R_0, we reduce the spread of the infection and the peak level of infected population. Decreasing R_0 will also delay the time for peak level of infection, buying us valuable

time to prepare tackle the infection effectively.

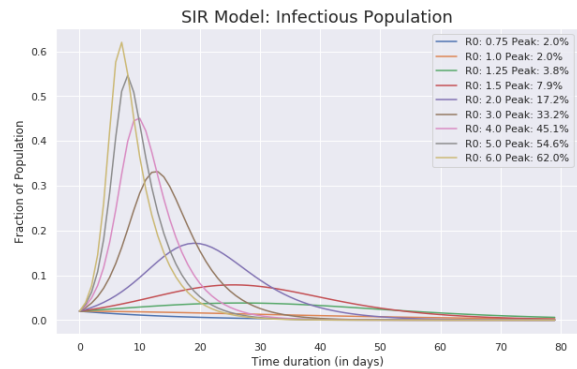Let's now check how the peak level of infection and extent of infection vary with R_0.

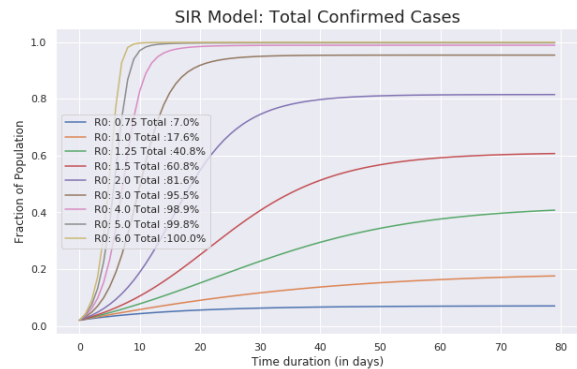**Figure 5:** Total infectious population wrt R_0

Figure 6: Total confirmed population wrt R_0

As R_0 decreases, the curve for infectious popula-

tion becomes less steeper and comes down. When R_0 is 6, more than 62% of the population is infections by around 7th day, whereas when R_0 is 2, maximum infectious population is 17.2% by around 19th day. That mean reduction in R_0 from 6 to 2 gives us additional 12 days to prepare to tackle the peak infection. It can also be observed that the extent of infection also decreases with reduction in R0. When R_0=6, total population gets infected whereas when R_0=2, 18.4% of the population remains uninfected. Figure 7[10] shows the current global status of this disease.
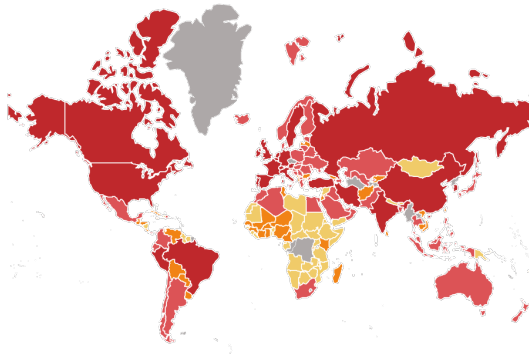

Figure 7: Current global status of COVID-19 spread

4   Results

We have seen that COVID-19 can be controlled if we manage to reduce the basic reproduction number[7,16]. This may be done in following ways-

- Reducing Susceptible population- The best way for decreasing susceptible population is vaccination, however no vaccination is available for COVID-19. Overall susceptible population can be contained in a region level by enforcing travel restrictions, lock-downs etc.

- Increasing recovery rate (γ)- Increasing recovery rate depends on available health infrastructure and treatment methods. Significant improvement in this area is both time consuming and capital intensive.

- Reduction in transmission rate(β)- Transmission rate depends on the number of persons from susceptible population an infected individual comes

into contact and probability that a contact becomes infected . Contact rate may be reduced by social distancing measures like closing of schools, offices etc., suspension of public transport, self-isolation of susceptible individuals, quarantine etc. Frequent hand washing, covering nose and mouth while sneezing, disinfecting environment, use of face mask and taking proper diet to improve the immunity, are few things that may be practiced to improve personal and environmental hygiene resulting in reduction in R_0.

5   Limitations

We have just considered basic SIR model to visualize the spread of pandemic. We have shown the percentage of population that might be affected in normal scenario. It is too early to predict the stable values of β, γ and R_0. The actual results may vary in different regions of the world. We have used the values predicted by researchers on available data till date and we have made some suitable assumptions to make the things simpler. Some of results may not be valid after some time.

References

[1] Eric Weisstein, *SIR Model*, From MathWorld–A Wolfram Web Resource, https://mathworld.wolfram.com/SIRModel.html, (Accessed: April 15, 2020).

[2] Eric Weisstein, *Kermack-McKendrick Model*, From MathWorld–A Wolfram Web Resource, https://mathworld.wolfram.com/Kermack-McKendrickModel.html, (Accessed: April 14, 2020).

[3] *COVID-19 dynamics with SIR model*, https://www.lewuathe.com/covid-19-dynamics-with-sir-model.html, (Accessed: April 15, 2020).

[4] James Holland Jones, *Notes On R0*, Department of Anthropological Sciences, Stanford University(May 1, 2017) https://web.stanford.edu/ jhj1/teachingdocs/Jones-on-R0.pdf,(Accessed: April 15, 2020).

[5] David Smith, Lang Moore, *The SIR Model for Spread of Disease-The Differential Equation Model*, https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model, (Accessed: April 15, 2020).

[6] https://www.merriam-webster.com/words-at-play/epidemic-vs-pandemic-difference, (Accessed: April 18, 2020).

[7] *SIR model*, https://www.kaggle.com/abhijithchandradas/sir-model-don-t-understand-calculus-don-t-worry, (Accessed: April 18, 2020).

[8] Yaqing Fang, Yiting Nie, Marshare Penny, *Transmission dynamics of the COVID19 outbreak and effectiveness of government interventions: A datadriven analysis*, Wiley Online Library, https://doi.org/10.1002/jmv.25750.

[9] Tara Haelle *The COVID-19 Coronavirus Disease May Be Twice As Contagious As We Thought*, https://www.forbes.com/sites/tarahaelle/2020/04/07/the-covid19-coronavirus-disease-may-be-twice-as-contagious-as-we-thought/5998861e29a6 (Accessed: April 18, 2020).

[10] *COVID-19: Lessons and Recommendations*, ISGlobal Barcelona Institute for Global Health, https://www.isglobal.org/en/coronavirus-lecciones-y-recomendaciones, (Accessed: April 17, 2020).

[11] Weiss, Howard Howie, *The SIR model and the foundations of public health*, Materials matematics (2013): 0001-17.

[12] *Compartmental models in epidemiology*, https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology, (Accessed: April 15, 2020).

[13] *COVID-19 INDIA* (Data Source MoHFW) https://data.gov.in/major-indicator/covid-19-india-data-source-mohfw, (Accessed: April 16, 2020).

[14] *KermackMcKendrick theory*, https://en.wikipedia.org/wiki/Kermack-McKendrick_theory, (Accessed: April 14, 2020).

[15] *LaTeX*, https://en.wikibooks.org/wiki/LaTeX, (Accessed: April 18, 2020).

[16] Coronavirus Resource Center, https://coronavirus.jhu.edu/map.html, (Accessed: April 19, 2020).