SIR Model for Spread of COVID-19 Infection among Households

Project Seminar Documentation

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Mathematical Modeling, Simulation and Optimization

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Acknowledgment

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1 Introduction

In December 2019, the first case of COVID-19 was identified in Wuhan, China and it spread worldwide rapidly. With the rise in COVID-19 infection, mathematical models are increasingly used to analyze the trend of spread which helps to monitor and control the infection. The model deals with the infection within households and how the average number of households in different regions impact the infectious period and the spread of infection.

The household infection model is based on the conventional Susceptible-Infected-Recovered(SIR) model. Probability distribution and recovery time of infections within a household are calculated for a specific period of time which is expanded to find the pattern of infection in a region having different distribution of household sizes.

2   SIR Model

2.1   Basic SIR Model

During the occurrence of a disease, the individuals in a population can be of three categories : Susceptibles , Infectives and Recovered.

Susceptibles : Susceptibles are uninfected people who gets infected when they come into contact with an infected person.

Infectives : Individuals affected with disease and able to transmit it.

Recovered : individuals recovered from disease and no more susceptible or infective.

$$S \rightarrow I \rightarrow R$$

Susceptibles have a possibility to get infections, infectives moves to recovered category but no new susceptibles are introduced in the population. The level of transmission from an infected to a susceptible person depends on several factors like age group, immunity, health conditions, intensity of contact etc.

2.2   SIR Model in Households

Members of a household are assessed at fixed sampling intervals and the numbers in each household at n^{th} sampling intervals are S_n,I_n and R_n. The size of the household (N) is assumed to be constant during the infectious period such that

$$S_n + I_n + R_n = N$$

After n^{th} sampling interval, status of the infections in a household is observed and the new values S_{n+1},I_{n+1} and R_{n+1} are assessed.

It is assumed that:

- Each individual in a household makes effective contact with any other individual with the same probability. Probability of effective contact depends on several factors like immunity of a person, health condition, age group etc.

- Each sampling interval is of same length as duration of infectious period(10 days) for COVID-19.

- No new susceptibles are introduced into a household during the period of observation.

- Re-infection is not possible in a household during short period of observation.

We use a probability distribution model to find the pattern of infection in a household during a sampling interval.

3 Probability Distribution for Infection in Households

The number of susceptibles or infected remaining in a household after each sampling interval can be determined by following a probability distribution where the probability of an infectious contact is considered as the probability of success and the probability of avoiding an infectious contact is considered as the probability of failure. Since the household size and the number of infected during the start of sampling interval are known, binomial distribution is used.

3.1 Binomial Distribution Model

Probability for x susceptibles to remain in a household in the next sampling interval:

$$P[S_{n+1} = x] = \binom{S_n}{x} q^x (1 - q)^{S_n - x}$$

where
p is the probability of effective contact between any susceptible and any infective in one sampling interval.
q is the probability that a susceptible avoids contact with any other infective in one sampling interval (q = 1-p).

In the next sampling interval (n+1),
S_{n+1} = x
I_{n+1} = S_n - x
$R_{n+1} = R_n + I_n$

   Analogously, Probability for j individuals to get infected in the next sampling interval:

$$P[I_{n+1} = j] = \binom{S_n}{j} q_n^{S_n - j} (1 - q_n)^j$$

where
p is the probability of effective contact between any susceptible and any infective in one sampling interval
q is the probability that a susceptible avoids contact with any one infective

in one sampling interval (q = 1-p).

In the next sampling interval (n+1),
$I_{n+1} = j$
$S_{n+1} = S_n - j$
$R_{n+1} = R_n + I_n$

3.2 Probability Distribution and Recovery time in a Household

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Infection in a Household of size :  4
Sampling interval : 1 (Period of infection is 10 days)
Number of susceptibles :  3
Number of infectives :  1
Probability of  effective contact between susceptible and infectives :  0.25
Possible outcomes during sampling interval  2
    S  I  R  Probability of this observation  Recovery Time
1  0  3  1                       0.015625           20.0000
2  1  2  1                       0.140625           22.5000
3  2  1  1                       0.421875           25.3125
4  3  0  1                       0.421875           10.0000
```

Figure 3.1: Possible outcomes for household size = 4 and p = 0.25

For example, in a household of size 4, one person is infected during the first sampling interval and all others are susceptibles. In the second sampling interval, the infected person moves to the recovered category since the infectious period(10 days) is over. Now there are six possible cases that can happen in this household, i.e., the number of infected persons (I_2) can take the values 1 to 3 or none of them will be infected(figure 3.1). Similarly, each of these cases have different possible inner cases.

Case 1: Suppose in the third sampling interval , case 1 happens($S_3=0$ and $I_3=3$), the probability is calculated as following :

Probability of effective contact between a susceptible and infective is assumed to be 0.25. $S_{n+1} = 3$, x = 0, $q_n = 0.75$

$$P[S_{n+1} = x] = \binom{3}{0} \times 0.75^0 \times (0.25)^3 = 0.015625$$

Case 2: In this case(S_n=1 and I_n=2) the probability is calculated similarly as in case 1. Since there is one susceptible remaining in this case, in the next sampling interval there is a possibility for this one susceptible to either get infected or to remain susceptible and the probability of each of these cases are calculated(Figure 3.2).

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Case 2
Sn 1
In 2
Possible outcomes during sampling interval  3
    S  I  R  Probability of this observation  Recovery Time
1   0  1  3                            0.25               30
2   1  0  3                            0.75               20

Case 3
Sn 2
In 1
Possible outcomes during sampling interval  3
    S  I  R  Probability of this observation  Recovery Time
1   0  2  2                          0.0625             30.0
2   1  1  2                          0.3750             32.5
3   2  0  2                          0.5625             20.0

Sn 1
In 1
Possible outcomes during sampling interval  4
    S  I  R  Probability of this observation  Recovery Time
1   0  1  3                            0.25               40
2   1  0  3                            0.75               30
```

Figure 3.2: Inner Cases

The process continues until all the susceptibles are infected or there are no more people to spread the infection. If there are any susceptibles remaining in the house, they can get infected again in the future but it is not considered in this model since the observation is limited to a short period.

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Recovery time is calculated as follows :

- When there are no more susceptibles in a household, the infectious period will end in the current sampling interval and Recovery time(R) = n * L where n is the sampling interval and L is the length of one sampling interval. For example, in case 1(S_1=0 and I_1=3)(Figure 3.1), R = 2 × 10 = 20 days.

- When there are no more infectives in a household , the infectious period ends in the previous sampling interval and Recovery time(R)= $(n-1)×$ L. For example, in case 4 (S_1=3 and I_1=0), R = 1 × 10 = 10 days.

- For all other cases , recovery time is calculated using the weighted average of recovery times in the sub-cases.
  Recovery time (R) = $\sum_{i=1}^{x} P_i \times R_i$
  where i is the number of sub-cases for a particular case, P_i and R_i are the probability and recovery time of each sub-case respectively. For example, in case 2,
  R = $\sum_{i=1}^{2} P_i \times R_i$= $0.25 \times 30 + 0.75 \times 20 = 22.5$ days.

```
probabilty of contact :   [0, 0.05, 0.25, 0.3, 0.5, 0.75, 1]
Recovery time :    [10.0, 11.57, 18.37, 19.94, 24.38, 24.72, 20.0]
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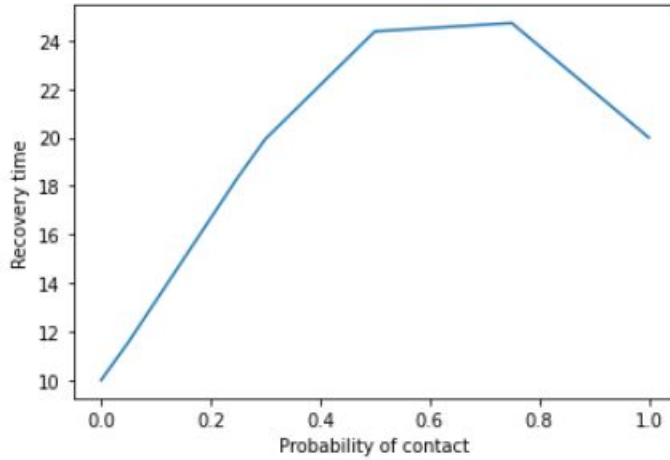

Figure 3.3: Recovery Time for household size 4

- Total recovery time for a household size 4 with probability of contact 0.25 is calculated as below : R = $(20 \times 0.015625 + 22.5 \times 0.140625 + 25.3125 \times 0.421875 + 10 \times 0.421875) = 18.37$ days.
  Similarly , total recovery time can be calculated for different probability of contact and different household sizes.

4 Simulation

The model considers only the local contacts i.e. infection within households. The average size of households in different countries vary largely. Depending on the size of household in different countries the spread of infection varies. For simulating the model, we are comparing the infection pattern in a country with higher average size of household like India and a country with lower average size of household like Germany.

4.1 Distribution of Household

Country or area	Average household size (number of members) Total	Distribution of households by number of members (%)[i]			
		1	2 to 3	4 to 5	6+
	Col (2)	(3)	(4)	(5)	(6)
India	4.8	4	24	42	31
Germany	2.1	37	48	13	1

Figure 4.1: Distribution of Households by Number of Members in India and Germany

Source : *https* : *//www.un.org/en/development/desa/population/publications/pdf/ageing/ household_size_and_composition_around_the_world_2017_data_booklet.pdf*

From figure 4.1, it is evident that in India there are only fewer households with less number of members as compared to Germany. The household size and its impact on recovery time in different countries are compared and simulated.
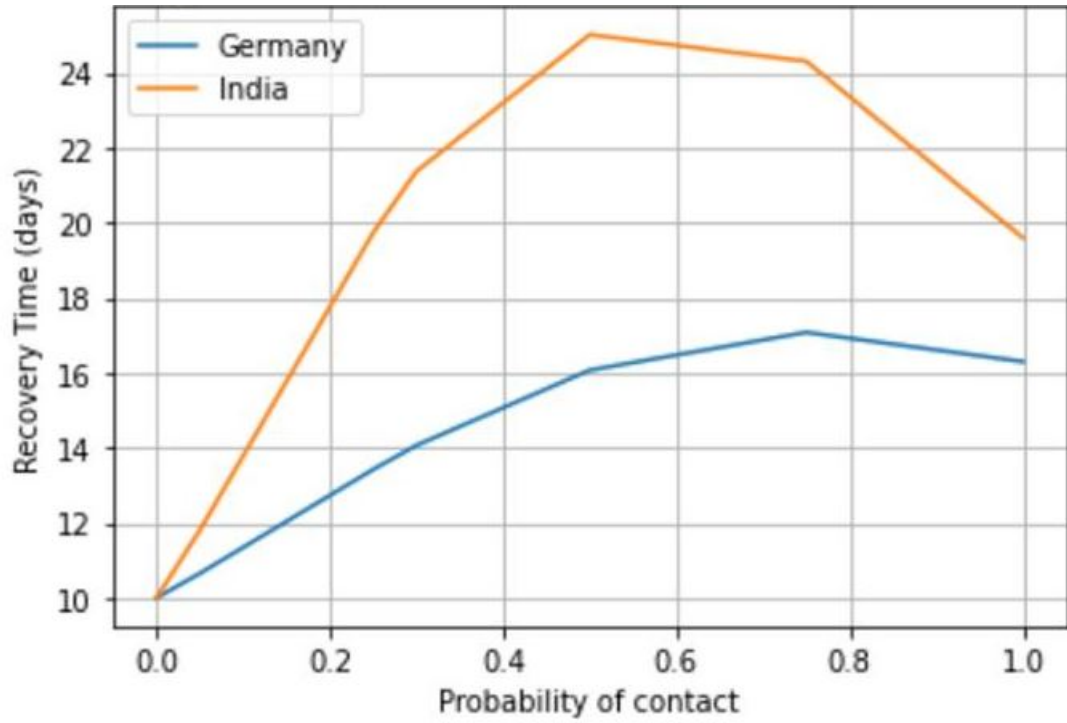
4.2 Simulation : Recovery time vs. Probability of Contact

Figure 4.2: Average Recovery Time of Households in Germany and India

Table 1: Distribution of Households by number of members.

Country	1	2	3	4	5	6
Germany	37	24	24	7	7	1
India	4	11	12	21	21	31

Table 2: Recovery time for different household sizes

Country	1	2	3	4	5	6
Recovery time	10	12.5	15.31	18.27	21.61	24.93

The graph compares the average recovery time of 100 households in India vs Germany based on the recovery time calculated (section 3.2) for different household sizes for different probabilities of contact. From figure 4.1, we consider the size of households and the corresponding distribution in different countries as in Table 1. Similar to the results in figure 3.3 , we could obtain the average recovery time for different sizes of households as shown in Table 2.

As an example, consider a probability of contact of 0.25, the average recovery time is calculated as below :

Average recovery time(Germany) = $(37 \times 10 + 24 \times 12.5 + 24 \times 15.31 + 7 \times 18.27 + 7 \times 21.61 + 1 \times 24.93)/100 = 13.42$ days

Average recovery time (India) = $(4 \times 10 + 11 \times 12.5 + 12 \times 15.31 + 21 \times 18.27 + 21 \times 21.61 + 31 \times 24.93)/100 = 19.71$ days

4.3 Expected Number of Infections vs. Sampling Interval

It is assumed that in each of the 100 households a single person is infected at the beginning of observation period. For a probability of 0.25, expected number of infections for the next sampling intervals are as shown in figure 4.3. As seen from the graph, the infectious period lasts longer in a country where the average household size is greater.

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Probability of effective contact: 0.25
Expected number of infections in Germany :  [100, 32, 8, 1, 0, 0]
Expected number of infections in India :  [100, 84, 35, 11, 2, 0]
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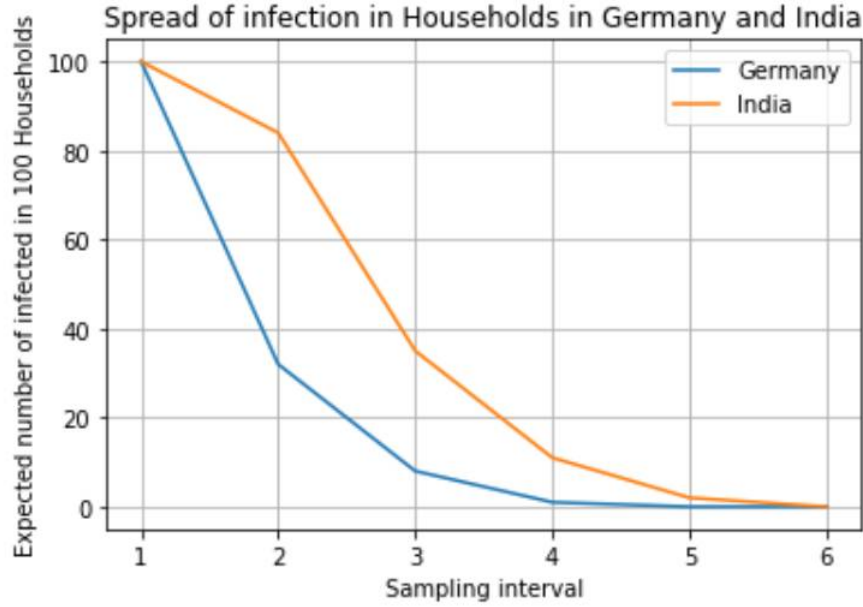

Figure 4.3: Expected number of infections in Germany and India

4.4   Modification : Two regions with same population

As a modification to the model, we are considering two regions (Region 1 and Region 2) with same population and different distribution of household size. Here, the total number of individuals in each region is 100 but the number of households with lesser size is more in region 1 compared to region 2.

Table 3: Distribution of Household size for region 1 and region 2

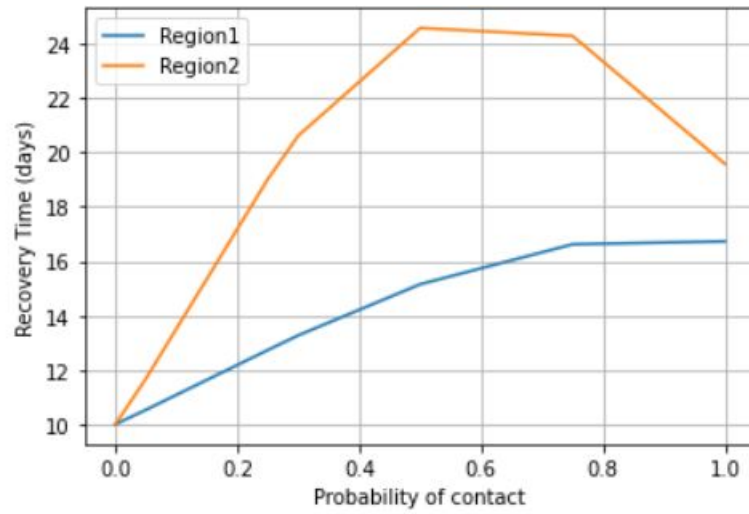| Region	1	2	3	4	5	6
Region 1	16	18	13	1	1	0
Region 2	1	1	3	9	8	2

Figure 4.4: Average Recovery Time of Households in Region 1 and Region 2

For Region 2, the infectious period lasts longer since there are more number of households with larger size as compared to region 1.

5   Conclusion

In this model, we demonstrate that for the SIR covid model among a population which is divided into different households, the distribution of individuals and the probability of effective contact play a significant role in determining how long the infection lasts in a region considering only the local contacts. For a region with more number of households with lesser size the epidemic is expected to subside in a short period of time as compared to the region with higher household size.

For a very low and very high probability of effective contact the infection period ends faster in all the region irrespective of the household size.

6   References

- Frank C Hoppensteadt , Charles S Peskin ; Modeling and Simulation in Medicine and the Life Sciences , Second Edition.

- Frank Ball, Laurence Shaw1 : Estimating the within-household infection rate in emerging SIR epidemics among a community of households