Effectiveness of lock down strategy : A mathematical view

Nazrul Haque¹, Tushar Karmakar², Soudip Karmakar³

^{1,2}Dept. Of Mathematics, ³Dept. of Zoology

Ramakrishna Mission Vivekananda Centenary College

Abstract

This study provides an analysis of lock down strategy during a pandemic situation. We have conducted two different approaches to address the effectiveness of lock down. We have constructed a compartmental epidemic model to show how reproduction number varies between a lock down scenario and without lock down scenario. We have also used a conditional probabilistic approach to show how lock down help in identifying the infectious and more susceptible individuals.

Introduction

Pandemics are different from epidemics in terms of their geographic spread. An epidemic affects many people at same time. It spreads from person to person and remains local to a specific region. In comparison, when an epidemic engulfs entire country, continent, or the whole world, it is termed as pandemic. Containment of the virus has proven very challenging. The main problem of is, if a large number of people become infected in very small time then most of them will not get the proper treatment in time. So, anyone can understand, how serious issue this is! According to the health experts, the only way of spreading contagious disease is human to human transmission. If a carrier comes in contact with any other person then there may be a chance of making more carriers. The increasing of carriers will increase the Growth rate gradually. We may have two possibilities :

⇒(a) growth rate is high and the time span is low. This situation is dangerous enough for decision making such as medical treatments, identification of carriers, testing, vaccination etc.

⇒(b) growth rate is low and the time span is high. This is an ideal situation for a good decision making in medical treatments, identification of carriers, testing, vaccination etc.

In any pandemic situation, where there is no official vaccine, it is hard to decrease the growth rate of the carriers, especially where the population density is a big factor. We can only slow down the growth rate. Lock down is a great weapon for a situation like this. It is not only the best way of social distancing but also the ideal way to slow down the contact rate subsequently the growth rate of the disease. Lock down is an emergency protocol that prevents people from leaving the place where they are staying for a time period. They are not allowed to exit from their place without any emergency situation such as food, medical emergency etc. A lock down is not the cure of any pandemic but it will give us enough time to take our best decisions to find the cure, that is vaccine.

Figure 1: Model with lock down

Effectiveness of lock down

In this section, we will construct a realistic compartmental model to show how reproduction number varies by taking the lock down strategy and then we will use a simple conditional probabilistic argument showing that lock down also help in identifying the infectious and more susceptible individuals.

Compartmental model approach :

We have extended the well known S-E-I-R by introducing lock down compartment and asymptomatic compartment. We will show two models - (a) Model with lock down (b) Model without lock down. Let's construct the models.

Assumptions :

- (i) $N = S(0) = \text{Total population}$
- (ii) Constant rates.
- (iii) There is no new birth and no deaths in the population.

Model with lock down

Here, we have tried to extend the S-E-I-R model by introducing lock down(L) and asymptomatic(A) compartment. We assume that a portion of susceptible individuals(S) become isolated due to lock down at success rate l . Since, the population which are isolated due to lock down do not come to contact with infectious individuals(I), therefore average effective contact rate of a single infected and asymptomatic(A) individual become $\frac{\beta}{N-L}$ and $\frac{\rho\beta}{N-L}$ respectively. Where, N stands for total population and L stands for the number of people who are isolated. Here, we assume that the

infect rate with probability k is $k\sigma$ and asymptomatic rate is $(1 - k)\sigma$. We have also assumed a fast variability factor(ρ) for variability in disease transmission rate. On the other hand, it is also assumed that the population in lock down compartment(L) again become susceptible after lock down period ($\frac{1}{\omega}$) is over. The recovery rate for asymptomatic and infected populations are γ_2 and γ_1 respectively and $\frac{1}{\mu}$ is average life expectancy at birth.

So, based on these assumptions, the model is as follows,

$$\begin{aligned}\frac{dS}{dt} &= \omega l - \frac{\beta IS}{N-L} - \frac{\rho \beta AS}{N-L} - (l + \mu)S \\ \frac{dL}{dt} &= Sl - (\omega + \mu)L \\ \frac{dE}{dt} &= \frac{\beta SI}{N-L} + \frac{\rho \beta SA}{N-L} - (\sigma + \mu)E \\ \frac{dA}{dt} &= (1 - k)\sigma E - (\gamma_2 + \mu)A \\ \frac{dI}{dt} &= k\sigma E - (\gamma_1 + \mu)I \\ \frac{dR}{dt} &= \gamma_1 I + \gamma_2 A - \mu R\end{aligned}$$

Where, average life expectancy at birth is ($\frac{1}{\mu}$).

Now, we shall find out basic reproduction number(R_0) which give us the average number of secondary infectious individuals produced when one infected individual is introduced into a host population where everyone is susceptible. We will try to find out the basic reproduction number (R_0) using one generation matrix. Before using the procedure, we firstly divide our model(Figure.01) into two parts for better understanding :

Figure 2: Part 1

Using one generation matrix(see Ref.1 for the detailed method) in part 1(Fig.2), we only need two compartment E and I which are related to infectious cases.

Therefore the spectral radius of FV^{-1} i.e. $\rho(FV^{-1})$ is the eigen value of the one generation matrix, FV^{-1}

$$R_1 = \rho(FV^{-1}) = \frac{k\sigma\beta S(0)}{(N-L)(\sigma+\mu)(\gamma_1+\mu)}$$

Similarly, we can use the same concept for part 2(Fig. 3) where we will use two compartments E and A.

Figure 3: Part 2

So, it is clear that,

$$R_2 = \rho(FV^{-1}) = \frac{\rho(1-k)\sigma\beta S(0)}{(N-L)(\sigma+\mu)(\gamma_2+\mu)}$$

Therefore, our basic reproduction number(R_0) for the model with lock down will be as follows,

$$R_0 = R_1 + R_2 = \frac{k\sigma\beta S(0)}{(N-L)(\sigma+\mu)(\gamma_1+\mu)} + \frac{\rho(1-k)\sigma\beta S(0)}{(N-L)(\sigma+\mu)(\gamma_2+\mu)} \dots\dots\dots(1)$$

Model without lock down

Here, we have tried to extend the S-E-I-R model by adding only asymptomatic cases(A). We assume that the disease transmission rate(β) only occur in contact with asymptomatic(A) and infected(I) individuals. We have also assumed a fast variability factor(ρ) for variability in disease transmission rate, in case of asymptomatic(A) and infected(I) individuals. The recovery rate for asymptomatic and infected populations are γ_2 and γ_1 respectively and $\frac{1}{\mu}$ is average life expectancy at birth.

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta IS}{N} - \frac{\rho BAS}{N} - \mu S \\ \frac{dE}{dt} &= \frac{\beta SI}{N} + \frac{\rho\beta SA}{N} - (\sigma + \mu)E \\ \frac{dA}{dt} &= (1 - k)\sigma E - (\gamma_2 + \mu)A \\ \frac{dI}{dt} &= k\sigma E - (\gamma_1 + \mu)I \\ \frac{dR}{dt} &= \gamma_1 I + \gamma_2 A - \mu R \end{aligned}$$

Using the one generation matrix , we get ,

$$R'_0 = R'_1 + R'_2 = \frac{k\sigma\beta}{(\sigma+\mu)(\gamma_1+\mu)} + \frac{\rho(1-k)\sigma\beta}{(\sigma+\mu)(\gamma_2+\mu)} \dots\dots\dots(2)$$

Finally, from (1) and (2) we get,

$$\begin{aligned} R_{lockdown} &= \frac{k\sigma\beta S(0)}{(N-L)(\sigma+\mu)(\gamma_1+\mu)} + \frac{\rho(1-k)\sigma\beta S(0)}{(N-L)(\sigma+\mu)(\gamma_2+\mu)} \\ R_{without-lockdown} &= \frac{k\sigma\beta}{(\sigma+\mu)(\gamma_1+\mu)} + \frac{\rho(1-k)\sigma\beta}{(\sigma+\mu)(\gamma_2+\mu)} \end{aligned}$$

Figure 4: Model without lock down

Lemma. *If lock down is applied in a pandemic situation, then $R_{lockdown} < R_{without-lockdown}$*

Proof. Since, $S(0) = N \implies N > N - L \implies \frac{N}{N-L} < 1 \implies \frac{\beta k \sigma N}{N-L} < \beta k \sigma$

$$\implies \frac{\beta k \sigma N}{(N-L)(\sigma+\mu)(\gamma_1+\mu)} < \frac{\beta k \sigma}{(\sigma+\mu)(\gamma_1+\mu)} \dots\dots\dots (a)$$

Similarly,

$$\implies \frac{\rho(1-k)\beta\sigma N}{(N-L)(\sigma+\mu)(\gamma_2+\mu)} < \frac{\rho(1-k)\beta\sigma}{(\sigma+\mu)(\gamma_2+\mu)} \dots\dots\dots (b)$$

Adding (a) and (b), we get,

$$\implies \frac{\beta k \sigma N}{(N-L)(\sigma+\mu)(\gamma_1+\mu)} + \frac{\rho(1-k)\beta\sigma N}{(N-L)(\sigma+\mu)(\gamma_2+\mu)} < \frac{\beta k \sigma}{(\sigma+\mu)(\gamma_1+\mu)} + \frac{\rho(1-k)\beta\sigma}{(\sigma+\mu)(\gamma_2+\mu)}$$

$$\implies R_{lockdown} < R_{without-lockdown} \dots\dots\dots (proved)$$

□

Probabilistic Approach

Identifying the susceptible and infectious individuals are very important during any pandemic situation. It helps to take possible precautions to decrease the growth rate. If the situation is too difficult to identify the infectious individuals, then it is almost impossible to control the growth rate of the disease. We will now construct a conditional probabilistic argument to show how lock down help in identifying the infectious and more susceptible individuals. Some terms and notations that we have clarified at first. More susceptible(S_m) are those(including their family members) who go outside relatively more during a lock down and Infectious(I) persons are those who are already infected.

Assumptions :

(1) The number of people(including their family members) who become infectious or more susceptible individuals are poisson random variable with mean λ . (see Ref.5)

(2) Each person(including their family members) is, independently become infectious individuals with probability p and More susceptible individuals(S_m) with probability $(1 - p)$.

We will now see this argument for two different scenarios - (a)Lock down (b) Without lock down

With lock down

Let, K_1 denote the total number of more susceptible(S_m) individuals and K_2 denote the total number of infectious individuals. Also, let $K = K_1 + K_2$. We will now try to find the probability of identifying n more susceptible(S_m) individuals and m infectious individuals i.e. I_{m+n} . The probability of identifying only more susceptible individuals is I_m and only infectious individuals is I_n .

Figure 5: Without lock down (red=infected; blue=more susceptible)

Figure 6: With lock down (red=infected; blue=more susceptible ;black=isolated individuals)

Conditioning on K gives,

$$P\{K_1 = n, K_2 = m\} = \sum_{i=0}^{\infty} P\{K_1 = n, K_2 = m | K = i\} P\{K = i\}$$

Because $P\{K_1 = n, K_2 = m | K = i\} = 0$ when $i \neq n + m$, the preceding equation yields

$$P\{K_1 = n, K_2 = m\} = P\{K_1 = n, K_2 = m | K = n + m\} e^{-\lambda} \frac{\lambda^{n+m}}{(n+m)!}$$

Given that, $n + m$ people will be identified follows, because each of these $n + m$ is independently a more susceptible individuals with probability p , that the conditional probability that n of them are more susceptible individuals (and m are infectious individuals) is just the binomial probability of n successes (or m successes) in $n + m$ trials. Therefore,

$$\begin{aligned} P\{K_1 = n, K_2 = m\} &= \binom{n+m}{n} p^n (1-p)^m e^{-\lambda} \frac{\lambda^{n+m}}{(n+m)!} \\ &= \frac{(n+m)!}{n!m!} p^n (1-p)^m e^{-\lambda p} e^{-\lambda(1-p)} \frac{\lambda^n \lambda^m}{(n+m)!} \\ &= e^{-\lambda p} \frac{(\lambda p)^n}{n!} e^{-\lambda(1-p)} \frac{(\lambda(1-p))^m}{m!} = I_{m+n} \end{aligned}$$

Because the preceding joint probability mass function factors into products, one of which depends only on n and the other only on m , it follows that K_1 and K_2 are independent. Moreover, because

$$\begin{aligned} P\{K_1 = n\} &= \sum_{m=0}^{\infty} P\{K_1 = n, K_2 = m\} \\ &= e^{-\lambda p} \frac{(\lambda p)^n}{n!} \sum_{m=0}^{\infty} e^{-\lambda(1-p)} \frac{(\lambda(1-p))^m}{m!} \\ &= e^{-\lambda p} \frac{(\lambda p)^n}{n!} = I_n \end{aligned}$$

and, similarly,

$$P\{K_2 = m\} = e^{-\lambda(1-p)} \frac{(\lambda(1-p))^m}{m!} = I_m$$

Without lock down

Let, K_1 denote the total number of more susceptible (S_m) individuals and K_2 denote the total number of infectious individuals. Also, let $K = K_1 + K_2$. We will now try to find the probability of identifying n' more susceptible (S_m) individuals and m' infectious individuals. Note that, $n < n'$ and $m < m'$. Similarly, from the previous section, we can say that,

$$P\{K_1 = n', K_2 = m'\} = e^{-\lambda p} \frac{(\lambda p)^{n'}}{n'!} e^{-\lambda(1-p)} \frac{(\lambda(1-p))^{m'}}{m'!} = I_{m'+n'}$$

$$P\{K_1 = n'\} = \sum_{m'=0}^{\infty} P\{K_1 = n', K_2 = m'\} = e^{-\lambda p} \frac{(\lambda p)^{n'}}{n'!} = I_{n'}$$

$$\text{and, } P\{K_2 = m'\} = e^{-\lambda(1-p)} \frac{(\lambda(1-p))^{m'}}{m'!} = I_{m'}$$

Lemma. *In a pandemic situation, $n < n' \implies I_{n'} < I_n$*

$$\text{Proof. } n < n' \implies \frac{1}{n'} < \frac{1}{n} \implies \frac{e^{-\lambda p} \lambda^{n'}}{n'!} < \frac{e^{-\lambda p} \lambda^n}{n!} \dots\dots\dots (a)$$

$$0 < p < 1 \implies p^{n'} < p^n \dots\dots\dots (b)$$

So, from (a) and (b) we get,

$$e^{-\lambda p} \frac{(\lambda p)^{n'}}{n'!} < e^{-\lambda p} \frac{(\lambda p)^n}{n!}$$

$$\implies I_{n'} < I_n$$

□

We can also prove that, $I_{m'} < I_m$ and $I_{m'+n'} < I_{m+n}$ respectively in this way.

Conclusion

An infected person can spread the disease by infecting susceptible individuals. So, both of these quantity are useful in disease control policy during a pandemic. If we can track more susceptible individuals easily then we will have a rough idea on who can be the next infected individuals. This will help reducing the transmission rate in the host population. The above inequality implies that - the disease spreads rapidly if lock down is not implemented during a pandemic as the probability of identifying infectious and susceptible individuals decreases. On the other hand, if we implement lock down strategy as early as possible, then the growth rate may decrease. Reproduction number(R_0) is useful in analyzing the current scenario during a pandemic as it has great influence on the growth rate and transmission rate of a disease. Therefore by comparing reproduction numbers, it's easy to understand that lock down is too much important to reduce the number of infectious individuals. So, from the inequalities and the diagrams stated in this paper, it is easy to understand the necessity of lock down strategy in disease control. Since, $I_i \propto \frac{1}{i}$ (i.e. probability of identifying i individuals), we have to implement necessary policies that will force people to stay at home during lock down because if more people go out day by day, then the whole lock down enforcement strategy may turn into a big fallacy.

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