RESEARCH ARTICLE

DOI: 10.34256/famr2314

Frontiers in Advanced Materials Research

A Simple Model of Endemicity to Analyse Spread and Control of COVID-19 in India

Sourabh Banerjee [a], Chinmay Das [b], Swarniv Chandra [a]

[a] Department of Physics, Govt. General Degree College at Kushmandi, P.O. Kalikamora, South Dinajur, Pin 733121, West Bengal, India.

[b] Department of Mathematics, Kabi Jagadram Roy Government General Degree College, Mejia, Bankura-722143, India.

* Corresponding Author: bandosou@gmail.com

Received: 03-03-2023, Revised: 07-05-2023, Accepted: 15-05-2023, Published: 30-05-2023

Abstract: A simple model based on 2 parameters, time-dependent infectability and efficacy of containment measures, is written to analyse the spread and containment of an endemic outbreak. Data from the first wave of the outbreak of COVID-19 in India is analysed. Interestingly, growth and decay of infections can be seen as a competition between the ratio of logarithm of infectability and the logarithm of time vis-a-vis the efficacy of containment measures imposed. Containment time estimates are shown to exhibit the viability of the simple model.

Keywords: COVID-19, Average Infectability, Efficacy of Containment Measures, Containment Time

1. Introduction

The outbreak of the novel coronavirus, also called COVID-19, has forced most nations to impose a complete closure of all social and commercial activities over certain temporal durations, generally referred to as a lockdown. The imposed lockdowns primarily targeted areas of relatively high occurance rate of infections or of high population densities with a few infected individuals. However, many governments worldwide were forced to impose lockdown on a national level, extending over weeks, sometimes months. In this work, we strive to write a minimal model which is an interplay of 2 parameters, the dynamic infectability leading to the growth of infections and efficacy of containment measures which is a kind of umbrella parameter subsuming in it the benefits of mass isolation through lockdown and benefits of awareness measures. Large-scale testing in infected areas and tracking of the isolated are two key measures which can assess the number of infected individuals better and are thus subsumed in the parameter of dynamic infectability.

The salient features of the COVID-19 which need to be factored in while considering a model are :

I. a period of about 2 weeks (with a median of 5 to 6 days) during which the virus remains active in an infected individual and chances of infecting people coming in contact with the infected person

II. infected individuals exhibiting symptoms are generally considered for clinical testing; as a result, their number on a given day is known with reasonable accuracy; however, the number of asymptomatic, yet infected, individuals cannot be ascertained with a high level of confidence, so, a ratio of infected individuals at two successive time instants may be considered as a dynamic measure of infectability at the later instant

III. containment of the infection comprises of several measures : (a) as a primary measure individuals known to be infected are advised to stay in isolation till recovery or seek hospitalisation in case of severe symptoms; also, those who may have come in contact with infected individuals are tested and tracked; (b) as a secondary measure, governments worldwide have forced lockdown in regions where high incidence of occurance were reported extending over varying periods of time between several weeks to a few months; (c) oftentimes governments had to take recourse to national lockdown in apprehension of situation spinning out of control, as an extreme measure.

2. The Model

As the median time of spread of the infection is about a week, so we will work in discrete time, t_i, where an unit time step denotes one week. Since most of the infected individuals remain asymptomatic over the 1st week, that is the time when the maximum spread by contagion occurs. Assuming a dynamic infectabilityk(t_j), at time instant t_i, one can , therefore, write, $N_I(t_j) = k(t_j)\, N_I(t_{j-1})$, where the subscript "I" denotes infected. In epidemiological terms, k(t_j) could be considered a discretely varying reproduction number [2]. As pointed out earlier, one has to consider the clinically tested and positively diagnosed number of the population as $N_I(t_j)$, at time instant t_i. Thus, if control measures are not taken, the infection is expected to spread as, $N_I(t_j) = \prod_{j=0}^{t_j} k(t_j) N_I(0)$ over time. Mass isolation, on the other hand, ideally, means zero spatial diffusion of the infection. So to mimic the role of mass isolation(under a lockdown) which comes into effect at an instant of time t_{lock} after the outbreak, the model incorporates a decreasing function of time, assumed as a power law [3] with time-dependent exponent $-\alpha_j$, thus,

$$\begin{aligned} N_I(t_j) &= k(t_j) N_I(t_j - 1), 0 < t_j < t_{lock} \text{ and } t_j > t_{withdrawal} \\ &= k(t_j) t_j^{-\alpha(t_j)} N_I(t_j - 1) t_{lock} < t_j < t_{withdrawal} \end{aligned} \quad (1)$$

where $t_{withdrawal}$ denotes the instant of time at which the lockdown is withdrawn. Generally, lockdowns are imposed and withdrawn in a phased manner. To avoid cluttering the

model with more parameters we have let $\alpha_j(t_j)$ evolve dynamically too. $\alpha_j(t_j)$ may be regarded as a measure of "efficacy of containment", factoring in effects of isolation alongwith benefits of awareness measures. In case of a partial withdrawal of lockdown, $\alpha_j(t_j)$ would change discontinuously and remain non-zero. Complete withdrawal of imposed measures would only make $\alpha_j(t_j) = 0$ Any model for infected population of an endemic outbreak must be able to account for a growth leading to a peak and subsequent decay. Our simple 2-parameter ($k-\alpha$) model encapsulates the growth and decay of infected individuals when the following conditions are satisfied. The infected population grows so long as,

$$\frac{log(k(t_j))}{log(t_j)} > \alpha_j(t_j) \tag{2}$$

obviously, at low values of t_j, and decays when

$$\frac{log(k(t_j))}{log(t_j)} < \alpha_j(t_j) \tag{3}$$

as time progresses. Recovery, is a delayed-time phenomenon and can, on an average, vary from society to society. However, a maximum of 3 weeks with a median of 2 weeks is a reasonable time-frame for recovery, keeping in view the mandatory quarantine of 2 weeks for an infected individual. Therefore, the dependence of number of cured individuals, denoted by subscript 'c', as a function of infected individuals may be written as,

$$N_c(t_j) = p_c N_I(t_j - 1) + p_c^{'} N_I(t_j - 2) + p_c^{''} N_I(t_j - 3), \tag{4}$$

where p_c, $p_c^{'}$ and $p_c^{''}$ are average probabilities of cure of individuals diagnosed as infected 1, 2 and 3 weeks before the present time respectively and could also vary over time. Given the time-frame for recovery is, generally, more than a week, one would expect $p_c^{''} \geq p_c^{'} > p_c$.

Fatalities on the other hand, have been known to happen within days for infected elderly people or others with co-morbid conditions. Mortality, low though it is, for healthy individuals could take upto a couple of weeks, with a median of 1 week, after symptoms begin to show. The deceased, denoted by subscript "d", as a function of infected individuals may be written as,

$$N_d(t_j) = p_d N_I(t_j) + p_d^{'} N_I(t_j - 1) + p_d^{''} N_I(t_j - 2), \tag{5}$$

where p_d is the average probability of mortality of the elderly and those with pre-existing co-morbid conditions, while the probability of mortality of other individuals infected 1 and 2 weeks ago are denoted by $p_d^{'}$ and $p_d^{''}$.

3. Results

3.1 Extracting the parameters - first 4 weeks

Let us see what values of the parameters suitably describe the progression of the pandemic in India during the month of March 2020. On 2nd March only 5 individuals were reported COVID-19 positive. Considering 2nd March as our starting time instant, $N_I(0)=5$. The Indian government clamped a national lockdown from the midnight of 24th March, i.e., the end of 3rd week from $t_j=0$, therefore, $t_{lock}=3$. Data from the Situation Update Report (SUR) of World Health Organisation (WHO) [1] in corroboration with the Ministry of Health and Family Welfare (MOHFE), Government of India, for March 2020 of total number of individuals infected, cured and expired due to COVID-19 in India is displayed in Table 1. From the data for $N_I(0)$ and $N_I(1)$ it is obvious that the initial infectability $k(0)$ satifies $5k(0)+5=44$ implying $k(0)>7$. Globally, the average infectability due to COVID-19 has been found to be below 4 [4,5,6,7]. So we choose an initial value of infectability, $k(0)=3.7$, such that its fluctuations over the 1st three weeks is least. The variation of $k(t_j)$ over time instants $j=1\ to\ 4$ which fit the WHO SUR & MOHFE, GoI data are also enlisted in Table 1. In so doing, we note

- A definite rise in infectability leading to the 3rd week, k(3), presumably indicative of a progression of the pandemic from Stage1 to Stage2 during the period.
- To assess the initial value of α, one needs to consider one time instant after imposition of lockdown, i.e., $t_j=4$. Using the infectability value of k(3) and setting $\alpha=0$, one finds that $\sum N_I(4)$ exceeds its reported value by a factor of 1.78. This is a clear indication that lockdown effects were showing and the contagion level remained at Stage2. To arrive at the reported value, holding $k=k(3)$, we find $\alpha=0.596$.
- The probabilities for cure $p_c=0.15, p_c^{'}=0.25$ and $p_c^{''}=0.25$ and death, $p_d=0.01,\ p_d^{'}=0.03\ and\ p_d^{''}=0$ were found to fit the data well and remained unchanged over the 4 week period.
- The overall mortality averaged about one-fourth of that for cure.

Table 1: Comparison of total number of infected, cured and deceased individuals as obtained from WHO SUR data [1] and the numbers obtained from our model using k(0)=3.7. 1st week under lockdown is fitted using .

Date (SUR no)	9/3/2020 (6)	14/3/2020 (7)	22/3/2020 (8)	28/3/2020 (9)
end of week (t_j)	1	2	3	4
$\sum N_I(t)$ (SUR data)	44	84	360	909
$\sum N_c(t)$ (SUR data)	NA	10	NA	80
$\sum N_d(t)$ (SUR data)	NA	2	7	19
Infectability (k)	3.7	3.145	4.558	4.558
α	NA	NA	NA	0.596

At this stage, one needs to understand how to interpret the simultaneous variations of 'k' and α.

Let k_j and α_j denote the values of k and α at $t = t_j$. Let at some later time instant (t), the infected population is determined by scaling only the infectability, k_j, by a factor C_1 without changing the value of α_j. If the same infected population is fitted by differently scaling the parameters, viz., $C_3 k_j$ and $C_2 \alpha_j$, then, the distribution of the $C_2 - C_3$ scale factors, for that particular t, and known value of C_1, may be easily derived from equation (1) and will be of a log-linear form

$$C_2 = 1 + \frac{\log(C_3 / C_1)}{\alpha_j \log(t)} \qquad (6)$$

Clearly, $C_3 > C_1$ implying $C_2 > 1$, indicates that a fit of same number of infected individuals can be effected by a simultaneous increase of both parameters, k and α. Thus, rather than the numerical values of infectability or efficacy of containment at a given instant of time, variation of these parameters over time and the ensuing trend is more amenable for interpretation. So for $t_j > 4$, we will hold α_j fixed at its value at $t_j = 4$ and study the variation in 'k'.

3.2 Next 4 weeks - the fluctuation regime

In order to fit the WHO SUR data for weeks 5 to 8 (Table 2), we note,

- That a 3.407 times increase in the average infectabilityoccured for week 5, i.e., $k(5) = 12.6059$, assuming lockdown effectiveness remains unchanged, i.e., $\alpha = 0.596$
- Fortuitously, over the subsequent weeks (6th, 7th \& 8th), a perceptible fall in the infectability was registered - an assurance that Stage 3 contagion had been successfully averted thus far. The corresponding "k" values are enlisted in Table 2, assuming that $\alpha = 0.596$. The ratios $\frac{k(7)}{k(6)} \approx 0.945$ and $\frac{k(8)}{k(7)} \approx 0.969$ indicate a steady decline of 3 to 4% in average infectability from week 6.

- Values of $\log(k(t_j))/\log(t_j)$ till week 8, although decreasing, is still greater than the value of α implying thereby that the peak of infected population was yet to arrive.
- Alongside the anomalous increase in infected individuals over the 5th week, we find that ratio of the total number of individuals cured to that of infected, viz., $\sum N_c(t)/\sum N_I(t)$, exhibits a steady increase by a factor of 2.86 from its value of 0.0766 after the 5th week to 0.2197 at the end of 8th week (Table 2). Although the individual values of p_c as well as $\sum p_c$, required to fit the data, exhibit a cyclical change over the period, the mean values of p_c as well as that of $\sum p_c$ over the weeks 5 to 7, remain unchanged vis-a-vis their corresponding values for weeks 1 to 4. This is a reaffirmation of our choice of p_c values, and, consequently, of $\sum p_c$ values over the entire 7 week period. Over the 8th week, however, there has been a very definite increase in the probability of cure. The fluctuations over the mean is not surprising as data collated over a large country like India under difficult circumstances and evolving curative methods could lead to such mild fluctuations.
- Mortality, on the other hand, increased sharply over the 5th and 6th weeks, also as a consequence of the abrupt rise in the number of infected people. To fit the data for N_d, the distribution of the death probabilities, p_d, was so adjusted that the ratio $p_d^{'}/p_d$ remained unchanged at its initial value of 3 and the individual values were increased in steps maximally by 12.5%. The remaining deaths were attributed to a time delay of 2 weeks through $p_d^{''}$. Fortuitously, a sharp decrease in mortality was observed for the next two weeks. The mortality-to-cure ratios, as per available data is listed in Table 2.

Date (SUR no)	5/4/2020 (10)	12/4/2020 (11)	19/4/2020 (12)	26/4/2020 (13)
end of week (t)	5	6	7	8
$\sum N_I(t)$ (SUR data)	3577	8447	16116	26917
$\sum N_c(t)$ (SUR data)	274	765	2302	5914
$\sum N_d(t)$ (SUR data)	83	273	519	826
$\sum N_c(t)/\sum N_I(t)$	0.0766	0.0905	0.1428	0.2197
$\sum N_d(t)/\sum N_c(t)$	0.303	0.357	0.225	0.14
k	12.6059	5.3132	5.2029	4.8655
$\log(k(t_j))/\log(t_j)$	1.574	0.932	0.829	0.761
p_c	0.18	0.117	0.15	0.188
$p_c^{'}$	0.28	0.217	0.25	0.288
$p_c^{''}$	0.28	0.217	0.25	0.288
$\sum p_c$	0.74	0.551	0.65	0.764
p_d	0.012	0.0125	0.0075	0.0058
$p_d^{'}$	0.036	0.0375	0.0225	0.0174
$p_d^{''}$	0.04	0.05	0.03	0.0232
$\sum p_d$	0.087	0.1	0.06	0.0464

Table 2. Comparison of total number of infected, cured and deceased individuals as obtained from WHO SUR data and the parameters used to fit the data for weeks 5 to 8 assuming remains unchanged at 0.596.

The last two sub-sections are representative of the varied nature of the progression of a pandemic. So, a projection based on parameters fitted from collated data needs to factor in fluctuations based on likelihood and consider multiple scenarios for containment.

3.3 Future tense

The time at which the infection peaks, t_{peak}, given by, $\frac{log(k(t_{peak}))}{log(t_{peak})} = \alpha(t_{peak})$, while containment occurs when the number of infected individuals at a given time instant reduces to zero and continues to remain zero, implying that the total number of infected individuals remains constant thereafter.

Containment period, t_C, formally is given by

$$\lim_{t \to t_C} N_I(t_j) \to 0 \tag{7}$$

However, to assess t_{peak} and t_C one has to make reasonable assumptions regarding the evolution of $k(t)$ and $\alpha(t)$ and calculate $\log k(t)/\log t$ and $N_I(t)$ till the latter falls to zero. Earlier, it was pointed out, that from week 6 there has been a steady decline in infectability. So to determine containment time of COVID-19, let us assume that infectability decreases by 3% every subsequent week in keeping with the trend, till containment. The assumption of a non-linear decrease in infectability is justified only if there is a concomitant increasing trend in $|\alpha(t)|$, so that efficacy of lockdown is not reversed and the pandemic is contained. In the Indian context it is worth noting, that the enhancement of $|\alpha(t)|$, is expected to be severely restrictive, as it is very difficult to strictly enforce mass isolation in a country of 1.3 billion. We will consider increments in $|\alpha(t)|$ maximally upto 4%. However, such a dual trend of decrease in k(t) and simultaneous increase in $|\alpha(t)|$ can bring in fluctuations in the variation of $\log k(t)/\log t$ with time, so the peak value of infections cannot be ascertained only with some degree of error. Figure 1 shows a plot of $\frac{log(k(t)}{log(t)}$ vs 't' from the 6th week since the outbreak based on 3% decrease in values of "k" every week and a 2% increase in $|\alpha(t)|$. Figure 2 clearly brings out the possibility of an oscillation between $\frac{log(k(t)}{log(t)} < \alpha(t)$ and $\frac{log(k(t)}{log(t)} > \alpha(t)$ before the latter condition stabilises. So to find the peak in infections as well as the containment time one has to rely on calculation of $N_I(t)$.

Assuming unrealistically that lockdown remains in effect till containment of infections, the following table shows the time of containment for different rate of increase of $|\alpha(t)|$ and a fixed rate of decrease of "k" values at 3%.

The enhancement of $|\alpha(t)|$, is expected to be severely restrictive, as it is very difficult to increase testing, tracking and isolation steadily in a country of 1.3 billion. We will consider increments maximally upto 4%. The key results of scenarios 1 and 2 are displayed in Table 3.

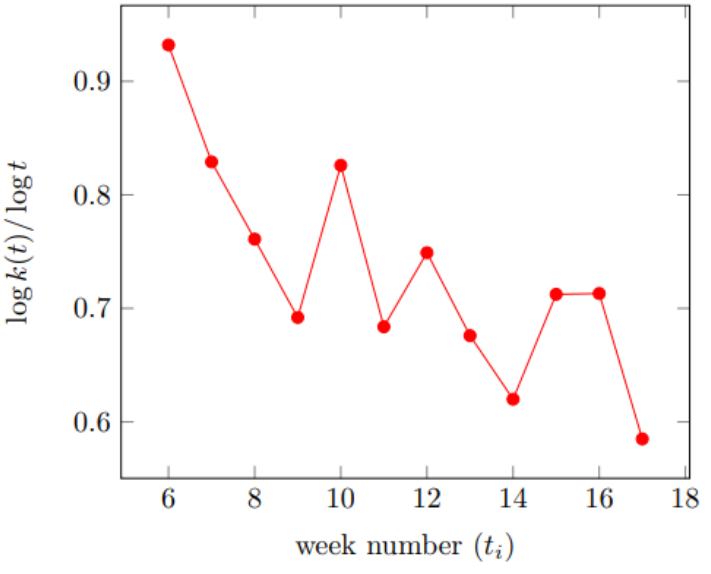

Figure 1. Plot of WHO SUR data for the number of infected, cured and deceased individuals over the first 8 weeks

Table 3. Containment time with different rate of increase of and decreasing values of "k" at 3%.

Rate of increase in α	0%	2%	4%
Containment Time (weeks)	29	24	21

The data represented in Table 3 may be considered as indicative only, since a lockdown of 24 weeks (nearly 6 months) is rather unrealistic. To mimic partial withdrawal of lockdown, the variation of $|\alpha(t)|$ was considered as a steady increase (of 2%) from the 9th week till the beginning of phased withdrawal, thereafter, a steady decrease (of 2%) till containment. The effect of phased easing of lockdown measures beginning (i) 1st of June (14th week) and (ii) 15th of June (16th week) is summarised in Table 4 below.

Table 4. Containment time for phased withdrawal of lockdown measures

Partial withdrawal of lockdown from & 1st June & 15th June	1st June	18th June
Containment Time (weeks)	32	28

One should note that, simple parametrisation suffers the pitfall of getting absolute numbers, like number of infected people at a particular instant of projected time, erroneous. However, calculations involving ratios, like the time of containment, which depends on the ratio

of infected population at successive instants of time, can be obtained with better accuracy if the initial parameters are carefully chosen.

4. Conclusion

In this simple analysis we have attempted to assess the spread and containment of the COVID-19 through an interplay of a positive scaling (spread of infection) and a power law with negative coefficient (efficacy of lockdown). The COVID Pandemic has left us. This research article started sometime in 2021 and was long lost in the hard drive. Recently we received it and completed the writing. In these tough days we lost many of our close ones. We have overcome the pandemic. We consider this work will help mathematicians and researchers to model any crisis in future.

References

[1] World Health Organization, (2020) India Situation Report, *World Health Organization,* India.

[2] J.K. Aronson, J. Brassey, K.R. Mahtani, (2020). When will it be over?": An introduction to viral reproduction numbers, R0 and Re. The Centre for Evidence-Based Medicine, 14.

[3] D. Brockmann, L. Hufnagel, T. Geisel, The scaling laws of human travel. *Nature*, -(2006) 462-465. https://doi.org/10.1038/nature04292

[4] N. Harding, R.E. Spinney, M. Prokopenko, Phase Transitions in Spatial Connectivity during Influenza Pandemics. *Entropy*, 133(2020) 133. https://doi.org/10.3390/e22020133

[5] Y. Liu, A.A Gayle, A. Wilder-Smith, J. Rocklov, The reproductive number of COVID-19 is higher compared to SARS coronavirus. *Journal of Travel Medicine*, 27 (2020) 1-4. https://doi.org/10.1093/jtm/taaa021

[6] J. Hellewell, S. Abbott, A. Gimma, N.I. Bosse, C.I. Jarvis, T.W. Russell, J.D. Munda, A.J. Kucharski, W.J. Edmunds, Centre for the Mathematical Modelling of Infectious Diseases COVID-19 Working Group, S. Funk, R.M. Eggo, Feasibility of controlling COVID-19 outbreaks by isolation of cases and contacts. *The Lancet Global Health*, 8 (2020) e488-e496. https://doi.org/10.1016/S2214-109X(20)30074-7

[7] E. Klein, G. Lin, K. Tseng, E. Schueller, G. Kapoor, R. Laxminarayan, (2020) COVID-19 for India updates. *Center for Disease Dynamics, Economics, and Policy and Johns Hopkins University*, USA.

Acknowledgements

We thank Dr.Gouranga Biswas, Officer-in-Charge, Government General Degree College at Kushmandi for actively supporting to carry this work.

Conflict of interest: The Authors has no conflicts of interest to declare that they are relevant to the content of this article.