

# Indian Supermodel for Covid-19 Pandemic

National Supermodel Committee

## 1 Introduction

In the current Covid-19 pandemic, an unusual phenomenon is observed: while the infection badly affects a section of population, a large fraction of population show little or no symptoms upon infection. For example, in Delhi, a sero-survey in July-beginning reported 23.5% population having antibodies while the reported recoveries at the start of the survey were around 55 thousand. Taking current population of Delhi to be close to 2 Crores, this is about 0.3% of the population, showing a factor of around 85 in reported and actual infections. Similar story is repeated in the recent ICMR sero-survey in Delhi where around 33% of population was found to be with antibodies while the reported infection was around 1.6 Lakhs, showing a factor of around 40 in reported and actual infections. Sero-survey done in Mumbai in July also threw up similar numbers.

The large presence of such *asymptomatic* patients, who do infect others they come in contact with, changes the dynamics of disease. Instead of the total infected population, number of seriously impacted persons, which is significantly less, becomes more important since only they require major medical intervention. Thus estimates for medical inventory, including oxygen, ventilators, ICUs beds etc needs to be made based on projections of this number. At the same time, asymptomatic patients need to be advised isolation so they do not spread the infection.

The standard model for pandemic dynamics is called SIR, which classifies the population in three categories: Susceptible ( $S$ ), Infected ( $I$ ), and Removed ( $R$ ). A subcategory of Removed is Deceased ( $D$ ). In order to differentiate between asymptomatic and symptomatic patients, we introduce a new category: Asymptomatic ( $A$ ) with population in category  $I$  of SIR model divided into  $A$  (asymptomatic patients) and  $I$  (symptomatic patients). Further, we assume that whether a person goes in  $A$  or  $I$  upon infection solely depends on the physiology of the person (immunity level, genetic disposition, comorbidities etc.). This splits category  $S$  into two:  $S_A$  (these transition to  $A$  upon infection) and  $S_I$  (these transition to  $I$  upon infection).

## 2 Covid-19 Dynamics

Based on above categorization, we write down equations governing progression of the pandemic. We make three simplifying assumptions that help us compute the parameter values governing the dynamics: (1) the average probability of an infected person infecting others remains the same irrespective of the infected person being in  $A$  or  $I$ , (2) the removal rate from both  $A$  and  $I$  categories is the same, and (3) a person in  $A$  or  $I$  category can infect others until he or she moves to  $R$ .

Split  $R$  also into two subcategories:  $R_A$  (those who move from  $A$  to  $R$ ) and  $R_I$  (those who move from  $I$  to  $R$ ). At  $t = 0$  (at the start of pandemic), let

$$\frac{S_I(0)}{S(0)} = \epsilon, R_A(0) = R_I(0) = 0.$$

Also, by dividing all categories with population of the region we are studying, all values become between 0 and 1 satisfying:

$$S_A + S_I + A + I + R_A + R_I = 1.$$

The governing equations for the pandemic are:

$$\frac{dS_A}{dt} = -\beta S_A(A + I) \quad (1)$$

$$\frac{dS_I}{dt} = -\beta S_I(A + I) \quad (2)$$

$$\frac{dA}{dt} = \beta S_A(A + I) - \gamma A \quad (3)$$

$$\frac{dI}{dt} = \beta S_I(A + I) - \gamma I \quad (4)$$

$$\frac{dR_A}{dt} = \gamma A \quad (5)$$

$$\frac{dR_I}{dt} = \gamma I, \quad (6)$$

$$\frac{dD}{dt} = \eta I, \quad (7)$$

where  $\beta$  is the average probability of an infected person passing it to another,  $\gamma$  is the average removal rate, and  $\eta$  is average mortality. Note that everyone in category  $A$  recovers and hence  $A$  does not contribute to  $D$ .

Letting  $M = A + I$ ,  $R = R_A + R_I$ , and  $S = S_H + S_L$ , the model becomes the standard SIR model with equations:

$$\frac{dS}{dt} = -\beta SM \quad (8)$$

$$\frac{dM}{dt} = \beta SM - \gamma M \quad (9)$$

$$\frac{dR}{dt} = \gamma M. \quad (10)$$

Dividing equation (2) by (8):

$$\frac{dS_I}{dS} = \frac{S_I}{S},$$

giving

$$S_I = \epsilon S.$$

Thus,  $S_I$  is *always* an  $\epsilon$  fraction of  $S$ . Substituting in equations (9) and (4):

$$\begin{aligned} \frac{dI}{dt} + \gamma I &= \beta S_I M \\ &= \epsilon \beta S M \\ &= \epsilon \left( \frac{dM}{dt} + \gamma M \right). \end{aligned}$$

Rearranging, we get:

$$\frac{d(I - \epsilon M)}{dt} = -\gamma(I - \epsilon M).$$

This gives:

$$I - \epsilon M = (I(0) - \epsilon M(0))e^{-\gamma t}.$$

Above equation shows that  $I$  converges to  $\epsilon M$  rapidly since both  $I(0)$  and  $M(0)$  are negligible. Same can be shown for  $R_I$  and  $R$ :

$$\begin{aligned}\frac{d(R_I - \epsilon R)}{dt} &= \gamma(I - \epsilon M) \\ &= \gamma(I(0) - \epsilon M(0))e^{-\gamma t}.\end{aligned}$$

Hence:

$$R_I - \epsilon R_M = -(I(0) - \epsilon M(0))e^{-\gamma t},$$

given that  $R_I(0) = 0 = R(0)$ . We get the same conclusion:  $R_I$  converges to  $\epsilon R$  rapidly. Therefore, for some small time value  $t_0$ , we can assume that above convergences have taken place, and take:

$$\begin{aligned}I &\approx \epsilon M \\ R_I &\approx \epsilon R\end{aligned}$$

### 3 Estimating Parameter Values

There are four parameters in above equations:  $\beta$ ,  $\gamma$ ,  $\eta$ , and  $\epsilon$ . For data, we have three daily time series available: active infections, cumulative removed, and cumulative deaths. These three provide us with daily values of  $I$ ,  $R_I$ , and  $D$  respectively. Strictly speaking, active infections and cumulative removed also include subsets of  $A$  and  $R_A$  – we will discuss effects of it in subsection 3.4.

#### 3.1 Estimating $\gamma$

Parameter  $\gamma$  can be estimated using equation (6):

$$R_I(T) - R_I(T - 7) = \int_{T-7}^T \frac{dR_I}{dt} dt = \gamma \int_{T-7}^T I dt.$$

We can collect data for multiple values of  $T$ , fit the best line passing through origin through these points, and take  $\gamma$  as the slope of the line.

#### 3.2 Estimating $\eta$

This is done exactly as above using the equation (7).

#### 3.3 Estimating $\epsilon$ and $\beta$

Rewrite equation (4) as:

$$\begin{aligned}\frac{dI}{dt} &= \beta S_I M - \gamma I \\ &= \beta S I - \frac{dR_I}{dt},\end{aligned}$$

resulting in

$$\begin{aligned}\frac{d(I + R_I)}{dt} &= \beta(1 - M - R)I \\ &= \beta\left(1 - \frac{I}{\epsilon} - \frac{R_I}{\epsilon}\right)I \\ &= \beta I - \frac{\beta}{\epsilon}(I + R_I)I.\end{aligned}$$

Rewriting this as

$$I = \frac{1}{\beta} \frac{d(I + R_I)}{dt} + \frac{1}{\epsilon} (I + R_I)I,$$

we integrate over a window of seven days:

$$\int_{T-7}^T I dt = \frac{1}{\beta} \{(I + R_I)(T) - (I + R_I)(T - 7)\} + \frac{1}{\epsilon} \int_{T-7}^T (I + R_I)I dt.$$

Computing it for several values of  $T$ , we simultaneously estimate the value of  $\beta$  and  $\epsilon$  from above using linear regression.

The value of  $\epsilon$  thus obtained can be cross-validated by comparing against seropositive data, if available, which measures the value of  $R$  at certain instant.

### 3.4 Variability of Parameters

All the four parameters change with time.

- Parameter  $\beta$  is a function of interactions between people and so lockdowns directly impact it by reducing it.
- Parameters  $\gamma$  and  $\eta$  are functions of medical care available. Improvements in medical care increase  $\gamma$  and reduce  $\eta$ .
- Parameter  $\epsilon$  should not change as it is a fixed ratio at the beginning of pandemic. However, its measurement is not exact for two reasons: (i) initially the infection is limited to a very small part of the region if the region under study is large, and it takes time for it to spread to entire region. However, since we are always dividing all numbers by total population of the region,  $\epsilon$  will be much smaller than its actual value initially and slowly increase to eventually stabilize once entire region is covered – this makes  $\epsilon$  also dependent on lockdown, (ii) measured values of active infections and cumulative removed also include parts of  $A$  and  $R_A$  respectively. Hence, actual values of  $I$  and  $R_I$  are smaller than used in parameter estimation. This causes value of  $\epsilon$  to be overestimated. Adjustments can be made to get real value of  $\epsilon$  by estimating how is the infection spreading in the region and recording the fraction of asymptomatic cases in reported positive ones.

This variation in parameter values requires multiple estimations to be done for different time periods. These time periods should coincide with the various lockdown strategies implemented. Once we measure the variation in parameter values, we get additional useful information about relative success of lockdown strategies, improvement in medical interventions, and also how fast is the disease spreading in different parts of the region (by detecting change in  $\epsilon$  value).