

# COEFFICIENT IDENTIFICATION IN SIQR MODEL OF INVERSE PROBLEM OF COVID -19

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**Abstract**—*The effect in the present paper inflict with the inverse problem in the epidemiology based on SIQR model with time dependent infectivity and recovery rates , authorizing for a better prognosticate of the long term darwinism of a pandemic. We used the method to analyze the Covid-19 spread by the solution of an inverse problem to find the infectivity and recovery rates from the original data and then the approximate rates are used to compute the examine of the disease. We used the time dependent parameters to estimate the spread of disease Covid-19 in the country India.*

**Keywords**—*SIQR model, inverse problem, parameter estimation, infectivity and recovery rates projections.*

## I. INTRODUCTION

The Covid-19 corona virus disease is arise from the Wuhan city of the Hubai (China) in the end month of the year 2019. The corona virus quickly spread all over the every country in the world. In the last week of the April there were approximately more than three million infected people confirmed with the death of more than 200,00 people all over the world. Governments taken a effective step to close lots off enterprising peace, so called non essential businesses and facilities for weeks in order to slow down the growth of infections especially to save the life of population. In the last week of May more than 6 million infected case are confirmed and more than 370,00 deaths reported globally. Many mathematical models adopted to predict of the future of the Covid-19 epidemic all over the world. As there is no such effective drugs to control the infection and no vaccines for this highly communicable disease.

Many mathematical models are used to forecast the spread of epidemic disease , if we see in the history [13, 15, 20, 37]. In 1766 Daniel Bernoulli generate a mathematical model to describe the practice of inoculation against small pox [24]. Many other infectious disease like measles, malaria, varicella, HIV, Ebola and SARS etc., some of the infectious disease has no vaccine , only preventive practices[25].

In 1921 Kermack and McKendrik, first introduce their SIR model to explain the rapid rise and fall in the number of infected people with a contagious illness in a closed population over time. SIR model is the basic model to analyze and predict evolution of a disease.

For Covid-19 best mathematical modeling is to applies by using one of the variant SIQR [3] model. In which isolation of infected person plays a major part. This model helps to analyze the effect of the disease has been carried out for many affected nations countries USA, Canada, Italy, France, Germany,

Sweeden, India, Russia, Brazil, Bulgaria, New Zeland. The focus of the present work is to develop a method to point out the accurate time dependent parameters of SIQR model.

To estimate the parameter is an inverse problem. It indicates that calibrate the parameters of a model to recreate measure data .Inverse problem is climacteric for computing the model and for handle the model parameters. Proposal elaborate inverse problem can be opulencely applied different processes, with the spread of infectious disease, allowing epidemiologists and public health specialists to make prediction on epidemic [15]. In the present work proposed a method for evaluate the optimal values for the infectivity and recovery rates.

## II. PROBLEM FORMULATION

### Direct Problem-

SIQR model is the extended form of classical SIR appears to be particularly most suitable for the modeling of covid-19 [5].SIQR model indicates, S susceptible, I, infected, Q quarantine and R recovered. In the given model there are two types of infected individuals first who quarantine and second who don't (asymptomatic or negligence). In the present model susceptible indicates those individuals has the probability of getting infected. Susceptible becomes infected by the virus may be asymptomatic or have symptoms. Infected individuals who increase the symptoms and become lonely is observe as quarantine. Recovered indicates those infectious individuals or quarantine who become healthy or died from the disease. The total population size is denoted by N.

$$\text{Susceptible } \{0 \quad 0 \quad 0 \quad 0 \quad 0\} S'(t) \propto -S \& I$$

↓  $\beta$  - infectious rate

$$\text{Infected } \{0 \quad 0 \quad 0\} I'(t) \propto I \& S$$

↓  $\eta$  – rate of new case detected *Quarantine*  $\{0 \quad 0\} Q'(t) \propto Q \& I$

↓  $\alpha$  - rate of removal of asymptomatic cases *Recovered*  $\{0 \quad 0\} R'(t) \propto Q \& I$

Figure 1 indicate the dependence of each component of the SIQR model, where S is susceptible, I is infected, Q for recovered. Right hand side of the picture represents the dependence of the rate of change on S,I,Q,R and also mention four proportionality constants relating each parameter of the model.

Differential equations of each part of the model is as follow

$$\frac{dS}{dt} = -\frac{\beta SI}{N(1-l)} \quad (1)$$

$$\frac{dI}{dt} = \frac{\beta SI}{N(1-l)} - (\alpha + \eta)I \quad (2)$$

$$\frac{dQ}{dt} = \eta I - \gamma Q \quad (3)$$

$$\frac{dR}{dt} = \gamma Q + \alpha I \quad (4)$$

Where ,  $\beta$  is the infectious rate ,  $\eta$  indicates the rate at which new cases are recognized from the infected population.  $\gamma$  indicates the rate at which isolation are become removed (recovered or died) .  $\alpha$  indicating the removal rate of infected individuals who are asymptomatic and didn't become quarantined, N

consider as population size. The factor  $(1-l)$  to  $N$  with 'l' being the fraction of population following lockdown, is used to consider lockdown. But we assume that everyone not following lockdown so every person has equal probability to become infected in to contact with every other person.

Since the differential equation (1) and (2) independent from  $Q$  and  $R$ . So it is to separate the system in to two parts – equation (1) & (2) is separated system and (3) & (4) are others. If the coefficient  $\beta$  &  $\alpha$  given, we can solve the problem numerically after driving the initial conditions from the given data by any of the well known methods from initial value problems (IVPs). We can get more methods for numerical solution of IVPs from [12].

The important question arise here, how can we get the coefficient  $\beta$  &  $\alpha$  from the infection i.e. Covid-19. Estimation of parameter  $\beta$  &  $\alpha$  is an inverse problem which is solved in [32]. A same method is used for estimating parameters in an Euler-Bernoulli equation from over posed data [31] & [34].

#### Inverse Problem -

From the available data we suppose the values of  $S$  and  $I$  at different two points, at beginning time  $S(T_b)$  and at ending time  $S(T_e)$

$$S(T_b) = S_b, \quad I(T_b) = I_b \quad (4)$$

$$S(T_e) = S_e, \quad I(T_e) = I_e \quad (5)$$

If the parameters are known than equation (1) and (2) can be solved by taken equation (4) as boundary value. Mostly boundary values (5) assure exactly. So if the parameters  $\beta$  and  $\alpha$  are known, the problem can be find.

Let us suppose that the parameters  $\beta$  and  $\alpha$  are constant and unknown. In this situation, the general solution of the system the system (1) and (2) depends on four constants – two constants we get from integration and another two are the unknown parameters  $\beta$  and  $\alpha$ . The equation (4) and (5) also shows four conditions; therefore the problem for finding the parameters by the side with the functions is  $S$  and  $I$  is well posed, anticipate an exact solution can be obtained. Such kind of problem are known as *inverse problem*.

Even now problem could be ill- posed for determining  $(S, I)$  ( $\beta, \alpha$ ) by equation (1) and (2) under the condition (4) and (5). For arbitrary values of  $S_b, S_e, I_b, I_e$  there may be no solution of  $(S, I)$  and  $(\beta, \alpha)$  satisfying the equation (1), (2) and all of the conditions in (4) and (5). For this basis, we suppose that the problem is posed accurately after Tikhonov [45]. It means the solution exists.

For inverse problem (1), (2) and (4), (5), we establish an algorithm to find the approximation solution of  $(S, I)$  and  $(\beta, \alpha)$ . For finding the parameters  $(\beta, \alpha)$  of SIQR model using a very similar method used as in [32].

Parameters  $\beta$  and  $\alpha$  depend on time –

The SIQR model suppose that the parameters  $\beta$  and  $\alpha$  are constants. But in Covid-19 pandemic, the parameters depend on time, i.e.  $\alpha = \alpha(t)$  and  $\beta = \beta(t)$ . Governments limitations, lockdown, treatment and social experiences etc., can affect the parameters. For the functions  $(t_k), I(t_k)$ , let  $D$  be the data set at different time moment  $t_1, t_2, \dots$ . For finding the solution of inverse problem (1), (2) under the

condition (4), (5) and data set  $D$ , we assume an algorithm. Let us assume that  $\beta$  and  $\alpha$  be piece-wise constant (step) functions of time.

$$\alpha(t) = \alpha_k \text{ and } \beta(t) = \beta_k \text{ for } t_{k-1} < t < t_k \quad (6)$$

Solving the inverse problem (1), (2), (4), (5), constants  $\beta_k$  and  $\alpha_k$  can be estimated using  $S_b = S(t_{k-1}), S_e = S(t_k), I_b = I(t_{k-1}), I_e = I(t_k)$ , for  $k = 2, 3, \dots$

#### Reproduction rate and herd immunity

In the history of epidemics it is observed that, epidemics increase if the derivative  $dI/dt > 0$  and decrease if  $dI/dt < 0$ . Considering the people not following lockdown to be susceptible, i.e.  $S \approx N(1 - I)$  and approximating equation (2) to

$$\frac{dI}{dt} = [\beta - (\alpha + \eta)]I \quad (7)$$

An important parameter which is used to quantify the transmission ability of a disease is defined as the average number of infected individuals by the only individual and formulated as follows:

$$R_0 = \frac{\beta}{\alpha + \eta} \quad (8)$$

From equation (7) and (8), it follows that

$$\frac{dI}{dt} = [R_0 - 1](\alpha + \eta)I$$

Consequently, the epidemic increases if  $R_0 > 1$  and decreases if  $R_0 < 1$ .

One another major parameter of an infectious disease is *herd immunity*. Herd immunity means the minimum fraction of the population,  $\hat{f}$ , that is required to have immunity to prevent an epidemic [38]. Population acquires herd immunity in two ways. First one, the *natural* way is to let the epidemic spread until the required fraction of the population,  $\hat{f}$ , obtains immunity. Second way is vaccination, which is non-natural. But for Covid-19, recently there is no availability of vaccine. So most of the countries have been practicing to wear masks and maintain social distancing to slow down the spread of the epidemic.

### III Solving the inverse problem for the time dependent infectivity and recovery rates

Some theoretical appearance and method for solving the inverse problem to find the constant coefficient  $\beta$  &  $\alpha$  given in [32]. A numerical algorithm will be established to estimate the time-dependent coefficient, i.e.,  $\beta = \beta(t)$  and  $\alpha = \alpha(t)$  in the present paper. To find the time-dependent infectivity and recovery rates, we used the method to solve the inverse problem referred to by [34]. In the paper, the original problem was changed to minimization.

At two time moments using data values for the minimization problem

Now we come to a sub-problem in the case of using data values at two time moments. For the numerical solution of the system (1)-(4), we make an effort to do an approximation of the function  $I(t)$ ,  $Q(t)$  and  $R(t)$  at the discrete set  $\{t_0, t_1, t_2, \dots, t_n\}$  of points in the interval  $[T_b, T_e]$ , where  $T_b$  indicates the beginning time moment,  $T_e$  indicates the end time moment, and  $n$  is an integer which is greater than 1. The mesh of equidistant points is shown in figure .2

Figure 2. The mesh of equidistant point  $t_k = T_b + k\tau, k = 0, 1, 2, \dots, n$ .

We define the step size as  $\tau = \frac{T_e - T_b}{n-1}$ . The nodes are the equidistant points  $t_k = T_b + k\tau, k = 0, 1, 2, \dots, n$ . Now equation (1) and (2) organized for discretization

$$S_k = S_{k-1} - \frac{\tau\beta\hat{S}_k\hat{I}_k}{N(1-l)} \quad (9)$$

$$I_k = I_{k-1} + \tau \left( \frac{\beta\hat{S}_k\hat{I}_k}{N(1-l)} - (\alpha + \eta)\hat{I}_k \right) \quad (10)$$

Where  $\hat{S}_k = (\hat{S}_{k-1} + \hat{S}_k)/2, \hat{I}_k = (\hat{I}_{k-1} + \hat{I}_k)/2$  for  $k = 1, 2, \dots, n$ .

This approximation secured next approximation  $O(\tau^2)$ . Because the system (9) - (10) is non-linear, we use an iterative method and acquire the values of  $\hat{S}_k$  and  $\hat{I}_k$  by the previous iteration. Consider the function.

$$\begin{aligned} \varphi(\beta, \alpha, S_1, \dots, S_{n-1}, I_1, \dots, I_{n-1}) &= \sum_{k=1}^{n-1} (\epsilon_k^2 + \delta_k^2) \\ &= \sum_{k=1}^{n-1} \left[ (S_k - S_{k-1} + \frac{\tau\beta\hat{S}_k\hat{I}_k}{N(1-l)})^2 + (I_k - I_{k-1} - \tau \left( \frac{\beta\hat{S}_k\hat{I}_k}{N(1-l)} - (\alpha + \eta)\hat{I}_k \right))^2 \right] \end{aligned} \quad (11)$$

Where  $\epsilon_k$  and  $\delta_k$  are the residual of equation of (9) and (10), respectively.

Absolute minimum value of the function  $\varphi$  is zero, it's a homogeneous quadratic function of  $\epsilon_k$  and  $\delta_k$ . If and only if  $\epsilon_k = 0$  and  $\delta_k = 0$ , for all  $k = 1, 2, \dots, n-1$ , the function attains its minimum. Hence the problem is for minimization of the function  $\varphi$  for the conditions given by (5) and (6), if there exists one-to-one correspondence for the solution of the system of equations (9), (10), (5), (6)

Equations for susceptible  $S$  and infected  $I$

The necessary conditions for minimization of the function  $\varphi$

With respect to its arguments  $S_k$  and  $I_k$  are

$$\frac{\partial \varphi}{\partial S_k} = 0, \quad \frac{\partial \varphi}{\partial I_k} = 0 \quad (12)$$

Conditions (12) yield the following difference equations

$$S_{k-1} - 2S_k + S_{k+1} = \tau\beta \left( \frac{S_k I_k}{N(1-l)} - \frac{S_{k+1} I_{k+1}}{N(1-l)} \right), \quad (13)$$

$$I_{k-1} - 2I_k + I_{k+1} = \tau \left( -\frac{\beta S_k I_k}{N(1-l)} + \beta \frac{S_{k+1} I_{k+1}}{N(1-l)} + (\alpha + \eta)I_k - (\alpha + \eta)I_{k+1} \right) \quad (14)$$

For  $k = 1, 2, \dots, n-1$ . Adding beginning and ending condition (5) and (6), we obtain a well-posed linear system of  $2(n+1)$  equations for the unknown sets of values  $(S_0, S_1, S_2, \dots, S_n)$  and  $(I_0, I_1, I_2, \dots, I_n)$

Equation for  $\beta$  and  $\alpha$

We will write the function  $\varphi$  in the form

$$\varphi = \gamma_{00} + \gamma_{10}\beta + \gamma_{01}\alpha + \gamma_{20}\beta^2 + \gamma_{11}\beta\alpha + \gamma_{02}\alpha^2 \quad (15)$$

Where

$$\gamma_{00} = \sum_{k=1}^{n-1} (S_k - S_{k-1})^2 + (I_k - I_{k-1})^2 \tag{16}$$

$$\gamma_{10} = \sum_{k=1}^{n-1} -\frac{2\hat{S}_k \hat{I}_k (I_k - I_{k-1} - S_k - S_{k-1}) \tau}{N(1-l)} \tag{17}$$

$$\gamma_{01} = \sum_{k=1}^{n-1} 2 \hat{I}_k (I_k - I_{k-1}) \tau \tag{18}$$

$$\gamma_{20} = \sum_{k=1}^{n-1} \frac{2\hat{S}_k^2 \hat{I}_k^2 \tau^2}{(N(1-l))^2} \tag{19}$$

$$\gamma_{11} = \sum_{k=1}^{n-1} \frac{-22\hat{S}_k^2 \hat{I}_k^2 \tau^2}{N(1-l)} \tag{20}$$

$$\gamma_{02} = \sum_{k=1}^{n-1} \hat{I}_k^2 \tau^2 \tag{21}$$

The necessary condition for minimization of the function  $\varphi$  with respect to  $\beta$  and  $\alpha$  are as follows

$$\frac{\partial \varphi}{\partial \beta} = \gamma_{10} + 2\gamma_{20}\beta + \gamma_{11}\alpha = 0 \tag{22}$$

$$\frac{\partial \varphi}{\partial \alpha} = \gamma_{01} + \gamma_{11}\beta + 2\gamma_{02}\alpha = 0 \tag{23}$$

The solution of the system (22) and (23) is

$$\beta = -\frac{2\gamma_{02}\gamma_{10} - \gamma_{01}\gamma_{11}}{-\gamma_{11}^2 + 4\gamma_{02}\gamma_{20}} \tag{24}$$

$$\alpha = -\frac{\gamma_{10}\gamma_{11} - 2\gamma_{01}\gamma_{20}}{\gamma_{11}^2 - 4\gamma_{02}\gamma_{20}} \tag{25}$$

### Minimization problem using entire data set

Let us suppose that at some time moment the number of infectious individuals  $v_1, v_2, \dots, v_m$  is known and given by

$$I(v_f) = \sigma_f \tag{26}$$

For  $f = 1, 2, \dots, m$ , while the values of the coefficients  $\beta$  and  $\alpha$  are known.

Assume that for every  $1 < f < m$ , there exist index  $k_f$  such that  $v_f = t_{k_f}$  i.e. the set of time moments  $\{v_1, v_2, \dots, v_m\}$  is a subset of the set of mesh nodes  $\{t_1, t_2, \dots, t_n\}$ . To simplify the calculation, let us assume the notation  $\chi_k$  such as: if there exist  $k \in \{0, 1, 2, \dots, n\}$  such that  $t_k = v_f$ ,  $1 < f < m$  then  $\chi_k = \sigma_f$  and  $\mu_k > 0$ , otherwise  $\chi_k$  and  $\mu_k = 0$ , where  $\mu_k$  is the weight of the equation (26) in the LSM.

Similarly, we consider the function from equation (11)

$$\begin{aligned} \varphi(\beta, \alpha, S_1, \dots, S_{n-1}, I_1, \dots, I_{n-1}) &= \sum_{k=1}^{n-1} (\epsilon_k^2 + \delta_k^2 + \mu_k (I_{k_f} - \sigma_f)^2) \\ &= \sum_{k=1}^{n-1} [(S_k - S_{k-1} + \frac{\tau \beta \hat{S}_k \hat{I}_k}{N(1-l)})^2 + (I_k - I_{k-1} - \tau (\frac{\beta \hat{S}_k \hat{I}_k}{N(1-l)} - (\alpha + \eta) \hat{I}_k))^2 + \mu_k (I_k - \chi_k)^2] \end{aligned} \tag{27}$$

Where  $\epsilon_k$  and  $\delta_k$  are residual of the equation (9) and (10), respectively.

Equation for susceptible  $S$  and infected  $I$

The necessary condition for minimizations of the function  $\varphi$  with respect to  $S_k$  and  $I_k$  are given by the equation (12). We get

$$S_{k-1} - 2S_k + S_{k+1} = \tau\beta \left( \frac{S_k I_k}{N(1-l)} - \frac{S_{k+1} I_{k+1}}{N(1-l)} \right) \quad (28)$$

$$I_{k-1} - (2 + \mu_k)I_k + I_{k+1} = \tau \left( -\frac{\beta S_k I_k}{N(1-l)} + \beta \frac{S_{k+1} I_{k+1}}{N(1-l)} + (\alpha + \eta)I_k - (\alpha + \eta)I_{k+1} \right) - \mu_k \chi_k \quad (29)$$

For  $k = 1, 2, \dots, n - 1$ . After adding the starting and end conditions (5), (6), we get a well-posed linear system with  $2(n + 1)$  equations for the unknown set of values  $(S_0, S_1, S_2, \dots, S_n)$  and  $(I_0, I_1, I_2, \dots, I_n)$ .

### Equations for $\beta$ and $\alpha$ .

In this case the equations for  $\beta$  and  $\alpha$  are the same as the equations (24) and (25), derived in section III.

### Algorithm for solving the inverse problem

To solve the system (13), (14), (5), (6), we use following application:

- i) With given initial condition for  $\hat{S}, \hat{I}, \beta, \alpha$ , the system (13), (14), (5), (6) is solved for the function  $S$  and  $I$ .
- ii) Enumerate the deviation of the values of  $S$  and  $I$  from  $\bar{S}$  and  $\bar{I}$  as follow :

$$\left\| \frac{S - \bar{S}}{\bar{S}} \right\| < \epsilon_0, \quad \left\| \frac{I - \bar{I}}{\bar{I}} \right\| < \epsilon_0 \quad (30)$$

If both values are smaller than a sufferance  $\epsilon_0$

,then the algorithm goes to iii); apart from that  $\hat{S}$  and  $\hat{I}$  are replaced by  $S$  and  $I$ , respectively, and the computation back to i);

- iii) The coefficient  $\beta$  and  $\alpha$  are calculated from (24) and (25). If the difference between new and old values of  $\beta$  and  $\alpha$

$$|\beta - \bar{\beta}| < \epsilon_0, |\alpha - \bar{\alpha}| < \epsilon_0 \quad (31)$$

Is less than  $\epsilon_0$  then calculation will discontinue; otherwise iteration goes on and return to i).

For all calculation which presenting here, we use  $\epsilon_0 = 5 \times 10^{-10}$ .

### Parameters $\beta$ and $\alpha$ and $R_0$ as a function of time

The data set (26) contains the number of infected individuals for every day for a period of  $m$  days. Now distribute the set into subset of fixed length of  $P$  days (e.i.  $P = 14$  days)fg. For every sub-interval  $[k - P + 1, k]$  and  $= P, P + 1, \dots, m$ , implement the algorithm introduce in the part 3.

Therefore, we get  $\beta_k, \alpha_k$  as a function of time. For every sub-interval we evaluate the value of reproduction rate

$$R_k = \frac{\beta_k}{\alpha_k + \eta_k}$$

#### IV Projection and Data mining

With the help of the present model we can recognize the most unfavorable scenario and exact action proposal to achieve the best possible outcome under the given conditions.

The prediction of the spread of the disease are depend on the available data of COVID -19 of 18 November, 2020, [46] [47]. Our model shows the optimal value of  $\varepsilon_0 = 10^{-8}$ . We can calculate the parameters  $\beta, \alpha$  and  $R_0$  as a function of time with the help of  $\tau = 1/40$  and  $\mu = \tau$  and approximately found over the interval of 14 days. The dynamic of this epidemic is projected based on the values of the parameters taken at the last day of the period used for the transmission and cured rate estimation.

To recognize the dynamics of the infectious disease, we use some important characteristics are as follows;

- Estimated up- to-date transmission rate  $\beta(t)$ ;
- Estimated up-to-date removal rate  $\alpha(t)$ ;
- Estimated up-to-date reproduction rate  $R_0(t)$ ;
- Projected COVID-19 infectious cases  $I(t)$  using the up-to-date estimated rates,

If the coefficients are given, all the four functions  $S(t), I(t), Q(t), R(t)$  are satisfy direct problem. In order to forecast of upcoming behavior of the epidemic, we calculate numerical solution of the direct problem (1) – (4) with the help of the initial constraints after illustrate  $\beta$  and  $\alpha$ . In all computation, we use Runge-Kutta method of order second and predictor-corrector method. The first footstep is as follows:

$$S_k^p = S_{k-1} - \frac{\tau \beta S_{k-1} I_{k-1}}{N(1-l)} \quad (33)$$

$$I_k^p = I_{k-1} + \frac{\tau \beta S_{k-1} I_{k-1}}{N(1-l)} - \tau(\alpha + \eta) I_{k-1} \quad (34)$$

$$Q_k^p = Q_{k-1} + \tau \eta I_{k-1} - \tau \gamma Q_{k-1} \quad (35)$$

$$R_k^p = R_{k-1} + \tau \gamma Q_{k-1} + \tau \alpha I_{k-1} \quad (36)$$

After getting the prediction in the first step, now refine the calculation in the corrector method.

$$S_k^c = S_{k-1} - \frac{\tau \beta S_{k-1}^p I_{k-1}^p}{N(1-l)} \quad (37)$$

$$I_k^c = I_{k-1} + \frac{\tau \beta S_{k-1}^p I_{k-1}^p}{N(1-l)} - \tau(\alpha + \eta) I_{k-1}^p \quad (38)$$

$$Q_k^c = Q_{k-1} + \tau \eta I_{k-1}^p - \tau \gamma Q_{k-1}^p \quad (39)$$

$$R_k^c = R_{k-1} + \tau \gamma Q_{k-1}^p + \tau \alpha I_{k-1}^p \quad (40)$$

At the end

$$S_k = 0.5(S_k^p + S_k^c), I_k = 0.5(I_k^p + I_k^c),$$

$$Q_k = 0.5(Q_k^p + Q_k^c), R_k = 0.5(R_k^p + R_k^c), \quad (41)$$

for  $k = 1, 2, 3 \dots$ . We use  $\tau = 0.01$  for simplify the direct issue numerically by Runge-kutta method.

Figures 2, 3, 4 and 5 shows that these prediction are effective as far as the rates remains as approximated; since COVID-19 is highly infectious disease, we don't know more about the transmission rate, removal rate, reproduction can instantaneously affect due to compute and /or policy to control the disease can influence the spread. Anyhow after few months people become aware to protect themselves from disease; hence this indicate that the transmission and reproduction rate become slow and removal rate increasing.

Table 1: The values  $\beta$ ,  $\alpha$ , and  $R_0$  for the last day consideration

Days	$\beta$	$\alpha$
$R_0$		
14	1.8165681e-09	0.00020484
	1.1730921	



Fig.1: The mesh of equidistant point  $t_k = T_b + k\tau$ ,  $k = 0, 1, 2, 3 \dots n$ .

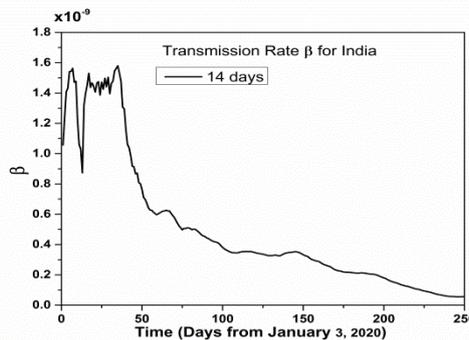


Fig.2: Transmition rate as function of time calculated over 14 days interval.

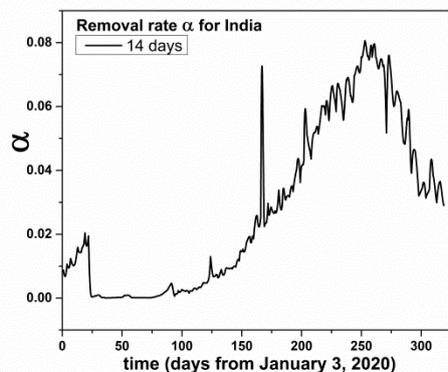


Fig.3: Removal rate as function of time calculated over 14 days interval.

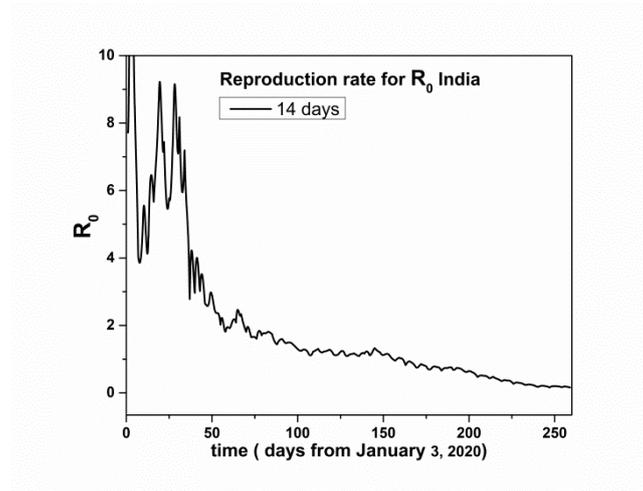


Fig.4 : Reproduction rate as function of time calculated over 14 days interval.

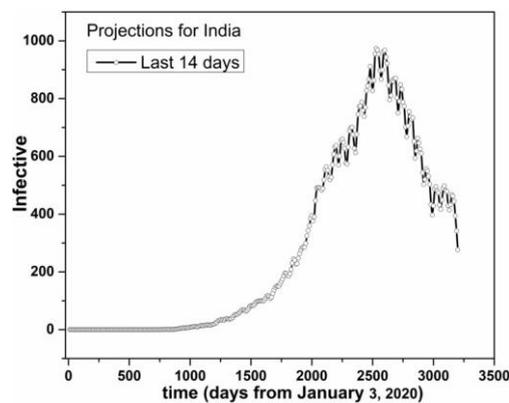


Fig.5 : Forecasts, based on 14 days interval estimations of  $\beta$ ,  $\alpha$ .

## Conclusion

The inverse problem for estimating the time dependent transmission rate and removal rate in *SIQR* model is derived and solved. With the obtained results, estimate the transmission rate and removal rates. The Numerically calculated rates are used to forecasting the COVID-19 pandemic in India. The result of this research give insight of the pandemic in India and could help in determining policy. The *SIQR* model is good choice for short period of time of this epidemic. In future, we can use other models and depending on future developments of the disease, we can consider models addressing non-constant population, latency, reinfection and vaccine.

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