



# Numerical Simulation and Design of COVID-19 Forecasting Framework Using Efficient Data Analytics Methodologies

Puneet Pathak<sup>a</sup>, Chetan Kumar<sup>b</sup>

<sup>a</sup> M.Tech. Scholar, Department of Computer Science & Engineering, KITE, Jaipur, India

<sup>b</sup> Associate Professor, Department of Computer Science & Engineering, KITE, Jaipur, India

puneetpathak27@gmail.com<sup>a</sup>, chetanmnit@yahoo.in<sup>b</sup>

## Abstract

The COVID-19 pandemic hit globally in December 2019 when a certain virus strain from Wuhan, China started proliferating throughout the world. By the end of March 2020, lockdowns and curfews were imposed all over the world halting trade, commerce, education, and various other essential activities. It has been nearly a year since the WHO declared a pandemic but there is still a consistent rise of the cases even with the administration of various types of vaccines and preventive measure. One of the main struggles that the healthcare workers face is to find out the how the virus is spreading amongst a community. The knowledge of this can be used to stop the spread of virus. This is a very important step towards getting things back into momentum to restore activities globally. Many attempts have been made under epidemiology to study the spread of COVID and many mathematical models have emerged as a result that can help with this. A popular model that is used for estimating the effective reproduction number ( $R_t$ ) has the shortcoming that it cannot simultaneously forecast the future number of cases. This work explores an extension of another model, the SIR-model, in which the model parameters are fitted to recorded data. This makes the model adaptive, opening up the possibilities for estimating the  $R_t$  daily and making predictions of future number of confirmed cases. The paper use this adaptive SIR-model (aSIR) to estimate the  $R_t$  and create forecasts of new cases in India. The paper purpose is to determine how precise aSIR-models are at estimating the  $R_t$  (when compared with FHM's model). It will also analyze how accurate aSIR-models are at simultaneously forecasting the future spread of Covid-19 in India. The coronavirus spread can be mathematically modelled using factors such as the number of susceptible people, exposed people, infected people, asymptotic people and the number of recovered people. The Khan-Atangana system is an integer-order coronavirus model that uses the above-mentioned factors. Since the coronavirus model depends on the initial conditions, the Khan-Atangana model uses the Atangana-Baleanu operate as it has a non-variant and non-local kernel. Instead, we replace the equations with fractional-order derivatives using the Grünwald-Letnikov derivative. The fractional order derivatives need to be fed with initial conditions and are useful to determine the spread due to their non-local nature. This project proposes to solve these fractional-order derivatives using numerical methods and analyse the stability of this epidemiological model.

**Keywords:** Covid-19, aSIR-Model, RMSE, FHM Model.

## 1. INTRODUCTION

Late in 2019, SARS-COV2 (COVID-19) broke out in Wuhan City, China, and then spread to other parts of the world. The COVID-19 epidemic has affected every aspect of our daily lives and has spread to more than 220 countries and territories worldwide. As of 22nd January 2022, a total of 34,64,64,304 (55, 85,224) contaminated (dead) COVID-19 instances were accounted worldwide [1]. The quantities of infected cases

passing notwithstanding everything increase generally and do not reflect a very much managed situation. This illness has been classified as a global epidemic by the WHO, along with the numerous controls used to determine the scope of the epidemic.

Human Covids, including as SARS-CoV and MERS-CoV, have emerged from the global pandemic caused by animal sources in the twenty-first century with an alarming death rate





and morbidity. The Coronavirinae subgroup, which is a part of the Coronaviridae group, is where the human COVID-19 infections belong. Due to the presence of spikes in the design on the exterior surface of the infection when seen with an electron microscope, it was given the name COVID-19. Its nucleic material varies in length from 26 to 32 KBS and has a single abandoned RNA with a diameter of 80 to 120 nm [2]. These are primarily divided into four different genera called,,. The majority of the time, as well as -CoV contaminate vertebrates, but as well as -CoV later began to affect birds. HCoV-229E, as well as HCoV-NL63 of -CoVs, HCoV-HKU1 and HCoV-OC43 of -CoVs, exhibit mild pathogenicity and moderate respiratory side effects as typical viruses among the six unprotected human infections. The other 2 identifiable -CoVs, including SARS-CoV and MERS-CoV, exhibit severe and potentially fatal respiratory diseases [3].

While the profoundly pathogenic infection predominantly influences individuals through respiratory droplets, disseminated via ecological contact [5, 6]. Unlike the various respiratory infections, other studies [7, 8] recommended that the SARS-CoV-2 communicated through the oral-fecal course. An ongoing investigation was done in ref. [9] on stool specimens of seventy-one individuals with COVID-19, 39 individuals +ve for fecal COVID-19 RNA, which supports the speculation that fecal-oral contamination could be an extra course for the extent of the infection. Generally, COVID-19 manifestations are cough, fever, as well as fatigue [10–12].

Various gastrointestinal indications showed in contaminated individuals like diarrhea, nausea, as well as deficiency of appetite [13, 14]. It is also important to note that the infection contamination could happen with no manifestation; asymptomatic people are a possible wellspring of infection transmission. Consequently, stringent adherence to the climate, hand cleanliness, as well as contact segregation is needed to guarantee viral control.

COVID-19 as well as various respiratory asperity condition viruses [15]. It acts a real job in the guideline of intestinal aggravation as well as the management of heart physiology. In any case, it has been accounted for that ACE2 is a cell-surface receptor for the infection, which works with the viral RNA section in the lungs [16, 17].

## Objectives

The objective of the research work is “To develop a SIR Model to Predict the Spread of COVID-19 in India and

conduct Numerical simulations and stability analysis of COVID-19 model using fractional derivatives”.

- To assess the historical database of Covid-19 in India.
- To extract the features and to develop SIR Model to Predict the Spread of COVID-19 in India.
- To conduct Numerical simulations and stability analysis of COVID-19 model using fractional derivatives.

## 2. LITERATURE REVIEW

**M. N. Alenezi (2021)** The Susceptible - Infected - Recovered (SIR) model is used in this research to analyze and predict the outbreak of coronavirus (COVID-19) in Kuwait. The time dependent SIR model is used to model the growth of COVID-19 and to predict future values of infection and recovery rates. This research presents an analysis on the impact of the preventive measures taken by Kuwait’s local authorities to control the spread. It also empirically examines the validity of various values of ranging from 2 to 5.2. The proposed model is built using Python language modules and simulated using official data of Kuwait in the period from February to May of 2020. Our results show the SIR model is almost fitted with the actual confirmed cases of both infection and recovery for the values of ranging from 3 to 4. The results shown indicate COVID-19 peak infection rates and their anticipated dates for Kuwait. It has been observed from the obtained prediction that if preventive measures are not strictly followed, the infection numbers will grow exponentially.

**J. P. Hespanha (2021)** address the prediction of the number of new cases and deaths for the coronavirus disease 2019 (COVID-19) over a future horizon from historical data (forecasting). We use a model-based approach based on a stochastic Susceptible–Infections–Removed (SIR) model with time-varying parameters, which captures the evolution of the disease dynamics in response to changes in social behavior, non-pharmaceutical interventions, and testing rates. We show that, in the presence of asymptomatic cases, such model includes internal parameters and states that cannot be uniquely identified solely on the basis of measurements of new cases and deaths, but this does not preclude the construction of reliable forecasts for future values of these measurements. Such forecasts and associated confidence intervals can be computed using an iterative algorithm based on nonlinear optimization solvers, without the need for Monte Carlo sampling. Our results have been validated on an





extensive COVID-19 dataset covering the period from March through December 2020 on 144 regions around the globe.

**A. B. Lawson (2021)** The Covid-19 pandemic has spread across the world since the beginning of 2020. Many regions have experienced its effects. The state of South Carolina in the USA has seen cases since early March 2020 and a primary peak in early April 2020. A lockdown was imposed on April 6th but lifting of restrictions started on April 24th. The daily case and death data as reported by NCHS (deaths) via the New York Times GitHub repository have been analyzed and approaches to modeling of the data are presented. Prediction is also considered and the role of asymptomatic transmission is assessed as a latent unobserved effect. Two different time periods are examined and one step prediction is provided. The results suggest that both socio-economic disadvantage, asymptomatic transmission and spatial confounding are important ingredients in any model pertaining to county level case dynamics.

**P. Pandey et al, (2020)** In this paper, an analysis and forecasting of Indian COVID-19 data is discussed by using scipy optimize curve fitting model of machine learning. We demonstrate the month wise analysis of coming cases, daily recovered cases, death cases and test cases conducted by the Government of India, of COVID-19 from 01 st March 2020 to 02 nd August 2020, and also forecast for the new cases, recover cases & death cases from 03 rd August 2020 to 01 st November 2020. Our study show that the total numbers of affected persons due to COVID-19 up to 01 st November 2020 will be total cases 13,690,491, recover cases 10,499,593 and death of 129,271.

**F. A. Binti Hamzah et al (2020)** COVID-19 outbreak was first reported in Wuhan, China and has spread to more than 50 countries. WHO declared COVID-19 as a Public Health Emergency of International Concern (PHEIC) on 30 January 2020. Naturally, a rising infectious disease involves fast spreading, endangering the health of large numbers of people, and thus requires immediate actions to prevent the disease at the community level. Therefore, CoronaTracker was born as the online platform that provides latest and reliable news development, as well as statistics and analysis on COVID-19. This paper is done by the research team in the CoronaTracker community and aims to predict and forecast COVID19 cases, deaths, and recoveries through predictive modelling. The model helps to interpret patterns of public sentiment on disseminating related health information, and assess political and economic influence of the spread of the virus.

### 3. METHODOLOGY

We describe the dataset used to estimate the work, prediction algorithms, and model accuracy metrics.

#### Improved SIR-model

The aSIR-models proposed are based on the basic SIR-model described with some slight modifications to allow for parameter fitting.

This work will test two different versions of an aSIR-model, one model where both  $\beta$  and  $\gamma$  are estimated (similar to Santos et al.) and another model where  $\beta$  is estimated and  $\gamma$  is taken from literature (similar to Shapiro et al.). This approach was chosen since previous research has shown that it can be problematic to estimate multiple parameters simultaneously [1]. Therefore motivating this work to also test an aSIR-model with only one estimated parameter. Both the aSIR-models used the assumption that the R Compartment of the SIR-model corresponds to the confirmed cases of Covid19, this idea was taken from Shapiro et al. [1]. When the R-compartment is used,  $\gamma$  corresponds to the average time before severe symptoms emerge resulting in the individual getting quarantined, tested or hospitalized. Possible values for  $\beta$  are in the interval  $[0,1.5]$  for the aSIR-models. In the aSIR-model, where  $\gamma$  is taken from the literature,  $\gamma$  is set as  $\frac{1}{8}$ . In the other aSIR-model, possible values for  $\gamma$  are between the interval  $[\frac{1}{6}$  and  $\frac{1}{5}]$ . this interval is also taken from the literature

To account for rapid changes in transmission rates and contact patterns a 7-day sliding window with a step size of 1 was used, described in Shapiro et al. [18]. A 7-day sliding window was also used by FHM [5]. At the end of the current window  $i$ , the values of the S-, I- and R-compartments must be updated to new initial conditions for the next window  $i + 1$ . The S-and Icompartments initial values for the next window  $(i + 1)$  are updated to the best estimated values taken from the second day of the current window (i). The initial value of the R-compartment for the next window  $(i + 1)$  will be equal to the reported number of cases up until the date of the second day of the current window (i). See the method chapter of Shapiro et al. [18] for more details. At the end of each window, the  $R_4$  is calculated from the values of  $\beta$  and  $\gamma$  that fitted best to the reported number of cases. The calculated  $R_4$  was assigned to the date that resembled the last day of the 7-day sliding window. To get a smooth estimation of the  $R_1$  a 5-day moving average was used on the data points, similar to Shapiro et al. [18] and Santos et al. [19].





This work forecasted the future number of confirmed cases of Covid-19 in India. There were 5 different forecasts of varying length for each aSIR model; a 1-day forecast, a 3-day forecast, a 7-day forecast, a 14-day forecast and a 21-day forecast.

5 initial values were needed in order to do a forecast for date  $D$ . These initial values were the values of the S-, I- and R-compartment corresponding to date  $D$  and the values of  $\beta$  and  $\gamma$  corresponding to date  $D$ . The values of the S- and I-compartment were the aSIR-model's estimated values of the S and I-compartment corresponding to date  $D$ . The value of the R-compartment was the number of confirmed cases up until date  $D$ . Only an estimated value of  $\beta$  was needed in the aSIR-model with  $\gamma$  held constant. This estimated  $\beta$  value was the data point corresponding to date  $D$  from the list with  $\beta$  values estimated by the aSIR-model. The aSIR-model where both  $\beta$  and  $\gamma$  were estimated got their values for  $\beta$  and  $\gamma$  determined in a similar way.

When a 7-day forecast was to be made on date  $D$ , the 5 determined initial values were used in order to make an ordinary SIR-simulation over 7 days.

The values of  $\beta$  and  $\gamma$  were held constant during the 7-day simulation and the values of  $S, I$  and  $R$  were updated according to the SIR-ODE. The simulation was halted on the 7th day and the value of the R-compartment was the forecasted value of confirmed cases 7-days into the future (after date  $D$ ). In a more general case, if a forecast of length  $T$  was to be made, the simulation would run for  $T$  days.

A series of forecasts were made for every recorded day excluding the first 20 days of the data set. The exclusion of the first 20 days were because the  $R_t$  is commonly known to get overestimated when using data from early on of an outbreak.

### The physical model and variables used to calculate the spread

The goal of the model is to understand how the trend of the active COVID cases is going to change. For this, first, a set of affected cases for a given period of time are taken to parameterize the mathematical model. Then the relationship between the different parameters is established by using integral differential equations. As we will see in the following equations, the model is parameterized using a fixed location which makes the model local in nature. To counter this, fractional-order derivatives are used. By changing the integral time-derivative with the fractional-order derivatives the equation becomes non-local in nature. The fractional-order derivatives have to be provided with a set of initial

conditions to be solved. The equations are then solved by iteration using computational methods.

The physical model of the system is derived from the Khan-Atangana model for COVID-19 spread by using the same parameters. The relationship between these parameters is then developed as mentioned above and instead of using the A tangent-Baleanu derivative for solving the equations (used in the Khan-Acangana model), the Grulnwald-Leenikov derivative is used to convert the integral derivative to fractionat-order derivative and solve them. Considering the fact that COVID-19 can be imported quickly from the seafood market (reservoir or source) and without the loss of generality, the bat-host relationship was not considered.[2] Parameters

- $\mu_1$  : Natural birth rate
- $a_1$ : Natural death rate
- $a_2$  : Host visiting reservoir
- $b_1$  : Disease spread coefficient
- $b_2$  : Disease spread coefficient relating sub groups A and F
- $\sigma$ : Transmissibility multiple
- & Proportion of the asymptomatic infection
- $f_1$  : Spread rate after incubation period
- $e_1$  : Spread rate joining slab groups C and D
- $g_1$  : Recovery rate
- $g_2$  : Removal rate
- $e_2$ : Disease spread coefficient relating sub groups C and F
- $f_2$  : Disease spread coefficient relating sub groups D and F
- $\mu_2$  : Removing rate of virus from the reservoir (F)
- $N_h$  : Unknown hosts
- $I_h$ : Infected hoses

The susceptible people A and the infected people C are related using the factor  $b_1AC$ . The susceptible people A and the people showing no symptoms of the infection D are related by  $\sigma b_1AD$ , where  $\sigma \in [0,1]$  is the transmissibility multiple of D to C. The above parameters are consistent throughout the text.

### The Khan-Atangana Model

As per the Khan-Atangana model, the overall population is divided into 5 parts which are,

- $A(t)$  = susceptible people
- $B(t)$  = exposed people



- $C(t)$  = infected people
  - $D(t)$  = asymptomatic people (people showing no symptoms of the infection)
  - $E(t)$  = recovered or removed people
- Thus the total population  $N(t)$  can be written as  $N(t) = A(t) + B(t) + C(t) + D(t) + E(t)$ . The class  $F$  denotes the reservoir (outbreak of infection) or the seafood market or place. The following non-linear differential equations show the relationship between these 5 groups:

$$\begin{aligned} \frac{dA(t)}{dt} &= \mu_1 - a_1A - \frac{b_1A(C + \sigma D)}{N} - b_2AF \\ \frac{dB(t)}{dt} &= \frac{b_1A(C + \sigma D)}{N} + b_2AF - (1 - d)f_1B - de_1B - a_1D \\ \frac{dC(t)}{dt} &= (1 - d)f_1B - (g_1 + a_1)C \\ \frac{dD(t)}{dt} &= de_1B - (g_2 + a_1)D \\ \frac{dE(t)}{dt} &= g_1C + g_2D - a_1E \\ \frac{dF(t)}{dt} &= a_2 \frac{FC_h}{N_h} + e_2C + f_2D - \mu_2F \end{aligned}$$

Now, neglecting the relationship between host and bat population, we get the equations as:

$$\begin{aligned} \frac{dA(t)}{dt} &= \mu_1 - a_1A - \frac{b_1A(C + \sigma D)}{N} - b_2AF \\ \frac{dB(t)}{dt} &= \frac{b_1A(C + \sigma D)}{N} + b_2AF - (1 - d)f_1B - de_1B - a_1B \\ \frac{dC(t)}{dt} &= (1 - d)f_1B - (g_1 + a_1)C \\ \frac{dD(t)}{dt} &= de_1B - (g_2 + a_1)D \\ \frac{dE(t)}{dt} &= g_1C + g_2D - a_1E \\ \frac{dF(t)}{dt} &= e_2C + f_2D - \mu_2F \end{aligned}$$

Following is the flow diagram that shows the relationship between the above-mentioned subgroups as developed by the given equations:

As mentioned before, to non-localize, we convert the time derivative in the above integral order equation to that of fractional-order. The equations thus become as follows:

$$\begin{aligned} {}_aD_t^{p_1} A(t) &= \mu_1 - a_1A - \frac{b_1A(C + \sigma D)}{N} - b_2AF \\ {}_aD_t^{p_2} B(t) &= \frac{b_1A(C + \sigma D)}{N} + b_2AF - (1 - d)f_1B - de_1B - a_1B \\ {}_aD_t^{p_3} C(t) &= (1 - d)f_1B - (g_1 + a_1)C \\ {}_aD_t^{p_4} D(t) &= de_1B - (g_2 + a_1)D \\ {}_aD_t^{p_5} E(t) &= g_1C + g_2D - a_1E \\ {}_aD_t^{p_6} F(t) &= e_2C + f_2D - \mu_2F \end{aligned}$$

The initial conditions are given as:  $A(0) = d_1, B(0) = d_2, C(0) = d_3, D(0) = d_4, E(0) = d_5$  and  $F(0) = d_6$ . Moreover we use  $0 < p_1, p_2, p_3, p_4, p_5, p_6 < 1$  to increase the degree of the freedom and obtain better results.

### Solution Methodology

We will convert the integer-order equations obtained from the Khan-A tangent model to fractional order equations. As mentioned in the physical model, due to the local nature of the integral differential equation, they are converted to fractional-order. By providing the initial conditions to the fractional order-derivatives, the system of the equation becomes non-local in nature. The additional parameters in the equations are used to provide an extra degree of freedom to obtain better solutions. We would be using the Grunwald-Letnikov (GL) derivative to obtain the solution to the fractional-order derivatives. Grunwald-Letnikov derivative is used to calculate the derivative of a function non-integer number of times [3].

The Trapezoidal method is used to solve the integer-order integral. By calculating the parameters of the Grunwald-Letnikov derivative and integrating the fractional derivative we would get the equations for  $A(t), B(t), C(t), D(t)$ , and  $E(t)$ . The unknowns in the coronavirus model can be obtained by writing a MATLAB code to solve the equations obtained.

To improve the accuracy of the model iterative methods with a small step size shall be used. For the stability analysis, we analyse the eigenvalues corresponding to the Jacobian matrices at specific equilibrium points. First, we identify the equilibrium points and find the Jacobian matrix  $J$ . The solution of this polynomial equation will give the eigenvalues corresponding to the Jacobian matrix  $J$ . We will solve these 6 degree polynomial equations using the Newton-Raphson method and analyse the stability of the system at the equilibrium points.

#### 4. SIMULATION AND RESULT ANALYSIS

##### Result Analysis of Prediction System

The goal of this study is to numerically solve these fractional-order derivatives and examine the stability of the epidemiological model. Major states above 3000 infected cases were taken for prediction. Data is collected from *covid19india.org* website along with the data of the whole country. Susceptible infected recovered (SIR) model is used for the prediction of cases, which gives the final epidemic size of infected cases in each state. MATLAB open source code is used to graphically plot the cases and predictions of India and its states. The geographical map shows the distribution of confirmed cases in INDIA among different state with colour as quantitative scale. The bar graph show the selected states which are above 2000 of infected cases named as highly infected states. COVID-19 prediction is shown in form of graphs using MATLAB software of India and its highly infected states (above 3000 cases). State included in the prediction are Maharashtra, Gujarat, Delhi, Tamil Nadu, Rajasthan, Madhya Pradesh, Uttar Pradesh, Andhra Pradesh, West Bengal. First graphs shows the total number of infected cases (here infected cases are shown on scale as multiple of 1000th of y axis on cumulative data) per day. Second graph shows the three phases on the plotted no. of infected cases per day.

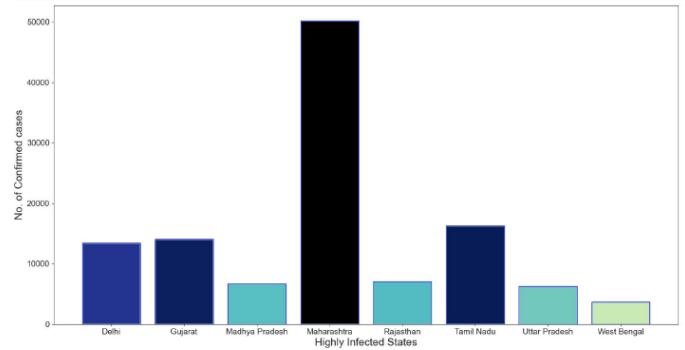


Figure 4.2 COVID Case Analysis- India

State	Data	Confirmed Infected Cases	Predicted Infected Cases	Relative Error (%)	Predicted Infected Cases on 30/5/2020	$R_0$ (Basic Reproduction No.)
Maharashtra	21st May	41642	41450	0.46	63100	1.3020
	22nd May	44582	43905	1.52		
	23rd May	47190	46950	0.51		
Gujarat	21st May	13910	13020	0.84	17600	1.6156
	22nd May	13273	13130	1.08		
	23rd May	13669	13360	2.26		
Delhi	21st May	11659	12530	6.95	16600	1.2664
	22nd May	12319	12800	2.23		
	23rd May	12910	12900	0.85		
Tamil Nadu	21st May	13967	13500	2.91	19800	1.7801
	22nd May	14753	14300	1.71		
	23rd May	15512	15700	1.20		
Rajasthan	21st May	6223	6190	0.53	9200	1.2320
	22nd May	6490	6300	0.15		
	23rd May	6758	6950	3.05		
India	21st May	118223	119350	1.09	172000	1.2471
	22nd May	124759	125900	0.98		
	23rd May	131422	130420	0.76		

Figure 4.3 Statistical Analysis of Proposed Model 5 States =1

State	Data	Confirmed Infected Cases	Predicted Infected Cases	Relative Error (%)	Predicted Infected Cases on 30/5/2020	$R_0$ (Basic Reproduction No.)
Madhya Pradesh	21st May	5981	5900	1.35	8200	1.2616
	22nd May	6170	6050	1.94		
	23rd May	6371	6200	2.68		
Uttar Pradesh	21st May	5515	5420	1.72	7400	1.1166
	22nd May	5735	5650	1.48		
	23rd May	6017	5890	2.11		
Andhra Pradesh	21st May	2605	2540	2.50	3500	1.9408
	22nd May	2667	2670	0.11		
	23rd May	2714	2760	1.67		
Punjab	21st May	2028	2015	0.64	2060	18.9254
	22nd May	2029	2035	0.29		
	23rd May	2045	2040	0.24		
West Bengal	21st May	3197	3050	4.60	4690	1.8628
	22nd May	3332	3390	1.71		
	23rd May	3459	3610	4.18		

Figure 4.4 Table 4.2 Statistical Analysis of Proposed Model for 5 States-2

After lockdown COVID-19 curves for different states are very dissimilar. India and its state maharashtra prediction graph curve is have a slow exponential growth leading to higher uncertainty in long-term predictions due to lockdown 4.0 .The spread of COVID-19 will continue for at least the next three to four weeks as shown in the prediction Most state lies in acceleration phase, thus still showing the growth in cases, Growth rate tends to decrease as the cases enters the steady phase. Most of the states will tend to to show high growth in infected cases as lockdown 4.0 is implemented with removal of some restriction. States which had reached their ending phase, might show the growth in cases again. Major states with high population like Maharashtra will show high growth

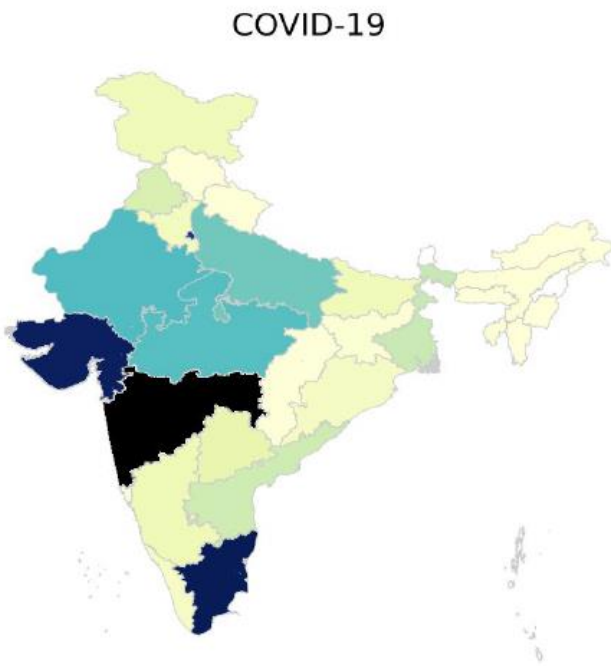


Figure 4.1 COVID Distribution Map- India



rate during lockdown 4.0. In (\*Figure) Punjab the cases have reached its ending phase but due to lockdown 4.0 the cases will grow in number. Cases must be updated regularly with right numbers for forecast/prediction to be more accurate and precise. Necessary action should be taken according to the forecast provided for different states infected with COVID-19. India will reach its inflection point on 29th May. Table shows the Relative error between the Confirmed and the predicted infected cases.  $R_0$  here above represents the basic reproduction number of infected cases .

After implementing the proposed model and solving the problems using the specific numerical methods, we obtain the following time of execution of the attached MATLAB code (averaged over several iterations): 11.893 seconds

The proposed technique is effective to show the behaviour of the solution in a very long time period which is helpful to predict the coronavirus model accurately. This method can be used in investigating many similar biological models showing wide applicability of the proposed method.

## CONCLUSION & FUTURE SCOPE

### 6.1 Conclusion

India is one of the high population counties in world. To stop Covid -19 is biggest challenges to county like India. But today's date (26 August, 2020); India spread of Corona viruses to extent. From the prediction times values tells that India would reach more than 32 lakhs with 64,213 deaths till 1 September 2020. Now after the all lock down, cases are increasing day by day. India has increasing day by day testing, which helps to get more information about Covid-19 spread. Also India is working on small trials on plasma therapy. India has developed aarogya setu to create more awareness about Covid-19. Due to lockdown spread to Covid-19 controlled and cases are less as compare to other countries. After the lockdown, biggest is challenge to maintain social distancing in society. But actually, medicine is required to completely stop the spread of Covid-19. This projection help government to make strategies against Covid-19. Finding out how the virus is spreading across a community is one of the biggest challenges faced by healthcare professionals. This information can be utilized to stop the virus's propagation. This is a crucial stage in the process of reviving activity on a worldwide scale. Numerous attempts have been undertaken in the field of epidemiology to research the transmission of COVID, and as a result, numerous mathematical models have developed that can be useful in this regard. The drawback of a widely used approach

for calculating the effective reproduction number ( $R_t$ ) is that it cannot concurrently predict the number of cases in the future. The SIR-model, an extension of another model, is examined in this paper. In this model, the model's parameters are fitted to collected data. As a result, the model becomes adaptive, providing the opportunity to calculate the  $R_t$  daily and forecast the number of confirmed instances in the future. The paper uses this adaptive SIR-model (aSIR) to forecast new cases in India and estimate  $R_t$ . The goal of the paper is to evaluate the accuracy of aSIR-models in estimating the  $R_t$  (in comparison to FHM's model). It will also examine how well aSIR-models predict the spread of Covid-19 in India in the near future. The number of susceptible people, exposed people, infected people, asymptotic persons, and the number of re-covered people can all be used to mathematically predict the coronavirus propagation. An integer-order coronavirus model that makes use of the aforementioned elements is the Khan-Atangana system. The Khan-Atangana model employs the Atangana-Baleanu operation because it has a non-variant and non-local kernel while the coronavirus model is dependent on the beginning conditions. We instead substitute fractional-order derivatives based on the Grünwald-Letnikov derivative for the equations. Due to their non-local character, fractional order derivatives can be used to calculate the spread but must be fed with initial circumstances. The goal of this study is to numerically solve these fractional-order derivatives and examine the stability of the epidemiological model.

### 6.2 Future Work

This research has numerous opportunities for growth in the future. More architectures are being implemented as the first expansion. In order to train more complicated architectures, I'd like to investigate model training choices that permit a higher GPU memory limit. This would enable the employment of inception modules in addition to numerous dense layers. The classification of various diseases will be the next field of investigation. This would make it possible to investigate if certain architectural designs are best for treating various diseases. If true, additional research might provide light on the reasons for the variations in performance caused by various disorders. It is also possible to use other data splitting methods, including k-fold data splitting. This will strengthen the results' validity and shed additional light on how data bias affects a model's ability to be trained correctly.

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