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Research Article

Progression of COVID-19 Pandemic in India: A Linear Functional Concurrent Regression Analysis Approach

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ABSTRACT

Background: COVID-19 is a disasterous pandemic that the world has ever faced. It is affecting the global health system irrespective of race, ethnicity, environment, and economic status. This study is conducted with the aim of assessing the progression of the COVID-19 pandemic in India.

Methods: This article uses the functional concurrent regression analysis approach to describe the pattern of daily reported confirmed cases of COVID-19 in India. The approach provides an excellent fit to the daily reported confirmed cases of the disease. The data used in this study have been taken from covid19india.org.

Results: Estimated value of the parameter b_k of the model is highly volatile. During the first phase of the pandemic which last up to 31st March 2020, value was very high. During 31st March to 19th July 2020 except for a few exceptions. Its value again increased rapidly from 17th February 2021 to 16th April 2021 and started decreasing after mid-March, 2021 and continued decreasing till present.

Conclusion: The data-driven approach used in this study is purely empirical and does not make any assumption about the progression of the pandemic or about the data. The article suggests that based on the parameter of the model, an early warning system may be developed and institutionalised to undertake the necessary measures to control the spread of the disease, thereby controlling the pandemic.

Keywords: COVID-19, India, Functional Concurrent Regression Analysis, Estimation

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Introduction

There are many studies related to the modelling of the COVID-19 pandemic in India since the outbreak of the pandemic in the early 2020.[1-3] These studies have generally followed the epidemiological modelling approach which is primarily based on the basic Susceptible-Infected-Removed (SIR) model and its numerous extensions.[4,5] The basic SIR model divides the entire population into three mutually exclusive states-Susceptible, Infectious and Removed (by recovery or death). The underlying assumption of the model is that a person once infected and subsequently recovered has little probability to become susceptible to the infection again.[6] Fitting of the SIR model and its different variants requires defining the transition rate between different states before hand. The progression of the pandemic in the model is characterised in terms of the basic reproduction number denoted by R_0 (pronounced *R nought* or *R zero*) which is the expected number of infected persons directly generated by an infected person in the population where it is assumed that all members of the population are susceptible to the infection.[7,8] Time-dependent SIR models have also been developed which take into account those infected persons who remain undetected.[9] The stochastic version of the model has been used to analyse the pace of virus transmissibility by estimating R_0 using the stochastic Markov Chain Monte Carlo method.[10]

There are also studies that have used different statistical tools and techniques to understand the propagation of the pandemic and suggest afuture course of action.[11-14] Progression of the pandemic has been analysed using statistical exponential growth model and adopting the serial interval from Severe Acute Respiratory Syndrome.[15,16] A three-parameter logistic growth function was used to predict the progression of the pandemic for China and for some other countries.[17] In the context of India,[18] it is concluded that the nationwide lockdown enforced on March 24, 2020 for 21 days was insufficient for controlling the spread of the pandemic. Mathematical modelling has also been used to describe the progression of the pandemic.[19-29] Most of these modelling exercises followed an exponential curve during the initial stages of the pandemic which, eventually, was assumed to flattened.[30] In one study, a stochastic mathematical model is used to describe the progression of COVID-19 pandemic in India.[31] The logistic growth regression model has also been used to estimate the final size and the peak of the pandemic in many countries and results have been found to be similar to those obtained by the SIR model.[32] Studies carried out by Sharma et al., Swain et al., Newtonraj et al.[33-35] revealed that ARIMA model is also appropriate for forecasting COVID-19 in India. Mishra et al.[36] have advocated SARIMA along with ARIMA for the modelling and forecasting of COVID-19 pandemic whereas Bedi P et al.[37] have used SEIRD and LSTM models.

In this article, we have followed a data-driven approach to describe the progression of the COVID-19 pandemic in India since March 2020. Data from published epidemiology and virologic studies provide the evidence that COVID-19 is transmitted from an infected person to other persons for a specific period by direct contact with the infected person, or by contact with contaminated objects and surfaces.[38] Since objects and surfaces are also contaminated by infected persons, the underlying assumption of the present analysis is that the reported number of new cases of COVID-19 is a function of the reported number of new cases of the disease during an immediately preceding period. The World Health Organization has also recommended that in general, a person infected with Novel Coronavirus, the virus that causes COVID-19 disease, may be released from isolation after a period of 13 days based on clinical criteria.[39] For example, if a person has symptoms for three days, then the person can be released from isolation after 10 days+3 days=13 days from the date of onset of symptoms. This, essentially means that there is very little chance that an infected person can infect other persons who come in contact with the infected person after a period of 13 days since infection. It has also been observed that the period between the onset of the symptoms of the disease and the confirmation of the disease through laboratory testing and subsequent reporting is around 3 days. Based on the above evidence, it can be assumed that the progression of the COVID-19 pandemic may be described by establishing a functional relationship between the reported numbers of new confirmed cases of the disease on a particular day with the number of reported numbers of new confirmed cases of the disease during the immediately preceding 10 days period. In this article, we have followed this line of reasoning to describe the progression of the COVID-19 pandemic in India and found that our approach has quite successfully been able to describe the progression of the pandemic in the country.

Data

The analysis is based on daily reported number of new confirmed cases of COVID-19 disease in India till 11th August, 2021.[40] The confirmation was done through laboratory testing using the RT-PCR test as recommended by the World Health Organization. An examination of the data released by the Government of India, however, suggests that there are many inconsistencies of known and unknown origin in the daily reporting of new confirmed cases of the disease. The testing for the novel coronavirus in India is voluntary, not population-wide. This means that persons who have not volunteered for testing for novel coronavirus but are positive are not included in the reported number of new confirmed cases of COVID-19 which implies that the actual number of new cases of the disease COVID-19 in India may be substantially higher than the reported number of new confirmed cases of the disease released by the Government of India. Moreover, the reported number of new confirmed cases of COVID-19 is also influenced by the number of persons tested for novel coronavirus.

A decrease in the number of persons tested for the virus affects the number of new confirmed cases of the disease reported. In fact, an examination of the time series of the reported number of new confirmed cases released by the Government of India also suggests that there is a dip in the reported number of new confirmed cases of the disease on Monday of almost every week. To minimise the errors associated with daily reporting of new confirmed cases of the disease, it is usually the practice to use 7 days moving average for analysing the progression of the pandemic instead of daily reported new confirmed cases of the disease. The same practice has also been adopted in the present analysis. For example, the reported number of new cases of the disease on 15th August 2020 is actually the simple average of the daily reported new confirmed cases of the disease during the period 12 August 2020 through 18 August 2020.

Method

We use linear functional concurrent regression modelling approach to analyse the progression of the COVID-19 pandemic in India. Concurrent models are also termed as the varying-coefficient model.[41-43] These models are particularly useful in the analysis of longitudinal data as is the case here. The linear functional concurrent regression model can be fitted through regression and smoothing spline methods.[24,44-45] A detailed exposition of linear functional concurrent models and different fitting procedures for these models is given elsewhere.[46]

In what follows, let the entire period of the pandemic is divided into concurrent time segments of 10 days each so that Y_{jk} denotes the reported number of new confirmed cases of the disease on day j of the time segment k, j =1,2,...10. Then the reported number of new confirmed cases of the disease during the time segment $k+1$ may be related to the number of confirmed cases of the disease reported during the time segment k as follows:

$$\frac{Y_{jk+1}-\overline{Y}_{jk+1}}{\sigma_{k+1}}=r_k\left(\frac{Y_{jk}-\overline{Y}_k}{\sigma_k}\right) \qquad (1)$$

Where r_k is the correlation coefficient between Y_{jk} and Y_{jk+1}, j =1,2,...10, $\overline{Y}_k$ denotes the average of the reported number of new confirmed cases of the disease during the time segment k, and σ_k is the standard deviation. It may be clarified here that different time segments used for analysing the progression of the pandemic have overlapping days. For example, *k*=1 indicates day 1 through day 10 of the pandemic while k=2 indicates day 2 through day 11.

Equation (1) can be rearranged as,

$$Y_{jk+1}=(\overline{Y}_{k+1}-b_k\overline{Y}_k)+b_kY_{jk} \qquad (2)$$

Where $b_k=r\dfrac{\sigma_{k+1}}{\sigma_k}$ (3)

Equation (3) suggests that when $Y_{jk+1}=b_kY_{jk}$ for all j =1,2,...10, $\overline{Y}_{k+1}-b_k\overline{Y}_k=0$ .In this ideal situation, the reported number of new confirmed cases of the disease during the time segment $j+1$ is b_k times the reported number of new confirmed cases of the disease during the time segment k. This essentially means that all reported new confirmed cases of the disease in the time segment $k+1$ are known contacts of the reported number of new confirmed cases of the disease in the time segment k. It is, however, rare that $\overline{Y}_{k+1}-b_k\overline{Y}_k=0$ for two reasons. First, all known contacts of the reported new confirmed cases of disease during the time segment k are not reported during the time segment $k+1$. Second, there may be confirmed cases of unknown contacts who are reported during the time segment $k+1$. When $\overline{Y}_{k+1}-b_k\overline{Y}_k>0$, there are some confirmed cases of unknown contacts of the disease reported in the time segment $k+1$. On the other hand, when $\overline{Y}_{k+1}-b_k\overline{Y}_k<0$, there are some known contacts of the confirmed cases of the disease reported during the time segment k who are not reported during the time segment $k+1$.

Model (2) suggests that the progression of the pandemic can be characterised in terms of the parameter b_k. When $b_k>1$, $Y_{jk+1}>Y_{jk}$, j =1,2,...10, which means an increase in the reported number of new confirmed cases of the disease during the time segment $k+1$ relative to the reported number of new confirmed cases of the disease during the time segment k. On the other hand, when $b_k<1$, $Y_{jk+1}<Y_{jk}$, j =1,2,...10, there is a decrease in the reported number of new confirmed cases of the disease during the time segment $k+1$ relative to the reported number of new confirmed cases of the disease during the time segment k. If all contacts of the reported number of new confirmed cases of the disease reported during the time segment k are traced, tested and positive cases of novel coronavirus are identified and reported, then the reported number of new confirmed cases of the disease during the time segment $k+1$ can be determined from the reported number of new confirmed cases of the disease during the time segment k. Model (2) serves as a data-driven model for analysing the progression of COVID-19 pandemic. The model does not make any assumptions about the progression of the disease. It is based on the relationship between the numbers of new confirmed cases of the disease reported during two concurrent time segments of 10 days.

Results

Figure 1 presents the trend in the estimated value of the parameter b_k of model (2) from 11th March 2020 to 11th August 2021. The trend is highly volatile. The parameter

b_k is the key factor in deciding the pace of progression of the pandemic. During its early days, COVID-19 pandemic in India progressed very rapidly. The first phase of the pandemic appears to have lasted till 31st March 2020. During this phase, the number of new confirmed cases of the disease increased from an estimated 7 cases on 11th March 2020 to estimated 426 cases on 31st March 2020 or the reported new confirmed cases of the disease multiplied more than 60 times during this period.

The second phase of the pandemic appears to have started around 31st March 2020 and lasted till 19th July 2020. During this period, the estimated value of b_k has always been more than 1 but less than 2 except for a few exceptions when it was less than 1 and for a few exceptions when it was more than 2 but always less than 3. This means that except for a few days during this period, there has been an increase in the reported number of new confirmed cases of the disease but the pace of the increase in the reported number of new confirmed cases of the disease was not fast as the estimated b_k was rarely more than 2 during this period.

The third phase of the pandemic appears to have started around 20th July 2020 and lasted up to 15th August 2020. During this period, barring a few exceptions, the estimated b_k was always less than 1 indicating a decrease in the daily reported number of new confirmed cases of the disease. This period was, however, followed by a period of spike in b_k till 31st August 2020. During this period, the estimated b_k was always more than 1 and even increased to more than 4 in some days leading to a rapid increase in the reported number of new confirmed cases of the disease. This period was followed by a rapid decrease in the estimated value of b_k up to 18th September 2020. The rapid decrease in estimated b_k during this period resulted in a rapid decrease in the daily reported number of new confirmed cases of the disease. However, b_k increased again from 26th September 2020 to 16th October 2020, but the increase in the daily reported number of new cases of the disease was not very rapid as estimated b_k was never more than 2 during this period.

The next phase of the pandemic appears to have started from 17th October 2020 and lasted up to 15th February 2021. This period is characterised by a decrease in the number of daily confirmed cases of the disease as estimated b_k remained less than 1 in most of the days of this period so that there was a digression of the pandemic. However, b_k increased rapidly from17th February 2021 to16th April 2021 so that there was a very rapid increase in the daily reported number of new confirmed cases of the disease. Although b_k started decreasing after mid-March, 2021 yet, b_k decreased to less than 1 only in mid-April 2021 resulting in a decrease in the daily reported number of new confirmed cases of the disease during the time segment $k+1$ relative to the time segment k.

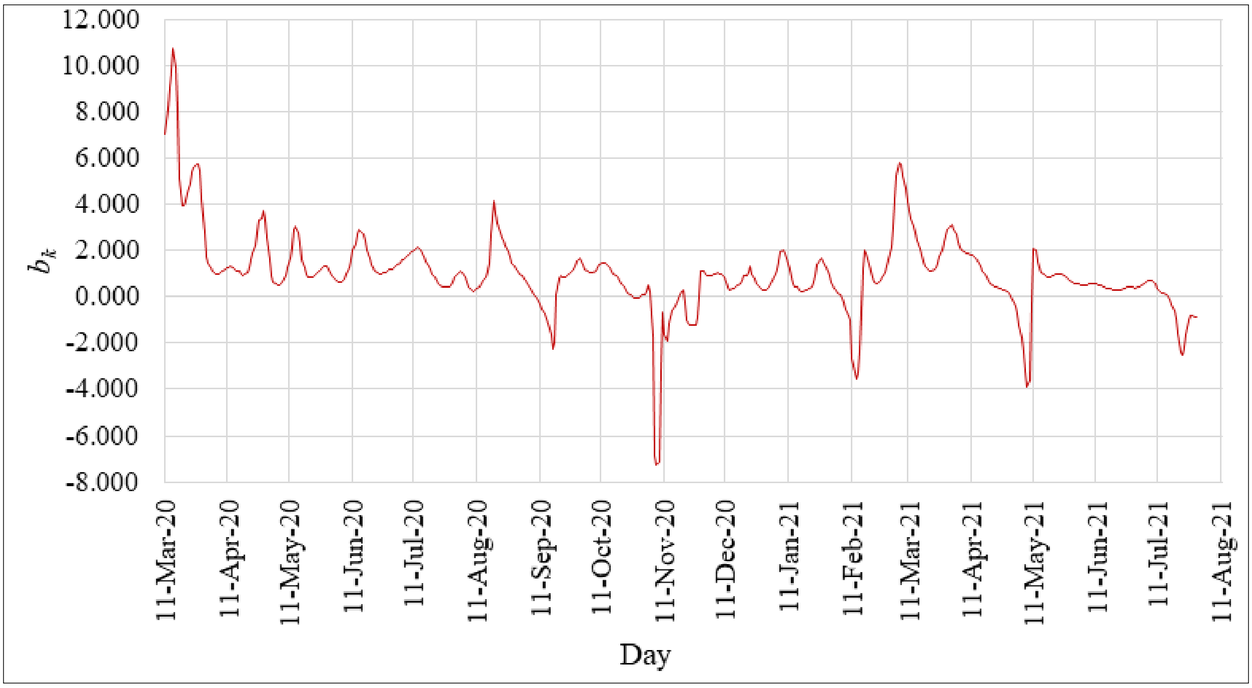

Figure 1.Trend in Estimated Values of b_k

Source: Estimated by authors from the daily reported number of new confirmed cases of the disease in conjunction with model (2).

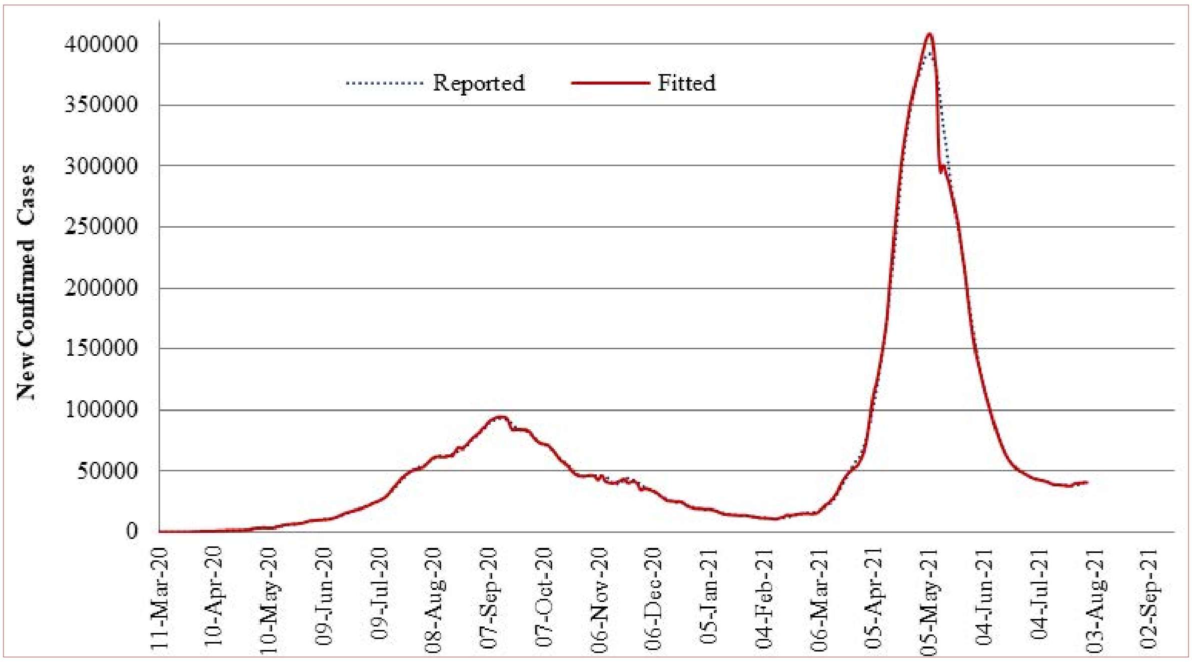

Figure 2.Reported and Fitted Reported Number of New Confirmed Cases ofCOVID-19 in India

Source: Reported number of new confirmed cases of the disease is released by the Government of India and are available at https://www.covid19india.org. Fitted number of new confirmed cases of the disease is calculated by authors in conjunction with model (2).

The daily reported number of new confirmed cases of the disease is also influenced by the difference $\overline{Y}_{k+1} - b_k\overline{Y}_k$. If this difference is greater than 0, then the daily reported number of new confirmed cases of the disease is more than that implied by the estimated b_k. For example, estimated b_k =1.020 between the time segment beginning 16th June 2020 and the immediately succeeding time segment beginning 26th June 2020. This means that the number of new confirmed cases of the disease reported on 26th June 2020 should be 1.020 times the number of new confirmed cases of the disease reported on 16th June 2020 (12320). However, the number of new confirmed cases of the disease, actually reported on 26th June 2020, was only 18154. This implies that an estimated 5572 new confirmed cases of the disease reported on 26th June 2020 were the cases of unknown contacts, although a part of this difference may also be due to reporting and other inconsistencies. On the other hand, if the difference $\overline{Y}_{k+1} - b_k\overline{Y}_k$ is less than 0, then this implies that all new confirmed cases of the disease implied by b_k are not reported. This means that all contacts of the new confirmed cases of the disease reported during the time segment k could not be traced/ tested and positive cases reported during the time segment k+1.

Figure 2 depicts the daily reported number of new confirmed cases of COVID-19 in India beginning 1st March 2020 through 11th August 2021 along with the fitted values of the daily reported number of new confirmed cases of the disease which have been obtained from the estimated b_k in conjunction with model (2). It is evident from the figure that model (2) fits very well with the daily reported number of new confirmed cases of the disease. More specifically, the model effectively captures the very rapid increase in the daily reported number of new confirmed cases of the disease in the recent past reflecting the second wave of the COVID-19 pandemic in the country.

Conclusion

This article has followed a data-driven approach to analyse and describe the progression of the COVID-19 pandemic in India. The approach is purely empirical and does not make any assumptions about the progression of the pandemic or about the data. Figure 2 empirically validates the data-driven approach adopted in this article. The present analysis suggests that two factors may be attributed to the progression of the COVID-19 pandemic in India. The first, obviously, is the multiplicity of the reported new confirmed cases of the disease which has been captured through the parameter b_k of the model (2). The second factor in the progression of the pandemic in the country appears to be the inability to contact and trace all contacts of daily reported new confirmed cases of the disease and their testing to identify the cases of the disease. This inability has resulted in a large number of reported new confirmed cases of the disease with unknown contacts.

Our analysis suggests that keeping a close watch on the trend in the parameter b_k may give an early indication about the increase in the number of new confirmed cases of the disease. An exceptional increase in b_k is an indication of some exogenous factors that may be responsible for the increase in the multiplicity of the reported number of new confirmed cases of the disease such as a new mutation or strain of the novel coronavirus. It is possible to forecast the daily reported number of new confirmed cases of the disease by projecting b_k using appropriate forecasting tools such as trend analysis or time series analysis. It may, however, be noted that the trend in the parameter b_k has been found to be highly volatile so that the long-term projection of the parameter b_k does not appear to be a feasible proposition. Because of the high volatility of the parameter b_k, conventional forecasting tools such as linear regression analysis may not be appropriate. Instead, techniques such as joinpoint regression may be used for this purpose.[21] In any case, very high volatility of the parameter b_k probably and so obviously appears to be the reason why most of the existing approaches have not been successful in forecasting the progression of the pandemic.

Contribution

ARC conceptualised the study, developed the model and carried out calculations.

BPS carried out literature and model review and read the manuscript.

RS read the manuscript.

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Conflict of Interest: None

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