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Understanding Covid-19 Situation Using Mathematical Modeling

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Abstract

In light of the absence of an effective vaccine or specific antiviral treatments, mathematical modeling assumes a crucial role in enhancing our comprehension of disease dynamics and in devising strategies to manage the rapid spread of infectious diseases. Particularly during this period, forecasting holds paramount significance for healthcare planning and for effectively addressing the COVID-19 pandemic. To elucidate the dynamics of the COVID-19 outbreak, this study introduces an extended Susceptible Exposed Infected Recovered (SEIR) compartment model, refined with the inclusion of contact tracing and hospitalization strategies. The model is calibrated employing daily COVID-19 data encompassing various Indian regions, including Kerala, Karnataka, Andhra Pradesh, Maharashtra, West Bengal, and the entirety of India. Employing the least squares method, we estimate sensitive parameters after conducting a sensitivity analysis, which we approach using partial rank correlation coefficient techniques. Our exploration focuses on the relative significance of system parameters, with a dedicated sensitivity analysis centered on the reproductive number R_o. To assess the model's resilience across parameter variations, we compute R_o sensitivity indices. Our findings underscore the effectiveness of strategies that involve reducing disease transmission coefficients (s) and clinical outbreak rates (qa) in controlling COVID-19 outbreaks. Our study generates short-term predictions for daily and cumulative confirmed COVID-19 cases across the five Indian provinces. These projections reveal distinct trends, with certain states demonstrating steady exponential growth, while others exhibit a decline in daily new cases. Examining the long-term perspective, our model predicts oscillatory dynamics for COVID-19 cases in India, suggesting the potential for the disease to follow a seasonal pattern. Consequently, our simulation points towards a power law trend in coronavirus cases in India by the close of September 2020, further contributing to our understanding of the disease's progression.

Keywords

Covid-19, Mathematical Modeling, Susceptible Exposed Infected Recovered (SEIR)

1. Introduction

Up to September 29, 2020, the World Health Organization (WHO) has reported a global total of 33,034,598 confirmed cases (with 996,342 confirmed deaths) of the novel coronavirus disease 2019 (2019-nCoV), out of which India accounts for 6,145,291 confirmed cases (with 96,351 deaths) [1-3]. The initial outbreak was declared on December 31, 2019, by the "Health Commission of Hubei Province" in China, when an unexplained cluster of severe pneumonia cases of unknown origin was identified in Wuhan, Hubei's capital and China's seventh-largest city [3–5]. Subsequently, the disease was named COVID-19 by the World Health Organization. On January 30, 2020, the WHO declared it a global health emergency, while on March 16, 2020, both the WHO and the Indian government announced a nationwide 21-day lockdown from March 25, 2020, to April 14, 2020. This was followed by a one-day "Janata Curfew" on March 22, 2020, aimed at curbing the spread of the virus. The lockdown was extended to Phase 4, covering May 18, 2020, to May 31, 2020 [6-8]. At present, India is in Unlock 4.0, spanning from September 01, 2020, to September 30, 2020, following Unlock 1.0 from June 01, 2020, to June 30, 2020.

Coronavirus is known to cause mild infections and occasionally severe communicable diseases, such as Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS), and is now responsible for the current COVID-19 pandemic. It is closely related to SARS-CoV and is found in bats, raising the potential for future outbreaks. The virus has an incubation period of 2–14 days and primarily spreads through respiratory droplets and direct contact. Symptoms range from mild, such as fever and sneezing, to more severe conditions like dry cough, fatigue, breathing difficulties, and lung issues in critically ill patients. The virus can survive on surfaces for varying periods, with metal surfaces retaining the virus for up to five to six hours [9-12].

The ongoing coronavirus outbreak was declared a pandemic by the WHO on March 16, 2020. By that date, the UN's Public Health Agency had confirmed 167,511 cases, with 6,606 deaths, across 151 countries. As nations impose travel restrictions and quarantines, understanding the virus's nature and behaviour is crucial to protecting communities [13-15]. Factors influencing transmission include air travel, human-to-human contact, low temperatures, and low humidity. India ranks 17th among countries at highest risk of importing the virus through air travellers. The likelihood of an infected air traveller arriving in India is 0.383 percent (as of September 30, 2020). The relative import risk is highest in Delhi (0.124 percent), followed by Mumbai (0.064 percent), Kolkata (0.021 percent), Madras (0.023 percent), Kochi (0.013 percent), Bangalore (0.029 percent), and Hyderabad (0.018 percent). Initially, the Health Ministry and Family Welfare (MoHFW) of the Government of India recommended quarantine for those travelling from China [14]. Individuals returning from Wuhan, China, on January 15, 2020, were tested for the virus. Those becoming ill within a month of returning from China were advised to seek treatment at a local health centre while self-isolating at home. Thermal screening of travellers from Wuhan and other affected areas was implemented at around twenty-one airports across the country, with international screening in place for flights from countries including Taiwan, Singapore, South Korea, Italy, Hong Kong, and Japan. Travellers displaying symptoms of illness are strongly encouraged to undergo a screening test, similar to the screening implemented at international harbours. Governments face a challenge in simultaneously reducing deaths caused by the coronavirus epidemic and minimizing its economic impact. It is crucial to keep the fatality rate as low as possible among populations. To address the inevitable economic downturn, governments must implement measures for mitigation. Coronavirus has evolved into a pandemic, with small transmission chains in various countries and widespread outbreaks in many nations, including the United States, Spain, Italy, South Korea, Germany, France, and others. Currently, no fully licensed vaccines, antivirals, or effective treatments are available for coronavirus infections. Given the absence of such therapeutics, we employed non-pharmacological interventions (NPIs) focused on decreasing contact rates between individuals to curb transmission. These measures included social distancing, closure of schools, universities, offices, religious institutions, and entertainment venues, avoidance of mass gatherings, and active case management (quarantine, surveillance, and contact tracing) [16].

Several crucial factors contribute to understanding the trajectory of a coronavirus outbreak, although some aspects remain challenging to comprehend fully. R0, the basic reproduction number, holds significant importance in infectious diseases as it quantifies a disease's contagiousness. R0 indicates the average number of secondary infections caused by a single infected individual in a susceptible population, effectively representing the area under the epidemic curve. If R0 is less than 1, the disease is expected to fade out; for R0 = 1, an infected individual can infect one other person on average, indicating stable transmission; if R0 is greater than 1, the disease can spread epidemically. R0 aids in understanding the disease's potential to spread or cease under different conditions. In the early stages of the coronavirus outbreak, R0 values in China were around 2.5. The extent of a coronavirus outbreak's spread is determined by the virus's infectiousness and the pool of susceptible individuals. Mathematical modelling is pivotal for comprehending disease dynamics and designing strategies to manage its spread, especially in the absence of an effective vaccine or specific antivirals. Numerous mathematical models have been developed to elucidate the intricate dynamics of novel coronaviruses. For instance, Chen et al. formulated a novel coronavirus model and estimated the basic reproduction number. Imai et al. explored a computational model for COVID-19 in Wuhan, focusing on human-to-human transmission. Tang et al. introduced a coronavirus compartmental model incorporating symptomatic individuals to understand patients' epidemiological status. Their model produced a high basic reproduction number of 6.47. Nadim et al. examined a mathematical model to study coronavirus disease dynamics and validated it with Hubei City data. Gumel et al. developed a model for the Severe Acute Respiratory Syndrome (SARS) outbreak. Wu et al. devised a coronavirus model based on four classes—susceptible, exposed, infected, and recovered—to analyze human-human transmission dynamics from December 31, 2019, to January 28, 2020. They calculated the reproduction number for coronavirus disease to be approximately 2.68 [4,5].

Several significant studies on the transmission dynamics of COVID-19 or SARS-CoV-2 have been conducted across various countries, including Italy, the United States, and Wuhan. Giordano et al. introduced SIDARTHE, a compartmental model with eight sub-classes, to study COVID-19 communication dynamics in Italy. They forecasted that strict social distancing could mitigate the spread. Kucharski et al. conducted a model-based analysis of COVID-19 dynamics and calculated a basic reproduction number (R0) of 2.35, considering positive cases in Wuhan until March 5th, 2020. In the absence of therapeutics or vaccines, non-pharmaceutical interventions like public use of face masks could significantly reduce community transmission and the burden of the pandemic. The authors demonstrated that greater adherence to social-distancing protocols led to a substantial reduction in the pandemic's impact.

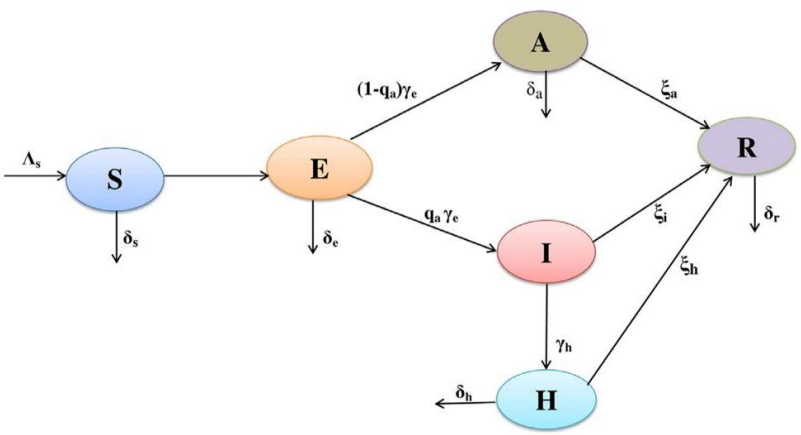


Figure 1. Schematic representation of the model. The schematic flow diagram represents the biological mechanism of the novel coronavirus (COVID-19) infection in India, which influences the formulation of the mathematical model (7). The mathematical model consists of six sub-populations: susceptible *S(t),* exposed *E(t)*, asymptomatic *A(t),* symptomatic or clinically ill *I(t),* hospitalized or isolated *H(t)* and recovered *R(t)* individuals in a total population of $N(t) = S(t) + E(t) + I(t) + H(t) + R(t)$ individuals.

Furthermore, their model illustrates the required mask coverage in conjunction with the social-distancing strategy to eliminate SARS-CoV-2. Gatto et al. estimated model parameters using a metacommunity Susceptible Exposed Infected Recovered (SEIR) model to examine COVID-19 transmission dynamics in Italy. Their model involves a network of 107 interconnected regions with high-resolution mobility data. The authors employed their model to differentiate transmission between presymptomatic and asymptomatic individuals, resulting in a calculated basic reproduction number R0 = 3.60. Arino et al.'s simple mathematical models provide insight into explaining the threatening pandemic, even when faced with uncertain parameters. These models can be adapted to disease outbreaks and used to ascertain the number of doses needed for antiviral treatment, with initial doses significantly influencing the outcome.

Several mathematical models have already been developed to analyze the transmission dynamics of the COVID-19 pandemic in India, taking into consideration intervention strategies like lockdowns, social distancing, and economic perspectives. Chatterjee et al. employed a system of stochastic differential equations to investigate the COVID-19 outbreak in India, utilizing an extended SEIR model. While few mathematical models have explored the impact of lockdowns as a compartment, the COVID-19 epidemic in India has garnered widespread interest. Mathematical modeling that incorporates media effects also plays a pivotal role in containing disease outbreaks.

Our study delves into a dynamic model to examine the coronavirus epidemic and its control in India's five most affected states: Maharashtra, Karnataka, Kerala, Andhra Pradesh, West Bengal, as well as the entire nation. This endeavor seeks to enhance our understanding of crucial factors related to coronavirus control within communities and globally. We applied the least squares method to estimate pivotal parameters highlighted by sensitivity analysis. The calculated basic reproduction number R0 is determined for each of the five Indian states and the entire Republic of India.

2. Dynamic model in the absence of effective control measures

To explore the epidemiological characteristics of the classical deterministic (SEIR) compartmental model, we expand its scope by introducing contact tracing and hospitalization strategies for COVID-19. Our mathematical model is calibrated using daily data on confirmed coronavirus cases in India, and we estimate the basic reproduction number for disease transmission. To make our mathematical model more realistic, we adopt the following assumptions:

- The model incorporates a net inflow rate of vulnerable individuals.
- The model considers only human-to-human epidemic spread, excluding zoonotic infections of coronavirus.
- Effective control measures are not in place before September.
- The model includes demographic effects by accounting for proportional natural mortality in each sub-population.

The total population N(t) is partitioned into six sub-populations (classes) within the underlying dynamic model: susceptible S(t), exposed E(t), asymptomatic A(t), clinically ill or symptomatic S(t), hospitalized H(t), and recovered R(t). Figure 1 illustrates a schematic representation of the biological mechanism of coronavirus in humans, which serves as the foundation for our model. The dynamics of the novel coronavirus model are governed by the following system of nonlinear ordinary differential equations.

Although coronavirus transmission is primarily associated with symptomatic populations, a low transmission rate through asymptomatic individuals cannot be dismissed entirely. The parameter αa, representing different levels of hygiene during asymptomatic periods, contributes to this adjustment, with analogous parameters αi and αh for symptomatic and hospitalization stages, respectively. Given the progressive implementation and enhancement of asymptomatic, symptomatic, and hospitalization programs, along with corresponding hygiene measures, during the coronavirus epidemic, spreading coeffi-

cients (as, αaβs, αiβs, αhβs) and rates for asymptomatic, symptomatic, and hospitalized cases may be modeled as time-dependent parameters. Furthermore, the interaction between susceptible and infected populations (asymptomatic, symptomatic, and hospitalized) is characterized by a standard homogeneous mixing incidence represented by the total individuals N. The rate of change for susceptible individuals is expressed through the ordinary differential equation (ODE):

$$\frac{dS}{dt} = \Lambda_s - \frac{\beta_s S(\alpha_a A + \alpha_i I + \alpha_h H)}{N} - \delta_s S.$$

2.1. Individuals who have been exposed dynamics

Individuals who have been exposed to COVID-19 but have not yet developed clinical symptoms are categorized as asymptomatic individuals. Asymptomatic individuals decrease the population of exposed individuals at a rate of γe, and natural death also contributes to the reduction of exposed individuals at a rate of δe. The constant per-capita rate e is used to model the transition from exposed individuals (E) to either asymptomatic individuals (A) or symptomatic individuals (I). The parameter qa (0 < qa < 1) represents the proportion of the population moving from the exposed class (E) to either the asymptomatic partially infectious class (A) or the symptomatic class (I) at the per-capita rate γe. The following ordinary differential equation (ODE) describes the dynamics of the exposed population within the related model:

$$\frac{dE}{dt} = \frac{\beta_s S(\alpha_a A + \alpha_i I + \alpha_h H)}{N} - \delta_e E - \gamma_e E.$$

2.2. Individuals that are asymptomatic have different dynamics A(t)

The coronavirus was exposed to asymptomatic populations, but they were not contagious to the rest of the community. The exposed classes progress to the asymptomatic classes at a constant rate e (1- qa).

At the per capita rate ξa and natural mortality rate δa, asymptotic individuals ascend to the recovered class. The following ODE governs the rate of change in asymptomatic individuals:

$$\frac{dA}{dt} = (1 - q_a)\gamma_e E - \delta_a A - \xi_a A.$$

2.3. Dynamics of symptomatic individuals I(t)

Symptomatic individuals emerge when previously asymptomatic individuals exhibit clinical signs of the coronavirus (diagnosed by physicians). Exposed individuals transition to the symptomatic group at a constant per-capita rate. Additionally, at the per-capita rate I and the natural mortality rate, symptomatic or clinically unwell individuals progress to the hospitalized or isolated class (H). It is reasonable to deduce that the per-capita rate denoted by I, at which symptomatic or clinically unwell persons seek medical attention and are subsequently placed in the hospitalized class, exceeds the per-capita rate at which exposed individuals proceed to the asymptomatic classes. In the absence of diagnosis, clinically unwell classes (class I) transition to the recovery classes at the per-capita rate. The following ordinary differential equation (ODE) governs the dynamics of symptomatic populations:

$$\frac{dI}{dt} = q_a\gamma_e E - \delta_i I - \xi_i I - \gamma_i I.$$

2.4. H (t) Individuals in Hospital Dynamics

These are individuals who have experienced clinical symptoms related to coronavirus and have undergone hospitalization for medical treatment. Hospitalized individuals emerge at a per-capita rate denoted by I, originating from the clinically unwell class or symptomatic community (class I), and they experience a natural mortality rate of h. Hospitalized or isolated populations recover at a per-capita rate of ξh. We hypothesize that $\xi h > \xi i$ since isolated or hospitalized groups are more likely to receive partially effective treatment. The subsequent ordinary differential equation (ODE) illustrates the dynamics of hospitalized individuals:

$$\frac{dH}{dt} = \gamma_i I - \delta_h H - \xi_h H.$$

2.5. Individuals that have been rehabilitated have different dynamics R(t)

The recovered population is thought to have long-term immunity to coronavirus. The coronavirus was isolated from asymptomatic, symptomatic, and hospitalized people at the per capita rates, ξi and ξh, respectively. Individuals who have been rehabilitated die at a rate of r per capita. The following ODE can be used to write the rate of change for recovered individuals:

$$\frac{dR}{dt} = \xi_a A + \xi_i I + \xi_h H - \delta_r R.$$

We create a mathematical model of novel coronavirus based on the preceding biological assumptions and schematic depiction of coronavirus (see Fig. 1), as well as specific forms, using the following six-dimensional nonlinear system of ODEs:

$$\begin{cases} \frac{dS}{dt} = \Lambda_s - \frac{\beta_s S(\alpha_a A + \alpha_i I + \alpha_h H)}{N} - \delta_s S, \\ \frac{dE}{dt} = \frac{\beta_s S(\alpha_a A + \alpha_i I + \alpha_h H)}{N} - \delta_e E - \gamma_e E, \\ \frac{dA}{dt} = (1 - q_a)\gamma_e E - \delta_a A - \xi_a A, \\ \frac{dI}{dt} = q_a \gamma_e E - \delta_i I - \xi_i I - \gamma_i I, \\ \frac{dH}{dt} = \gamma_i I - \delta_h H - \xi_h H, \\ \frac{dR}{dt} = \xi_a A + \xi_i I + \xi_h H - \delta_r R, \end{cases}$$

The following nonnegative beginning conditions are satisfied by the model:

$S(0) = S0$, $E(0) = E0$, $A(0) = A0$, $I(0) = I0$, $H(0) = H0$, $R(0) = R0$. (8)

All state variables are considered to be positive because the model system (7) monitors the dynamics of the human population.

2.6. Number of basic reproductions

The basic reproduction number, denoted as R0, is defined as "the anticipated secondary cases arising from an infectious indi-

vidual within a completely susceptible community." The infinite basic reproduction number functions as a threshold for discerning whether a disease will endure or wane within a community. R0 can also be delineated as the count of fresh infections produced by a typical infective population at an equilibrium devoid of infection. R0<1 signifies that during the infective duration, an infected population generates fewer than one new infected population on average, leading to the extinction of the infection. Conversely, R0 > 1 indicates that each infected population generates more than one new infection on average.

$$\mathcal{F} = \begin{bmatrix} \frac{S}{N}\beta_s(\alpha_a A + \alpha_i I + \alpha_h H) \\ 0 \\ 0 \\ 0 \end{bmatrix}, \quad \mathcal{V} = \begin{bmatrix} (\delta_e + \gamma_e)E \\ -(1-q_a)\gamma_e E + (\delta_a + \xi_a)A \\ -q_a\gamma_e E + (\delta_i + \xi_i + \gamma_i)I \\ -\gamma_i I + (\delta_h + \xi_h)H \end{bmatrix}.$$

The Jacobian matrix for the system (7), can be computed at an infection free state (*E = A = I = H = 0)*, we have

$$F = \begin{bmatrix} 0 & \beta_s\alpha_a & \beta_s\alpha_i & \beta_s\alpha_h \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix},$$

Table 1. Parameter values and coefficient of determination (R^2) for the power law $X_{t+1} = \propto X_t^{\beta}$, and the corresponding curve fitting has been shown in the figure 2.

Provinces	α	β	R^2
India	1.456	0.9672	0.9919
Kerala	1.479	0.9522	0.9429
Maharashtra	1.676	0.9466	0.9620
West Bengal	1.556	0.9451	0.9907
Karnataka	3.316	0.8653	0.9638
Andhra Pradesh	3.616	0.8591	0.9793

$$V = \begin{bmatrix} \delta_e + \gamma_e & 0 & 0 & 0 \\ -(1-q_a)\gamma_e & (\delta_a + \xi_a) & 0 & 0 \\ -q_a\gamma_e & 0 & (\delta_i + \xi_i + \gamma_i) & 0 \\ 0 & 0 & -\gamma_i & (\delta_h + \xi_h) \end{bmatrix}.$$

$$V = \begin{bmatrix} \delta_e + \gamma_e & 0 & 0 & 0 \\ -(1-q_a)\gamma_e & (\delta_a + \xi_a) & 0 & 0 \\ -q_a\gamma_e & 0 & (\delta_i + \xi_i + \gamma_i) & 0 \\ 0 & 0 & -\gamma_i & (\delta_h + \xi_h) \end{bmatrix}.$$

The basi ectral radius for a next generation matrix FV^{-1}. Thus, from

$$R_0 = \frac{(1-q_a)\gamma_e\beta_s\alpha_a}{(\delta_e+\gamma_e)(\delta_a+\xi_a)} + \frac{q_a\gamma_e\beta_s\alpha_i}{(\delta_e+\gamma_e)(\delta_i+\xi_i+\gamma_i)} + \frac{q_a\beta_s\alpha_h\gamma_e\gamma_i}{(\delta_e+\gamma_e)(\delta_i+\xi_i+\gamma_i)(\delta_h+\xi_h)}.$$

Equilibria

The system (7) has two biologically feasible equilibrium points which are as follows:

1. disease-free equilibrium point $E^0(\Lambda_s/\delta_s, 0, 0, 0, 0, 0)$,
2. endemic equilibrium point $E^*(S^*, E^*, A^*, I^*, H^*, R^*)$, where

$$\begin{aligned}
S^* &= \frac{1}{\delta_s}\left[\Lambda_s - \frac{(\delta_e+\gamma_e)(\delta_i+\xi_i+\gamma_i)}{q_a\gamma_e}\right],\\
E^* &= \frac{\delta_i+\xi_i+\gamma_i}{q_a\gamma_e}I^*, \qquad H^* = \frac{\gamma_i}{\delta_h+\xi_h}I^*,\\
A^* &= \frac{(\delta_i+\xi_i+\gamma_i)(1-q_a)}{q_a(\delta_a+\xi_a)}I^*,\\
R^* &= \frac{1}{\delta_r}\left[\xi_i + \frac{\xi_a(1-q_a)(\delta_i+\xi_i+\gamma_i)}{q_a(\delta_a+\xi_a)} + \frac{\xi_h\gamma_i}{\delta_h+\xi_h}\right]I^*,\\
I^* &= \frac{\Lambda_s(R_0-1)}{\delta_s}\\
&\times \left[1 + \frac{\xi_i}{\delta_r} + \frac{(\delta_e+\gamma_e)(\delta_i+\xi_i+\gamma_i)(R_0-1)}{q_a\gamma_e\delta_s} + \frac{\delta_i+\xi_i+\gamma_i}{q_a\gamma_e}\right.\\
&+ \left.\left(1+\frac{\xi_a}{\delta_r}\right)\frac{\gamma_e(\delta_i+\xi_i+\gamma_i)(1-q_a)}{(q_a\gamma_e)(\delta_a+\xi_a)} + \left(1+\frac{\xi_h}{\delta_r}\right)\frac{\gamma_i}{\delta_h+\xi_h}\right]^{-1}.
\end{aligned}$$

Table 2. Table of biologically relevant parameter values and their description for the coronavirus model system (7).

Parameter	Biological meaning	Values (Unit)	Source
Λ_s	Inflow rate of susceptible individual	–	–
β_s	Disease transmission coefficient	day^{-1}	Estimated
α_a	Adjustment factor for asymptomatic classes	0.20 (0, 1)	[7]
α_i	Adjustment factor for symptomatic classes	0.45 (0, 1)	[28]
α_h	Adjustment factor for hospitalized individuals	(0, 1)	Estimated
δ_s	Natural death rate of susceptible classes	0.1945×10^{-4} day^{-1}	[56]
δ_e	Mortality rate of exposed individuals	0.1945×10^{-4} day^{-1}	[56]
δ_a	Mortality rate of asymptomatic individuals	0.1945×10^{-4} day^{-1}	[56]
δ_i	Mortality rate of symptomatic individuals	0.018 day^{-1}	[57]
δ_h	Mortality rate of hospitalized individuals	0.1945×10^{-4} day^{-1}	[56]
δ_r	Mortality rate of recovered individuals	0.1945×10^{-2} day^{-1}	[56]
γ_e	Conversion rate from exposed to asymptomatic individuals	1/7 day^{-1}	[1]
γ_i	Rate at which symptomatic individuals become hospitalized	day^{-1}	Estimated
q_a	Proportion of exposed individuals	(0, 1)	Estimated
ξ_a	Rate of recovery from asymptomatic individuals	day^{-1}	Estimated
ξ_i	Rate of recovery from symptomatic individuals	day^{-1}	Estimated
ξ_h	Rate of recovery from hospitalized individuals	day^{-1}	Estimated

Table 3. Estimated parameter values from the daily confirmed and cumulative confirmed coronavirus observed data.

Parameters	India	Kerala	Andhra Pradesh	West Bengal	Maharashtra	Karnataka
β_s	0.879	0.899	1.221	1.799	1.021	0.879
ξ_a	0.302	0.341	0.876	0.241	0.359	0.128
q_a	0.710	0.146	0.439	0.091	0.551	0.291
ξ_h	0.114	0.010	0.102	0.471	0.269	0.130
γ_i	0.201	0.389	0.862	0.469	0.010	0.481
ξ_i	0.210	0.211	0.209	0.210	0.211	0.209
α_h	0.350	0.349	0.351	0.349	0.350	0.349

The disease-free equilibrium point E^0 is always feasible and the endemic equilibrium point E^* feasible only if $R_0 > 1$ and $\Lambda_s >$

$$\left(1 + \frac{\delta_e}{\gamma_e}\right)\left(\frac{\delta_i+\xi_i+\gamma_i}{q_a}\right)$$

3. Coronavirus data source and model calibration

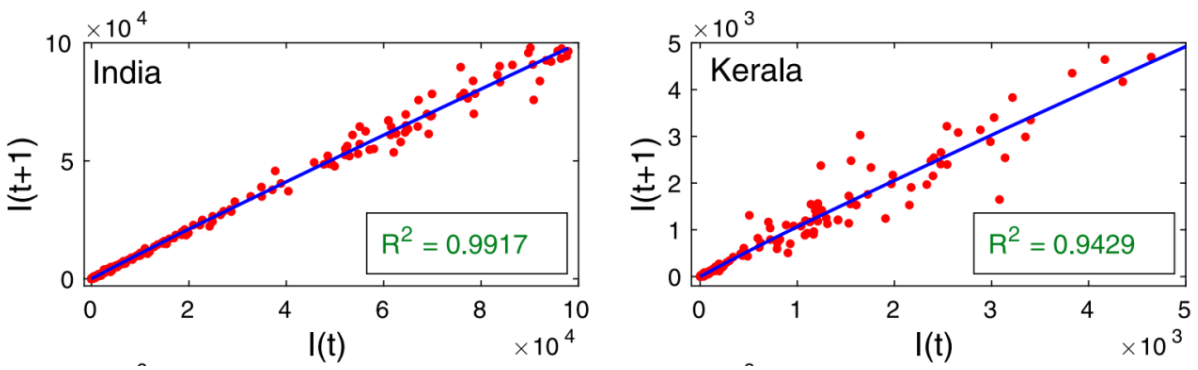
This section provides a comprehensive exploration of computer simulations for the coronavirus model system (7). We commence by estimating the parameters, followed by presenting computer simulation results that illuminate the eradication and dynamics of the coronavirus (COVID-19) outbreak. Several parameters are estimated from observed data, while others are deduced from existing literature. Table 2 presents the parameter values accompanied by descriptions, and Table 3 compiles the values of the remaining parameters, derived from observed data across five distinct Indian states: Kerala, Andhra Pradesh, West Bengal, Maharashtra, and Karnataka. The initial population sizes for Kerala, Maharashtra, Andhra Pradesh, and West Bengal.

3.1. COVID-19 data shows power-law growth

We begin with a simple analysis to gain some insight into the ongoing COVID-19 outbreak. The association between the infected population of $(t+n)^{th}$ and t^{th} day, with a temporal lag of nth days, was explored.

In Fig. 2, we plotted the infected populations of the t^{th} and $(t + 1)^{th}$ days along the horizontal and vertical axes, respectively, using n = 1. The power law governs the afflicted populace.

Xt+1 = Xt, (10) where Xt represents the number of symptomatic infected patients on the t^{th} day, Xt+1 represents the number of symptomatic infected cases on the $(t+ 1)^{th}$ day, and α and β are variables to be considered.



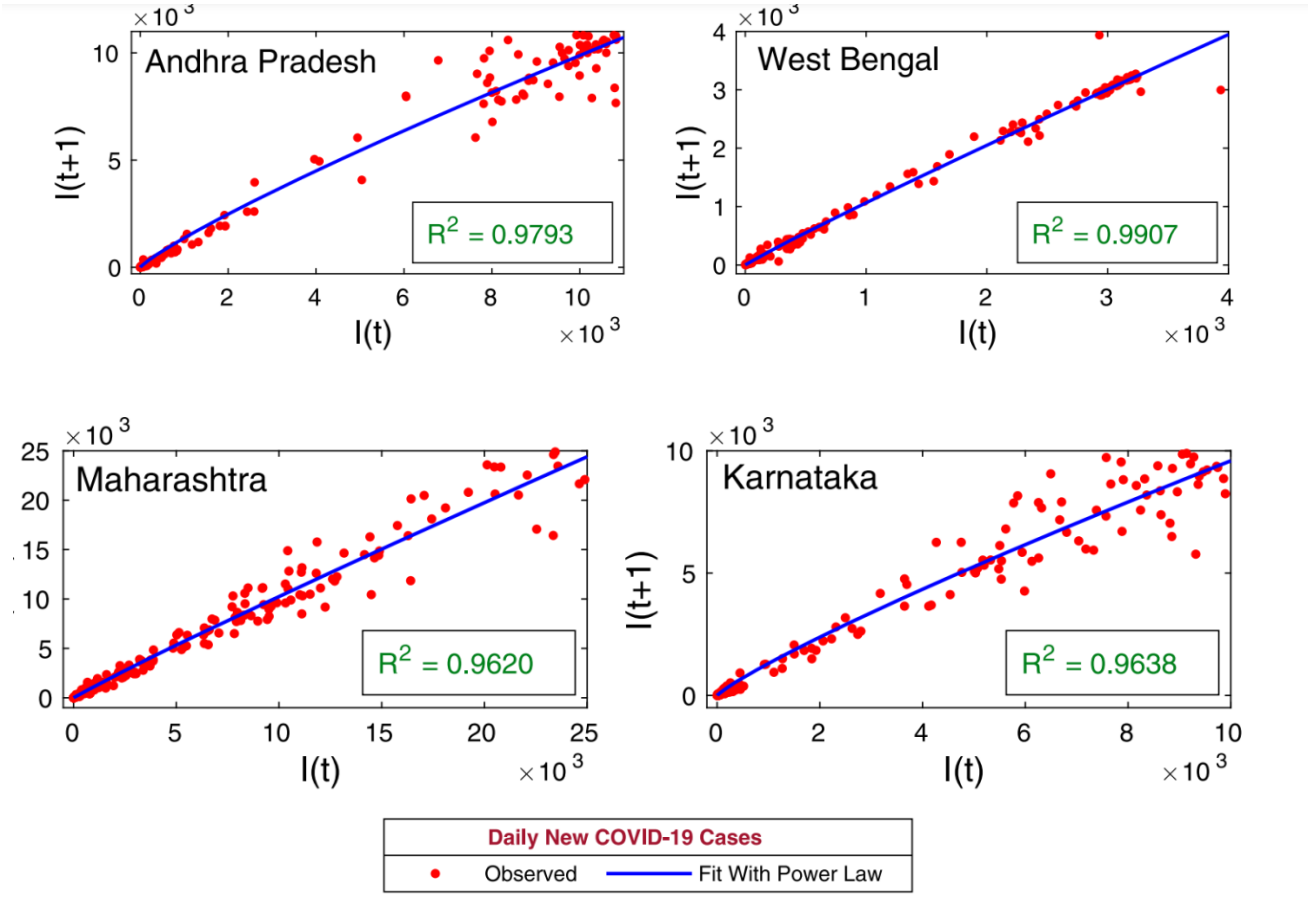


Figure 2. Power law growth. The figure represents the recurrence plots for the daily new coronavirus cases for five provinces of India, namely, Kerala, Andhra Pradesh, West Bengal, Maharashtra, Karnataka and the Republic of India. Solid blue curves are the best fit of the power law of the kind (10). The coefficient of determination (R^2) for each provinces are shown in the inset. The trend of power law shows that the best fit curves are increasing for all the provinces of India as well as overall India.

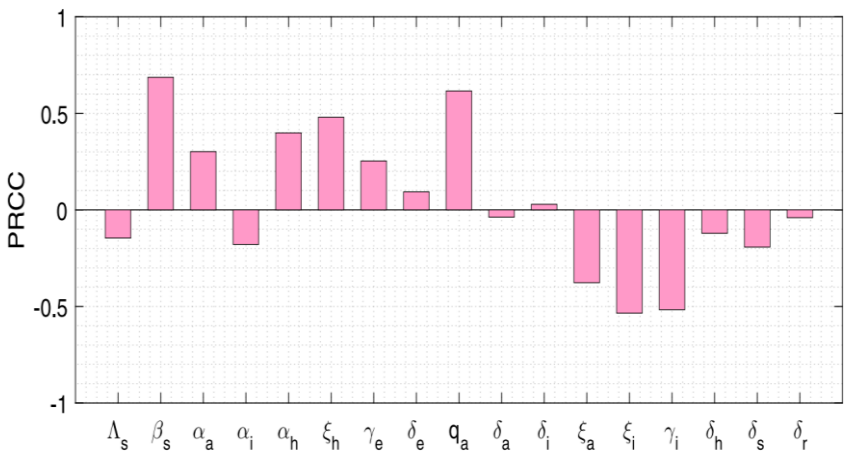


Figure 3. Parameter Sensitivity. Partial rank correlation coefficients illustrating the dependence of symptomatic individuals *I* on each of the system parameters at the day 60 with *p<0.02.*

Table 4. Accuracy of the COVID-19 model (7) for the five different states of India and the Republic of India.

Performance Metrics	India	Kerala	Andhra Pradesh	West Bengal	Maharashtra	Karnataka
E_{MAE}	2339.5	172.9	894.7	151.2	858.8	594.1
E_{RMSE}	3861.2	287.5	1235.8	219.2	1346.5	771.3

Table 5. Estimated values of the initial population size and the constant inflow rate for the five provinces of India and the Republic of India.

Parameters	India	Kerala	Andhra Pradesh	West Bengal	Maharashtra	Karnataka	Source
$S(0)$	160 000	400 000	130 000	120 000	1 000 000	200 000	Estimated
$E(0)$	250	800	1000	1000	1700	1600	Estimated
$A(0)$	10	100	100	100	250	150	Estimated
$I(0)$	1	1	1	1	2	1	Data
$H(0)$	1	1	1	1	1	1	Estimated
$R(0)$	0	0	0	0	0	0	Data
$M(0)$	0	0	0	0	0	0	Estimated
Λ_s	35 000	13 000	19 000	21 000	20 000	21 000	Estimated

It shows the values of, and coefficient of determination (R2) for five Indian states of Kerala, Andhra Pradesh, West Bengal, Maharashtra, Karnataka, and the Republic of India. For all provinces, the R2 value is very close, and the curve Xt+1 = Xt matches exactly with the COVID-19 examples observed in all provinces. Power law population growth provides crucial information on population growth in the future. As a result, the preliminary examination of the COVID-19 cases utilizing the power law method is extremely important. The exponent varies by province, and a list of all provinces is given in Table 1, which is arranged in decreasing order.

In comparison to its five states, the Republic of India has the largest exponent. Kerala has the fewest COVID-19 cases among the five states, but it has the second-largest exponent, behind Maharashtra, West Bengal, Karnataka, and Andhra Pradesh.

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4. PRCC sensitivity analysis

This section provides a detailed exploration of the computer simulations applied to the coronavirus model system (7). We initiate by estimating the parameters, followed by computer simulation findings that shed light on the dynamics and mitigation of the coronavirus (COVID-19) outbreak. Several parameters are approximated from observed data, while others are derived from existing literature. Table 2 offers a compilation of parameter values alongside descriptions, while Table 3 presents the values of the remaining parameters obtained from observed data originating from five distinct Indian states: Kerala, Maharashtra, Andhra Pradesh, Karnataka, and West Bengal. The initial population sizes are accounted for in these states and the Republic of India. In comparison to the five states, the Republic of India possesses the highest exponent. Among these states, Kerala registers the fewest COVID-19 cases, yet it holds the second-largest exponent, following Maharashtra, West Bengal, Karnataka, and Andhra Pradesh. The utilised template serves to structure your paper and format the text. All margins, column widths, line spacing, and text fonts are predefined; kindly avoid altering these specifications. Some peculiarities may be ob-

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To further investigate the epidemiological properties of the deterministic SEIR compartmental model, we extend it to incorporate contact tracing and hospitalization strategies specifically for COVID-19. By utilizing the Partial Rank Correlation Coefficient (PRCC) technique, we conduct a sensitivity analysis to identify the most influential input parameters concerning symptomatic individuals. The collection of these significant characteristics is determined using data from multiple Indian states (Kerala, Maharashtra, Andhra Pradesh, Karnataka, West Bengal) and the Republic of India. Our approach involves simultaneous alteration of all 17 system parameters in our coronavirus model (Equation 7). The PRCC quantifies the relationship between each model parameter and the state equation of interest, aiding in identifying critical parameters contributing to system variability. We focus on PRCC values within the range of -1.0 to +1.0 for model simulation.

We adopt the Latin hypercube sampling method introduced by Marino et al. [58] to generate 2800 samples for PRCC computation and p-value determination concerning symptomatic classes on day 60. Several parameters, such as the disease transmission coefficient rate βs, proportion rate of exposed individuals qa, the rate vi by which symptomatic individuals become recovered, and others, exhibit significant positive correlation. Conversely, parameters like the rate vi by which susceptible individuals become exposed, the rate i by which susceptible individuals become symptomatic, exhibit strong negative correlation. Our PRCC analysis highlights 7 vital parameters out of the total 17.

To proceed, we employ the least square method to estimate these 7 parameters. Our coronavirus illness model (Equation 7) has now been calibrated using daily confirmed new coronavirus cases for both India as a whole and five specific states: Kerala, Andhra Pradesh, West Bengal, Maharashtra, and Karnataka. The data spans January 30, 2020, to September 20, 2020, and originates from the World Health Organization (WHO) situation report as well as the India COVID-19 Tracker (https://www.covid19india.org/). The initial COVID-19 case in India was identified in Kerala on January 30, 2020. Consequently, we gathered COVID-19 data for both Kerala and India as a whole within that timeframe. A similar approach was taken for the other states. The acquired COVID-19 data for Andhra Pradesh spans from March 12, 2020, to September 20, 2020, while Maharashtra and Karnataka data were collected for the period of March 9, 2020, to September 20, 2020. The daily new coronavirus cases (class I in the model) were integrated into our coronavirus model system (Equation 7) for the five states and India. Additionally, cumulative coronavirus instances were fed into the model. The observed data were fitted using the least squares approach in Matlab, and the parameters found to be sensitive through PRCC analysis were computed: βs, va, qa, vh, γi, vi, and αh. The biological explanations for these model parameters are outlined in Table 2, while Table 3 presents the estimated values for each dataset. It's important to note that the initial population estimates align with the confirmed new coronavirus infections (see Table 5). The model's output for daily new cases is depicted in Figure 4, with observed daily cases overlaid. Additionally, Figure 5 illustrates observed daily cumulative confirmed coronavirus cases against model simulations.

To gauge the performance of our coronavirus system (Equation 7), we calculate:

$$E_{MAE} = \frac{\Sigma_{i=1}^{n} |O(i) - Q(i)|}{n},$$

$$E_{RMSE} = \sqrt{\frac{\Sigma_{i=1}^{n} (O(i) - Q(i))^2}{n}},$$

where $O(i)$ represents the observed value, $Q(i)$ is the model output and n is the sample size of the observed data. The values of $EMAE$ and $ERMSE$ for the five states (Kerala, Andhra Pradesh, West Bengal, Maharashtra and Karnataka) and the Republic of India are presented in Table 4.

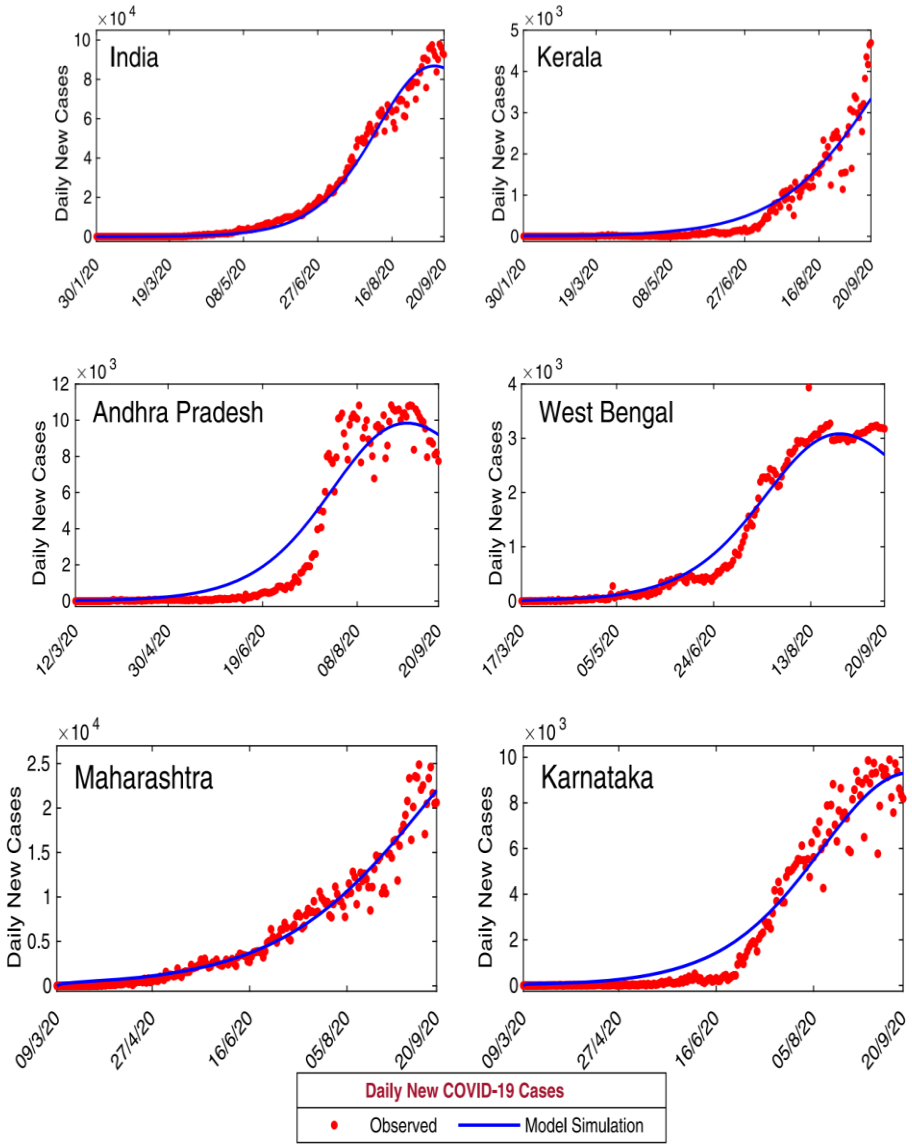

Figure 4. Model estimation based on observed data. Daily new confirmed positive coronavirus cases for India and five states of India, namely, Kerala, Andhra Pradesh, West Bengal, Maharashtra and Karnataka, Observed data are shown in red circles, whereas the blue curve is the best fitting curve of the model system (7). The parameter values are used for numerical simulation and listed in Tables 2 and 3. The initial population sizes used for numerical simulation are listed in Table 5.

We can calculate the basic communicability number R0 from the expression of the fitting data (9). The basic reproduction number for coronavirus in different states is R0 = 3.3870 in Kerala, R0 = 1.8155 in Andhra Pradesh, R0 = 1.5525 in West Bengal, R0 = 1.2937 in Maharashtra, R0 = 1.5934 in Karnataka, and R0 = 1.6795 across India. Let us note that, in comparison to the other four states and India as a whole, Kerala has a moderately high rate of basic reproduction. The fundamental reproduction number R0 in India indicates that coronavirus outbreaks are pandemic, and the government should take the necessary steps to maintain social distance and take essential safeguards. Table 6 shows the fundamental reproduction number R0 for five provinces and India as a whole. The data fitting results indicate that our model performs quite well in all states: Kerala, Andhra Pradesh, West Bengal, Maharashtra, and Karnataka. This alignment with observed data and the curve fitting of the coronavirus disease model is notable. However, the model's performance is less optimal for the entirety of India, possibly due to the relatively high number of confirmed coronavirus cases. Nevertheless, the model accurately captures the increasing trend of daily

confirmed coronavirus cases across all datasets. We also computed the numerical errors for our model's simulations, revealing that the lowest values of $EMAE$ and $ERMSE$ were obtained for the state of West Bengal, likely due to its smaller dataset size.

5. Bifurcation at the Trans critical point

At R= 1, the coronavirus model system (7) experiences trans critical bifurcation. The symptomatic individuals (I) are plotted in the (R0, I) plane in Fig. 6. R0, the basic reproduction number, increased progressively as disease transmission coefficients increased from 0.25 to 1.1, and then R0 changed from 0.5 to 2.0. The values of the system parameters are qa = 0.71, a = 0.302, I = 0.20, and h = 0.114, s = 35000, and additional parameters are provided in Table 2. At R0 = 1, the system (7) suffers trans critical bifurcation, as shown in Fig. 6.

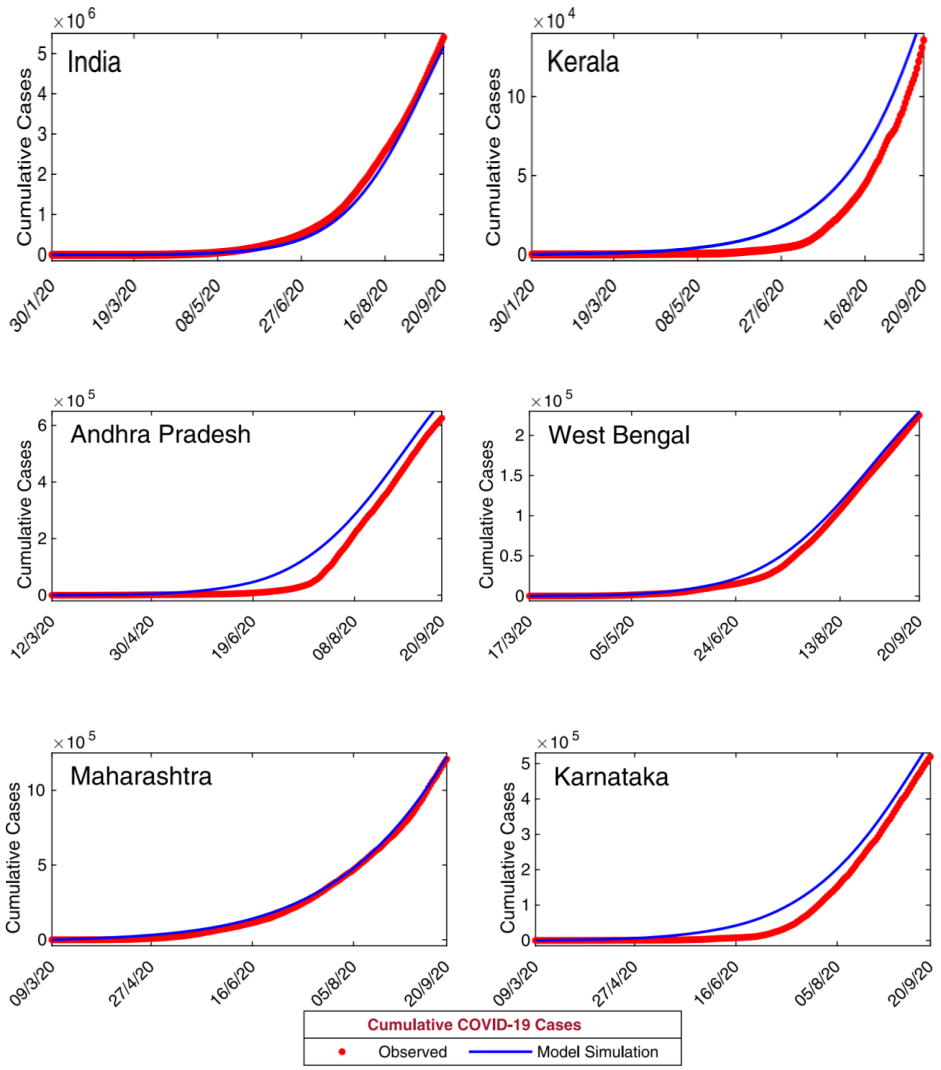

Figure 5. Model estimation based on observed data. Daily cumulative confirmed coronavirus cases for India and five states of India, namely, Kerala, Andhra Pradesh, West Bengal, Maharashtra and Karnataka. Observed data points are shown in red circles, whereas the blue curve is the best fitting curve of the model system (7). The parameter value used for numerical simulation are listed in Tables 2 and 3. The initial population sizes used for numerical simulation are listed in Table 5. (For interpretation of the references of color in this figure legend, the reader is referred to the web version of this article.)

Table 6. Basic reproduction number of the five different provinces of India and the Republic of India.

Reproduction Number	India	Kerala	Andhra Pradesh	West Bengal	Maharashtra	Karnataka
R_0	1.6795	3.3870	1.8155	1.5525	1.2937	1.5934

The stable disease-free equilibrium point (E0) is shown by the black line, the unstable endemic equilibrium point (E) is represented by the red dashed line, and the stable branch of the endemic equilibrium point (E) is represented by the blue curve. As a result, for R0 > 1, the endemic equilibrium point (E) is stable, while for R0 1, it is unstable.

Also, for R0<1, the disease-free equilibrium point (E0) is stable, whereas for R0 > 1, it is unstable. When R0 > 1, the endemic equilibrium point E is stable, and the coronavirus illness spreads in the population.

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6. Prognosis for the near future

Predictive mathematical models can provide valuable insights into the intricate dynamics of coronavirus transmission and control, as well as its complex epidemiological cycle, especially in the absence of effective vaccination or treatment strategies for the novel coronavirus. To explore short-term predictions for our model system, we conducted simulations for the daily and cumulative symptomatic classes of coronavirus cases from September 21, 2020, to October 11, 2020. The estimated parameter values from Table 3 and initial population sizes from Table [reference to the appropriate table] were employed for these simulations.

Table 7. Table of sensitivity indices of basic reproduction number R_0 for the coronavirus model system (7) for five different states of India and the Republic of India. The baseline parameter values taken from Table 2 and other parameters are estimated and taken from Table 3.

Parameters	Sensitivity Indices					
	India	Kerala	Andhra Pradesh	West Bengal	Maharashtra	Karnataka
β_s	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000
α_a	0.10061	0.13384	0.08572	0.88393	0.19764	0.61277
α_i	0.38041	0.02776	0.12057	0.05795	0.77989	0.10000
α_h	0.51899	0.83839	0.79371	0.05813	0.02247	0.28723
q_a	0.65308	0.84328	0.84692	0.01786	0.56080	0.13695
γ_e	0.13613×10^{-3}	0.13613×10^{-3}	0.13613×10^{-3}	0.13613×10^{-3}	0.13613×10^{-3}	0.13613×10^{-3}
γ_i	0.11017	0.30263	0.07796	-0.01874	-0.95085×10^{-2}	0.02940
δ_e	-0.13613×10^{-3}	-0.13613×10^{-3}	-0.13613×10^{-3}	-0.13613×10^{-3}	-0.13613×10^{-3}	-0.13613×10^{-3}
δ_a	-0.64789×10^{-5}	-0.76561×10^{-5}	-0.19033×10^{-5}	-0.71629×10^{-4}	-0.10678×10^{-4}	-0.93098×10^{-4}
ξ_a	-0.10060	-0.13384	-0.08572	-0.88386	-0.19763	-0.61267
δ_i	-0.06132	-0.04121	-0.02491	-0.49065×10^{-2}	-0.09594	-0.01611
ξ_i	-0.42926	-0.28918	-0.17362	-0.03430	-0.67444	-0.11329
δ_h	-0.88531×10^{-4}	-0.16275×10^{-2}	-0.15132×10^{-3}	-0.24053×10^{-5}	-0.16186×10^{-5}	-0.42968×10^{-4}
ξ_h	-0.51890	-0.83677	-0.79356	-0.05812	-0.02247	-0.28719

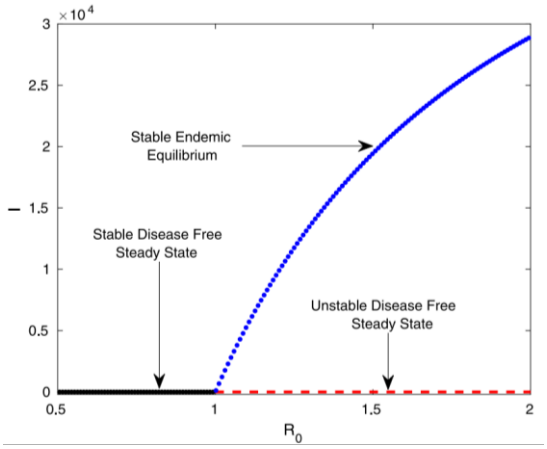

Figure 6. Transcritical bifurcation. The figure shows the transcritical bifurcation diagram of the system (7) with respect to the basic reproduction number R_0. The stability of the system (7) interchange at the threshold $R_0 = 1$. The parameters value are

$$\Lambda_s = 35000,\ q_a = 0.710,\ \xi_a = 0.302,\ \gamma_i = 0.201,\ \xi_h = 0.114$$

and other parameters are listed in Tables 2 and 3. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Table 2 lists the values for the other baseline parameters. Figures 7 and 8 show the simulated outcomes for the five Indian provinces of Kerala, Andhra Pradesh, West Bengal, Maharashtra, and Karnataka, as well as the Republic of India, during the period September 21, 2020, to October 11, 2020. The model forecast is represented by black solid curves. Daily confirmed new coronavirus cases are expected to increase in Kerala and Maharashtra, whereas daily confirmed new coronavirus cases are expected to decrease in all other provinces. As projected daily fresh coronavirus cases are positive, the cumulative coronavirus cases for all provinces are increasing.

7. Prognosis for the near future

Understanding the relative significance of various factors in new coronavirus transmission is crucial to formulating strategies that minimize human mortality and morbidity. We have conducted sensitivity analysis on the parameters of the system with respect to R0, as the initial spread of the illness is closely linked to the reproduction number R0. Sensitivity indices provide insights into the potential spread of infectious diseases within a population, and they play a pivotal role in assessing the resistance of the reproduction number R0 to alterations in system attributes. Sensitivity analysis not only helps us gauge the impact of changes in system parameters but also aids in identifying the proportional variation in a state variable when a parameter shifts. The normalized forward sensitivity index concerning R0 with respect to parameter p is defined as follows:

$$\Gamma_p^{R_0} = \frac{\partial R_0}{\partial p} \times \frac{p}{R_0}.$$

As we have the explicit expression for R_0 in (9), we obtain the analytical formulae for sensitivity indices of R_0, $\Gamma_p^{R_0}$, to each of fourteen parameters stated in Table 7. As for example, the sensitivity index of R_0 with regards to β_s is

$$\Gamma_{\beta_s}^{R_0} = \frac{\partial R_0}{\partial \beta_s} \times \frac{\beta_s}{R_0} = 1,$$

Regardless of any parameters This denotes that R0 is the rising function in relation to βs. It means that illness transmission likelihood has a significant impact on coronavirus control and management. Table 7 lists the sensitivity indices for the other parameters. The R0 sensitivity indices for each of the model parameters used in Table 7 are plotted in Figure 9. To prevent coronavirus outbreaks, we must focus on the most sensitive characteristics that have a significant impact on system dynamics. The illness transmission coefficient s, for example, is the most effective parameter in controlling coronavirus infections, as

shown in Fig. 9 and Table 7.

Contour plots illustrating the relationship between R0 and positively associated parameters, namely disease transmission coefficients s and clinical outbreak rate qa for all infected classes, are presented in Figure 10 as a means to control coronavirus outbreaks. The dependence of R0 on these parameters is depicted in the contour plot for the five states (Kerala, Andhra Pradesh, West Bengal, Maharashtra, and Karnataka) as well as the Republic of India. The basic reproduction number R0 increases with higher values of βs and qa on the contour plot, suggesting the potential for the coronavirus to enter stage-3 and spread throughout the community. In order to manage R0, it is essential to restrict the values of the transmission coefficient s and the fraction qa by which the exposed class transitions to symptomatic illness. Furthermore, the adjustment variables αa, αI, and αh display positive correlations with the basic reproduction number R0, as depicted in Figure 10 and Table 4. Consequently, minimizing these adjustment factors is also crucial. From these findings, we can infer that maintaining social distancing and restricting or eliminating events like fairs and theatre performances are necessary measures to reduce the occurrence of coronavirus outbreaks.

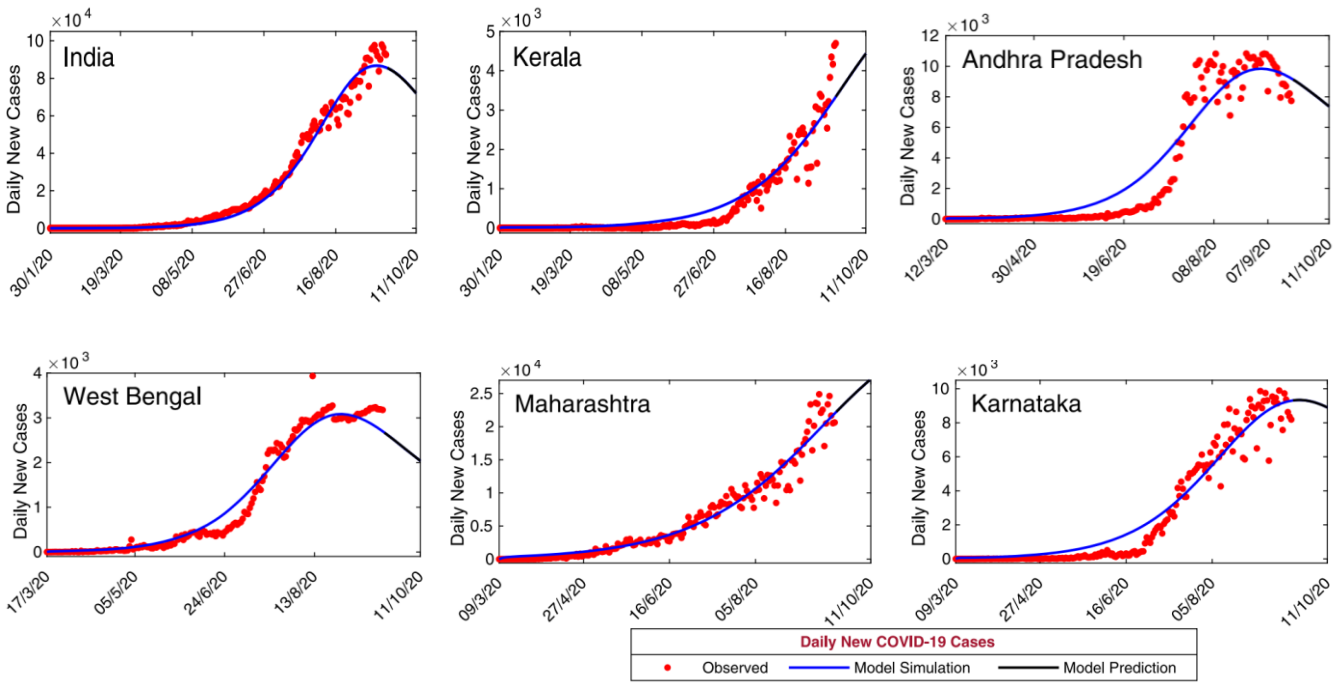

Figure 7. Model-Based Data-Driven Short-term prediction. Model simulations shows the short term predictions for the five provinces of India, namely Kerala, Andhra Pradesh, West Bengal, Maharashtra, Karnataka and the Republic of India. The solid black curve represents the model predictions for the daily new infected coronavirus cases. The baseline parameter values are listed in Table 2 and rest of estimated parameters are listed in Table 3.

8. Conclusion

As of September 29, 2020, India had reported 6,148,640 confirmed cases, 5,101,118 recovered cases, and 96,378 confirmed deaths due to the novel coronavirus outbreak, according to the INDIA COVID-19 TRACKER report. Each day witnesses a significant number of new cases and deaths being reported from various cities across India. This is an alarming situation considering India's population of approximately 1.39 billion people and the looming transition into stage 3 of coronavirus transmission. As of now, no specific vaccine, antivirals, or effective treatments have been developed for addressing coronavirus infections.

During this critical time, accurate forecasting is crucial for healthcare planning and the management of new coronavirus infections. In the absence of any medication or definitive diagnostic tests, mathematical modeling can play a pivotal role in devising strategies to curb the spread of coronavirus infections. In this paper, we propose a compartmental epidemic model to analyze the transmission dynamics of new coronavirus infections, both in the short-term and the long-term. Our model incorporates two categories of infectious individuals: asymptomatic and symptomatic, with the former acting as rapid spreaders of coronavirus infections.

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