

A Year Into the Pandemic: A Mathematical Model and Study of COVID-19 in India

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Abstract

COVID-19 has been declared as a global pandemic by the World Health Organization (WHO) since its outbreak in December 2019. In India, as of May 12th 2021, the total number of coronavirus cases and associated deaths are 2,35,57,676 and 2,56,617 respectively. To control the spread of the virus effectively, social distancing, self-isolation and quarantine, lockdowns and mass inoculation are vital. In this paper we propose a deterministic epidemic model which is an extension of the SEIR model to understand the disease dynamics. The proposed model has eight compartments, Susceptible₁, Susceptible₂, Exposed, Infected, Quarantined, Isolated, Recovered and Dead and is termed as the S₁S₂EIQJRD model. The basic reproduction number R_0 is derived for the proposed model and it is shown that for $R_0 < 1$ the disease dies out and for $R_0 > 1$ the disease is endemic. Numerical simulations for the growth of the virus across India through the span of the outbreak are obtained. The simulation is done on real data and the results obtained may be used to make suitable inferences about the dynamics of the disease and appropriate measures can be taken to control its spread.

Keywords : COVID-19, Mathematical Model, Comorbidities, Basic Reproduction Number, Numerical Simulation

Introduction

COVID-19 was detected for the first time in December 2019 in Wuhan City at Hubei Province in China. The virus soon spread to the rest of the world and on March 11, 2020 the World Health Organization (WHO) declared the novel coronavirus outbreak a global pandemic^[1]. As on May 12, 2021, over a year since the outbreak occurred, the world has witnessed 160,417,576 confirmed cases and 3,333,805 deaths^[1].

The first case of coronavirus in India was detected on January 30, 2020. The entire nation has been following various preventive measures and the Government of India had also imposed lockdowns

throughout the country at various time frames. Despite all the efforts made to curb spread of the virus, India has been extensively affected. As of May 12, 2021, the total number of cases in India are 2,35,57,676 and 2,56,617 deaths^[2].

The optimal way to control the spread of the virus is to understand its dynamics. Epidemiological models can be used for prediction of coronavirus (COVID-19)^[3]. These models help to estimate the number of COVID-19 patients. Some of the popular mathematical models e.g. SIR, SEIR, SEIJR, SEIAR, and SEIRD^[4] are widely used to estimate the future outbreak of communicable diseases.

Kermack et al^[5] adopted a fundamental epidemic model for human-to-human transmission through an SIR model that tracks the number of susceptible, infected and recovered individuals during an epidemic with the help of ordinary differential equations (ODE). The SEIR model presented by Zhang et al^[6] illustrates the relation among susceptible, exposed, infectious, and recovered individuals. Yang et al.^[7] suggested the modified SEIR model for Hubei province in China by introducing the two new parameters move-in and move-out for the inflow and outflow of susceptible individuals respectively. SEIJR model was put forward by Read et al^[8]. This is an extended version of the SEIR model. It includes one more factor asymptomatic individual during the incubation period in the SEIR model. It precisely segregates an isolated individual from the other populations. However, it is difficult to collect precise data for individuals which makes it difficult to get the best-fit parameters. Chen et al.^[9] recommended the SEIAR model which incorporates asymptomatic infections and population migration into SEIR. Memon et al^[10] adopted an SEIQJR model for Pakistan to assess the role of isolation and quarantine to control the spread of COVID-19. The model examines the dynamics of six classes: susceptible, exposed, quarantined, infected, isolated and recovered individuals. Kumari et al^[11] illustrated the SEIAQRDT model by extending the generalised model given by Peng et al^[12] for India and its states by incorporating asymptomatic cases as a new compartment. The eight compartmental model incorporates factors such as susceptible, exposed, infected, asymptomatic, quarantined, recovered, dead, and insusceptible. Chowell et al^[13] have proposed a modification to the SEIJR which has two susceptible classes, S_1 and S_2 , which accommodates for the population with comorbidities for SARS.

In this paper we propose an extension of the SEIRD model with the addition of compartments for Isolated and Quarantined population. The presence of

comorbidities has also become an important factor in the mortality of the infected individuals. Hence, the proposed model has two separate compartments to account for difference in susceptibility of individuals with and without comorbidities where individuals with comorbidities being more severely infected. In total, the proposed model has eight compartments, susceptible1 (S_1), susceptible2 (S_2), exposed (E), infected (I), quarantined (Q), isolated (J), recovered (R) and dead (D).

The rest of the paper is organised as follows. In Section 2, a model is proposed and discussed to understand the growth of the coronavirus. In Section 3, the expression for the reproduction number of the proposed model is derived and Section 4 displays the numerical simulations of the growth of the virus in various parts of India across the span of the outbreak and Section 5 finally concludes the paper.

Model Formulation

In this section, we introduce a mathematical model to understand the increase and spread of the coronavirus. The proposed model is an extension of the SEIR model^[6] with inclusion of populations with difference in susceptibility. It also has separate classes for quarantined and infected. The reproduction number^[14] of this model is also discussed in this section.

The proposed model has eight compartmental states, S_1S_2EQIJD is shown in Fig 1. $S_1(t)$ represents a population $N\rho$ with increased susceptibility and $S_2(t)$ represents a population $N(1 - \rho)$ with lower susceptibility at time t where N is the total population. $E(t)$ represents the exposed population who are infected with the virus but do not infect others within the latent period. $Q(t)$ represents the population who are exposed but are quarantined, thus not infecting others. $I(t)$ represents the exposed population who show symptoms of infection and

are infecting others by not being quarantined. $J(t)$ represents the population who have been confirmed to be infected and hence isolated. $R(t)$ represents the

population who have recovered and $D(t)$ represents the deceased population. The compartmental diagram is shown below.

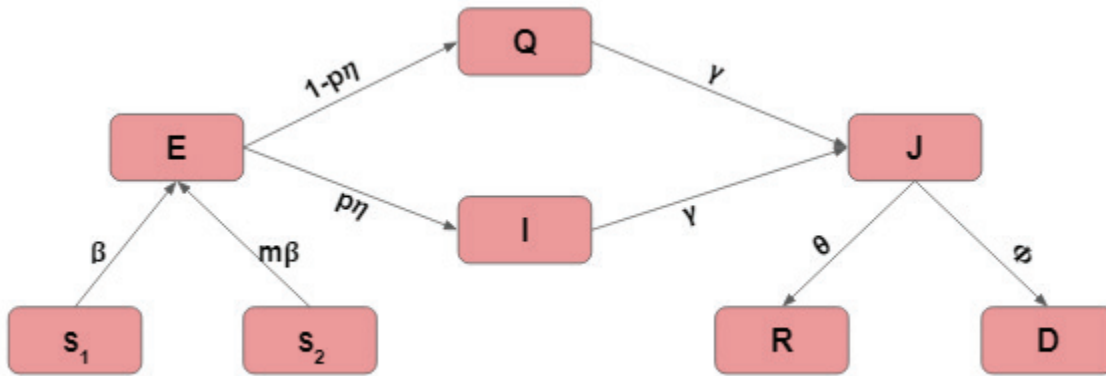


Fig 1: Compartmental Diagram

The system of ordinary differential equations which describe the compartmental model are as follows:

$$\frac{dS_1(t)}{dt} = \frac{-\beta S_1(t)[I(t) + qQ(t)]}{N} \tag{1}$$

$$\frac{dS_2(t)}{dt} = \frac{-m\beta S_2(t)[I(t) + qQ(t)]}{N} \tag{2}$$

$$\frac{dE(t)}{dt} = \frac{[\beta S_1(t) + m\beta S_2(t)][I(t) + qQ(t)]}{N} - \eta E(t) \tag{3}$$

$$\frac{dI(t)}{dt} = p\eta E(t) - \gamma I(t) \tag{4}$$

$$\frac{dQ(t)}{dt} = (1-p)\eta E(t) - \gamma Q(t) \tag{5}$$

$$\frac{dJ(t)}{dt} = \gamma [Q(t) + I(t)] - \phi(t)J(t) - \theta(t)J(t) \tag{6}$$

$$\frac{dR(t)}{dt} = \theta(t)J(t) \tag{7}$$

$$\frac{dD(t)}{dt} = \phi(t)J(t) \tag{8}$$

□

With initial conditions $S_1(0) > 0, S_2(0) > 0, E(0) > 0, I(0) > 0, Q(0) > 0, J(0) > 0, R(0) > 0$ and

$$D(0) > 0.$$

The total population is assumed to be constant, which is represented by $N = S_1 + S_2 + E + Q + I + J + R + D$

Table 1: Parameters and their definition

m	Probability of lowering risk of infection in S2
p	Probability of symptomatic disease
β	Infection Rate
η	Inverse of average latent time
γ	Isolation Rate
$\theta(t)$	Recovery Rate (time dependent)
$\phi(t)$	Death Rate (time dependant)
ρ	Initial proportion of the population at higher risk
$q\beta$	Transmission rate for Q class

Basic Reproduction Number

The basic reproduction number R_0 is a dimensionless quantity that plays a vital role in the study of infectious diseases^[15]. It is ‘the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual’^[16]. The original infectious person can transmit disease in a population where each individual is susceptible. If $R_0 < 1$ the disease-free equilibrium is locally asymptotically stable and the disease is under control. On the other hand if $R_0 > 1$, then the

disease-free equilibrium is unstable and a pandemic exists in the population^[17]. Thus in order to control the pandemic, COVID-19, the reproduction number should be made smaller than one.

For the given system a disease-free equilibrium exists where $S_1 = N\rho, S_2 = N(1 - \rho)$ and $E = I = Q = J = R = D = 0$. R_0 is mathematically computed using the next generation matrix method^[18]. We consider the nonnegative matrix \mathcal{F} and the non-singular M -matrix \mathcal{V} . \mathcal{F} is expressed as the production of new-infection and \mathcal{V} as the transition part for the given system.

$$\mathcal{F} = \begin{pmatrix} \beta[S_1(t) + mS_2(t)][I(t) + qQ(t)/N] \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

$$\mathcal{V} = \begin{pmatrix} \eta E(t) \\ \gamma I(t) - p\eta E(t) \\ \gamma Q(t) - (1-p)\eta E(t) \\ \frac{-\beta S_1(t)[I(t) + qQ(t)]}{N} \\ \frac{-m\beta S_2(t)[I(t) + qQ(t)]}{N} \\ \gamma[Q(t) + I(t)] - \phi(t)J(t) - \theta(t)J(t) \\ \theta(t)J(t) \\ \phi(t)J(t) \end{pmatrix}$$

The variation matrix of the given model at disease free state gives

$$F = \begin{bmatrix} 0 & \beta[\rho + m(1 - \rho)] & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \eta & 0 & 0 \\ -\eta p & \gamma & 0 \\ -\eta(1 - p) & 0 & \gamma \end{bmatrix}$$

The reproduction number for the proposed system is calculated using equation $R_0 = \rho(FV)^{-1}$ where ρ represents the spectral radius of the matrix $(FV)^{-1}$ [19].

$$R_0 = q\beta[\rho + m(1 - \rho)][p + q(1 - p)]/\gamma \tag{9}$$

R_0 depends upon the major parameters such as infection rate β and the isolation rate γ . Additionally the parameters m, p, q, ρ also affect the value of R_0 . As seen from the equation of R_0 the probability of lowering the risk of infection in class S_2 , probability of symptomatic infection, transmission rate for

quarantined population and the initial proportion of population at a higher risk are all important parameters in determining the value of the reproduction number using the proposed model.

NUMERICAL SIMULATION AND DISCUSSION

In this section we present the numerical simulations for India across different phases of the pandemic as well as the numerical simulations for 4 different states of India during the 2nd wave of the pandemic. The simulated data is compared with the real data in both these cases. The dataset used for the coronavirus cases in India is available at the COVID-19 REST API for India [2]. Due to lack of available data regarding

quarantined and isolation population as well as populations with comorbidities or those at a higher risk of contracting the virus, we opt for a simpler compartmental model for numerical simulations[20]. For the purpose of simulation we define a SEIR model as shown in Fig 2 and minimize the nonlinear least squares to estimate the parameters from real data of COVID-19 cases in India. Levenberg–Marquardt (LM) algorithm[21] is used to solve the nonlinear least squares optimization.

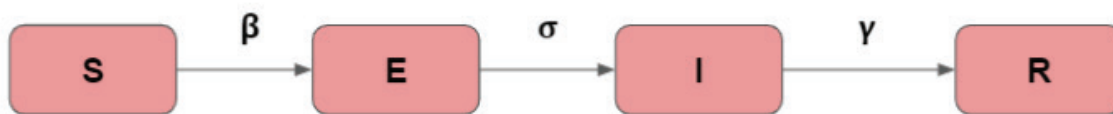


Fig 2: SEIR Compartmental Model

The compartments S, E, I, R refer to the susceptible, exposed, infected and recovered populations respectively. In this model β is the infection rate, γ is the recovery rate and σ is the incubation rate.

The reproduction number for the simplified SEIR model is found to be $R_0 = \beta/\gamma$

Simulation of Data across different phases of the pandemic

The model fitting for cumulative cases from

March 10th 2020 to May 12th 2021 is split into 5 phases. Phase 1 is from 10th March and 8th June 2020, Phase 2 is from 9th June to 6th September 2020, Phase 3 is from 7th September to 5th December 2020, Phase 4 is from 6th December 2020 to 4th March 2021 and Phase 5 is from 5th March to 12th May 2021. Table 2 displays the parameter values for the five phases. Figure 4 contains the plots the observed and fitted infections for the five phases.

Table 2: Parameter values of the five phases

Phase	Beta	Gamma	Sigma	R0
1	0.10929	0.05111	2.39085	2.138
2	0.13640	0.08281	0.09042	1.647
3	0.07602	0.09226	0.16513	0.824
4	0.07037	0.10854	0.09117	0.648
5	0.19425	0.08982	0.13147	2.162

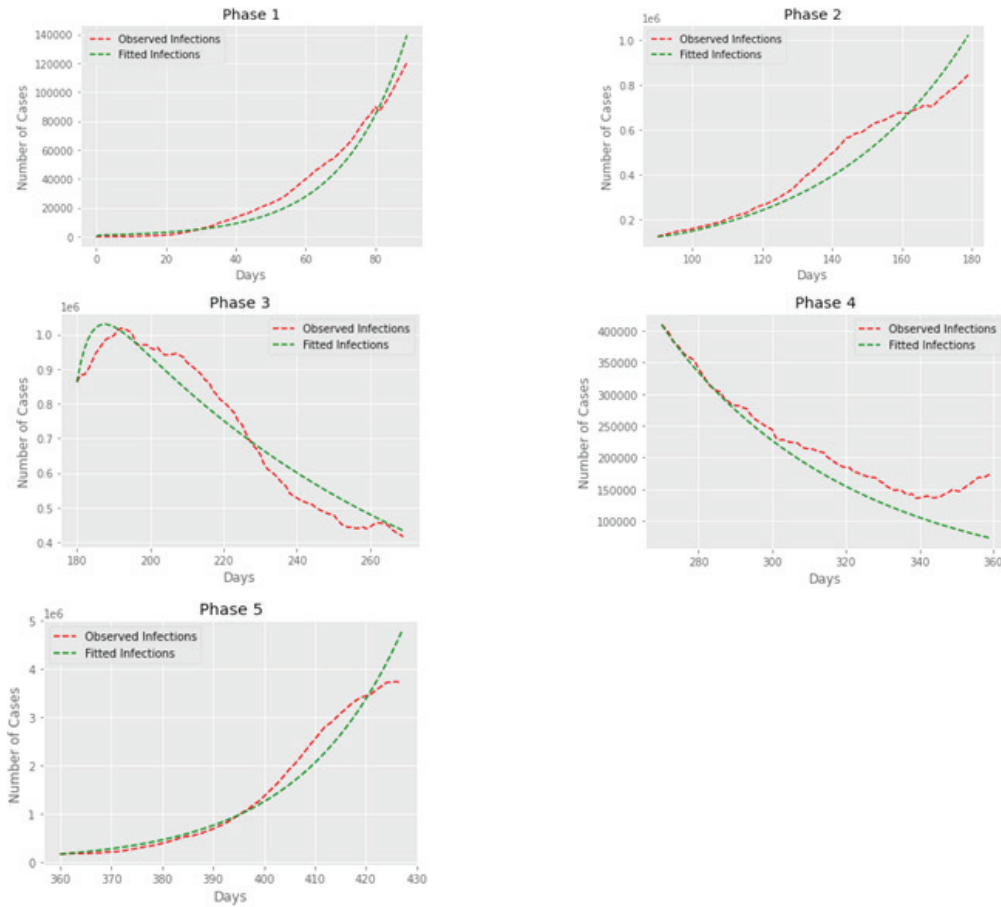


Fig 3: Graphs for observed and fitted infections for the five phases

Numerical Simulation for Indian States

The second wave in India had come into picture in early February when India reported an average of 10,000 cases a day. However, the situation worsened by the end of April when India recorded a total of

4,00,000 cases in a day. This surge in the number of cases can be attributed to the emergence of new coronavirus variants such as B.1.1.7 and B.1.617. This section discusses the coronavirus trends in a few states of India for the time period of 4th March 2021 to 12th May 2021.

Table 7: Estimated parameters for Indian states

State	R0 value	Beta	Sigma	Gamma
Karnataka	3.7846	0.1775	0.1278	0.0469
Tamil Nadu	2.6199	0.3285	0.0826	0.1255
Andhra Pradesh	1.9431	0.1556	0.9987	0.0801
Odisha	1.8280	0.1850	0.7172	0.1012
Haryana	3.1344	0.2962	0.0890	0.0945
Himachal Pradesh	2.0519	0.1658	0.3396	0.0808
Rajasthan	6.5052	0.3090	0.0564	0.0475

The relationship between R_0 (reproduction number) and β (infection rate), γ (recovery rate) was found using correlation coefficient. The correlation coefficient between R_0 and β is 0.529, and between R_0 and γ is -0.650. This signifies that as β increases R_0 also increases and conversely as γ increases R_0 decreases. Figure 8 is a plot to visualize the relation between β , γ , and R_0 .

Beta and Gamma

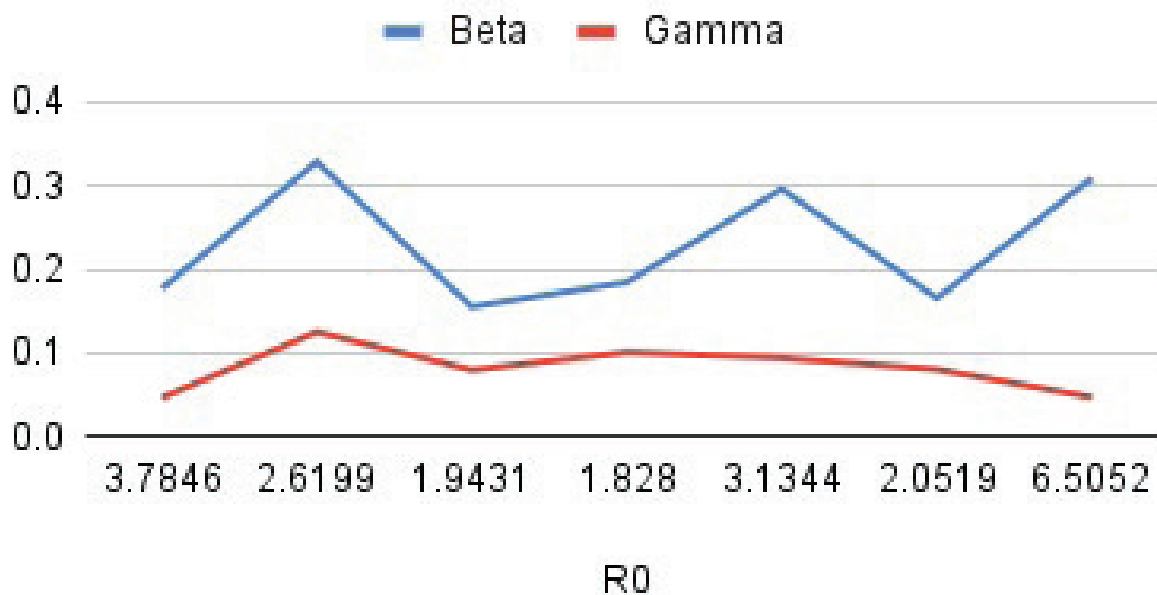


Fig 4: Relationship between beta, gamma and R_0

The following figures are numerical simulations of the observed infections versus the fitted infections by the SEIR model. From the graphs it can be seen that the states of Tamil Nadu and Odisha have an early spike in the number of cases, from day 395 which is early April. The states of Karnataka, Andhra Pradesh, Rajasthan and Himachal Pradesh followed the trend a week later. This period of early April to mid-May

was when India was worst hit by the second wave. On May 9, 2021, the daily number of cases recorded was 4,14,188 making it the highest ever. After reaching the peak it can be observed that there has been a gradual drop in the number of cases in all of the above states beyond day 420. This indicates the end of the second wave in late May.

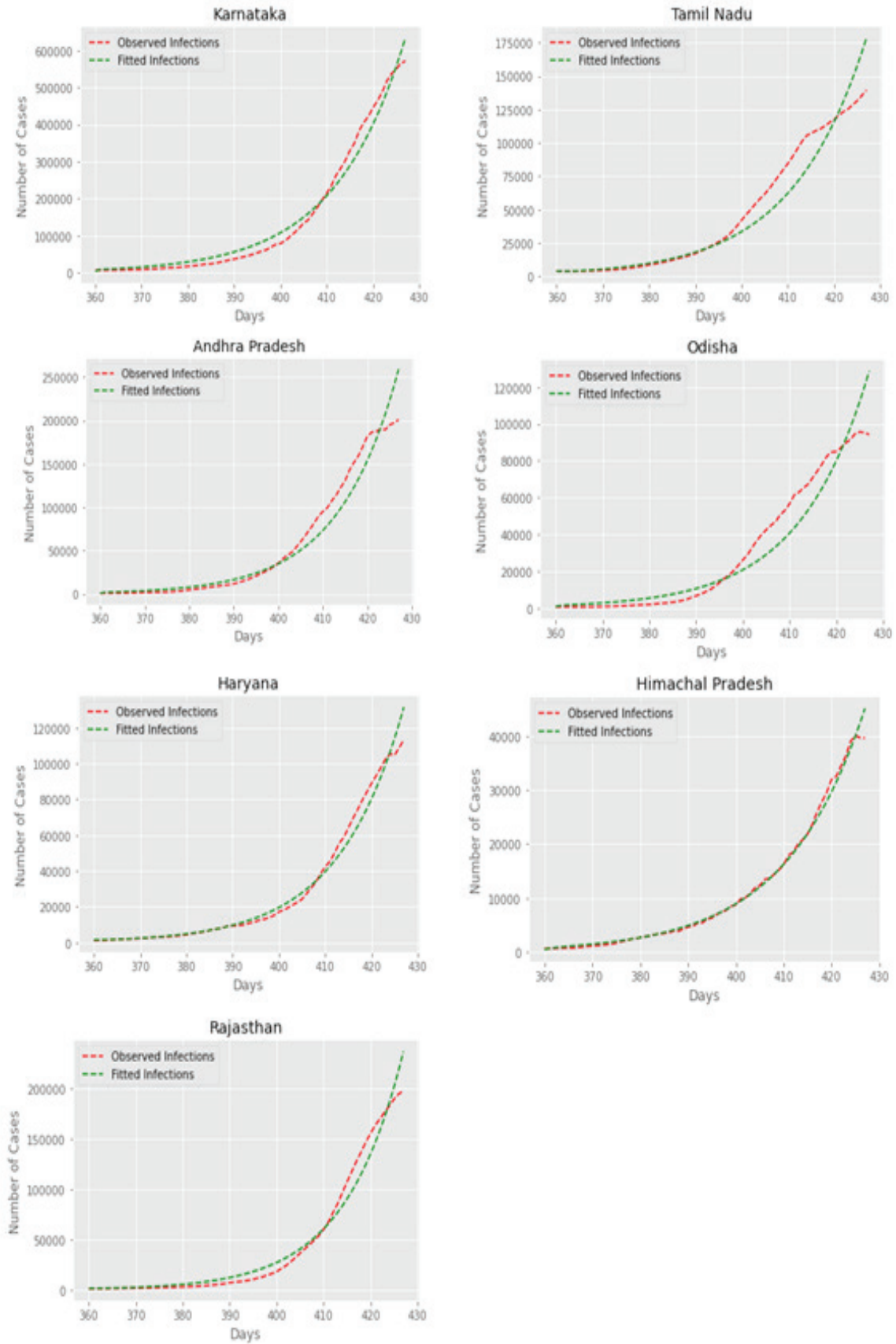


Fig 5: Observed and Fitted Infections for Indian states

Conclusion and Future Work

Combining the SEIR model with the dataset by the Government of India, the median reproduction number, R_0 for India has been estimated to be 1.647 till the 12th of May 2021. A detailed analysis of R_0 across India over 5 phases has displayed fluctuations in its estimated values driven by the rise and fall of the number of cases. In phase 1, initial stages of pandemic, the value of R_0 is 2.138. With the introduction of travel restrictions and strict regulations, R_0 dropped to as low as 0.648. However, due to relaxation of the lockdown norms, the value of R_0 increased to 2.162 in phase 5 indicating the second wave of the pandemic. In the analysis done for a few states of India, it can be observed that the states experienced a sudden increase in the number of cases and also a gradual drop around the same time.

On comparing the model predictions with the observed cases reported, it can be seen that the model does not accurately capture the rapid rise or fall in the number of cases. This drawback can be attributed to the fact that the SEIR model does not take into account the comorbidities present in susceptible populations, as well the isolated and quarantined cases. With adequate amounts of data for the mentioned cases, the 8 compartmental proposed model can be used for accurate predictions.

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Ethical Clearance: All data has been taken from official government sources. Data available at <https://www.covid19india.org/>.

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