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Prediction of COVID-19 Infected Population for Indian States through a State Interaction Network-based SEIR Epidemic Model ⋆

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Abstract: Objective of this present study is to predict the COVID-19 trajectories in terms of infected population of Indian states. In this work, a state interaction network of sixteen Indian states with highest number of infected caseload is considered, based on networked Susceptible-Exposed-Infected-Recovered (SEIR) epidemic model. An intervention term has been introduced in order to capture the effect of lockdown with different stringencies at different periods of time. The model has been fitted using least absolute shrinkage and selection operator (LASSO). Machine learning methods have been used to train the parameters of the model, cross-validate the data, and predict the parameters. The predictions of infected population for each of the sixteen states have been shown using data considered from January 1, 2021 till writing this manuscript on June 25, 2021. Finally, the effectiveness of the model is manifested by the calculated mean error and confidence interval.

Keywords: Networked SEIR model, COVID-19, Epidemic model, Prediction, Intervention stingency.

1. INTRODUCTION

The devastation of the pandemic COVID-19 has left the mankind exasperated to find for any remotely possible solution and intensify the combating efforts against the deadly transmission of the disease. Originated in China (ECDC, 2020), (WCHC, 2019) and gradually engulfing the entire world, this deadly disease has been dangerously affecting all of our daily lives and various other day-to-day activities for the last one year or so now, infecting hundred millions of people and claiming more than millions of lives globally till June 25, 2021 (worldometer, 2021). With regard to the impact of the disease in national scenario of India, millions of people have been infected with the virus while lakhs have died of the disease till June 25, 2021 (India, 2021). Though, India managed to flatten the curve of COVID-19 during the first wave, and minimised the per day caseload; but the inevitable second wave hit hard and devastated India. The impact of second wave is approximately four times worse than the previous one. Quite naturally then, understanding the evolution and spreading dynamics of the disease and its future course in Indian states is of utmost importance at this point of time for major health and security concerns in the society as well as risk assessment and focussed medical support in regions.

The transmission dynamics of every viral disease can be dictated by existing dynamical epidemiological model (Draief and Massoulie, 2009), (Bailey et al., 1975). In this regard, Bernoulli developed the first known mathematical epidemiological model in eighteenth century that captures the spreading of smallpox (Bernoulli, 1760). Incidentally, two of the classical compartmental epidemiological transmission models are (i) Susceptible (S)-Infected (I)-Susceptible (S), i.e., SIS model(Kermack and McKendrick, 1932) and (ii) Susceptible (S)- Infected (I)-Recovered (R) model, i.e., SIR model(Kermack and McKendrick, 1927), both developed by Kermack and Mckendrick. In the former model, basically all the individuals start as susceptible and becomes infected when comes in contact with an infectious individual, and finally on getting recovered again becomes susceptible to the disease. On the other hand, in the later model, the infected individuals when recover from the disease stay recovered for some duration due to either enhanced immunity after the disease or due to the effect of the vaccine. These models are associated with two very important parameter namely (i) transmission rate (β) which represents the probability of infection and (ii) curing rate (δ) that represents the probability of recovery from the disease. However, in the case of COVID-19, it has been observed that COVID-19 infected patients can be both symptomatic and asymptomatic. The symptomatic patients are those which have apparent symptoms of the disease and require immediate medical attention. On the other hand, asymptomatic patients are those which are infected by other symptomatic or asymptomatic patients and carries the disease with them during a period known

as *latency period* or *incubation period* which can be as long as fourteen days. In other words, a person remains infected with the disease and carries the disease with her/him unaware of it and unnoticed in the society during the entire latency period before the symptoms begin to show up and the person requires medical attention. This state is called Exposed (E) state, and the rate at which the exposed individuals begin to show symptoms of being infected is called incubation rate (σ). Specifically speaking, exposed state is more dangerous than the infected state in the sense that during the entire incubation period, the exposed person can also expose other individuals who have come in contact with her/him, and eventually getting infected with the disease (Agrawal et al., 2021a), (Agrawal et al., 2021b). Hence, in this work the prediction of the future trajectories of COVID-19 in Indian states has been done based on the networked SEIR epidemiological discrete-time dynamical model (Vrabac et al., 2022). Various epidemiological models are provided in details in Hethcote (2000) and for recent and relevant review, Pastor-Satorras et al. (2015) and Nowzari et al. (2016) are excellent repositories. A rigorous study of stability analysis of various model has been provided in Paré et al. (2017). Network-based epidemic models are provided in Mesbahi and Egerstedt (2010). Moreover, investigation along with detailed stability analysis of a multi-competitive mutating virus epidemic model over a time-varying network has been carried out in Paré et al. (2021).

Network-based epidemic model relaxes many simplistic assumptions of well-mixed population model, e.g., homogeneous transmission rate and curing rate which reflect equal chances of getting infected and getting cured. Incidentally, the propagation of the disease which is mainly attributed to social interactions can take place among people from the same geographical locations or across states, and in that sense the nodes of the networks can be considered to be the states and their connectivity or interactions represent the edges of the network. Towards that end, the quantitative knowledge of the interactions between states in terms of population flow or the interactions within the state in terms of population density can be thought to be good indicators of the propagation of this disease across states. However, the knowledge regarding the population flow which should take into account not only the airline transportation data, but also various other modes of communication such as railways or roadways can not be expected to be very precise and reliable (Mandal et al., 2020). As an alternative to availing this data, the prediction analysis of the disease can be recast as a network inference problem for a particular network-based epidemic model where useful parameters of the model and the contact pattern can be estimated. Based on given epidemiological data, Welch et al. (2011) dwells upon the statistical inference methods to estimate interaction network. In the similar research area, for Chinese province Hubei (where the disease originated), Prasse et al. (2020) predicted the future course of COVID-19 in the early days of the disease based on a networked SIR model where an interaction network of Hubei's cities is considered, recently in Pizzuti et al. (2020) a transmission modifier term has been introduced, that incorporates the intervention policies to predict the future course of COVID-19 in Italy. Moreover, underlying contact network reconstruction and prediction of epidemic

course for generalized models has been discussed in Prasse and Van Mieghem (2020). Other than this, control algorithm for disease retardation in networked model has been formulated in Zino et al. (2020); Wang et al. (2020a).

In this study, the focus is on predicting the epidemic size of each of the sixteen most-infected Indian states through a state interaction networked-based SEIR epidemic model. The epidemic dynamical model underpins the transmission dynamics of COVID-19 with its tenets of disease spreading mechanism rooted in the estimated contact network among states. Moreover, other parameters of the models such as curing rate and incubation rate are also inferred from this study to predict the future course of infected caseload. Predicting the caseloads of each states for next fourteen days will help Government and policy makers to plan for the necessary arrangements of medical facility like requirements of numbers of beds, ICU, oxygen, medicines, and health care workers. Further, this prediction will help Government to plan for the necessary interventions by optimal trade off. The epidemic prediction results of the states are based on the data considered from January 1, 2021 to June 25, 2021 available in (India, 2021).

In the remainder of the paper, Section 2 describes the models of the work, Section 3 is about the different methods used, Section 4 is all about the simulated results and discussion, and the concluding discussion and future work are in Section 5.

2. MODELS OF THE WORK

2.1 Network SEIR Model

The following is the state connectivity network-based SEIR epidemic transmission model with difference of time index from k to $k+1$ being equal to one day:

$$S_i[k+1] = S_i[k] - S_i[k] \sum_{j=1}^{N} \alpha_i[k] \beta_{ij} I_j[k]$$

$$E_i[k+1] = E_i[k] + S_i[k] \sum_{j=1}^{N} \alpha_i[k] \beta_{ij} I_j[k]) - \sigma_i E_i[k]$$

$$I_i[k+1] = I_i[k] + \sigma_i E_i[k] - \delta_i I_i[k]$$

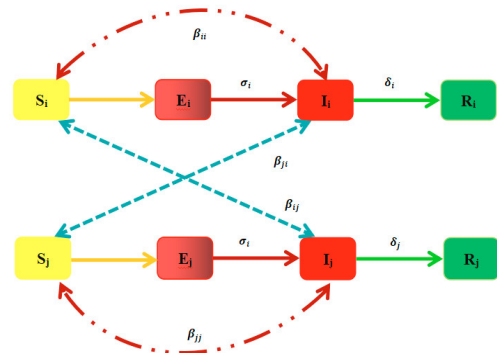$$R_i[k+1] = R_i[k] + \delta_i I_i[k], \tag{1}$$

Fig. 1. Network-based SEIR model of COVID-19 transmission dynamics between two states i and j with different parameters

where $S_i[k]+E_i[k]+I_i[k]+R_i[k]=1$; $i, j \in \Im_N = \{1, 2, \ldots, 16\}$ are the index of the sixteen states as provided in Table 1, $\sigma_i > 0$ and $\delta_i > 0$ are the incubation rate and curing rate for state i, respectively. $\beta_{ij} \geq 0$ denotes the rate at which susceptible individuals are getting infected when coming in close contact with infected individuals between states i and j ($i \neq j$) while self-transmission rate due to infected individuals within the same state i are represented by $\beta_{ii} > 0$, respectively. $\alpha_i[k]$ is the intervention term to simulate the different intervention strategy implemented by different state Governments.

The entire process of networked-based dynamical transmission of the disease between the compartments is shown in Fig. 1, where the transmission is shown between two states i and j.

3. METHODS

3.1 Intervention Term

It is witnessed that unlike the first wave of COVID-19 there was no nationwide lockdown in the second wave. Instead, based on experts advice different states impose lockdown at different time and that too with different stringency.
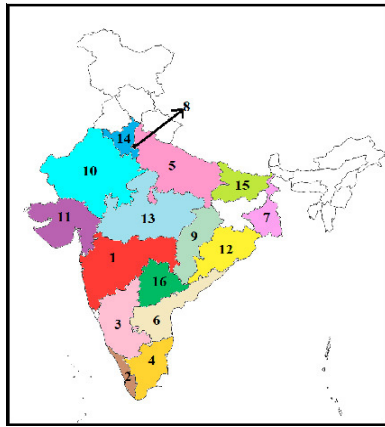

Fig. 2. The sixteen most affected states of Indiad maps (2021). The name of the states are stated in Table 1

To integrate this effect of different lockdown strategy by different state Government at different instant of time, an intervention term $\alpha_i[k] \in [0, 1]$ has been introduced (Pizzuti et al., 2020), (Wang et al., 2020b), where i represent i^{th} state and k represent the timeline or more specifically the day of imposition of intervention. After detailed research (MHA-GoI, 2021), it is found that most of the states impose night curfew within April, 2021; then they went for weekend lockdown, followed by partial lockdown; and finally they opted for strict or complete lockdown. However, after May 1 while some of the states start to open completely others went for partial relaxation of lockdown. The considered phases are as follows:
$\alpha_i^0[k]$ as phase 1 when there was no intervention;
$\alpha_i^1[k]$ as phase 2 during the period of night curfew;
$\alpha_i^2[k]$ as phase 3 during the period of partial lockdown;

$\alpha_i^3[k]$ as phase 4 during the period of strict lockdown;
$\alpha_i^4[k]$ as phase 5 when the states are opening completely or partially.

Depending on the stringency of lockdown human mobility decreases. Moreover, a decrease in human mobility will definitely decrease the rate at which the disease is transmitting, as COVID-19 spread through human interaction. Thus, the considered intervention term $\alpha_i[k]$ have dependencies on strictness of lockdown as well as the time of imposition of lockdown.

3.2 Data Processing

Table 1 shows the sixteen most-infected Indian states with their indices in descending order of infected population and total population of respective states. In this study, data has been considered from January 1, 2021 to June 25, 2021. From the available data for this entire duration and for each state, the fraction of reported infected cases per day has been calculated by dividing (I_{daily}) with the total population of the state (N_{state}), i.e., Input data, $I = \frac{I_{daily}}{N_{state}}$.

3.3 Modelling for Inference

The block diagram representation in Fig. 3 encapsulates our methods for the prediction of future course of COVID-19 progress in the most-infected sixteen Indian states based on the considered data from January 1, 2021 till June 25, 2021. Input data I is passed through data processing block and gives a seven-day moving average data as an output, then the processed data is used to calculate exposed fraction (E_i), recovered fraction (R_i), and thus susceptible fraction (S_i) using networked SEIR model (1), for each state and for entire duration of considered data. It is to be noted that to calculate the fraction of individuals in each compartment, $S_i + E_i + I_i + R_i = 1$ is used. Subsequently, data consisting information of S_i, E_i, and I_i are used to train and validate the data using a machine learning algorithm, and thus to predict the future course of epidemic size in Indian states in terms of the total number of infected population.
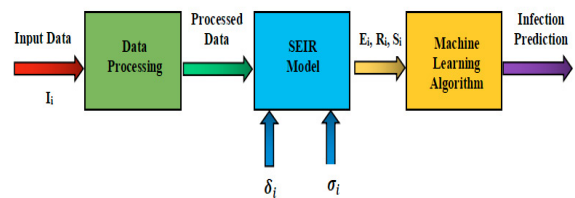

Fig. 3. Block diagram of the proposed method to predict infected population for every state

Mathematically, from the dynamical equation of E_i in (1), the following can be written:

$$V_i \triangleq \begin{bmatrix} E_i[2] & - & (1-\sigma_i)E_i[1] \\ E_i[3] & - & (1-\sigma_i)E_i[2] \\ & \vdots & \\ E_i[n] & - & (1-\sigma_i)E_i[n-1] \end{bmatrix} \in \mathbb{R}^{(n-1)} (i \in \{1, 2, ..., N\}), \quad (2)$$

$$F_i \triangleq \begin{bmatrix} S_i[1]I_1[1] & S_i[1]I_2[1] & \cdots & S_i[1]I_N[1] \\ S_i[2]I_1[2] & S_i[2]I_2[2] & \cdots & S_i[2]I_N[2] \\ \vdots & \vdots & \vdots & \vdots \\ S_i[n-1]I_1[n-1] & S_i[n-1]I_2[n-1] & \cdots & S_i[n-1]I_N[n-1] \end{bmatrix}, \quad (3)$$

where $F_i \in \mathbb{R}^{(n-1) \times N}$ and

$$\beta_i \triangleq \begin{bmatrix} \alpha_i[1]\beta_{i1} \\ \alpha_i[2]\beta_{i2} \\ \vdots \\ \alpha_i[n-1]\beta_{iN} \end{bmatrix} \in \mathbb{R}^N. \quad (4)$$

Then, from (1), (2),(3), and (4), the following can be written:

$$V_i = F_i \beta_i. \quad (5)$$

However, with almost every modelling, there is associated modelling error namely $\sigma_i (i \in \Im_N)$ in our case such that

$$\sigma_i = \hat{V}_i - \hat{F}_i \beta_i, \quad (6)$$

where $\hat{V}_i$ and $\hat{F}_i$ are values obtained from modelling. Consequently, following , modelling error σ_i is reduced by using least absolute shrinkage and selection operator, commonly known as LASSO Foucart and Rauhut (2017) to estimate the network transmission parameters such that

$$\min_{\beta_i} \|\hat{V}_i - \hat{F}_i \beta_i\|_2^2 + \lambda_i \sum_{\substack{j=1 \\ j \neq i}}^{N} \beta_{ij}$$

$$s.t. \ 0 \leq \beta_{ij} \leq 1, \forall \ i,j \in \Im_N \quad (7)$$

where $\lambda_i > 0$ is the regularization parameter obtained by cross-validation method. The solution of the LASSO problem (7) provides the network inference in terms of network transmission rates for each state.

In order to infer other parameters, for every state $i \in \Im_{16}$, curing rates δ_i is selected from 0.01 to 1 with linearly spaced values, while values of incubation rate σ_i is chosen from linearly spaced values in [0.05 0.25]. Moreover, regularized parameter λ_i is chosen from 40 logarithmically spaced values in $[10^{-4} \times 2 \max (F_i^T V_i), 2 \max (F_i^T V_i)]$. Hold-out cross validation method has been used with hold-out ratio being 0.2.

4. SIMULATION RESULTS AND DISCUSSION

Fig. 4 to Fig. 7 shows the cumulative infected population of all the states as tabulated in Table 1 with consecutive four states in each figure, based on the considered data from January 1, 2021 to June 25, 2021. The abbreviation of the states are provided in Table 1. For accuracy purpose, three days are skipped from the data points, i.e., data is considered till June 23, 2021 and then subsequently the prediction is shown for next fourteen days (two weeks). Blue lines show the actual plot of data available whereas, red lines show the prediction part for respective states. Thus, from the predicted results it is evident that for almost all the states the cumulative number of caseload is saturating except for the states Kerala and Odisha. Furthermore, Fig. 6 shows that after few days Odisha surpass Gujrat with respect to the cumulative infected caseload. Moreover, it is found that the average error percentage for the neglected three days is very small.

Table 1. Sixteen most infected Indian states with their population from January 1, 2021 to June 25, 2021

| Index i	State	Infected population	Total population
1	Maharashtra (MH)	40, 84, 923	12, 21, 53, 000
2	Kerala (KL)	21, 04, 938	3, 46, 78, 000
3	Karnataka (KA)	19, 07, 258	6, 57, 98, 000
4	Tamil Nadu (TN)	16, 37, 318	7, 56, 95, 000
5	Uttar Pradesh (UP)	11, 20, 254	22, 49, 79, 000
6	Andhra Pradesh (AP)	9, 89, 189	5, 22, 21, 000
7	West Bengal (WB)	9, 39, 156	9, 69, 06, 000
8	Delhi (DL)	8, 08, 221	1, 98, 14, 000
9	Chhattisgarh (CT)	7, 13, 109	29, 436, 000
10	Rajasthan (RJ)	6, 43, 583	7, 72, 64, 000
11	Gujarat (GJ)	5, 77, 972	6, 79, 36, 000
12	Odisha (OR)	5, 63, 887	4, 36, 71, 000
13	Madhya Pradesh (MP)	5, 47, 820	7, 26, 26, 000
14	Haryana (HR)	5, 05, 817	2, 86, 72, 000
15	Bihar (BR)	4, 68, 132	11, 95, 20, 000
16	Telangana (TG)	3, 32, 483	3, 72, 20, 000
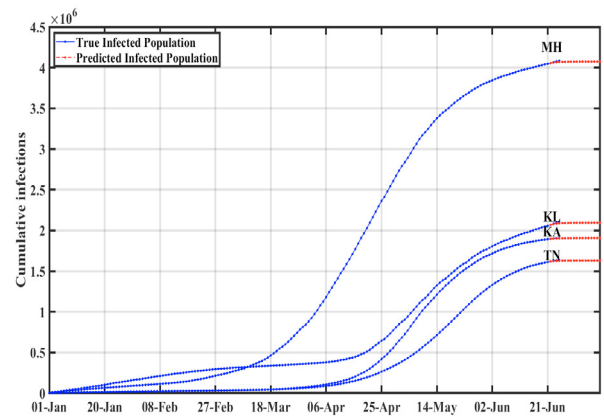
Fig. 4. Prediction of infected population of Maharashtra, Kerala, Karnataka, and Tamil Nadu
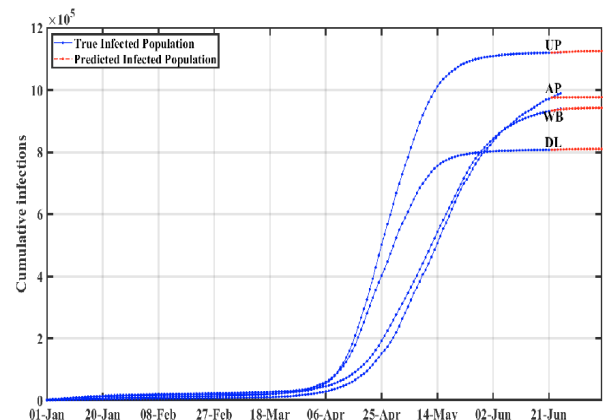

Fig. 5. Prediction of infected population of Uttar Pradesh, Andhra Pradesh, West Bengal, and Delhi

Data from January 1, 2021 to June 25, 2021 has been used for prediction and the prediction is done from June
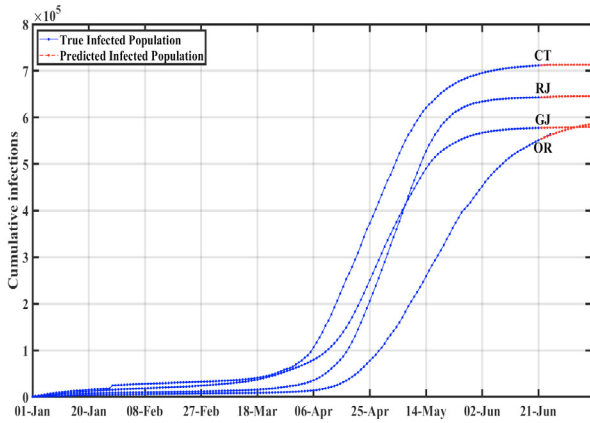
Fig. 6. Prediction of infected population of Chhattisgarh, Rajasthan, Gujrat, and Odisha
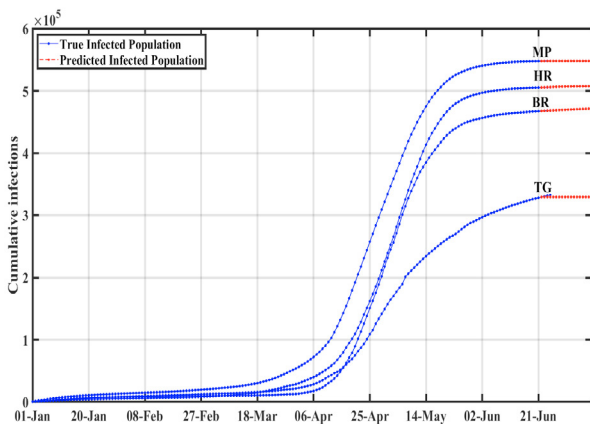

Fig. 7. Prediction of infected population of Madhya Pradesh, Haryana, Bihar, and Telengana

26 to July 9 (fourteen days). The predicted result has been compared with the real COVID-19 data. Thus, from the comparison, per day error percentage for each of the sixteen states has been calculated. Therefore, from the calculated per day error the mean error percentage of each of the states has been calculated. Table 2 shows the mean error percentage of each of the sixteen states. It is clear from the table that, for most of the states the mean error is close to or less than 1%, whereas the maximum mean error is found to be 3.84% for the state Kerala and minimum mean error is found to be 0.04% for the state Gujarat. Again, the 95% confidence interval(CI) (Papoulis and Pillai, 2002) as well as 99% confidence interval (CI) has also been calculated to find the effectiveness of this method, as shown in Table 2. Fig. 8 shows the plot of mean error percentage of each states. Moreover, it is found that the error of prediction for this method very less. Thus, it can be inferred that this model works well to predict the cumulative infection caseload for each of the states.

5. CONCLUSION

In this study, a state interaction network-based SEIR epidemic model is investigated to predict the spread of COVID-19 in sixteen most-infected Indian states in terms

Table 2. Percentage error calculation of predicted values for each state, 95% and 99% confidence interval (CI) of mean error.

| No.	State	Mean Error %	95% CI	99% CI
1	MH	1.59%	[1.12, 2.06]	[0.97, 2.21]
2	KL	3.84%	[2.64, 5.04]	[2.26, 5.42]
3	KA	1.10%	[0.79, 1.41]	[0.69, 1.51]
4	TN	2.10%	[1.53, 2.67]	[1.36, 2.84]
5	UP	0.21%	[0.17, 0.25]	[0.15, 0.27]
6	AP	3.33%	[2.56, 4.10]	[2.32, 4.34]
7	WB	0.87%	[0.61, 1.13]	[0.53, 1.21]
8	DL	0.04%	[0.035, 0.045]	[0.034, 0.046]
9	CT	0.31%	[0.21, 0.41]	[0.17, 0.45]
10	RJ	0.11%	[0.10, 0.12]	[0.09, 0.13]
11	GJ	0.04%	[0.02, 0.06]	[0.01, 0.07]
12	OR	1.54%	[1.06, 2.02]	[0.91, 2.17]
13	MP	0.05%	[0.04, 0.06]	[0.03, 0.07]
14	HR	0.10%	[0.08, 0.12]	[0.07, 0.13]
15	BR	0.09%	[0.06, 0.12]	[0.05, 0.13]
16	TG	2.27%	[1.70, 2.84]	[1.53, 3.01]
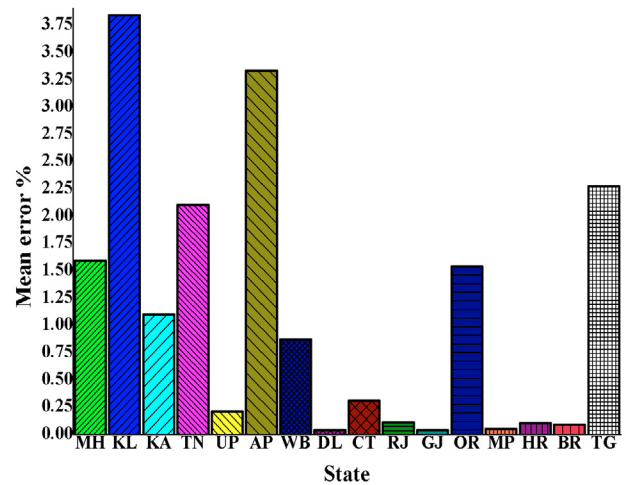
Fig. 8. Mean error for each of the sixteen states

of total cumulative number of infected people. Exposed state has been considered to incorporate the huge number of asymptomatic cases in India. Moreover, incorporation of new exposed compartment along with the intervention term $\alpha_i[k]$ helps to train the model parameters, and thus to predict the cumulative caseload quite accurately for all the considered states. Furthermore, the disease network transmission rates across/within the state which are otherwise difficult to quantify, are inferred from this network-based epidemic model approach. Other important modelling parameters such as curing rate and incubation rate are also inferred from this approach for each state. The mean error percentage of the prediction has been found to be very less, this shows the effectiveness of this method. As future work, there remains many challenges to understand the transmission dynamics of COVID-19 when considering the virus is mutating. Also, to find what are the factors that is leading to consecutive waves. Finally, to find optimal control strategies to control the disease propagation.

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