Federated Multitask Learning for forecasting the infection rate based on mobility data of COVID-19

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Abstract

The prediction of infection rate of COVID-19 disease is worthwhile if the mobility of patients in different regions is taken into account. Also, due to the patients' privacy concerns, the data is still scarce. To address these issues, we propose a federated multitask learning (FMTL) to predict the number of state wise COVID-19 infected people in various locations of USA based on mobility and using a SEIR epidemic model. To find a suitable control threshold for infection rate, the preventive measures like vaccination, social distance and lock down are playing a vital role. Using SEIR model with an additional constraint to check the availability of beds, we can ensure that the beds are available in case of need. We have used the real time mobility data sets in various states of USA during the years 2020 and 2021. We have chosen five states for the study and we observe that there exists correlation among the number of COVID-19 infected cases even though the rate of spread in each case is different. We have considered each US state as node in federated learning environment and a linear regression model is built at each and every node. Our experimental results show that the root mean square percentage error for the actual and prediction of COVID-19 cases is low for Colorado state and high for Minnesota state. Based on SEIR simulation model , we conclude that it will take at least 400 days to

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reach extinction when there is no proper vaccination or social distance.

1. Introduction

COVID-19 is the most challenging infectious disease which has been threatening human beings all over the globe ever since it has been declared as a pandemic by World Health Organization (WHO) [1]. Today, adequate awareness about the virus has been reached to a majority of people and all the countries around the world are imposing various precautionary measures to curb the spread of the virus. The COVID-19 pandemic accelerates itself into different phases of waves, where, many countries experienced the first two waves and now emerging into the third wave [2]. In the first wave, many people were affected with symptomatic and asymptomatic and the number of people hospitalized and death cases were at the peak. Due to various preventive measures, there was a decrease in the number of cases, however, after a certain period there was a substantial increase in the number of infected people and this is called the second wave. During the second wave, vaccinations are started and more understanding about the virus is known. Despite various measures, the early stages of the third wave have been started in many countries.

The WHO recommendations to avoid the spreading of the virus include social spacing, wearing the mask, good aeration, sanitizing, restricted movement, and home quarantine. Many countries around the world have put strict restrictions on travel, closure of malls, theaters, and shops leading to severe impact on economic impact on all sectors. Also, the closure of schools and colleges leads to a severe impact on the learning process and the results are yet to wait and be seen. The major sectors affected by the restrictions are Agriculture, Petroleum and Oil, the Manufacturing industry, Education, Finance industry, Tourism, Real estate, and the Food industry. Severe social impacts like increase of violence, mental stress, increased usage of video games and emotional issues are faced in this lockdown period[3]. A fine-tuned strategy is needed to relax the

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restrictions in such a way that both economic and social factors are taken care. There is a mutual relationship between the number of COVID-19 cases and human mobility. The accurate prediction of the epidemic concerning mobility helps to take preventive measures [4].

Plethora of data stored and transmitted from different mobile devices of humans due to mobility. The mobility data are heterogeneous including demographic information, diagnoses results, and clinical notes. A distributed machine learning approach known as Federated learning is used for training the model from heterogeneous mobile devices. This approach ensures data privacy by keeping the data in the local devices. The effective aggregation of locally trained models in the centralized server is playing vital role in this approach [13][14].

$$W = \sum_{k=1}^{n} \frac{n_k}{n} w_{t+1}^k \quad \text{Global Model}$$
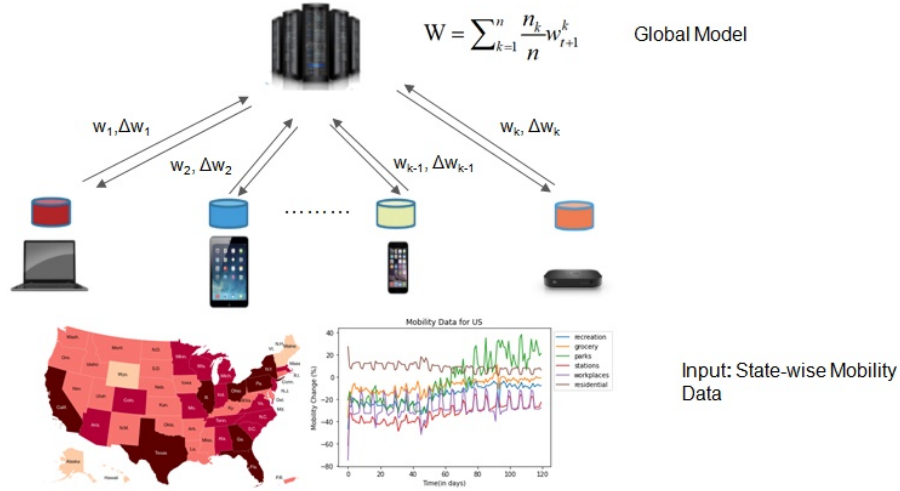
Figure 1: Schematic Representation of the Proposed Model

2. Related Work

Myriad research works in the literature are studied to predict the spread of COVID-19. There are many algorithms from the basic model to machine

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learning models. Network inference-based prediction algorithm was discussed by Achterberg et al.[20]. They have shown that the Network based algorithm is superior to other algorithms. Machine learning techniques to predict different levels of hospital care of COVID-19 were presented by Elena Hernandez-Pereira et al[21]. A robust model predictive control feedback using social distancing was proposed by Kohler et al[22]. Similar work was presented by Morato et al [23]which emphasizes various measures of social distancing. Variations of SIS and SEIR models were used by Yan and Zhou[24], Khouzani et al.[25] Multi-task learning, and nonlinear optimal control of the COVID-19 outbreak using mobility data was proposed by Mikhail Hayhoe et al[26].

To preserve data privacy, a federated multitask learning to detect COVID-19 from chest radiography images was proposed by MahbubUlAlam et al[27]. Several federated learning approaches to predict COVID-19 were available in the literature. Abdul salam et al [28] used federated learning to predict COVID-19. Federated learning is mainly used when the data is distributed and to protect data privacy. They have shown that the federated learning approach has more accuracy compared to other machine learning models. AkhilVaid et al [29] predict the mortality of COVID-19 patients based on electronic health records received from the hospital using a federated learning approach.

In our work, we have considered various mobility data of states in the US and considered federated learning environments. We have also studied the availability of beds facilities in the hospital using our prediction of proposed model. Our approach uses a federated environment to predict the COVID-19 spread based on mobility and our experimental results show the accuracy of our predictions compared with the actual cases. Data privacy is ensured in our approach. The schematic representation of the proposed work is presented in Figure 1. The main contributions of this paper are listed as follows:

i) Using Multi-task learning under federated environments, the infection spreading rate β of COVID-19 is predicted under mobility constraints.

ii) The availability of beds facilities in the hospital is determined using pre-

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dictive models.

iii) Various machine learning algorithms are compared with FMTL approach.

3. Mathematical Model

The proposed epidemic FMTL framework inherits the traditional FMTL[30][31]. Several epidemic prediction methods are estimating the parameter of their model, estimation are based an existing medical data. The idea of FMTL is to learn infection rate from mobility data. In FMTL the mobility data will include the effect of social distancing and lockdown restrictions, and movement of people in a region visiting different places or locations. Federated learning activities of $M_{l_i}(l_i = 1, 2, ..., m)$ region in a network based on their data, and each location generates data with distinct distribution, so far each sub region get separate models, $\{w_1, w_2, ..., w_m\}^T$ for each local data set. Let us denote that the vector $M = \{M_1, M_2, ..M_m\}^T$ and $W = \{w_1, w_2, ..., w_m\}^T$. Each device model has similarity between other models. By using multitask learning, performance of the structure of model is improved.

$$\min_{W,\Omega} \sum_{k=1}^{m} \frac{1}{n_k} \sum_{i=1}^{n_k} l_k(w_k^T, x_k^i, y_k^i) + R(W, \Omega)$$
$$such \ that \ \ trace(D^{-1}) = 1, D^{-1} \geq 0 \quad (1)$$

where l_k is the loss function, $R(W, \Omega) = tr(W^T(\lambda_1 \Omega + \lambda_2 I)W)$ and $D^{-1} = \lambda_1 \bar{\Omega} + \lambda_2 I, \lambda_1, \lambda_2 > 0, \Omega \in R^{m \times m}$ is the matrix that shows the relationship of models amongst the tasks and it is clear that strongly convex with respect to D^{-1}. The infection rate β can be determined by the following:

$$\Theta_t = W^T M; t = 1, 2, ...T$$
$$\beta = \sum_{t=1}^{T} \frac{\Theta_t}{T} \quad (2)$$

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3.1. Dual problem

Considering dual formulation of the (1) will give the global problem into local sub problem for federated computations:

$$\min_{\eta} \left\{ D(\eta) := \sum_{k=1}^{m} \sum_{i=1}^{n_k} l_k^*(-\eta_k^i) + R^*(X\eta) \right\} \tag{3}$$

where l_k^* and R^* are the conjugate dual function of l_k and R. We can define a local sub problem of the original dual optimization problem, which is formed by using quadratic approximation of the dual problem to separate nodes for computational purpose.

$$\min_{\Delta \eta_k} G_k^{\sigma'} = \sum_{i=1}^{n_k} l_k^*(-\eta_k^i - \Delta \eta_k^i) + \langle w_k(\eta), X_k \Delta \eta_k \rangle + \frac{\sigma'}{2} \|X_k \Delta \eta_k\|_{M_k}^2 + C(\eta) \tag{4}$$

where $C(\eta) = \frac{R^*(X\eta)}{m}$ and $M_k \in R^{d \times d}$ is the kth diagonal block of the symmetric positive definite matrix.

In every sub problem, we are finding the update for the model and aggregate all sub region models. Finally we have an aggregated model to a given region. This new model is also benefited from other sub region models through the multitask learning framework. It will provide the best parameter estimation to estimate infection rate from the mobility data and also overcome the issue of over fitting.

3.2. SEIR Model for COVID-19

The SEIR model is prevalent model describing various diseases, including COVID-19. Many overwhelming research works describe the SEIR epidemic model for various epidemic propagation. Here, the model divides the population into susceptible, exposed, infected, and recovered population. Hence we define the following:

- s(t)- fraction of susceptible at time t

- e(t)- fraction of exposed at time t

- i(t)- fraction of infected at time t

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- r(t)- fraction of recovered at time t

The proposed SEIR model is described as follows:

$$\frac{ds}{dt} = -(1-u)\beta si$$
$$\frac{de}{dt} = (1-u)\beta si - \alpha e$$
$$\frac{di}{dt} = \alpha e - \gamma i$$
$$\frac{dr}{dt} = \gamma i \qquad (5)$$

where α is a disease induced average fatality rate, β is spreading rate , γ is a disease recovery rate and u is the proportion of vaccinated population. By solving the equation, we have determined the fraction of infected population, fraction of recovered population at time t.

4. Methodology

We aim to simulate the COVID-19 scenario by taking data privacy into consideration. This experiment is conducted in two stages. The flow diagram of proposed algorithm is shown in Figure 2. In stage one, we predict the US state-wise infection numbers in a federated learning setup. The infection number is modeled as a function of the categories in the mobility data using the federated multi-task learning approach in [30]. Even though the cases in each state are observed independently, it is only logical that there will be some relatedness in COVID-19 trend between the states. Therefore multitask learning would be a good fit.

In stage two of the experiment we emulate the pandemic using the classic $SEIR$ model to analyse the rise and extinction of the pandemic. The infection number obtained in stage-1 is used as the β(Probability of disease transmission per contact $\times$ the number of contacts per unit time) for the $SEIR$ model. Also the susceptible, exposed, infected and recovered ratios of the states are compared. Finally, we try to put a threshold on the infection rate and discuss the time till which vaccination must be continued in order to prevent regions

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from running out of bed availability at medical care centers. For this we took the instance of Louisiana state and analysed the scenario. The Infection Rate - FMTL algorithm comprising of two stages is given below:

Algorithm 1 Infection Rate - FMTL Algorithm

Require: Mobility data M_{l_i} where $l_i \in$ location $i, i = 1, 2, ...m$ distributed across m nodes with initial matrix $\Omega_0, \eta(0) = 0 \in R^m, v(0) = 0 \in R^p$

1: **STAGE 1:**

2: FOR Global Epochs $g = 0, 1, 2...$ do

3:   **Set** sub-problem parameter σ_0 and the number of federated iterations $\boldsymbol{F}$

4:     FOR each location $l_i; i \in \{1, 2, ...m\}$ do

5:       **Get** $\Delta\eta_{l_i}$ of the local sub-problem from local servers

6:       **Update** $\eta_{l_i} \leftarrow \eta_{l_i} + \Delta\eta_{l_i}$

7:       **Return** $\Delta V_{l_i} = M_{l_i}\Delta\eta_{l_i}$

8:       **Reduce** $V_{l_i} \leftarrow V_{l_i} + \Delta V_{l_i}$

9:       **Update** Ω centrally based on $w(\eta)$ for latest η

10: **Compute** $w_{l_i} = w(\eta)$ based on the latest η at the central node

11: **Predict** infection number for day j, $\Theta_j = (W^T M)_j$, for next t days

12: **STAGE 2:**

13: **Compute** infection rate $\beta = \dfrac{\sum_{j=1}^{T} \Theta_j}{T}$

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5. Experimental Results

We use the mobility data [32] and the US state wise COVID-19 data[33] to model stage 1 of the experiment. Data provided by google [32], which is curated from March 2020 till August 2021 is used for modelling represent mobility vector as notation. The mobility vector contains the percentage change from a baseline in the volume of people visiting a particular category of public place(namely retail and recreation, grocery and pharmacy, parks, transit stations, residential). The mobility data of the US for the year 2020 can be seen in Figure 3.

The US state wise case count maintained live by the New York Times is utilized. This data contains all the COVID-19 cases starting from 14-01-2020
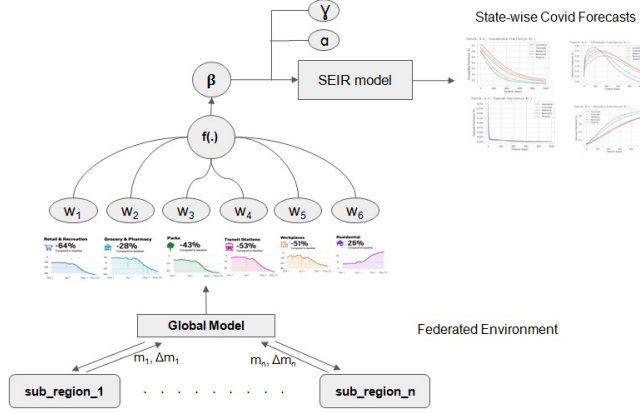
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Figure 2: Flow diagram of the Proposed Algorithm

till present day. For phase 2, US state wise population and bed availability are required. The former was taken from [34] and the latter was collected from [35].
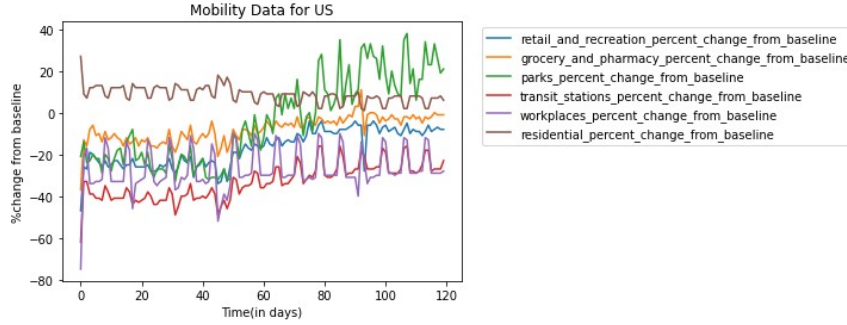

Figure 3: US mobility Data

5.1. Data Preparation

Our objective for stage 1 is to find the function that maps from mobility vector to infection number. Inherently, people's movement incurs the spread of the disease and we try to capture that correlation. The state-wise COVID-19 data are given as aggregated figures i.e, the data contains the total number of cases up to day D, where D ranges from 2020-03-14 to 2021-08-21. But the state-

wise recorded number for a particular day is required for building the analytic model. So a rolling difference is taken between day D and D-1 for COVID-19 cases and this first-order difference is employed throughout the experiment.

The mobility data-set consists of the data for every country and sub-regions. But for our experiment, we only took the US mobility data for the years 2020 and 2021 and appended it into a single source. We also only stick to analyzing the state-level data, so we further filter it based on sub-regions and remove other micro-level divisions.

Finally, both the mobility and infection data are joined by their corresponding states and date. This data contains all US states with their corresponding mobility and infection numbers. But the states show erratic trends and patterns in terms of both infection spread and movement of people. This could be the result of the state's population, foreign population lockdown policies, etc. The geographic distribution of COVID-19 cases across states can be visualized from the map plot in Figure 4. As a result, to obtain a better model, the scenario is to identify the states that show similar trends and proceed with the prediction for these chosen states. This is done to reduce the heterogeneity in the system. Firstly the mean and total case counts as shown in Table-1 are considered, followed by the similarity in a pattern followed during the two waves of COVID-19 spread as depicted in Figure 5 and Figure 6. Five states were chosen for the experiment which include Alabama,Colorado, Kentucky,Minnesota, and Washington.

Records with less than 50 cases per day and greater than 10000 cases per day were removed, considering them as extreme values. Training was done on data ranging from the date 2020-05-01 to 2021-06-01 and validation was performed on the date ranging from 2021-06-01 and 2021-08-01.

5.2. Stage-1

Each state is considered as a task(node) in the federated set up. Even Though the spread of cases in each state is different, still there exists a correlation between those states. Using multi-task learning the relatedness among the
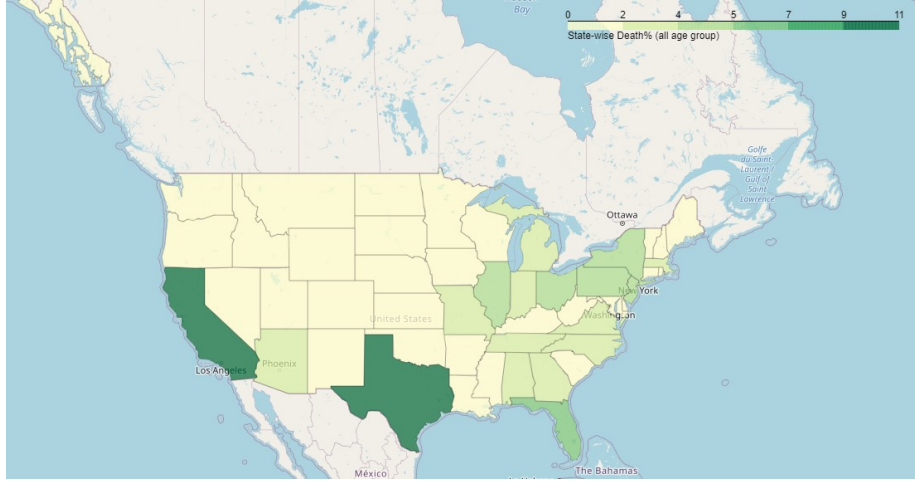
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Figure 4: Geospatial Visualization of COVID-19 cases across states in US

nodes will unravel which can be included while building the model.

Therefore in each node a linear regression model is built corresponding to a state which is then aggregated using the MOCHA framework as proposed in [3]. Initial parameters, hyperparameters and settings are mimicked from [3] as well. Each node has a minimum of 395 points for Minnesota and a maximum of 420 points for Washington. This data is then used to learn the regression model in three ways: multitask,local and global models. Five-fold cross validation is done so as to obtain the optimal regularization parameter from $1e-5, 1e-4, 1e-3, 1e-2, 0.1, 1, 10$. The process is iterated for 10 times and the average of errors for predictions across iterations is reported. The weight parameter from the training is given in Table 2. Infection number $W^T M$ is obtained from the dot product of the mobility vector and weights learned from training where M : Mobility data, W : weight corresponding to mobility feature vector in table 2.

Table 1: Similarity in chosen states in terms of cases

State	Total Cases	Average Case Count
Alabama	839947	1372.46
Colorado	793899	1280.48
Kentucky	768090	1240.86
Minnesota	847010	1368.35
Washington	756733	1184.25

Table 2: Weights corresponding to the mobility vector

Weights (W)	Public Places
-24.58	retail and recreation percent change from baseline
21.79	grocery and pharmacy percent change from baseline
-4.13	parks percent change from baseline
-4.44	transit stations percent change from baseline
-37.42	workplaces percent change from baseline
-60.55	residential percent change from baseline

5.3. Stage 2

The COVID-19 pandemic for 1000 days starting from 2021-06-01 is simulated using the SEIR model. The population of states is taken from [4] which is used as one of the initial parameters for the start of simulation. β is determined by averaging the infection numbers predicted from phase 1 of the experiment. Incubation time was fixed at a standard 7 days and reproduction ratio was taken as 2. α, β and γ are calculated as,

$$\alpha = \frac{1}{t_{incubation}}$$

$$\beta = \frac{1}{N} \times (predicted\ \ infection\ \ rate)$$

$$\gamma = \frac{((1-u)*\beta*s_0)}{R_0} \tag{6}$$

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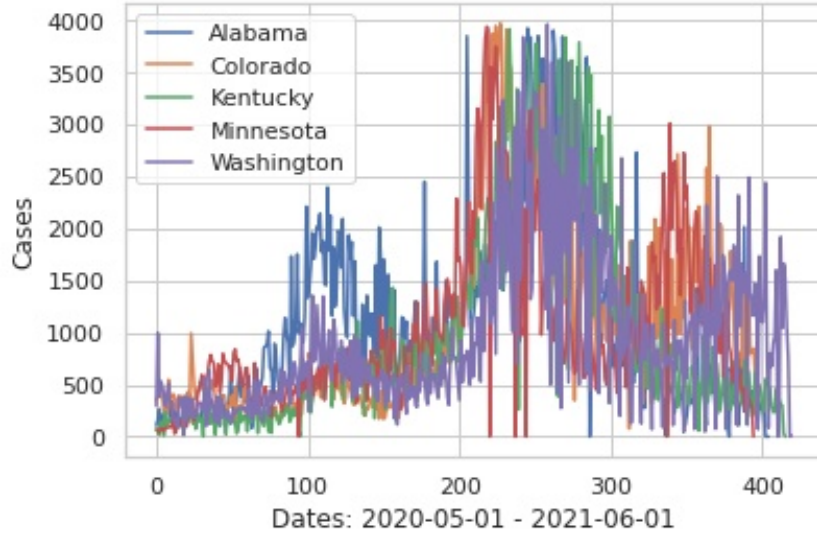Figure 5: Depiction of similar pattern between the states

where u is the vaccination parameter. Here $e0$ which is the initial exposed population is calculated as $1.5 * R_0$ in this experiment. We also have included a vaccination parameter in the model to indicate the percentage of the population who have been vaccinated. u value varies from 0 to 1, 0 indicating no vaccination and 1 indicating that everyone is vaccinated. The α, β and γ of states are as in Table 3.

6. Results and Inferences

6.1. State-wise infection number prediction

The predictions for the state-wise COVID-19 cases are tabulated in Table 4 and to check the confidence of the prediction model we have compared the cumulative case counts between the actual and prediction, which are visualised in Figure 7 - Figure 11.

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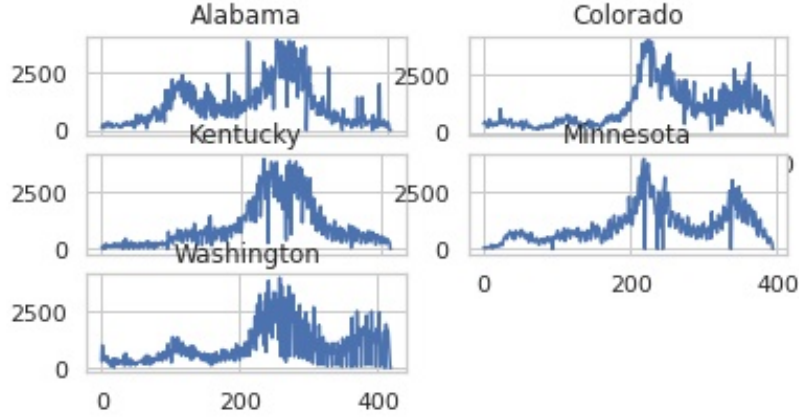
Figure 6: Depiction of patterns in individual states

6.2. SEIR Model - Simulation

The fraction that is susceptible, infected, exposed and recovered from simulations for the states(Stage 2) are compared in Figure 12-15. These simulations show that it will take at least another 400 days for the pandemic to reach near extinction given no proper vaccination or social distancing is followed.

6.3. Error Comparison

In Table 5, we defined five different model parameters' values. We have compared the error results of the five models using two metrics: root mean squared percentage error(RMSPE) and mean absolute percentage error(MAPE), as in Figure 16, and the values can be seen in Table 6. Federated learning has lesser error than all the other models, proving a better fit. Federated learning has the least MAPE of 4.4%, while the neural network has the highest MAPE of 15.12 %. Overall the statistical models perform better than the machine learning models, which the scarcity of data could reason.

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Table 3: Statewise α, β and γ

State	$\alpha\%$	$\beta\%$	$\gamma\%$
Alabama	0.14285714285714285	0.011674899882130375	0.0025818812733749853
Colorado	0.14285714285714285	0.00810977051954281	0.002442870349158038
Kentucky	0.14285714285714285	0.008496661147563526	0.00245179535677162
Minnesota	0.14285714285714285	0.0020389879314963886	0.0005762155029835365
Washington	0.14285714285714285	0.00946	0.00034070090325599126

Table 4: The prediction for these 5 states

State	MAPE(%)	RMSPE(%)
Alabama	3.23	2.41
Colorado	2.10	1.83
Kentucky	3.13	2.28
Minnesota	4.22	12.28
Washington	2.68	3.10

6.4. Bed Availability

One additional constraint has been introduced in the SEIR model to check the availability of beds in a particular state so that the situation can be managed effectively as in [4]. The simple constraint is that infection number < no of beds available. Given the bed availability constraint, our vaccination parameter u, will fine tune and show the percentage of vaccination to be done in order to maintain the bed availability in hospitals.

We simulated a scenario for *Colorado* state where bed availability is 50% and infection rate goes beyond that. So we fix the constraint and simulate it, which can be seen in Figure 17. This implies that vaccination drives should be done effectively for at least another 200 days in order to maintain the infection number less than 50%. Similar insights can be derived for other states as well.
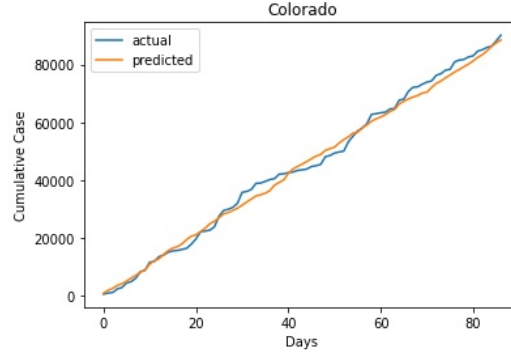
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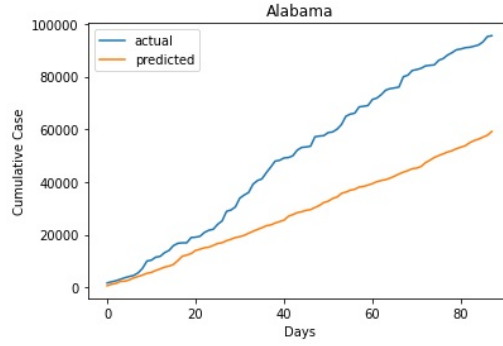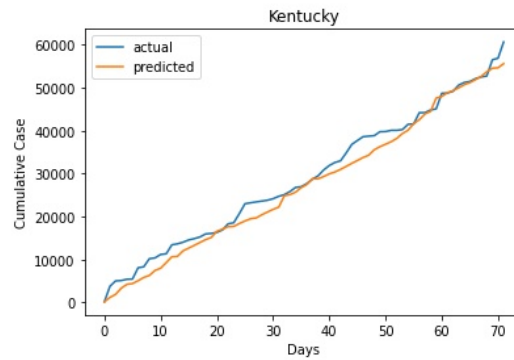Figure 7: Cumulative Case Counts: Prediction vs Actual Comparison for state Colorado

Figure 8: Cumulative Case Counts: Prediction vs Actual Comparison for state Alabama

7. Conclusion

In this paper, we have proposed a FMTL to predict the number of state wise COVID-19 infected people in US based on mobility. The mobility is considered by using data privacy into consideration. The infection number obtained in federated learning process is used as the β for the SEIR model. Also the susceptible, exposed, infected and recovered ratios of the states are compared. Our experimental results shows that the actual and predicted COVID-19 cases for the five states in US are very close. Also, based on the infected rate threshold value, we conclude that it will take at least 400 days to reach extinction when there is no proper vaccination or social distance. Also, the simulated scenario

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Figure 9: Cumulative Case Counts: Prediction vs Actual Comparison for state Kentucky
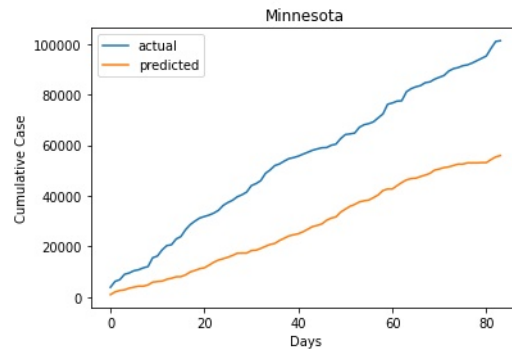
Figure 10: Cumulative Case Counts: Prediction vs Actual Comparison for state Minnesota

for Colorado state indicates that the vaccination should be continued for at least another 200 days in order to maintain the infection number less than 50%.
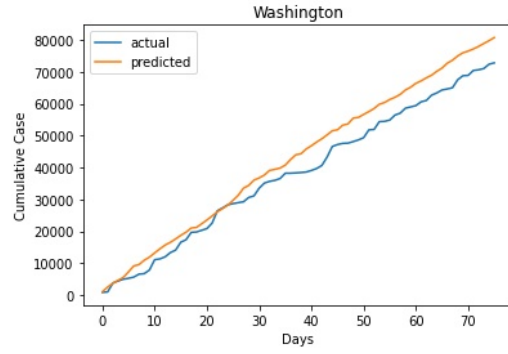
Figure 11: Cumulative Case Counts: Prediction vs Actual Comparison for state Washington
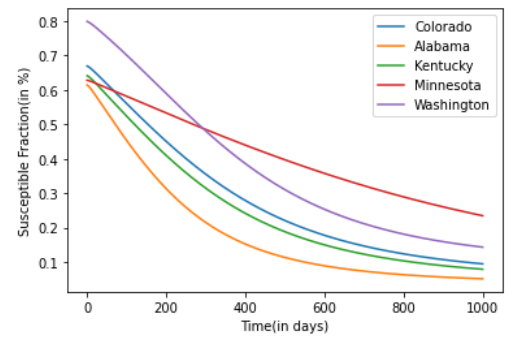

Figure 12: Simulation results comparison for Susceptible Fraction
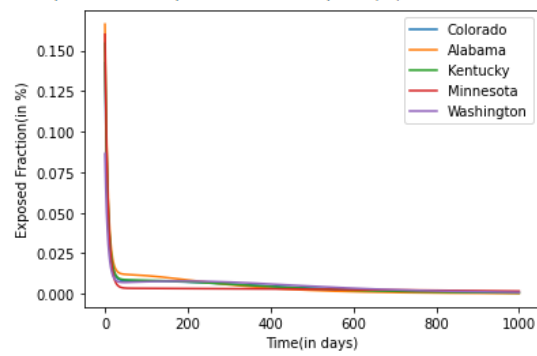
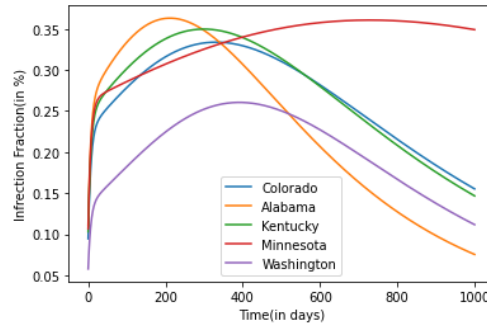Figure 13: Simulation results comparison for the Fraction of Exposed Population

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Figure 14: Simulation results comparison for the Fraction of Infected Population
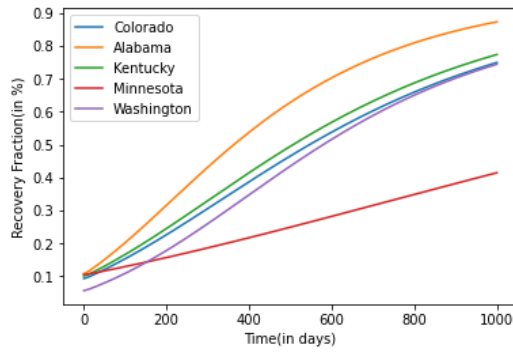

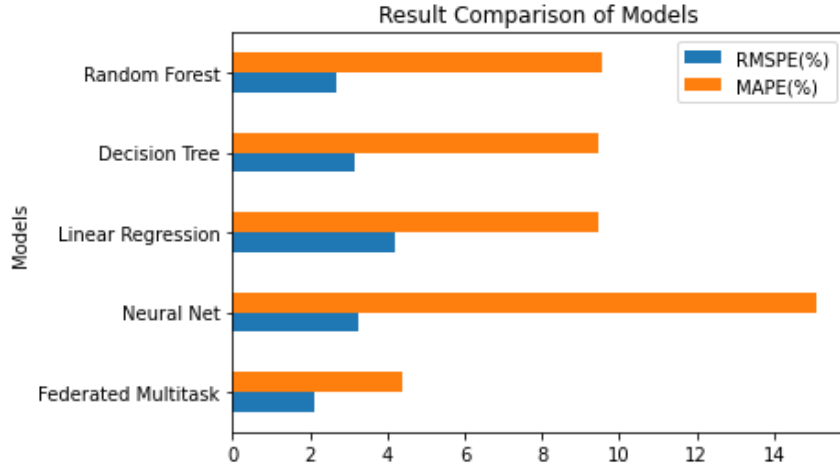Figure 15: Simulation results comparison for the Fraction of Recovered Population

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Figure 16: Error Comparison in Models

Table 5: Various Models with corressponding parameters' values

Model	Parameters
Neural Network	number of Hidden Layers=3,neurons count at each layer=[128,64,1]
	activation=relu, solver=adams optimizer, α=0.001
	learning rate=0.5, number of iterations=100
Multiple Linear Regression	Optimization algorithm= Stochastic Gradient Descent
Decision tree	CART Algorithm
Random Forest	max depth $= [1, 2, 3...., 10]$
	number of trees $= [5, 10, 15, 20]$
FMTL	$\lambda = [1e-5, 1e-4, 1e-3, 1e-2, 0.1, 1, 10]$,
	5-fold cross validation, trials =10

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Table 6: Results of error values

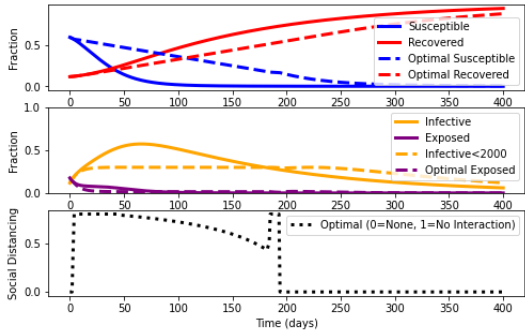| Models	RMSPE(%)	MAPE(%)
FMTL	2.10	4.4
Decision Tree	3.23	15.11
Linear Regression	4.22	9.46
Neural Net	3.13	9.46
Random Forest	2.68	9,57

Figure 17: Bed Availability Constraint

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