LSTM-based Forecasting using Policy Stringency and Time-varying Parameters of the SIR Model for COVID-19

Pavodi Maniamfu
Degree Programs in Systems and Information Engineering
Graduate School of Science and Technology
University of Tsukuba
Tsukuba, Japan
maniamfu@adapt.cs.tsukuba.ac.jp

Keisuke Kameyama
Faculty of Engineering, Information and Systems
University of Tsukuba
Tsukuba, Japan
Kameyama@cc.tsukuba.ac.jp

***Abstract*—Accurate forecasting of the number of infections is an important task that can allow health care decision makers to allocate medical resources efficiently during a pandemic. Two approaches have been combined, a stochastic model by Vega et al. for modelling infectious disease and Long Short-Term Memory using COVID-19 data and government's policies. In the proposed model, LSTM functions as a nonlinear adaptive filter to modify the outputs of the SIR model for more accurate forecasts one to four weeks in the future. Our model outperforms most models among the CDC models using the United States data. We also applied the model on the Canadian data from two provinces, Saskatchewan and Ontario where it performs with a low mean absolute percentage error.**

***Keywords*—COVID-19, Long Short-Term Memory, epidemiological model, policy pruning**

I. Introduction

Controlling the dynamic waves of a pandemic, recently COVID-19 turns out to be a very difficult task as the spread of the aforementioned is influenced by numerous factors such as governments' policies. Real-world events during a pandemic time are generated with a lot of complexity in the form of linear and non-linear representations. Since the outbreak of the pandemic, despite the rapid expansion of the virus worldwide, governments and health institutions have played a significant role to contain and limit the negative effects on their populations. Most of these efforts, known as responses, have been translated into policies that range from containment and closure policies, and vaccination policies to health system policies. These policies have contributed significantly to combat the COVID-19 exponential growth in some countries where they were strictly imposed. Apart from policy measures, many scientific approaches have been implemented as part of these efforts to predict the number of infected people in the near, medium, and long future in order to support government timely decisions in terms of resource allocations. In [1], Vega et al. outline these approaches in three groups, mainly compartmental models [2], [3], statistical methods [4], [5], and machine learning-related approaches [6], [7]. Compartmental models, for example, The Susceptible-Infected-Removed (SIR), is one of the mathematical models in epidemiology grounded on the principles of basic differential equations for modeling infectious diseases. Several works have tried to combine the stochastic nature of the SIR model with advanced mathematical methods in statistics and machine learning in order to improve the forecasts of new infections [8], [9], [10].

In this paper, firstly, we have proposed a policy pruning analysis within the neural network model in order to understand the impact of three types of policy on the dynamic trends of the infected number of people from one to four weeks in the future. Secondly, we have trained a Long Short-Term Memory (LSTM) model that was combined with a basic SIR model while considering the policy that was in place in order to make forecasts one to four weeks in the future. This model has produced the least error compared to the CDC baseline model. It has also been compared to the SIMLR (Machine Learning Inside the SIR model) model in [1] which uses a stochastic Markov chain approach. The model has achieved one of the least errors in terms of near-future forecasts of newly infected people. Unlike the SIMLR model, the LSTM-based model leverages neural network capabilities with long-term dependencies as well as policy data in order to make predictions up to four weeks in the future.

The term dependency is crucial in this specific work, as it is related to the current effects of policies that have been in place for two to three weeks. This assumption is confirmed with the pruning analysis of policy, which has revealed that policies in effect during the first week do not have any additional impact in predicting the new number of infected people one week in the future. However, the effect substantially grows as time moves on, from two to four week-ahead predictions, the model obviously relies on the effect of the policy in order to capture the trends of the pandemic.

In Fig. 1 below, we show the impact of policies in driving the number of infections amidst the pandemic by removing a single policy such as vaccination, stay-at-home policy, etc. at a time in the machine learning model like SIMLR and recording their performance across time. Compared to the result in Fig. 4, which runs the original model without any alteration, we show what we call "policy pruning" by removing two policies mainly the vaccination policy and stay-at-home requirement from the model, and have noticed that the model error significantly increases from

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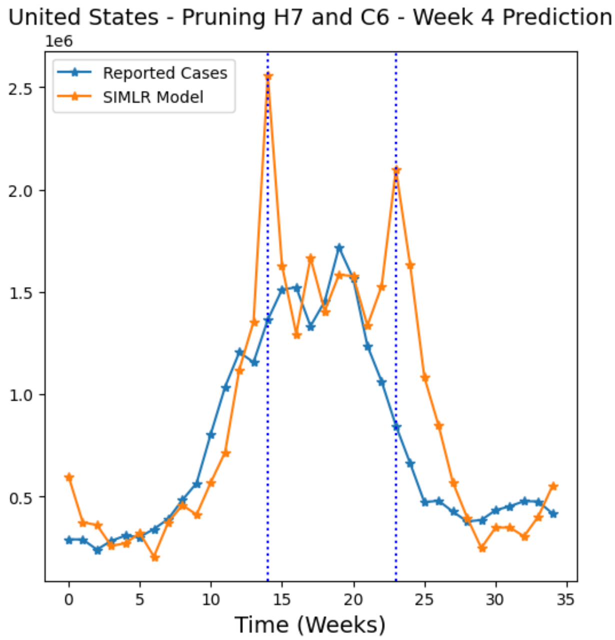

Figure 1. Policy pruning from the SIMLR model

mean error 33 to 37, and it is clear that the SIMLR model relied on those policies at week 14 and 23 to make more accurate forecasts.

The possibilities of including different policies in a mathematical model to analyze their impact on the trends of the pandemic is a crucial task though challenging. In most cases there is a scarcity of data at the beginning of the outbreak, therefore researchers need to rely on domain knowledge, which when inaccurate will lead to inaccurate results from the model.

This paper brings two contributions. First, we show the effects of policy implementation in the forecasts of the number of newly infected people. Our model shows that the policies in place during the current week do not contribute much to the short-term predictions but the effects become more considerable in the long-term predictions. Second, instead of relying on a stochastic approach, we proposed the use of the LSTM model that is combined with the time-varying SIR model in order to make more accurate forecasts one to four weeks in the future.

II. SIR Model with Time-varying parameters

Within a homogenous and constant population, modeling infectious diseases can be done by a basic mathematical model commonly known as The Susceptible-Infected-Recovered (SIR) compartmental model [11]. In this classic sense, the population is divided into three distinct groups. The susceptible group is a subpopulation of individuals that have not yet been in contact with the disease but they can acquire it when they come in contact with the second group. This group is the Infected, a set of individuals that contracted the disease and are capable of transmitting it. The last group is the Recovered (or the Removed), which is the number of individuals that have gained immunity against the disease, or in worst scenarios have died from the infection [12]. The differential equations that govern this model are as follows:

$$\frac{dS}{dt} = -\frac{\beta S(t)I(t)}{N} \quad (1)$$

$$\frac{dI}{dt} = \frac{\beta S(t)I(t)}{N} - \gamma I(t) \quad (2)$$

$$\frac{dR}{dt} = \gamma I(t) \quad (3)$$

both the transmission rate (β) and the recovery rate (γ) control the dynamic transition between the susceptible group and the recovered, and N = S + I + R, the total population under a constant assumption. In a basic approach with fixed parameters, this model can perform poorly in order to allow near-future predictions. However, the parameters β and γ can be optimized to reflect the change in the trend for more accurate predictions in the long future. This experiment applies the optimization algorithm as illustrated in [1] in order to find the optimal parameter of the SIR model.

Given the differential equations from Eqs. (1), (2), and (3), a basic SIR model can be rewritten with the following Eqs. (4), (5), and (6), respectively:

$$S_t = -\beta \frac{S_{t-1}I_{t-1}}{N} + S_{t-1} \quad (4)$$

$$I_t = \beta \frac{S_{t-1}I_{t-1}}{N} - \gamma I_{t-1} + I_{t-1} \quad (5)$$

$$R_t = \gamma I_{t-1} + R_{t-1} \quad (6)$$

As in the previous differential equations, S_t, I_t, R_t refer to the number of Susceptible, Infected, and Removed people, respectively, at a specific discrete time t. The parameters β and γ (the transmission rate and the recovery rate, respectively) control the flow of the transition between different groups. Since the SIR model is linear to these parameters under a constant N. the equation can be solved in a linear equation of the following type:

$$\begin{bmatrix} S_t \\ I_t \end{bmatrix} = \begin{bmatrix} -\frac{S_{t-1}I_{t-1}}{N} & 0 \\ \frac{S_{t-1}I_{t-1}}{N} & -I_{t-1} \end{bmatrix} \begin{bmatrix} \beta \\ \gamma \end{bmatrix} + \begin{bmatrix} S_{t-1} \\ I_{t-1} \end{bmatrix} \quad (7)$$

$$R_t = N - S_t - I_t \quad (8)$$

If a sequence of states denoted as $x_1,\dots,x_n$ where $x_t = [S_t\ I_t]^T$, the optimal parameters of the model are estimated in the Eq. (9):

$$(\beta^*, \gamma^*) = arg \min_{\beta,\gamma} \sum_{i=1}^{n} ||x_i - \hat{x}_i||^2 + \lambda_1(\beta - \beta_0)^2 + \lambda_2(\gamma - \gamma_0)^2 \quad (9)$$

- $\hat{x}_i$: a sequence of predicted values derived from the Eqs. (7) and (8)

- λ_1 *and* λ_2 : regularization terms derived as $\frac{1}{\sigma_\beta^2}$ *and* $\frac{1}{\sigma_\gamma^2}$, respectively.
- β_0 *and* γ_0: prior parameters from Gaussian priors.

The optimization algorithm in Eq. (9) computes the optimal values of the transmission rate and the recovery rate that justifies the number of COVID-19 cases, deaths and recovered people at a specific time frame. For example, given a daily sequence of data $x_1, \ldots, x_n$ where n = 7 (weekly), a pair of β_1, γ_1 is computed by fitting a simple ridge regression model to the previous weekly sequence. for the pair (β_2, γ_2), $x_8, \ldots, x_{14}$ are fitted to the model, the process goes on until the last week of sequences. The values of β and γ are continuously updated on a weekly basis to predict the number of new infected people in the following week.

III. Related works

Since the outbreak of COVID-19 in China, predicting the trends of the disease became one of the central themes in research as it contributes to the effective decision-making process and directs the allocation of medical resources [13-19]. In [20], the US Center for Disease and Prevention Control (CDC) shortly after the outbreak introduced a contest for accurate predictions of the number of newly infected people and deaths for effective control of the epidemic in the short, medium, and long terms. At the time of writing this paper, the repository contains 122 models submitted by different research groups from all over the world, for example [21], [22], [23]. Ref. [1] proposed a probabilistic graphical model that incorporated machine learning inside the SIR model for forecasting the number of newly infected people within one to four weeks in advance. The basic idea behind their work is to use machine learning to learn complex patterns of the model that augments the capabilities of the SIR model by using prior expert knowledge. Although relying on expert knowledge could lead to inaccurate results when this knowledge is misrepresented or inaccurate, their model outperformed several state-of-the-art models in the CDC repository, including the CDC baseline model.

Another line of work relevant to this study is [24], which incorporates machine learning into the epidemiological compartmental model SEIR (Susceptible-Exposed-Infected-Recovered) to forecast the trend of COVID-19. One major limitation of this work is a decline in terms of the performance of the model when there is a change in the number of new infections. In [1], this change in trend (e.g., the number of new infections declining) was hypothesized to be related to the government policies in place at a specific point in time. However, our study suggests that this reflection in government policies does not seem to play an important role in 1-week ahead prediction but they gradually reflect the trend as the prediction window moves to 2, 3, etc. weeks ahead. Another important work proposed by [10] proposes a time-varying parameter of the SIRD (Susceptible-Infected-Recovered-Dead) model using deep learning to improve forecasting accuracy. Unlike our research, they used mobility data from cellphones and positive test rates to capture the dynamic waves of the pandemic.

In this research, we compare the results of our model with the CDC baseline model on the United States' COVID-19 data. As for the Canadian provinces, we use the SIMLR as the baseline model.

IV. Methods

The use of the Long Short-Term Memory (LSTM) model proposed in this research is built on top of the SIR model. We use both a stochastic modelling and deep learning approach. In the first approach, candidate features are extracted from two types of datasets. First, government policies mainly the workplace closing, stay-at-home requirement and vaccination policy for the US, and for Canada the last policy is replaced by cancel public event. Second, the number of confirmed COVID-19 cases. In the second approach, the LSTM model functions as a nonlinear adaptive filter to modify the outputs of the SIR model to make more accurate predictions.

A. Data and Preprocessing

The Oxford COVID-19 Government Response Tracker (OxCGRT) [25] keeps track of the policies implemented by different governments during the pandemic sorted into the following groups: containment and closure policies, economic policies, health system policies, vaccination policies, and miscellaneous policies. In this research, we have used three policies for both the US data at the national level and the Canadian provinces. Each policy in the database is encoded with an ordinal number ranging from 0 (not implemented) to 1, 2, 3, or 4 (the higher the value, the stricter a given policy was enforced at a specific point of time), or a continuous value that represents a monetary amount (e.g., funding for research). For this work, each policy was transformed into a 3-dimensional vector wherein each value represents the probability estimation of whether a policy is relaxed, unchanged (remains the same since implemented) or strictly enforced at a given time.

The COVID-19 Data Repository by the Center for Systems Science and Engineering (CSSE) from Johns Hopkins University [26] was used to extract the cumulative number of reported infections, which was transformed into the number of new daily infections. The last-mentioned feature was used for both US and Canada. In addition, workplace closing, stay-at-home requirement, cancel public events and vaccination policies were used with the last two policies for Canadian provinces and US, respectively. Finally, in order to make the data consistent for the model, the normalization was applied to the time series by subtracting the mean from the series and dividing it by the variance. We combined the time series data with the policy data to make more accurate predictions from one to four weeks in the future. The goal is to allow the LSTM model to be able to learn from the policies implemented at a specific time that drive the number of new infections in the following weeks.

B. Proposed model

Our model is a combination of the time-varying parameters SIR model that we previously covered and the LSTM network. As for the LSTM model, it is a variant of recurrent neural network that was introduced by Hochreiter and Schmidhuber [27]. LSTM is a widely adopted artificial neural network

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algorithm in areas such as speech recognition, sequence models, time series prediction, etc.

The basic idea behind the LSTM network is to solve the problem of vanishing gradient encountered in classic RNN models. LSTM turns out to be a robust alternative in terms of handling long-term dependencies. We shortly introduce the LSTM cell in the following equations:

$$\tilde{C}^t = \sigma(W_c[a^{t-1}, x^t] + b_c) \tag{10}$$

$$\Gamma_u = \sigma(W_u[a^{t-1}, x^{t-1}] + b_u \tag{11}$$

$$\Gamma_f = \sigma(W_f[a^{t-1}, x^t] + b_f) \tag{12}$$

$$\Gamma_o = \sigma(W_o[a^{t-1}, x^t] + b_o) \tag{13}$$

$$C^t = \Gamma_u * \tilde{C}^t + \Gamma_f * C^{t-1} \tag{14}$$

$$a^t = \Gamma_o * \sigma(C^t) \tag{15}$$

In Eq. (10), $\tilde{C}^t$ is a candidate feature that computes the activation function σ (ReLu in this case) of the parameters W_c and a^{t-1}, which is the activation of the previous timestep and x^t which represents a point, e.g., the number of daily infected people at discrete time t. $\{\Gamma_u, \Gamma_f, \Gamma_o,\}$ stands for the update gate, forget, and output gates, respectively. $C^{<t>}$ is a memory cell that computes the element-wise product of those gates, and decides on the information to remember or discard. Finally, a^t computes the activation of the current timestep. This model is proposed on top of the Markov stochastic model, and has the advantage of being trained with a number of policies that are relevant to the tendency of new infections.

Initially, a stochastic SIR model with time-varying parameters computes the number of susceptible, infected and removed people, and returns the output which is fed into the LSTM model to make more accurate forecasts of the number of infected people one to four weeks ahead of time. The LSTM model makes new prediction by using three types of input, **the output from the SIR model**, **the output from the SIR model when the policy is either relaxed, strict or there is no change at all** and **the SLOW** (Same as the Last Observed Week) output from [1] which relies on β_{t+1} and γ_{t+1} (predicted parameters), such that the predicted number of new cases at week *t + 1* is identical to the one at week *t*. in short, this is only the copy of the prediction of the week at *t -1* (last week). The output of the LSTM model is a scalar, which is an estimation of the predicted number of cases within the range of time specified above. Fig. 2 depicts in a visual approach the proposed LSTM model:

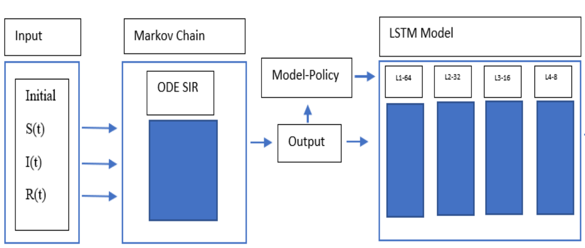

Figure 2. The Architecture of the Proposed Model

The LSTM network structure used in this experiment contains four layers. The first layer has 64 units which is divided by two in the following layers. The ReLu activation function was used, and the model was trained using the Adam optimizer with a mean squared error loss function.

C. Evaluation of the model

The performance of this model was evaluated in terms of the mean absolute percentage error (MAPE) from the data of the United States and two of the provinces of Canada (Saskatchewan and Ontario) in a window of one to four weeks in advance. For comparison and consistency purpose, since we compare the performance with SIMLR model, we have used the same time frame, which is 39 weeks from July 26, 2020 to May 1, 2021. In addition, this period is ideal as most publicly available models in the CDC repository had submitted their predictive points that we could use to compare the performance. The evaluation metric is presented in the equation below:

$$MAPE = \frac{1}{n}\sum_{t=1}^{n}\left|\frac{y_t - \hat{y}_t}{y_t}\right| \tag{16}$$

V. Results

In Fig. 3, we compare the performance of the proposed model (LSTM-TVP-SIR) with the publicly available models submitted at the CDC repository from the COVID-19 Forecast Hub. Predictions are submitted as either point forecasts or quantile forecasts. The comparison is made with models that consistently submitted point forecasts from July 26, 2020 to May 1, 2021. The models that simply submitted quantile forecasts were not considered. It is remarkable that our proposed model performs better than the baseline model (in red), and reports a consistently lower MAPE than most models in the US data at the country level. In Fig. 4 the performance of the proposed model is compared with the SIMLR model using the United States data

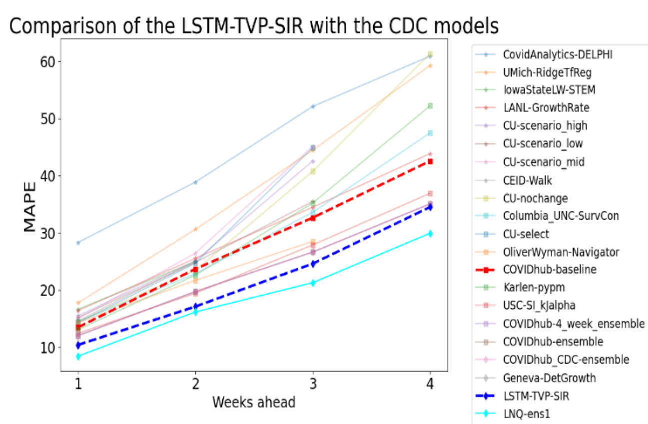

Figure 3. Comparison of the proposed model with CDC models.

for one to four weeks in the future. Although the difference in terms of MAPE is significantly low across time, our proposed model seems to capture the waves of infections without strong

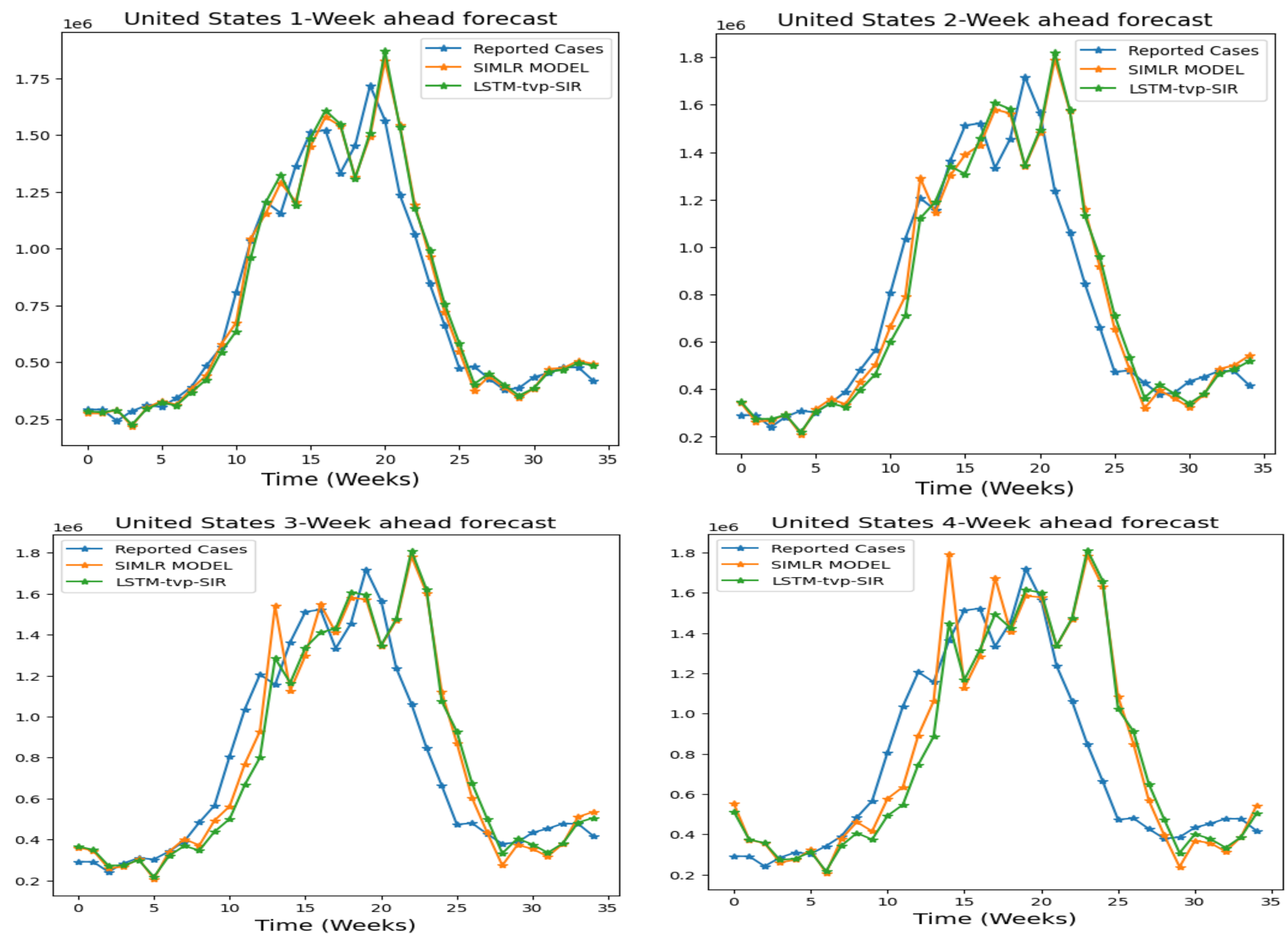

Figure 4. Comparison of SIMLR Model and our proposed model on the US Data (Country level)

TABLE I. MEAN ABSOLUTE PERCENTAGE ERROR FOR US DATA

MAPE		
Weeks ahead	*SIMLR MODEL*	*LSTM MODEL*
1	9.7	10.4
2	16.0	17.1
3	23.3	24.6
4	34.9	35.5

TABLE II. MEAN ABSOLUTE PERCENTAGE ERROR FOR CANADIAN PROVINCE: SASKATCHEWAN

MAPE		
Weeks ahead	*SIMLR MODEL*	*LSTM MODEL*
1	15.4	14.4
2	30.	28.6
3	38.6	36.8
4	47.1	49.4

TABLE III. MEAN ABSOLUTE PERCENTAGE ERROR: ONTARIO

MAPE		
Weeks ahead	*SIMLR MODEL*	*LSTM MODEL*
1	14.1	12.8
2	28.9	27.2
3	42.2	39.5
4	55.4	51.2

fluctuations which are found in the SIMLR model in the long run, at week 14 for example in a four-week ahead forecast.

The MAPE of both models are reported in the Table I. It is significantly noticeable that wherever the SIMLR model shows strong fluctuations, our proposed model seems to capture the reality (in blue) closely well. However, the result shows that SIMLR slightly performs better in whole at the country level. This can be attributed to the fact that policies are generally enforced at state level rather than at country level. Therefore, different states may have implemented different policies at different times, which can be a major limitation of this approach.

In Table II and Table III, we compare the result of our model with the data from two of Canadian provinces, Saskatchewan and Ontario. On average, the proposed model works better than the SIMLR model. Unlike the US case, the result of the Canadian provinces turns out to be low, and increasingly lower than the competing model from one to four weeks ahead.

VI. CONCLUSION

Predicting the number of new infections during the pandemic is a crucial task as it contributes to the effective decision-making process and helps to direct the allocation of medical resources efficiently. Therefore, making accurate forecasts can require more complex processes to consider such as the governments' policies. In addition, representing these policies in mathematical models turn out to be a more intricate task. By leveraging both the power of a stochastic model and neural network architecture, we trained an LSTM model that performed better in capturing the dynamic waves of the pandemic while relying on the policies implemented by the government. In a short-term prediction, e.g. one week, the effects of the policy can be slightly noticeable as in the case of SIMLR model but their effect substantially becomes visible in the long run predictions, two to four weeks ahead.

The proposed method based on the model by [1] with LSTM filtering has significantly performed better than the COVID-hub baseline model including several other models from the CDC repository. We have also compared our model with the SIMLR model using the Canadian data from two provinces, Saskatchewan and Ontario. Our model performs slightly better in the first-mentioned province but in the second, the difference is remarkable where our proposed model performs better than SIMLR model once more.

Real-world data come in many complex forms, more research needs to be done to develop mathematical models of infectious diseases that capture more accurately this complexity.

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