Data-driven Model for Influenza Prediction Incorporating Environmental Effects

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Abstract: Influenza is one of the most severe and prevalent epidemic that causes mortality and morbidity. The researcher focused on early forecasting to prevent and control the outbreak of the flu disease, which it may reduce their impact on our daily lives. We propose a model based on machine learning methods that is capable of making timely influenza prediction using the impact of many environmental factors such as climatic variables, air pollutants and geographical proximity. Our significant contribution is to incorporate the impact of this environmental factors changes on the spread of the disease with a machine learning method to improve the performance of the influenza prediction models. We use multiple data sources including Illness Like Influenza (ILI) data, climatic factors, air pollutant and geographic proximity that have significant correlation with ILI rate. In this paper, we compare the proposed model with two methods and with the actual value to prove the effectiveness of our approach.

1 INTRODUCTION

Influenza is one of the most prevalent and costly disease that affects many people in the world. Since 2010, Influenza accounts for about 9.2 million to 60.2 million announced diseases in the United States alone according to the Center for Disease Control (CDC)[1]. This illness can cause severe health risk and even death for high level populations. It is contagious disease resulting in serious respiratory morbidity and mortality. According to the New York times reports, the worst influenza season was in 2017-2018.

The current surveillance programs rely on weekly reports of the data collected from various resources by health departments on CDC. However, the data collected have a lag time of weeks, therefore, effective influenza prediction and early outbreak detection are valuable in surveillance research.

To reduce, prevent and control the outbreak of influenza in the world, the public health officials need an effective methods of prediction of influenza spread. It will be able to take measures, prioritizing resources such as emergency rooms, staff and vaccines. To perform disease surveillance, many researches and studies has been developed. Google Flu Trends (GFT) was quite successful and used search engine of Google (Dugas et al., 2013) to predict ILI activity for more than 25 countries(Ginsberg et al., 2009) and measure how often a particular term is entered. But it is criticized due to the lack of reliability that stopped Google from real time forecasting. Influenza forecasting research is an active research area, the existing models have limited ability and accuracy to effectively capture the dynamics of the influenza spread across different regions. There are several methods for time series data analysis based on machine learning that have earned significant importance in recent years. In our approach, we focus on neural network method called Long Short Term Memory (LSTM) (Hochreiter and Schmidhuber, 1997), it provides a robust model in temporal data processing. LSTM supersedes Recurrent Neural Network (RNN)(Siegelmann and Sontag, 1991), it shows remarkable performance in processing time series data therefore it attracted much interest in temporal prediction. To improve the accuracy of Influenza forecast-

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[1] https://www.cdc.gov/flu/weekly/index.htm

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ing, we integrated effective external variables that are shown to have strong influence and impact on flu outbreak. The data explored from different sources are historical ILI counts, weather information, air pollution variables, infection status in neighbour regions. Previous studies such as (Liu et al., 2018) and (Ram et al., 2015) proved the direct influence of weather predictable data such as temperature, humidity and precipitation and for air pollutant like carbon monoxide (CO), PM10, Sulphur Dioxide (SO2) and Nitrogen Dioxide (NO2) which they are significantly correlated with ILI count. Our research objective is to take advantages of LSTM method, air quality data, climatic factors and geographical proximity to estimate Influenza in a geographic area within short time periods (weeks). To this end, we have gathered ILI data from CDC, pollution censor data from Environmental Protection Agencies (EPA)[2], climatic variable and geographical proximity taking from the same geographic regions and time period to create model for forecasting Influenza. The experimental results indicate that our approach can predict the influenza trend very well.

2 LITERATURE REVIEW

Airborne infectious diseases can be extremely expensive, and the more the disease discovery is delayed the more this cost will increase. The world's public health system has taken considerable attempts to identify, get ready and control such contagions, and yet, outbreaks of recent infections, such as the respiratory syndrome, persist due to the increasing urbanization, but also to the mobility of the contemporary society (Donnelly et al., 2005). So finding an effective control of airborne infectious disease transmission is still a major issue despite the great work put in (Luo, 2016). In order to detect influenza in the early stages, we can set up a public health surveillance system (or bio-surveillance) whose role is to keep under observation regularly gathered data about patient. For instance, BioSense (Bradley et al., 2005) is one of these systems for Disease Control and Prevention: it was developed by the United States; it gathers public health reports from electronic health files in order to make local and national bio-surveillance an easier task. Better accuracy of disease detection results in better reliability of the bio-surveillance system (Wagner et al., 2011). Another concern over performance is reducing the time lag to notice the outbreak and retaining large precision of individual disease discovery. In modelling infectious diseases, researchers are analysing the spreading diseases processes, to predict the expected outbreak course, and assess the different strategies deployed to epidemic control.

The prediction research is classified in several categories. The first category includes Compartmental models like Susceptible-Infected-Recovered(SIR) done by (Hethcote, 2000) and (Keeling and Rohani, 2011) and the other model is Susceptible-Infected-Recovered-Susceptible (SIRS) studied in (Hooten et al., 2010) and (Shaman et al., 2013) and Susceptible-Exposed-Infected-Recovered (SEIR) in (Chowell et al., 2008), (Chowell et al., 2006); in this models, the population is divided into compartments based on disease states. The movement of individual between each compartment is defined by a rate. However, due to the homogeneity of population, the model cannot know the patterns with the variation of age groups and environments. The second category is the time series and statistical methods such as Auto-Regression Integrated Moving Average (ARIMA) (Choi and Thacker, 1981) and another method called Generalized Autoregressive Moving Average (GARMA) (Dugas et al., 2013). These methods can capture in flexible way the behaviour of infected populations and presume that the values can be predicted based on past patterns. But their accuracy is very poor due to the inconsistency of influenza activity from season to season, especially during the outbreak of diseases. The third category includes methods of machine learning that became very important in recent years due to their capability to analyse very large data called ”Big Data”. There are very popular machine learning methods such as Sport Vector Regression(SVR)(Signorini et al., 2011), Neural Network, Binomial Chain (Nishiura, 2011). Opposite to the statistical methods ARIMA, machine learning methods considered flexible in the role of capturing the impact of external factors but expensive in term of computational, they have to be retrained when new variable arrives. Recently, special and close attention was paid to machine learning (ML) classifiers in the area of influenza detection. In (Elkin et al., 2012) they had demonstrated how logistic regression classifier had improved considerably the prediction performance comparing with applying a model to Chief Complaints from Emergency department.

In the same way, in (Tsui et al., 2011) they had applied a Bayesian network specific to influenza in order to analyse this disease in individual patient files; an expert-constructed tool. (Elkin et al., 2012) and (Tsui et al., 2011) had chosen the same process: the first step was to extract the clinical features, then mapped them to codes using one of the NLP tool, finally,

[2] https://www.epa.gov/outdoor-air-quality-data

they used a machine learning method to predict approximately the risk of epidemic presence. But the disadvantage is that they take a longer time to detect outbreaks and they didn't give much attention to the evaluation of the ML classifiers used. Other than NLP tools to extract clinical features of influenza, recent work by (Hu et al., 2018) used the data set of twitter and of the US CDC for influenza reports to anticipate an approximate real-time improbable percentage flu in the United States by region: this was possible due to the use of an artificial neural network who owes its success to the improved artificial tree algorithm (AT)(Li et al., 2017). Search engines and social networking sites (SNS) are ways faster (7 to 10 days faster) than government organizations (CDC) in tracking trends of different diseases with real time analysis on SNS to track ILI (Alessa and Faezipour, 2018). SNS users' number is increasing exponentially, and people are sharing their daily details including their health issues. By consequence, SNS can provide us with efficient information about health status; Hence, it can be a useful resource for disease prediction and control and a better way of communication to prevent eventual disease outbreaks (Alessa and Faezipour, 2018). The work done by (Santillana et al., 2015) apply and test several machine learning methods on Social Network Twitter. These models are able to exactly estimate ILI pattern for two weeks ahead. But, they employed only the features of basic Bag-of-Word taken from tweets. In (Paul et al., 2016), the existing NLP techniques has to be enhanced and developing new methods to effectively explore social media word and to extract richer Bag-of-Word from tweets.

The focus of recent studies was on modelling disease spread in order to analyse the future outbreak course and assess the potential strategies for disease mitigation. Besides, the modification of parameters gives rise to new outcomes; which requires more scenario comparison analysis. For infectious disease simulations, we need to compare results over space and time so that we assess decision measures the way they are implemented with a multitude of state spaces (Lu et al., 2017).

Analysts need to explore closely the effect of mitigated measures; Hence, they need to take advantage of the environment factors like the effect of changing weather and the mobility of population.

3 MATERIALS AND METHODS

Our proposed method consists of two steps. In the first step, we apply a machine learning method which is the neural network approach LSTM, this technique is used to predict the initial real time value. In the next step, we incorporate three different external factors: (1) Climate variables: temperature, humidity and precipitation; (2) air pollution sensors includes different variables such as: PM2.5 concentration, Carbon Monoxide (CO) concentration, Nitrogen Dioxide (NO2) concentration, PM10 concentration, Sulfur Dioxide (SO2) concentration; and (3) geographical proximity impact is taken from the influence of neighbouring regions. The objective of integrating the environmental factors is to reduce the error from the initial forecast. Figure. 1 shows the architecture followed in this paper,

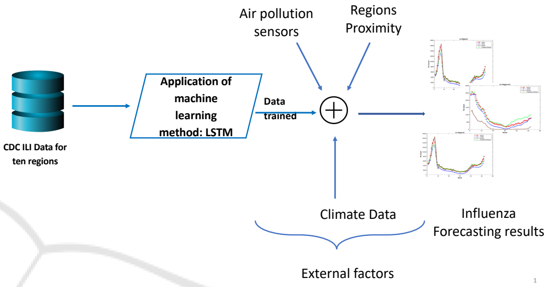

Air pollution sensors
Regions Proximity
Application of machine learning method: LSTM
Data trained
CDC ILI Data for ten regions
Climate Data
Influenza Forecasting results
External factors
1

Figure 1: Architecture of the Proposed Model.

3.1 Data Source

Based on previous and recent research, we combine various dataset with LSTM to forecast Influenza trends. In this research, we focus on CDC-reported ILI flu counts for ten regions classified by Health and Human Services (HHS)[3]. The data in reports of CDC represents the only national dataset with free access in the United States from 1997-2016. The weather data is freely accessed and downloaded from Climate Data Online (CDO)[4] . The climate variables collected are: Maximum temperature, minimum temperature, precipitation and humidity. The data of each stations in the boundaries of the CDC region is aggregated for each station in each city in each region, by averaging the sum of the time series data into single weekly. The data of air pollution is collected from the United States Environmental Protection Agency, the pollution variables downloaded as mentioned above are freely accessed. The data is summarized for each station in each state in each CDC region and calculated per week. All of the data set collected: flu count, weather, air pollution variables are pre-processed and organized by weekly.

[3] https://www.hhs.gov/about/agencies/iea/regional-offices/index.html

[4] https:www.ncdc.noaa.gov/cdo-web/datasets

3.2 Model

The proposed multi-steps approach for Influenza forecasting includes the following stages. In the first stage, we consider a geographical region as a node for the LSTM approach, this node is trained on the real ILI counts of regions to predict the original influenza counts. In the next step, we add the impact of climate data, geographical proximity and air pollution sensors to the estimated flu time series after the application of LSTM model while the objective is reducing the error. The LSTM and the proposed approach are compared with ARIMA model.

3.2.1 Long Short Term Memory Network

The model LSTM is considered as a variation of RNN architecture. It was designed by Hochreiter and Schmidhuber (Hochreiter and Schmidhuber, 1997) in 1997, LSTM algorithm is considered faster than the popular RNN network because it maintains the back-propagated error in time and layers. LSTM contains memory blocks which is composed of memory cells and gates as mentioned in the figure 2. The cell is performed as a memory while its role is to read, write and delete information depending on the decisions of three gates: the gate of input, the gate of output and the gate of forget. Then each weight of each gate, had to be trained after the learning process. The memory cell is implemented as shown in the following equations: From Eq. (1) to Eq. (5) :

$$I_t = \sigma_g(W_1 X_t + U_i C_{t-1} + b_1) \quad (1)$$

$$F_t = \sigma_g(W_2 X_t + U_f C_{t-1} + b_2) \quad (2)$$

$$O_t = \sigma_g(W_3 X_t + U_o C_{t-1} + b_3) \quad (3)$$

$$C_t = F_t \odot C_{t-1} + I_t \odot \sigma_c(W_c X_t + b_4) \quad (4)$$

$$H_t = O_t \odot \sigma_h(C_t) \quad (5)$$

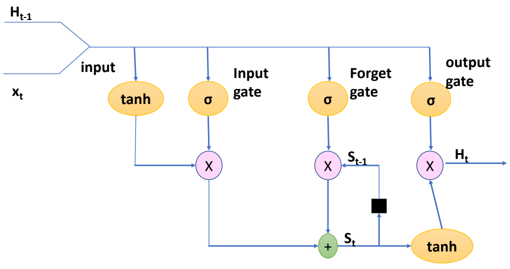


Figure 2: LSTM Cel Diagram.

Where W and U are the adaptive weights initialized between 0 and 1. F_t denotes the forget gate vector, X_t represents the input vector to the LSTM unit, It denotes the input gate vector, O_t is the output gate vector and H_t represents the output vector of LSTM unite. The operator $\odot$ denotes the Hadamard product (Hochreiter and Schmidhuber, 1997) and (Gers et al., 1999) and b represents the bias vectors.

The back propagation algorithm is used to train LSTM cells, where the training criterion is the Mean square cost function. At the time $t-i$ and to compute the flu activity O_{t-i}, LSTM cell received ILI counts computed by the previous cell O_{t-i-1} and the input X_{t-i}.

The process is repeated for all the LSTM cells in the model. It is considered that the number of cells for LSTM is the same number of time steps.

3.2.2 Air Pollution Sensors

The dataset collected contains measures of five types of pollutants: PM2.5, PM10, NO2, CO, SO2. The influenza transmission and infection may be due to the peak of air pollutant concentrations that may play a significantly important role. We calculated the mean weekly average for each pollutant, downloaded from each station in each state belonging to the CDC ten regions. To measure the linear dependence between two variables, we use the Pearson correlation coefficient. The value result of this method is between positive 1 which signifies total linear correlation and negative 1 that represents negative correlation, 0 means no linear correlation. In the Table. 1, we examined the relationship between flu counts and each air pollutant data. Four pollutant indexes, i.e., CO, NO2, SO2 and PM10 show significant correlation with flu counts. The correlation is significant at the 0.01 level.

Table 1: Correlation Results between Flu Counts and Air Pollution Data.

	CO	NO2	SO2	PM10
Pearson correlation	*0.95*	*0.16*	*0.592*	*0.361*
N	52			

The next step, is the decision a priori to investigate the effect of each pollutant on the same week and lagged by one and two or more weeks as these were the lags commonly investigated in previous studies. The dependence of the flu counts on pollutant is very often with laps of time, that is called lag. To determine the appropriate lag, we decide to use a criterion like the Akaike Information Criterion (AIC). In our case, we determine the possible lag impact between the augmentation of air pollutant variables and the starting of influenza-like illness, the delay ranging between 0 and 2 weeks, lag0-lag2: lag0 is considered as the current week information, lag1 is considered as the concentration of the previous week and lag2 corresponds to the concentrations of two weeks earlier. The lags between influenza-like illness and each pollutant concentrations is calculated for all the data of each region, the total effect $Ptot$ represents the estimated of air pollution concentrations for node n at time t. The following formula Eq. (6) explains the process.

$$P^{tot}_{n,t} = \Sigma^{D}_{i=1} W_{n,i} \times P_{n,i,t} \tag{6}$$

We used Widrow-Hoff (Widrow and Hoff, 1988) learning to train the weights, $W_{n,i}$ to decrease the Mean square Error (MSE). D represents the number of air pollutions sensors and $P_{n,i,t}$ denotes the impact of each pollution variables on the flu counts using the following formula Eq. (7).

$$P_{n,i,t} = \frac{S_{n,t-lag} - S_{n,t-lag-1}}{max(S_{n,t-lag}, S_{n,t-lag-1})} \tag{7}$$

$S_{n,t-lag}$ represents the effect estimation at region n from i^{th} air pollution variable at time t. The formula is the variation before the convenient lag of time and the actual numeric data P.

3.2.3 Climate Variable Impact

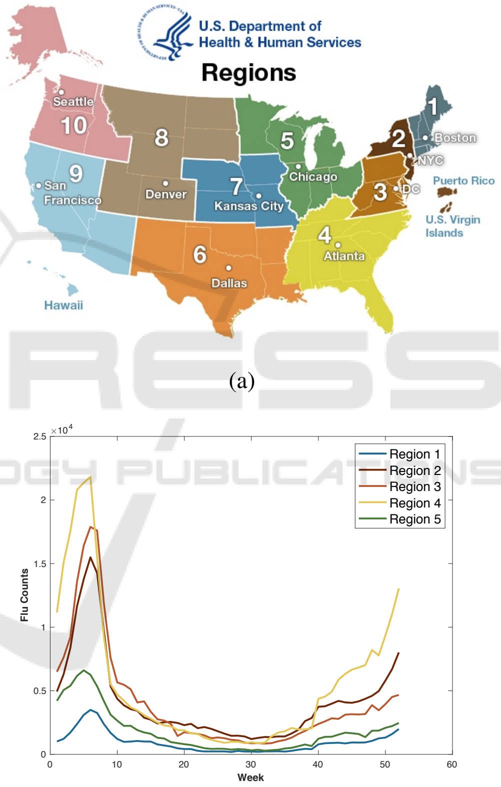
With the objective of including the environmental factors as input information to the method, first we look for the relation between the flu counts and the climatic variables in term of correlation. In the previous studies, the literature (Soebiyanto et al., 2010), (Lowen et al., 2007) and (Lowen and Steel, 2014) prove a strong cross-correlation between minimum, maximum temperature and influenza counts from CDC. Influenza epidemics is often associated with seasonal changes in temperature and relative humidity. The integration of different linear time series values is not an effective method to determine the impact of meteorological variables due to the impact delay of temporal variables. According to the study of (Venna et al., 2019), they compute a situational time lags between flu counts and each climatic variables, the daily climatic variable data: temperature, relative humidity and precipitation from CDO, were converted into values per week by calculating the average. And each time series were converted to a tuple XY of symbols: X represents the value magnitude (high, medium, low) and Y represents the change of value from the previous time step (increasing, stable, decreasing). After the generation of the symbolic tuples for each value in time series, we compute the frequent associations between a climate symbolic time series and Flu symbolic time series at different time lags from 0 to 5 using the Apriori algorithm [34]. When the time lags between influenza times series and each weather predictors are calculated, we calculate the ratio $C_{n,i,t}$ of change between the appropriate time lags and the actual value as explained in the Eq. (8).

$$C_{n,i,t} = \frac{X_{n,t-lag} - X_{n,t-lag-1}}{max(X_{n,t-lag}, X_{n,t-lag-1})} \tag{8}$$

Then the total impact is calculated following the Eq. (9) :

$$C^{tot}_{n,t} = \Sigma^{D}_{i=1} W_{n,i} \times C_{n,i,t} \tag{9}$$

Where t denotes the time steps, n denotes the region, D the number of climatic variables and W the weights trained using Widrow-Hoff learning (Widrow and Hoff, 1988).



(a)

(b)

Figure 3: Flu Counts: (a) Division Map of CDC-HHS Regions Taken from HHS Website. (B) a Plot of the Trends for ILI Counts in 2018 for Five CDC Regions.

3.2.4 Proximity Regions Factor

The geographical proximity has a strong threat of widespread influenza outbreak. We can observe, as shown in Fig. 3, a flu trends between regions in spatial proximity. We can calculate the proximity impact on the node n by a factor coming from each neighbour nodes which is the average of flu divergence. The factor A applied at each node n, represents the average variation in the flu counts given by the neighbour data at time $t-i$. Equation. (10) is as follow:

$$A_{n,i,t} = \frac{1}{y}\Sigma_{j=1}^{y}(F_{i,t-j} - F_{i,t-j-1}) \qquad (10)$$

An,i,t represents the individual adjustment for the neighbour i to the node n at time t, is computed with the ratio change in the previous y steps.

$F_{i,t-j}$ denotes the current ILI count for the neighbour i at time $t-j$. In the study done by (Venna et al., 2019) the y selected has to be 3, because it gave an optimal results. Once the individual adjustment is computed, the total adjustment $A_{n,t}^{tot}$ at time t and node n is the summation of weights of the individual adjustment $A_{n,i,t}$. The weights are trained using Widrow-Hoff algorithm (Widrow and Hoff, 1988).

$$A_{n,t}^{tot} = \Sigma_{i=1}^{N} W_{n,i} \times A_{n,i,t} \qquad (11)$$

N denotes the number of neighbours of data node n.

3.2.5 Predict Value Estimation

Final forecast value is calculated after applying the climate variable impact from Eq. (9), the total adjustment factor from Eq. (11) and Eq. (6) for the air pollution sensors to the predicted value generated by LSTM at time t for node n as shown in Eq. (12).

$$F_{n,t}^{final} = P_{n,t}^{tot} + C_{n,t}^{tot} + A_{n,t}^{tot} + F_{n,t}^{LSTM} \qquad (12)$$

4 RESULTS

In this study, we employed ARIMA a time series-based model compared to the three proposed data-driven models LSTM, proposed model: LSTM+PS+CI+SA and ARIMA+External factors (PS+CI+SA) on a freely available data sets about flu counts from the CDC.

We evaluate our approach on a multiple time series data: For influenza activity, we download flu counts real data sets from CDC for all ten HHS regions, the data is weekly presented. We collected 52 weeks of data in ten regions from 1st week of 2018 to the 52 nd week of 2018, the data selected for training is from the 1st week to 46 th week. The climate data is collected from (CDO) which is freely accessed. The data downloaded from the CDO is weekly aggregated for each region.

For the air pollution sensors, the data is downloaded from the EPA and is freely accessed, than it was aggregated and averaged into single week.

The external predictors are weekly summarized time series. Our samples are between 2016-2018, the training data selected was on 80

4.1 Evaluation Criteria

To evaluate our approach for prediction performance, we use the following evaluation metrics. Mean Absolute Percentage Error (MAPE): The metric used to measure the accuracy in percentage, is the average absolute error between actual and estimated values.

$$MAPE = \frac{1}{N}\Sigma\frac{|A-P|}{|A|} \qquad (13)$$

Root Mean Square Percentage Error (RMSPE): The metric used to compute the deviation between actual and predicted value and their square root.

$$RMSPE = \sqrt{\frac{1}{N}\Sigma(A-P)^2} \qquad (14)$$

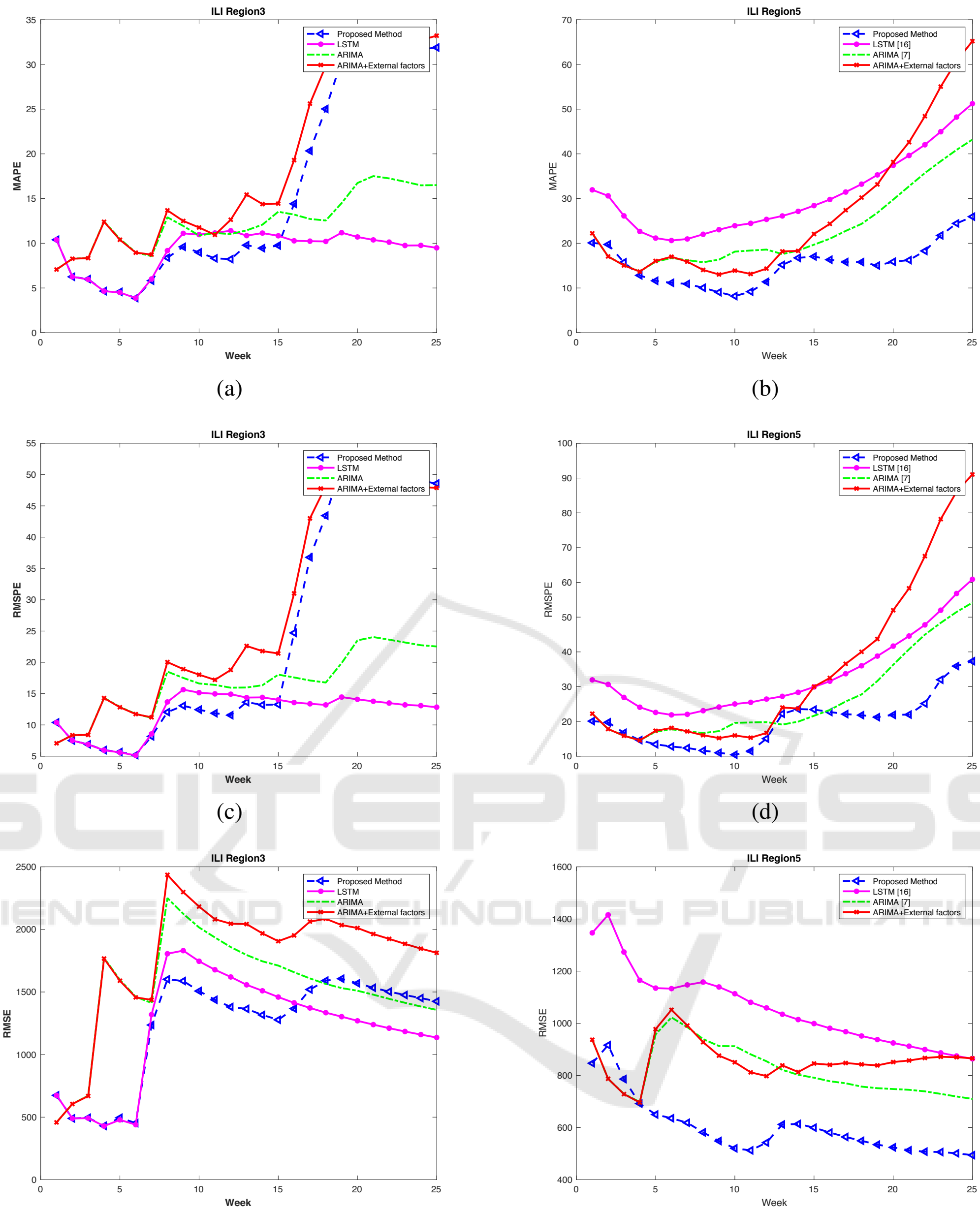
Root Mean Square Error (RMSE): the metric used to compute the difference between the real value and predicted value .

$$RMSE = \sqrt{\frac{1}{N}\Sigma\frac{(A-P)^2}{A}} \times 100 \qquad (15)$$

N denotes the number of weeks, A denotes the actual influenza data and P denotes the predicted value. As mentioned before, we compared the results of our approach with the state of art ARIMA method. Also we compared our results with the predicted value generated after application of the LSTM to prove that our method reduces the error after LSTM.

4.2 Results for the CDC Dataset

Table. 2 shows the comparison of three models of prediction: LSTM, ARIMA and our proposed approach (LSTM + external predictors). These models are applied on all the geographical HHS regions. The table compares the forecasting performance of the models until 25 weeks in the future. We do three experiments on CDC dataset for the ten regions: one for LSTM, second for ARIMA and the third experiments for the proposed model. We computed the performance in terms of MAPE, RMSPE and RMSE. We can observe an improvement of prediction accuracy after integrating the external predictors: pollution sensors, climatic data and geographical components, to LSTM data, the error was reduced that shows the importance of their impact. The improvement in forecasting is noticed from week 5 to week 15 ahead, while the first week



(a) (b)

(c) (d)

(e) (f)

Figure 4: Comparison Using Error Metrics: MAPE (a) and (B), RMSPE (C) and (D), RMSE (E) and (F) between Region 3 (Left) and Region 5 (Right) of the Flu Prediction Models over 25 Weeks Ahead.

ahead predicted doesn't show any significant amelioration.

Fig. 4 shows the six error charts metrics including MAPE, RMSPE and RMSE for two regions: Region 3 and Region 5. Table. 2 is correlated with the plots in Fig. 4 in numbers for Region 5. We can notice that for the Region 3 for the future prediction weeks, the MAPE error for ARIMA is less than the other models between the fourth week and the seventh week. And our proposed model performs slightly better than LSTM for the same region. As shown in Fig. 5, there are ten plots, presenting the ten regions from Region 1 to Region 10 respectively, of the forecasting models resulting from LSTM method, ARIMA and the proposed compared to the actual value for the year 2018.

It can be seen that the value predicted for all the regions of the year gives values very close to the actual one. The approach anticipates an approximate

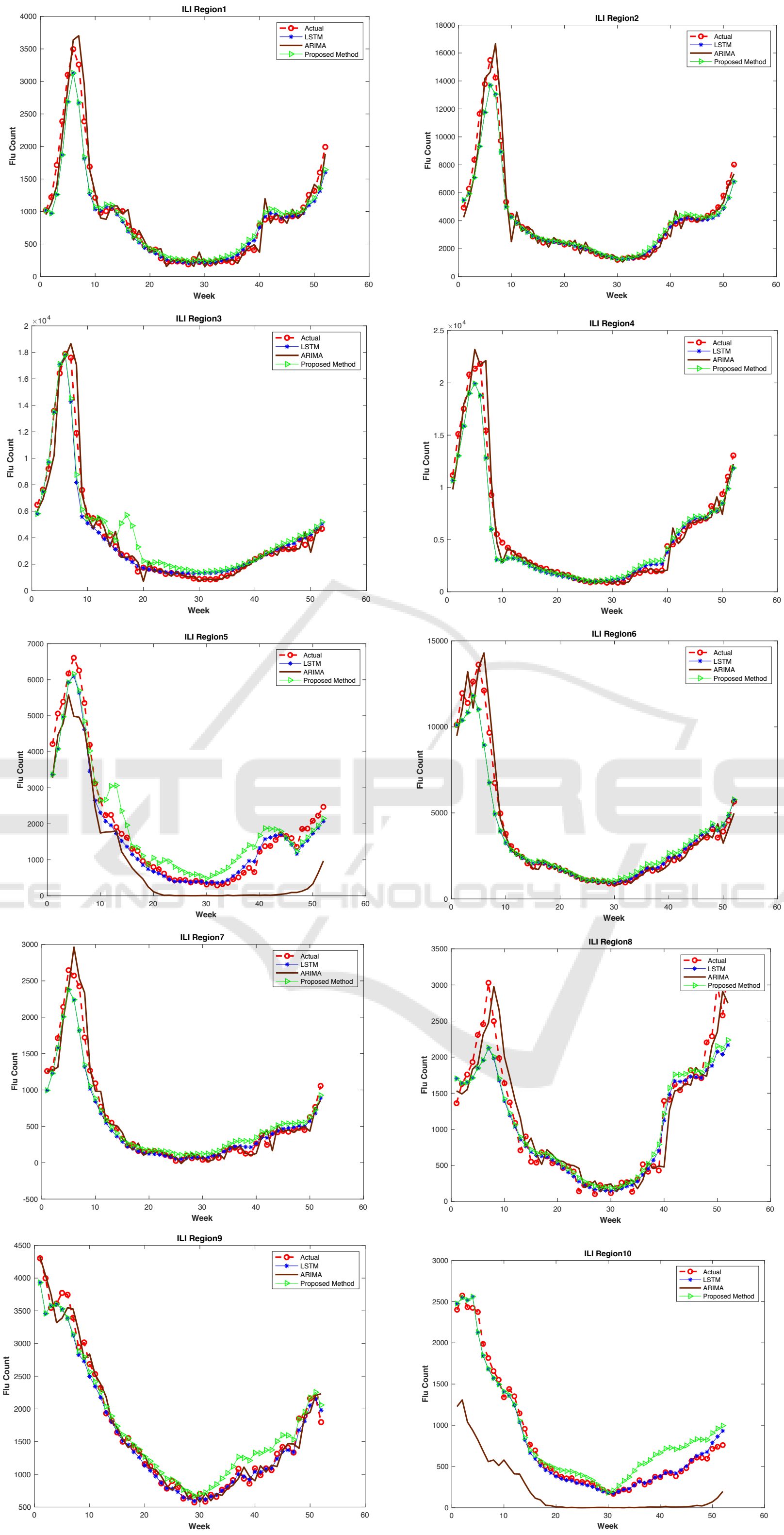


Figure 5: A Plots Represent Actual and Predicted Flu Count for 10 Regions.

Table 2: MAPE, RMSPE and RMSE for the ILI Count Predicted Using ARIMA and Proposed Model of Region 5.

Weeks	**1-week**			**5-week**			**10-week**			**15-week**		
Model	***MAPE***	***RMSPE***	***RMSE***	***MAPE***	***RMSPE***	***RMSE***	***MAPE***	***RMSPE***	***RMSE***	***MAPE***	***RMSPE***	***RMSE***
LSTM (Hochreiter and Schmidhuber, 1997)	*31.95*	*31.95*	*1364*	*21.15*	*22.59*	*1134.9*	*23.92*	*25.02*	*1113.35*	*28.42*	*29.92*	*998.89*
Proposed model	***20.09***	***20.09***	***846.8***	***11.59***	***13.42***	***650.18***	***8.18***	***10.42***	***520.37***	***17.04***	***23.41***	***599.73***
ARIMA (Choi and Thacker, 1981)	*22.23*	*22.23*	*937*	*15.87*	*17.05*	*957.68*	*18.13*	*19.58*	*912.08*	*19.68*	*21.62*	*791.33*
ARIMA+External factors	*22.23*	*22.23*	*937*	*16.03*	*17.30*	*977.41*	*13.88*	*15.97*	*850.58*	*22.07*	*30.01*	*845.77*

real-time data better than the other model. According to these three errors in Fig. 4 and Fig. 5, we can say that the proposed approach is favourable for the prediction of influenza-Like illness.

5 CONCLUSIONS

In this study, we proposed an approach to enhance influenza prediction. In our contribution, first step is the application of LSTM as machine learning technique, this method shows a better performance comparing to the existing time series prediction methods. Second step is the integration of the impacts of the external predictors : air pollution data, climatic variables and geographical proximity whose goal is to reduce the error of machine learning method. We evaluated the approach we proposed on the datasets from CDC-HHS ILI. The proposed approach is compared with ARIMA model. It can be seen that with the integration of external predictors in LSTM, we improved the accuracy performance. Also, the proposed approach may be useful for other viral illness such as Asthma, Chickenpox and Ebola. Our future study seeks to implement the proposed approach on Social Network Site like Twitter and Instagram dataset.

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