

Deep Learning Model for Predicting Spreading Rates of Pandemics, “COVID-19 as Case Study”

Maha A. Al-Bayati^{1*}

¹Department of Computer Science, College of Science, Mustansiriyah University, Baghdad, Iraq

*Correspondence: drmaha6699@gmail.com

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ABSTRACT

The outbreak of Coronavirus (COVID-19), has led to a catastrophic scenario over the globe, causing the cumulative prevalence of this virus to increase dramatically day by day. Both Machine learning (ML) and deep learning (DL) provide great chances to facilitate tracking disease, anticipating increase in pandemic, and hence planning for coverage techniques to control its spread. This work is based on the application of an advanced mathematical model to examine and predict the increase in a pandemic. On the bases of time-series data, an advanced DL model has been implemented to predict the risk of COVID-19 spreading in Iraq. A hybrid approach is presented where two deep learning algorithms; LSTM and GRU are brought up together to achieve good prediction with rewarding levels of (MAE = 0.109), (MAPE = 0.191) and (RMSE = 0.134).

Keywords: Pandemic, COVID-19, Coronavirus, Machine Learning, Deep Learning, Outbreak prediction

1. Introduction

The first case of coronavirus disease (CoVID-19) was first detected and acknowledged on December the 31, 2019, in Wuhan, China. It began to spread fast all over the world [1]. Accumulative occurrence of causative virus (SARS - CoV-2) is hastily growing and has severely affected about 196 nations and countries within USA and Europe [2]. Since then, the World Health Organization (WHO) has classified the coronavirus outbreak as a pandemic, while the virus continues to spread [3]. The distinction between the pandemic instigated by CoV-2 and other associated viruses, such as SARS and MERS, lies in CoV-2's capacity to spread rapidly through human interactions, resulting in nearly 20% of infected individuals remaining asymptomatic carriers [4]. Additionally, various studies have confirmed that diseases caused by CoV-2 pose a significantly greater risk for individuals with compromised immune systems. Furthermore, older adults and patients with life-threatening chronic like coronary cardiopathy, HIV, AIDS and others, are more likely to severe effects [5]. Due to absence of cure medicine, the only way afforded to control and slow down the spreading was practicing distancing in society and following health guidelines to break the transmission chain of the virus. This manner of behavior of CoV-2 necessitates the need for an increasingly robust mathematical basis for tracking its exposure and automates monitoring equipment to perform online dynamic selection.

There is a need for innovative and rapid solutions that allow for developing, managing, and analyses of big data related to the grown-up network of infected individuals, details of patients, community move-

rounds, and combination with clinical institutions' trials, genetic and general fitness information [6]. The availability of multiple data sources, such as text messages, social media interactions, online communications, and various articles on the web, enabled a thorough analysis of infection growth in relation to community behavior or through sampling methods. Wrapping this data with ML, DL and divers Artificial Intelligence (AI) and data science techniques, researchers can manage providing the needful prediction of regions and time likely for the disease to propagate, and to report those regions, as a consequent, to assist the needful authorities' arrangements. A method to examine epidemiological correlations with disease propagation behavior involves the automatic tracking of the travel history of infected individuals.

Some of communities' transportation-based effects have been discussed in a number of researches. For the huge amount of data, necessitates careful consideration of the infrastructure required for its storage and analysis, ensuring that development proceeds in an efficient and cost-effective way. This necessitates the establishment of solutions grounded in deep learning and artificial intelligence methodologies [7]. Various pneumonia types were addressed through machine learning and deep learning techniques for CT image analysis, offering valuable support to CoVID-19 patients [8]. Further related insights can be found in [9]. Moreover, the discovery of vaccine for CoVID-19 can further be elevated via analysis of genome sequences, using numerous ML, DL and other AI techniques [10].

2. Motivation and Contributions

This work concerns predicting spread rate of CoVID-19 in Iraq. Time-series dataset used are obtained from WHO – published global datasets to develop a novel forecasting model for CoVID-19 outbreak. Data-driven estimations and time-series data – based analysis is incorporated to predict the trends of virus dynamics in a range of up to come days such as confirmed positive cases, number of deaths, number of recovered cases and others that hopefully benefice governments, medical institutions and even citizens to respond proactively and take the necessary precautions to avoid outbreaks. To achieve the estimations, deep learning algorithms of Long-Short Term Memory (LSTM), and Gated Recurrent Unit (GRU) are suggested to model with, both in a combination, in an aim to gain the best prediction that effectively support governing such health threat crises.

3. Related Work

Development of the novel models for time-series prediction of Coronavirus (COVID-19) is of maximum importance. Machine learning (ML) methods have recently shown promising results. The present study aims to engage an artificial neural network (ANN) integrated by grey wolf optimizer (GWO) for Coronavirus (COVID-19) outbreak predictions by employing the Global dataset [14]. In this paper, the Coronavirus (COVID-19) outbreak is modelled as a complex time series. We have developed a hybrid Machine Learning (ML) model based on the artificial neural network (ANN). We trained the system with the grey wolf optimization (GWO) algorithm to get the highest performance. Based on the testing, we projected the outbreak until late May [14].

In this paper, the exact structure of Res Net-a hundred and is first prepared [15]. Education began for several hours. The unique information of R registration slips was manually collected to reap advanced results. Predicting the status of the viral load is designed to accurately reach the target area suitable for strict standard operating procedures, to reduce COVID-19. Attention parameters were the calculation of accuracy, precision and recall. Moreover, the hourly surrogate viral load was manipulated from October 15, 2020 to November 1, 2020. On November 3, the prediction was determined by the skilled Res Net-a hundred and one, and the accuracy became very close [15]. Secondly, Covid-19 was predicted by chest X-ray, but to save time for researcher destiny, 3 new technical frameworks were compared with R-CNN, Mask R-CNN and ResNet-50. Manipulation has become based entirely on precision, accuracy, and recall. The faster R-CNN does well compared to the Mask R-CNN and ResNet-50. The error framework is designed to test the amount of error after which it is reduced through classification techniques. The most important reason for these studies has become to make it less difficult for growing international sites that do not have a vaccination facility for contamination with the virus, and to allow time for rapid treatment of Covid-19 patients [15].

This paper aims to evaluate the currently advanced structures primarily based totally on deep studying strategies the usage of special clinical imaging modalities like Computer Tomography (CT) and X-ray [16]. This evaluate mainly discusses the structures advanced for COVID-19 prognosis the usage of deep studying strategies and affords insights on famous records units used to educate those networks. It additionally highlights the records partitioning strategies and numerous overall performance measures advanced with the aid of using researchers on this field. A taxonomy is interested in categorize the current works for correct

insight. Finally, we finish with the aid of using addressing the demanding situations related to using deep studying strategies for COVID-19 detection and likely destiny developments on this studies area. The goal of this paper is to facilitate experts (clinical or otherwise) and technicians in know-how the methods deep studying strategies are used on this regard and the way they may be doubtlessly in addition applied to fight the outbreak of COVID-19[16].

COVID-19, commonly referred to as coronavirus disease, is an infectious disease caused by the new coronavirus. Detection of coronavirus currently depends on elements such as patients' signs and symptoms, where the individual lives, visited records and close contact with any coronavirus patients. In order to screen a COVID-19 patient, the health care issuer uses an elongated swab to take a nasal pattern. The pattern is then examined in a laboratory setting. If an individual coughs, saliva (sputum) is released for examination. Prognosis will become more important while there may be loss of reagents or capacity verification, virus monitoring and severity, and communication with massive COVID-19 patients via the means of a healthcare practitioner. In this case of COVID-19 pandemic, streaming prediction based entirely on retrospective examination of laboratory facts in the form of chest x-rays using deep learning may be required [17].

This paper proposed a demystification method for locating COVID-19 using scientific pixel clustering with the help of deep networks. Study reports promising effects with 91.67% accuracy for diagnosis COVID-19 and 100 Score in Proven Survival Ratio [17].

4. Materials and Methods

4.1. Deep Learning Models

Techniques based on deep learning have shown significant performance increases in a variety of applications reported in the literature. This section provides a brief overview of the fundamental principles of deep learning models used to predict spreading rate of COVID-19 on the bases of time series data gathered from WHO concerning COVID-19 in Iraq for a period of about 2 months started at February the 4th of 2020 using a hybrid approach combining together LSTM and GRU.

4.1.1. LSTM Models

The LSTM [18] introduced a gated memory unit to address the vanishing gradient issues that constrain the performance of a standard RNN [19]. At a critical time step, the gradient either diminishes excessively or escalates dramatically resulting in a vanishing gradient problem. This issue appears consistently during the training process, as the optimizer's return propagation leads to the technique executing, even though the weights hardly alternate anymore. Basically, LSTM is composed of three gates. The three gates—input, forge, and output—serve to regulate the flow of information. These gates are fundamentally constructed using logistic functions derived from weighted sums, with the weights being obtainable during the training process through back propagation. The input and forget gates control the cell state. The output is generated by the output gate or the hidden state, which signifies the memory allocated for utilization. This method allows the network to maintain information for an extended period, a capability that conventional single RNNs do not possess. Indeed, the beneficial features of LSTM include their improved ability to capture long-term dependencies and their remarkable skill in handling time-series data.

Considering an input time-series sample X_t , along with the specified number of hidden units h , the equations governing the gates are as follows:

- Input Gate: $I_t = \sigma(X_t W_{xi} + H_{t-1} W_{hi} + b_i), \dots (1)$
- Forget Gate: $F_t = \sigma(X_t W_{xf} + H_{t-1} W_{hf} + b_f), \dots (2)$
- Output Gate: $O_t = \sigma(X_t W_{xo} + H_{t-1} W_{ho} + b_o), \dots (3)$
- Intermediate Cell State: $C^{\sim}_t = \tan h(X_t W_{xc} + H_{t-1} W_{hc} + b_c), \dots (4)$
- Cell State (next memory input) $C_t = F_t \circ C_{t-1} \circ C^{\sim}_t, \dots (5)$
- New State: $H_t = O_t \circ \tan h(C_t), \dots (6)$

where

- W_{xi} , W_{xf} , W_{xo} and W_{hc} , W_{hf} , W_{ho} refer respectively to the weight parameters and b_i , b_f , b_o denote bias parameters.
- W_{xc} , W_{hc} denote weight parameters, b_c is prejudice parameter, \circ reference to the element-wise multiplication. The assessment of C_t depends on the output information's from memory cells (C_{t-1}) and the current time step C^{\sim}_t .

4.1.2. GRU Models

GRU serves as another option to LSTM, introduced in [20], aimed at enhancing the performance of LSTM, decreasing parameters, and simplifying architecture. In GRU, the input gates and the forget gates of LSTM model are integrated into a single gate namely, the update gate (Figure 1). In contrast to LSTM, which has three gates, GRU has only two gates: update gate and reset gate. GRUs models bring new benefits such as the proposal of reset and update gate concepts. Finally, we present a new appreciation approach that enables the computation of hidden states in RNN models. The GRU enhanced the LSTM architecture by connecting the input and forget gates of the LSTM to the update gate, while utilizing the output gate as a reset gate. The update gate regulates the extent of previously retained memory, while the reset gate facilitates the integration of current inputs with prior memory. The mathematical relationships among the different components of the GRU are outlined as follows:

- Update gate: $Z_t = \sigma(X_t W_{xz} + H_{t-1} W_{hz} + b_z), \dots(7)$
- Reset gate: $R_t = \sigma(X_t W_{xr} + H_{t-1} W_{hr} + b_r), \dots(8)$
- Cell state: $\hat{H}_t = \tanh(X_t W_{xh} + (R_t \circ H_{t-1}) W_{hh} + b_h)$,
- New state: $H_t = Z_t \circ H_{t-1} + (1 - Z_t) \circ \hat{H}_t$,

where

- W_{xr}, W_{xz} and W_{hr} are weight parameters and b_r, b_z are bias parameters
- W_{xh}, W_{hh} are weight parameters, while b_h is a bias parameter. For a given time step t , the current update gate Z_t is utilized to combine the prior hidden state H_{t-1} and current candidate hidden state \hat{H}_t .

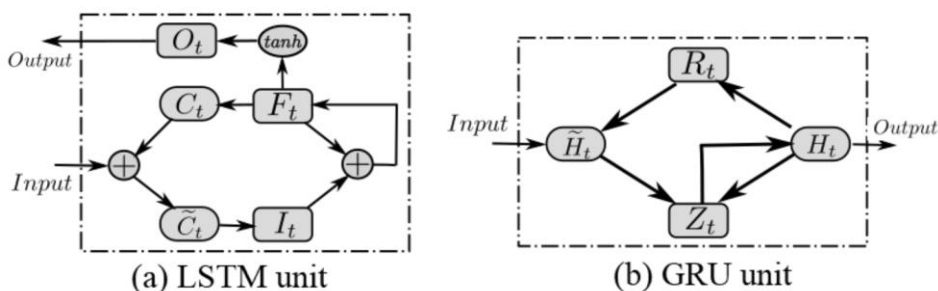


Figure 1. The basic structure of LSTM and GRU models. (a) I_t, F_t , and O_t represent the three LSTM gates (input, forget and output gates respectively), C and \tilde{C} represent the candidate memory cells and memory cell content. (b) R_t and Z_t are reset gate and update gates respectively, H_t and \tilde{H}_t is the candidate hidden state and hidden state respectively.

4.2. Evaluation Metrics

Generally speaking, the following indexes were used to evaluate ANN-based prediction models:

1. $RMSE = \sqrt{\frac{1}{n} \sum_{t=1}^n (y_t - \hat{y}_t)^2}$
2. $MAPE = \frac{100}{n} \sum_{t=1}^n \left| \frac{y_t - \hat{y}_t}{y_t} \right| \%$
3. $MAE = \frac{\sum_{t=1}^n |y_t - \hat{y}_t|}{n}$

In this context, (y_t) represents the actual values, (\hat{y}_t) denotes the expected values, and (n) indicates the total number of measurements taken. The RMSE indicator was selected due to its widespread application in assessing model quality within regression contexts and its role as a scoring metric in numerous data science competitions. Essentially, it is calculated using the logarithmic scale. The benefit of employing RMSE as a statistical measure lies in its strong resistance to outliers. Lower MAE or MAPE values approaching 1 signify improved predictive accuracy. Furthermore, we will examine the distribution of forecasting errors through the use of histograms.

4.3. Deep Learning-based COVID-19 Prediction

As stated, this work presents a DL architecture for predicting CoVID-19’s spreading rate in Iraq. The proposed approach uses deep learning models to predict, on daily bases, confirmed positive cases, death cases and recovered cases. Figure 2 shows the general structure for the suggested prediction technique. The prediction of CoVID-19 has been accomplished via a two-phase process: training phase and testing phase. Initially, the raw data undergoes pre-processing and standardization prior to its application in constructing the DL model. Parameters in DL models are selected to assure minimization of the loss function throughout training process. Adam optimizer is employed for this task. During the testing phase, the models generated earlier with the parameters just selected are employed to predict the spreading rate of CoVID-19. This prediction functions based on the WHO’s most effective tracking data, as for instant, the number of newly confirmed positive cases on day $t + 1$, which relies on the corresponding cases recorded for specific previous days leading up to day t .

5. Results

5.1. Data Description

WHO has declared CoVID-19 in around 210 countries and territories globally. Most countries around the globe are currently facing the rapid and extensive propagation of the CoVID-19 outbreak. Extensive air traffic among nations participated badly in the spread of CoVID-19 from origin to various impacted regions; documented instances of person-to-person transmission have also occurred among close contacts of returning passengers. As stated earlier, the goal of this work is to predict CoVID 19’s spreading and the consequent propagation of the pandemic. This work considers the number of confirmed daily registered cases and the recovered daily registered cases and other related data gathered and registered by the WHO in Iraq.

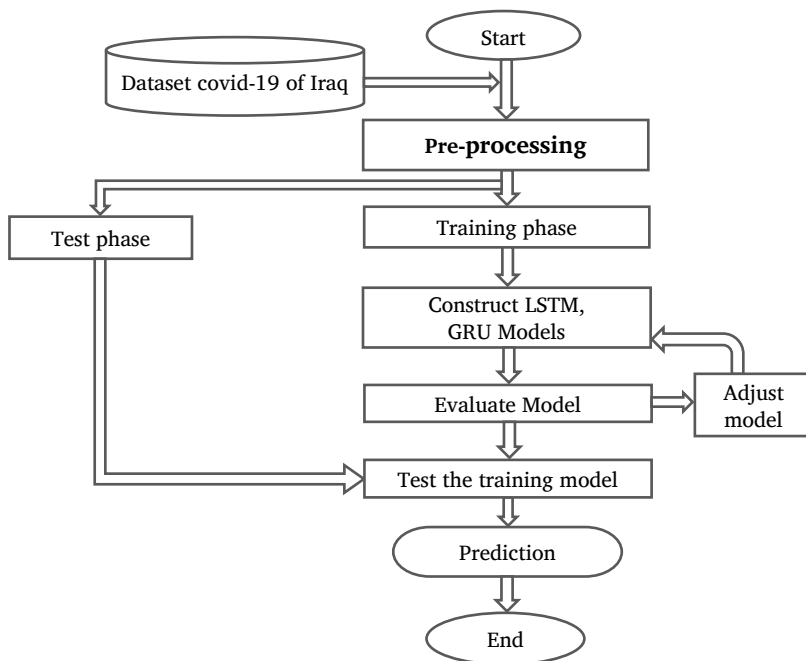


Figure 2. Conceptual underpinning for the proposed prediction algorithms

5.2. Data Analysis and Modeling

Descriptive data, as presented in Table 1, are considered as the descriptive coefficients that summarize a particular data set, which can either represent the overall or a sample pattern of population. It is necessary to examine the data before building a model as this assist getting maximum insights from the data, and to derive hypotheses that could possibly lead to experiment data using statistical graphs or other visualization techniques. Figure (3) depict aspects of applying such analysis to the leftover of the WHO dataset in Iraq.

```

Out[10]:
total_cases      count      mean      std
new_cases        count      mean      std
new_cases_smoothed count      mean      std
total_deaths     count      mean      std
new_deaths       count      mean      std
new_deaths_smoothed count      mean      std
total_cases_per_million count      mean      std
new_cases_per_million count      mean      std
new_cases_smoothed_per_million count      mean      std
total_deaths_per_million count      mean      std
new_deaths_per_million count      mean      std
new_deaths_smoothed_per_million count      mean      std
reproduction_rate count      mean      std
total_tests       count      mean      std
total_tests_per_thousand count      mean      std
new_tests_smoothed count      mean      std
new_tests_smoothed_per_thousand count      mean      std
positive_rate     count      mean      std
tests_per_case    count      mean      std
stringency_index  count      mean      std
population         count      mean      std
population_density count      mean      std
median_age        count      mean      std
aged_65_older    count      mean      std
aged_70_older    count      mean      std
gdp_per_capita   count      mean      std
extreme_poverty  count      mean      std
cardiovasc_death_rate count      mean      std
diabetes_prevalence count      mean      std
handwashing_facilities count      mean      std
hospital_beds_per_thousand count      mean      std
life_expectancy   count      mean      std
human_development_index count      mean      std

total_cases      min      25%      50%
new_cases        min      25%      50%
new_cases_smoothed min      25%      50%
    
```

Table 1. Summary of COVID-19 of IRAQ Datasets

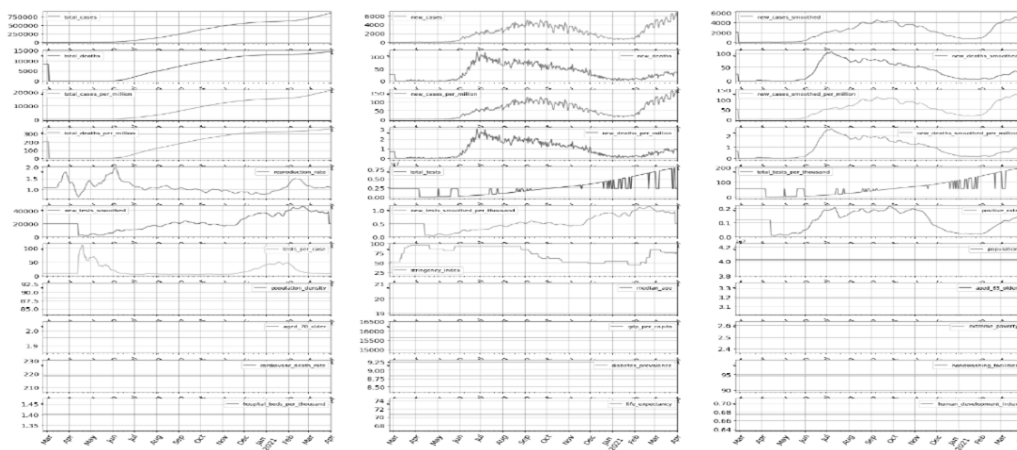


Figure 3. Visualization of Time-Series Data Analysis

5.3. Prediction over Time-Series Data

For the prediction over time series data, the model has to estimate the output, at certain point in time, as a function of the input over a certain range of preceding time points. So, to predict the output at time point t (that is $x(t)$), model should consider $x(t - 1)$. In this sense, time series data, for a duration of time ranging $1-n$, should be manipulated such that output samples at time $\{t, t + 1, \dots, t + n\}$ should be predicted out of input samples at time $\{t - n, t - n-1, \dots, t - 1\}$.

```

          1         2         3         4         5
var1(t-1) 0.000000 0.000000 0.000005 0.000007 0.000007
var2(t-1) 0.000150 0.000000 0.000600 0.000300 0.000000
var3(t-1) 0.354241 0.354241 0.354241 0.354241 0.354241
var4(t-1) 0.578955 0.578955 0.578955 0.578955 0.578955
var5(t-1) 0.229508 0.229508 0.229508 0.229508 0.229508
...
var29(t)   0.000000 0.000000 0.000000 0.000000 0.000000
var30(t)   0.000000 0.000000 0.000000 0.000000 0.000000
var31(t)   0.000000 0.000000 0.000000 0.000000 0.000000
var32(t)   0.000000 0.000000 0.000000 0.000000 0.000000
var33(t)   0.000000 0.000000 0.000000 0.000000 0.000000

[66 rows x 5 columns]
No of Features of cleandData: 33
No of Features of Reframed Date: 66
    
```

5.4. Model Training

Figure 4 presents the behavior of the deep networks of LSTM and GRU, in terms of the model loss according to WHO Iraq time-series data.

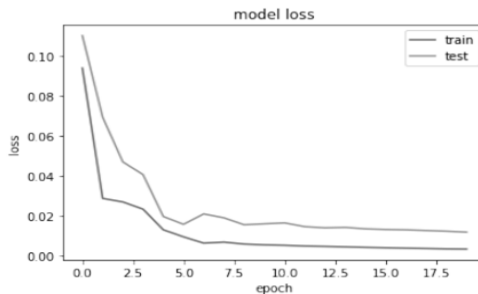


Figure 4. Training Model

5.5. Calculate Errors

This is done according to the error rate of the model:

- Test MAE for LSTM: 0.109
- Test MAPE for LSTM: 0.191
- Test RMSE for LSTM: 0.134
- Training elapsed Time: 11.428 Seconds

5.6. Model Testing

Figure 5 depicts testing model’s prediction for the overall 33 features over 20% of the data that covers the time from 12/1/2021 to 2/4/2021, amongst is the prediction results for a two of the most vital features of “total-cases- per-million” and “new-confirmed-cases” as presented in Figure 6 and Figure 7 respectively.

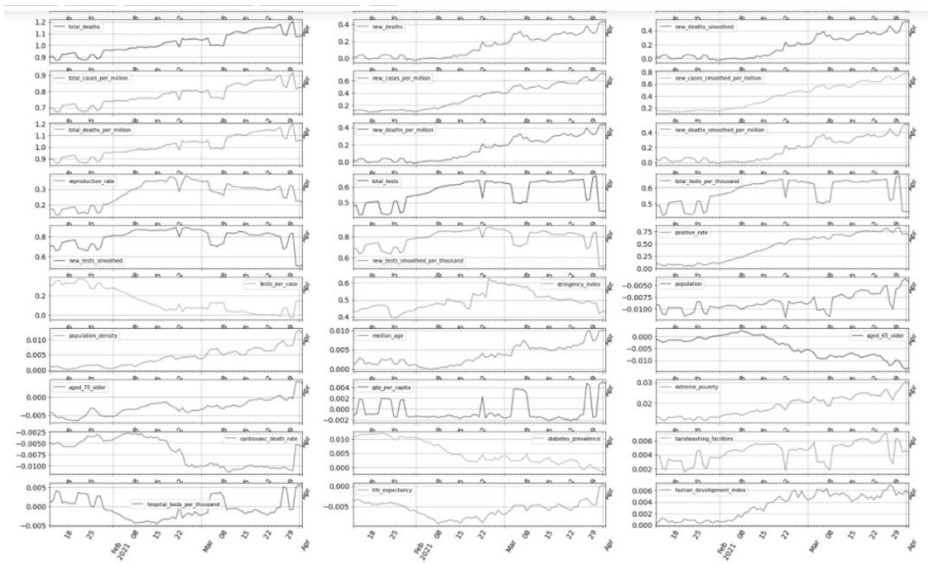


Figure 5. Testing model

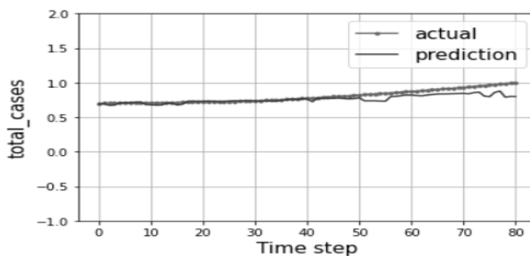


Figure 6. Total Cases per Million

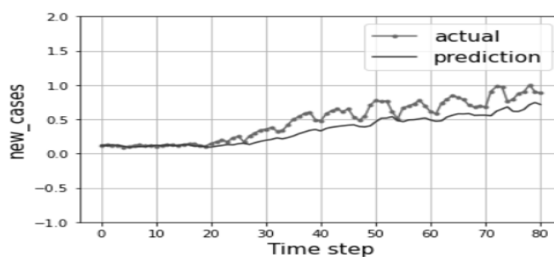


Figure 7. New Cases

6. Conclusion

CoVID-19 is a dramatically spreading disease around world, so it requires building a prediction model based on global health data. This work presented a hybrid model of LSTM and GRU algorithms built for the purpose of predicting the speed of disease spread among people in Iraq to assist accordingly identifying ways and actions of reducing spread of this disease via social distancing, online communication, and taking appropriate treatment and necessary vaccinations.

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