Research Article

Applying Machine Learning Prediction Methods to COVID-19 Data

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ARTICLE INFO	ABSTRACT
	The Coronavirus (COVID-19) epidemic emerged in China and has caused many problems such as loss of life, and deterioration of the social and economic structure. Thus, understanding and predicting the course of the epidemic is very important. In this study, the SEIR model and machine learning methods LSTM and SVM were used to predict the values of Susceptible, Exposed, Infected, and Recovered for COVID-19. For this purpose, COVID-19 data from Egypt and South Korea provided by John Hopkins University were used. The results of the methods were compared by using MAPE. A total of 79% of MAPE were between 0 and 10. The comparisons show that although LSTM provided better results, the results of all three methods were successful in predicting the number of cases, the number of patients who died, and the peaks and dimensions of the epidemic.

1. Introduction

Epidemics are large-scale communicable diseases that greatly increase morbidity and mortality over a wide geographical area and cause significant economic, social, and political disruptions [1]. In December 2019, an epidemic of atypical pneumonia of a novel coronavirus (SARS-CoV-2) of zoonotic origin occurred in Wuhan, the capital of China's Hubei province [2]. On January 30, 2020, the World Health Organization (WHO) declared the outbreak a "Public Health Emergency of International Concern". On 12 February 2020, WHO named the disease caused by the novel coronavirus "Coronavirus Disease 2019" (COVID-19) [3]. On March 11, 2020, the epidemic was declared a pandemic by the World Health Organization [4]. COVID-19 pandemic is a global public health crisis that threatens people's health [5]. In the analysis of epidemics, there are many epidemic modelling methods used to both predict the number of cases, the number of patients who died, and other parameters of the epidemic and to simulate the epidemic pro[1]cess. Among these models, the SIR model is one of the most preferred models. The SIR model has a compartment-type structure and was introduced to the literature by [6]. Compartment S represents Susceptible, compartment I Infected, and compartment R Recovered/Removed. Until today, many improvements have been made to the main model, such as adding new compartments and editing existing compartments, and new models have been created. In the literature, SIR [7], [8], SIRS [9], SEIR [10] – [12], and SIRD [13] are examples of use in this area. However, the SEIR model is more appropriate and comprehensive to describe information on the spread of the epidemic [14].

Time series are frequently preferred to produce helpful results for policymakers or managers in many

different fields such as water resources [15], soil mapping [16], traffic [17][18], and tourist numbers [19]. In addition, the number of studies using machine learning methods in addition to traditional methods is increasing. Along with epidemic modelling methods, many machine learning methods are used in the analysis of epidemic diseases in epidemiology. Examples of usage in this field are ARIMA [20]– [22], LSTM [23], [24], SVM [25], [26] methods. Both epidemic modelling methods and machine learning methods can be used together in the analysis of epidemics. Hybrid studies are generally performed for comparison and confirmation of results. SEIR model and Regression techniques [27], SEIR model and DNN method [28], and SEIR model and LSTM method [29] are examples of hybrid studies in the literature.

This study consists of four stages and aims to predict some COVID-19 data. Firstly, a dataset was created using COVID-19 data from South Korea and Egypt due to their consistency in the number of cases and deaths. In the second section, SEIR model were optimized using various optimization methods. In the third section, epidemic parameters were predicted using Long Short-Term Memory (LSTM) and Support Vector Machine (SVM), which are machine learning methods frequently mentioned in the literature. In the last section, the data of the outputs obtained from the methods were evaluated using the MAPE metric.

1.1. Motivation and Background

The SEIR model interactively models four different conditions (Susceptible, Exposed, Infected, and Recovered/Removed) using historical data from an outbreak. In the compartmental models, firstly, the main parameters are given as input to the system. Then the output created by the first compartment is given as input to the next compartment. This interaction continues until the last compartment. The study, it is aimed to optimize the values of the parameters produced by the SEIR model in the transitions between the compartments by using machine learning methods and thus enhancing the overall success.

2. Material and Methods

The data set used in the study was obtained from the data updated daily by John Hopkins University via the GitHub platform. "Number of Confirmed Cases", "Number of Patients Who Died", "Number

of Recovered Patients", "Date" and "Country Population" information were extracted from the data [30].

2.1. SEIR

Epidemic modelling methods simplify the mathematical modelling of infectious diseases. In these models, people are assigned to compartments according to their health status. People can advance between groups/compartments. The order of the labels usually shows the flow patterns between the compartments. Models attempt to estimate how far a disease has spread, the total number of infected, the duration of the epidemic, and various epidemiological parameters such as the reproduction coefficient. Such models can show how their response could affect the outcome of the epidemic.

The SEIR model simulates the time history of an epidemic. The model interactively models between four different conditions using historical data from an epidemic. These conditions are Susceptible (S), Exposed (E), Infected (I), and Recovered/Removed (R) [31]. The first compartment of the model, susceptible people, is equal to the entire population on the first day of the epidemic and has not yet encountered the disease. The second compartment consists of people who are exposed to the disease while being susceptible. In the third compartment, some people are infected. These consist of people with symptoms whose incubation period has ended after exposure to the disease. Finally, some are infected people who come out of the cycle because of death or recovery. The dynamic transfer of the population during the epidemic period is shown in Figure 1.
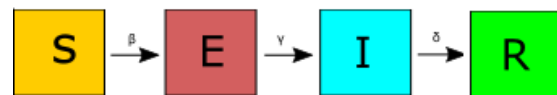

Figure 1. SEIR model

SEIR model parameters are calculated using the formulas in Equations. (1), (2), (3) and (4).

Equations

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

$$\frac{dE(t)}{dt} = \beta I(t)\frac{S(t)}{N} - \gamma E(t) \tag{2}$$

$$\frac{dI(t)}{dt} = \gamma E(t) - \delta I(t) \tag{3}$$

$$\frac{dR(t)}{dt} = \delta(t)I(t) \tag{4}$$

The formula for the number of susceptible in Eq. (1), the number of exposed in Eq. (2), the number of infected in Eq. (3), the number of removed in Eq. (4) at time t.

The terms in these equations are expressed as (S) parameter is target time histories of susceptible cases, (E) parameter is target time histories of exposed cases, (I) parameter is target time histories of infectious cases, (R) parameter is target time histories of removed/recovered cases, (β) infection rate, (γ) the inverse of the mean delay time and (δ) refers to the coefficients used depending on the mortality rate [31].

2.2. Curve Fitting Methods

In the predictions made on epidemic modelling methods, curve fitting methods can be used to keep the epidemic curves at a certain level or to optimize the curves. The curve fit is a data analysis method that attempts to construct a linear or nonlinear $f(x)$ model function. Some optimization algorithms such as L-BFGS-B are proposed to optimize the parameters of SIR and SEIR models and improve their prediction capabilities [32]. The curve fitting methods used in this study are explained as follows.

The L-BFGS-B algorithm defines constant and free variables at each step. The method only works by repeating the L-BFGS method on free variables to achieve high accuracy.

The Powell method is an algorithm proposed by Michael J. D. Powell to find the local minimum of a function. It is quite useful to use for minimizing functions of a large number of variables as it does not require storing any matrix with a conjugate gradient [33]. The conjugate gradient (CG) method commonly attributed to Magnus Hestenes and Eduard Stiefel is an algorithm used in mathematics for the numerical solution of certain systems of linear equations. COBYLA is a gradient-free optimization algorithm that can manage nonlinear inequality constraints. For this reason, Powell developed the COBYLA algorithm in 1994, which creates linear polynomial approximations to the objective and constraint functions by interpolating the vertices of the simplifications [34]. The SLSQP method is generally used when the objective function and constraints are continuously differentiable. In mathematical problems using the SLSQP algorithm, each step solves two subproblems [35].

2.3. Support Vector Machine

The Support Vector Machine (SVM) was originally introduced by Vapnik et al and later expanded by another researcher [36], [37]. Vapnik stated that SVM method is based on VC (Vapnik–Chervonenkis) theory, and their experimental work demonstrated superior generalization performance over the neural network and statistical learning technique [38]. SVM is implemented in the form of classification and regression. Classification is performed with a linear or nonlinear separation surface in the input field of the dataset [39]. Regression, on the other hand, uses Vapnik's non-precision approach, creating a flexible channel with a minimum radius symmetrically around the predicted function, thus ignoring values outside the threshold as a result of error calculation [40]. SVM is basically divided into two according to whether the data set can be separated linearly or not. Therefore, in this section, it is discussed in two parts as linear and non-linear SVM.

2.3.1. Linear SVM

In classification with SVM, it is aimed to separate the samples belonging to two classes, which are generally shown with class labels as {-1, +1}, with the help of a decision function obtained from the training data [36], [38] for the training of SVM in a linearly separable two-class classification problem, assuming that the training data consisting of k samples {xi, yi}, i = 1, ..., k. The inequalities of the optimum hyperplane are calculated as Equations (5) and (6).

$$\min \quad \frac{1}{2}||w||^2 \tag{5}$$

$$y_i(wx_i + b) - 1 \geq 0 \text{ and } y_i \in \{-1, 1\} \tag{6}$$

2.3.2. Non-Linear SVM

Data may not always be linearly separated in problem-solving. In such cases, the problem arising from the fact that some of the training data remain on the other side of the optimal hyperplane is solved by

defining a positive dummy variable (ξ). The objective function is specified in Eq. (7) and the constraints of the function are specified in equations (8) and (9) [36].

$$\frac{1}{2}||w||^2 + C(\sum_{i=1}^{t} \xi_i)^k \qquad k>1 \qquad (7)$$

$$y_i(wx_i + b) \geq 1 - \xi_i \qquad i = 1 \dots t \qquad (8)$$

$$\xi_i \geq 0 \qquad i = 1 \dots t \qquad (9)$$

2.4. Long Short-term memory

Long short-term memory (LSTM) was first processed by Hochreiter & Schmidhuber in 1997 and developed later by the Flex Gers team [41]. The LSTM layer consists of a series of repetitively linked blocks known as memory blocks. These blocks can be thought of as a different versions of memory chips in a digital computer. Each contains one or more repetitively linked memory cells and three multiplicative units (input, output, and forget gates) [42].

Memory cells store their entries for a period. Input gates control the flow of new values into the cell. Forget gates decide which values should be stored in memory. The output gates, on the other hand, control which values in memory should be used to calculate the output activation of the LSTM unit. The LSTM model is shown in Figure 2.
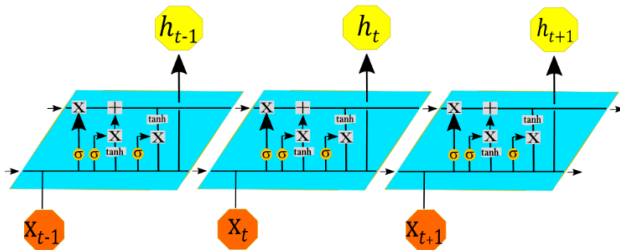

Figure 2. LSTM module

In Figure 2, each line carries a vector from the output of one node to the inputs of the others. Orange circles represent operations for points, such as vector addition, while blue boxes learn neural network layers. Merging lines indicate the merge, while a line stamp indicates that its content is copied, and the copies go to different locations.

In LTSM, the hidden state of memory cells is calculated by the formulas in Equations (10), (11), (12), (13) and (14).

Here i_t is the input gate, f_t is the forget gate, o_t is

the output gate, w is the weight on the corresponding gate, σ is the standard sigmoid value, x_t is the current timestamp input, c_t is the cell memory timestamp, and b is the deviation value [43].

$$i_t = \sigma(W_{ix}x_t + W_{hh}h_{t-1} + W_{ic}c_{t-1} + b_i) \qquad (10)$$

$$f_t = \sigma(W_{fx}x_t + W_{hh}h_{t-1} + W_{fc}c_{t-1} + b_f) \qquad (11)$$

$$c_t = f_t * c_{t-1} + i_t * g(W_{cx}x_t + W_{hh}h_{t-1} + W_{cc}c_{t-1} + b_i) \qquad (12)$$

$$o_t = \sigma(W_{ox}x_t + W_{hh}h_{t-1} + W_{oc}c_{t-1} + b_o) \qquad (13)$$

$$h_t = o_t * h(c_t) \qquad (14)$$

2.5. Performance Measurement

Mean Absolute Percentage Error (MAPE) is one of the statistical performance measurement methods that shows how consistent the results obtained in applications are. The closer the result obtained in this method is to 0, the more successful it is. The MAPE formula in Eq. (15):

$$MAPE = \left(\frac{1}{n}\sum_{t=1}^{n} \frac{|Y_t - \hat{Y}_t|}{Y_t}\right) * 100 \qquad (15)$$

3. Experimental Results

The initial parameters of the SEIR Model in this study were taken from studies published by WHO. R0, mean incubation time and infection time was taken as below to calculate pass rates between parameters [44].

Reproduction Number (R0) = 3,9 (people)
Incubation Period = 2,9 (day)
Infection Period = 5,2 (day)

A total 70% of the data set was reserved for training and 30% for testing. "Number of Confirmed Cases", "Number of Patients Who Died", "Number of Recovered Patients" and "Country Population" information included in the data set were introduced to the model. R0 and fatality rate were calculated on the SEIR model, along with the optimized number of cases and deaths. R0 and mortality rates were used to find transition rates between epidemic parameters. Daily values of epidemic parameters were calculated using pass rates. Five different optimization algorithms were used for the optimization of the "Case" and "Death" numbers on the SEIR model.The

MAPE ratios related to the results are shown in Table 1.

Table 1. MAPE results of optimization algorithms

| Method | Egypt | | South Korea | |
	Case	Fatality	Case	Fatality
L-BFGS-B	1.294	0.438	16.991	17.176
Powell	1.294	0.438	16.991	17.177
SLSQP	1.285	0.444	17.009	17.172
CG	1.294	0.438	16.991	17.177
COBYLA	4.822	3.868	18.187	17.698

As seen in Table 1, all methods produced acceptable results. The data of the L-BFGS-B method in calculating the transition ratios between parameters on the SEIR model are presented below. Calculated R0 and pass rates are shown in Table 2.

Table 2. Pass rates and R0 value of the parameters

Country/ Parameter	S>E	E>I	I>R	R0
Egypt	0.679	0.340	0.050	1.97
South Korea	0.651	0.344	0.016	1.89

The MAPE resulting from the prediction of the epidemic parameters of Egypt and South Korea are shown in Table 3 and Table 4. While the lowest MAPE value was obtained by the SVM to predict S and R, LSTM provided the lowest MAPE value for E and I.

Table 3. MAPE results of S, E, I and R for Egypt

Method/ Parameters	S	E	I	R
SEIR (L-BFGS-B)	2.570	6.100	5.270	6.550
SVM	0.002	12.500	5.880	0.430
LSTM	0.280	0.930	1.180	0.510

Table 4. MAPE results of S, E, I and R for South Korea

Method/ Parameters	S	E	I	R
SEIR (L-BFGS-B)	2.010	39.030	37.540	15.950
SVM	0.015	31.500	6.640	0.250
LSTM	0.110	0.860	0.450	1.540

In Figure 3, it is seen that the difference between the actual and predicted data widened after 150 days, although the predicted and actual data for the first 100 days were very close in predicting the number of susceptible people in Egypt with the SEIR. In Figure 3, it is also seen that the curves of the predicted and actual data of the people who were exposed, sick, and died in the epidemic in Egypt and South Korea are similar to each other.

Figure 3. Prediction results of S, E, I and R in Egypt and South Korea using SEIR model

In the prediction of the COVID-19 epidemic parameters, LSTM and SVM (SVR) methods were used as machine learning methods. Susceptible, Exposed, Infected, and Removed persons in Egypt and South Korea were predicted by SVR and LSTM. A total 70% of the dataset was reserved for training and 30% for testing. The prediction results of SVR and LSTM are shown in Figure 4 and Figure 5 respectively. As seen in the figures, the curves of the actual data and the predicted data are close to each other.
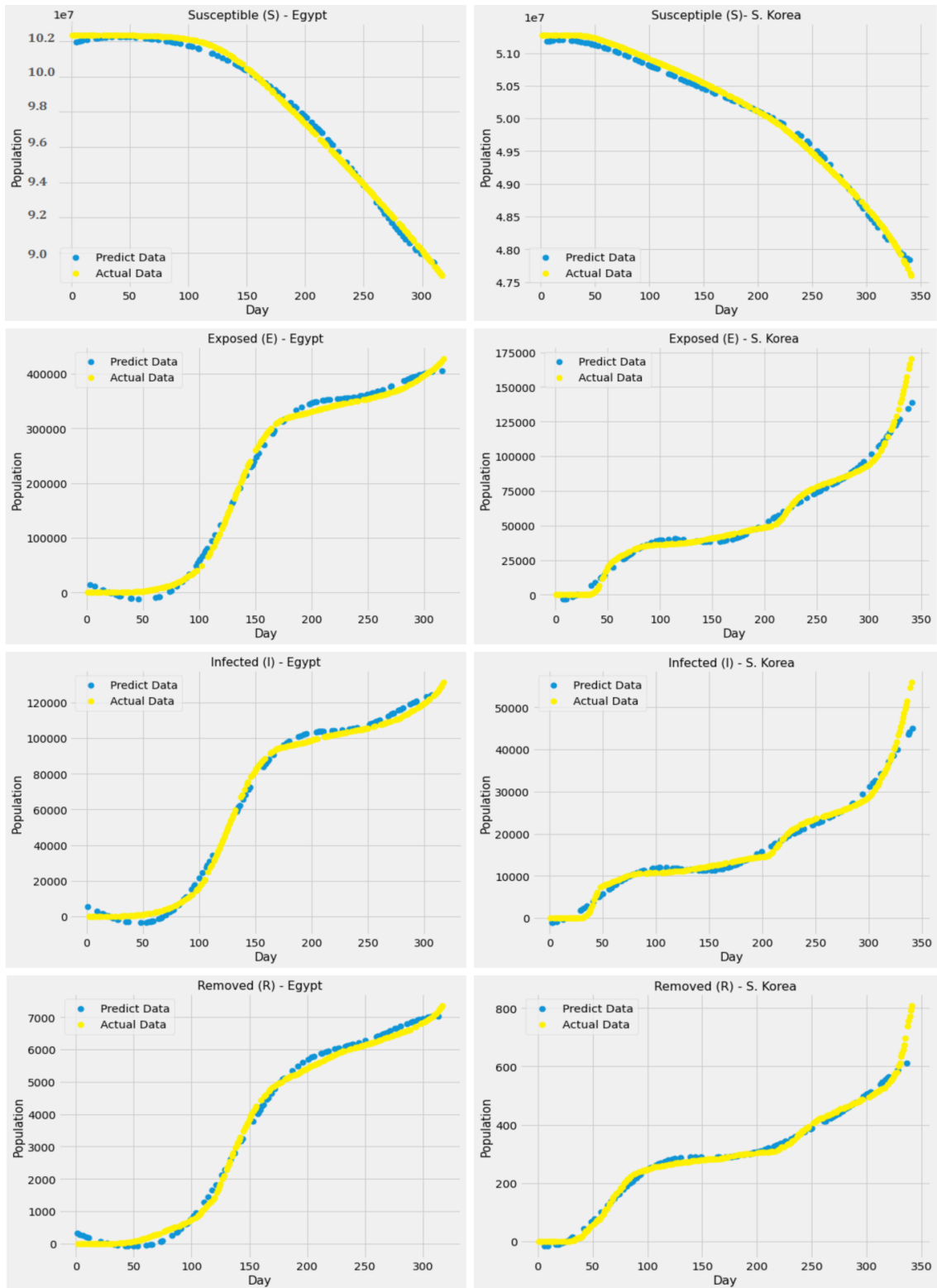
Figure 4. Prediction results of S, E, I and R parameters in Egypt and South Korea by SVM
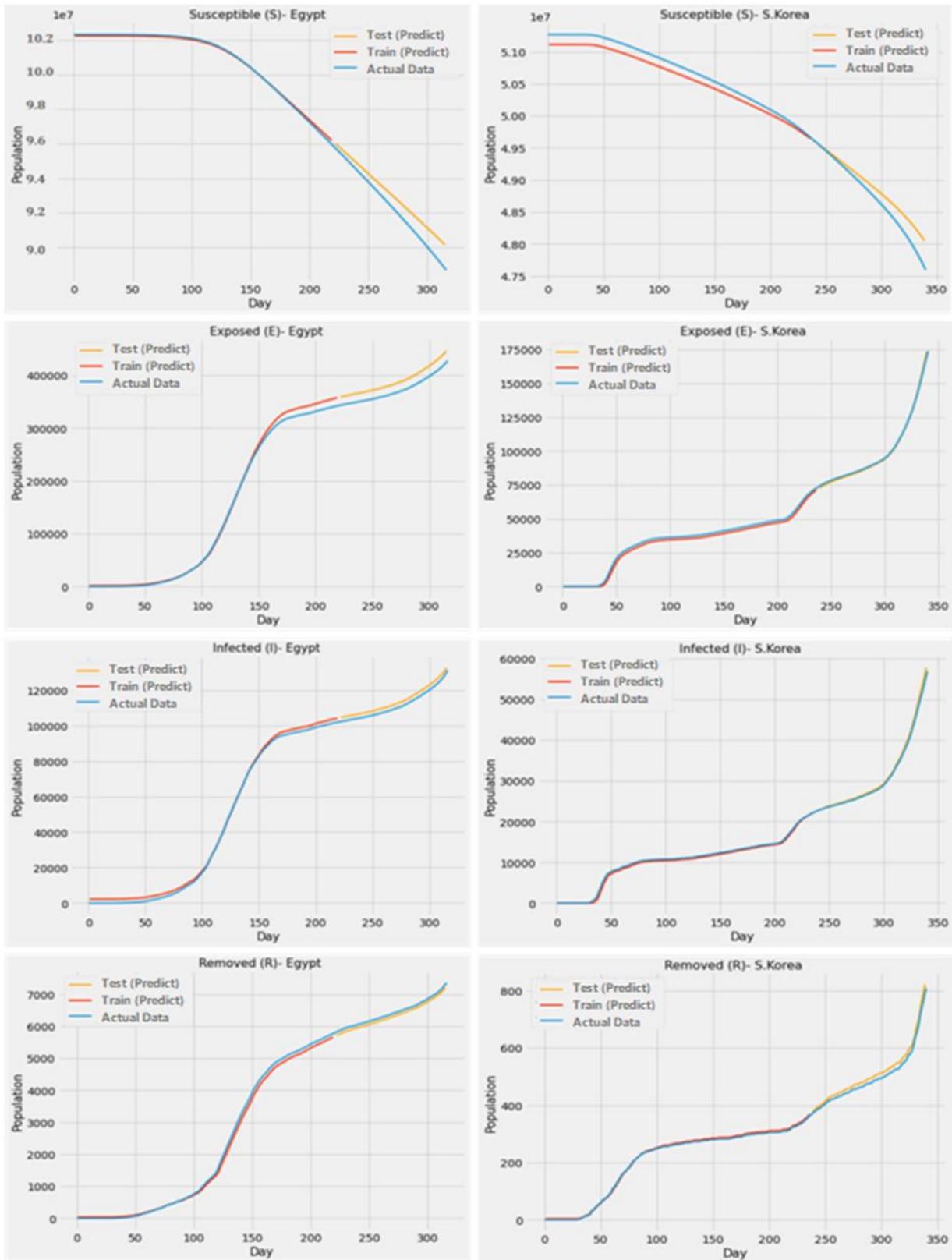
Figure 5. Prediction results of S, E, I and R parameters in Egypt and South Korea by LSTM

4. Discussion and Conclusion

Studies in the literature show that instead of estimating time series with a single method, estimating by combining multiple methods that can model different functional relationships in the data set gives more effective results. In addition, the success of the previously used machine learning methods compared to traditional methods also supports the results of the study [24], [26]. In the study, which was carried out by bringing an additional perspective to the existing studies, machine learning methods gave very successful results in estimating the parameters of epidemic diseases. Societies are cultural, social, economic, etc. It has different structures due to many factors. For this reason, the real-life consequences of epidemics differ according to the structure of society. However, compartment models used in the field of epidemiology accept these characteristics of societies as the same. It is aimed to provide memory features to the SEIR model, which has a memoryless structure, by using the LSTM method. Thus, instead of approaching every data in the same way, training the data according to the patterns it has will increase the accuracy and confidence rates of the results to be obtained.

4.1. Limitations and future research

The official numbers announced by each country may not reflect the truth, as countries may impose bans such as entry and import bans to countries with a high number of infected individuals to protect their own citizens in pandemic-level epidemics. In addition to the inherent limitations of the time series, this situation may cause erroneous data, and thus the results may be erroneous. To overcome such limitations in the study, the countries used were carefully researched to choose their data. Models derived from the SIR main model, such as SEIR, generally make some assumptions. Some of these assumptions are that during the spread of the disease, there is no birth, or death other than a disease, external migration, or immigration, and the society has a homogeneous structure. In future studies, using the obtained data by eliminating the possibilities such as misdiagnosis and different causes of death will increase the success rate of the model. In addition, it will show significant success in studies where all the

features that shape the basic structure of the society can be added to the model, considering the super-spreaders in the spread of the disease. It is thought that more reliable results will be produced because of adding a compartment that can provide memory properties to such models, providing the data of similar events in the past in the same population to the model, and training the model using these.

Contributions of the Authors

Adnan Kece: Methodology, Data curation, Writing Original draft preparation, Visualization, Software.

Yigit Alisan: Reviewing, Editing, Visualization.

Faruk Serin: Conceptualization, Original draft preparation.

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