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EXPLORING THE ACCURACY OF AN OPTIMIZATION-FREE NEURAL NETWORK FORECASTING MODEL IN MATHEMATICAL EPIDEMIOLOGY: A CASE STUDY IN TÜRKİYE

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Abstract. In this study, we explore the use of mathematical epidemiology models in predicting COVID-19 cases in Turkey. Our approach employs a Feed-Forward Neural Network solver, which is designed to quickly converge and make accurate predictions. To eliminate the need for time-intensive optimization procedures, the network weights are calculated using the Extreme Learning Machine algorithm, ensuring adherence to the initial conditions set by the epidemiology models. We examine the performance of both the Susceptible-Infected (SI) and Susceptible-Infected-Susceptible (SIS) models using this approach and evaluate their accuracy.

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1 Introduction

Mathematical models are essential tools for understanding the spread of infectious diseases and developing strategies to control and prevent outbreaks. Compartmental models are one such class of tools that have been extensively used in mathematical epidemiology (Brauer et al., 2019). These models divide the population into different compartments based on their disease status and model the flow of individuals between these compartments. The compartmental epidemiology models also describe how a disease spreads through a population and how different interventions, such as vaccination or social distancing, can affect the spread of a disease.

It must be emphasized that the predicting the spread of a disease through a population is important for several reasons. First, it can help public health officials and policymakers make informed decisions about interventions to control the spread of the disease. For example, if a model predicts that the disease will rapidly spread through a certain population group, such as elderly people or healthcare workers, officials may choose to prioritize vaccination or other preventive measures for that group. Second, predicting the spread of a disease can help healthcare providers prepare for a potential surge in cases. If a model predicts that the disease will rapidly spread and lead to a large number of cases, healthcare providers can take steps to increase their capacity to treat patients, such as by expanding hospital capacity or securing additional medical supplies. Finally, predicting the spread of a disease can help individuals take precautions to protect themselves and their families. For example, if a model predicts that the disease is likely to spread rapidly in a certain geographic area, individuals may choose to avoid traveling to that area or take additional precautions to avoid exposure.

The spread of diseases has been questioned and studied for many years. The first mathematical model to describe and investigate infectious diseases was given (Bernoulli, 1766). Bernoulli (1766) modeled the spread of the smallpox virus, which was widespread at the time.

However, traditional compartmental models often require simplifying assumptions that may not accurately reflect the complexity of real-world epidemiological processes. In recent years, there has been increasing interest in using machine learning approaches, specifically neural networks, to improve the accuracy of epidemiological models (Ghafouri et. al, 2021; Kuvvetli et al., 2021; Shawaqfah & Almomani, 2021; Aminu et al., 2022). All of these studies demonstrate the potential of neural networks for predicting the spread of infectious diseases, including COVID-19, using a range of approaches and datasets Segall & Sankarasubbu (2022). Because, neural networks have the ability to learn complex relationships between input data and output predictions, making them well-suited for modeling the complex dynamics of infectious disease transmission. In this context, neural networks can be trained on large datasets of epidemiological data to predict the spread of infectious diseases, identify effective control measures, and optimize resource allocation for disease surveillance and response. This approach has the potential to improve the accuracy and effectiveness of public health interventions, and ultimately reduce the impact of infectious diseases on human health.

On the other hand, the COVID-19 pandemic, which began in late 2019, has caused a global health crisis as the virus spread rapidly and affected millions of people. Direct human-to-human contact has been the most efficient mode of transmission. In response, deep learning techniques, such as feed-forward neural networks, have been widely applied due to their ability to approximate complex mappings and perform prediction and estimation tasks. The Universal Approximation Theorem supports the approximation capabilities of these networks (Nishijima, 2021).

In this study, we focus on the use of two-stage neural networks for solving the compartmental models in mathematical epidemiology for controlling the spread of infectious diseases. With this manner, this study aims to adapt the SI (Susceptible-Infected) and SIS (Susceptible-Infected-Susceptible) epidemiology models to COVID-19 dynamics, and to obtain numerical solutions using neural network (Net). The Net model is trained without time series analysis using the optimization-free extreme learning machine approach. The inputs to the network are defined solely as the daily number of positive cases, or the number of infected individuals.

2 Mathematical Prerequisites

Theorem 1. *Under certain conditions on the activation function, a neural network with a finite number of neurons that is designed with a feed-forward architecture has the ability to approximate continuous functions on compact subsets of* $\mathbb{R}^n$.

This theorem is known as the universal approximation theorem for artificial neural networks. We refer to Nishijima (2021) for more details on this theorem.

The process of solving linear equations represented by $\mathbf{Ax} = \mathbf{b}$ can present difficulties if the matrix $\mathbf{A}$ is singular or not a square matrix. To address these challenges, the utilization of the Moore-Penrose generalized inverse is recommended. A least square solution in a linear system $\mathbf{Ax} = \mathbf{b}$ is represented by $\mathbf{x} = \mathbf{x}_1$ if

$$\|\mathbf{Ax}_1 - \mathbf{b}\| = \min_x \|\mathbf{Ax} - \mathbf{b}\| \tag{1}$$

The solvability of the system $\mathbf{Ax} = \mathbf{b}$ does not require matrix $\mathbf{A}$ to be square or full rank. However, for $\mathbf{Ax} = \mathbf{b}$ to have a solution, the equation $\mathbf{AGb} = \mathbf{b}$ must hold true, where $\mathbf{G}$ is the Moore-Penrose inverse of matrix $\mathbf{A}$. Keeping all this in mind, we introduce the following theorem:

Theorem 2. *If* $\mathbf{Gb}$ *serves as the minimum norm least square solution for the linear system* $\mathbf{Ax} = \mathbf{b}$*, then it is necessary and sufficient that* $\mathbf{G}$ *equals the generalized Moore-Penrose inverse of matrix* $\mathbf{A}$*, or* $pinv(\mathbf{A})$*.*

Based on this insight, it appears that a workable solution for differential equations could be achieved through the use of a neural network in tandem with the extreme learning machine algorithm (Panghal & Kumar, 2021).

3 Mathematical Epidemiology Models

In this section, various mathematical epidemiology models used in the study will be discussed.

3.1 SI (Susceptible - Infected) Model

In SI (Susceptible-Infected) model, the number of individuals who are susceptible to a disease (S), and the number of individuals who are currently infected with the disease (I) are represented as a system of ordinary differential equations (ODEs). This system can be written as:

$$\begin{cases} \frac{dS(t)}{dt} &= -\frac{\beta S(t)I(t)}{N} \\ \frac{dI(t)}{dt} &= \frac{\beta S(t)I(t)}{N} \end{cases} \tag{2}$$

where β is the rate of spread of the disease, $N(t) = S(t)+I(t)$ is the total number of individuals in the population, and $S(0) = s_0 > 0$, $I(0) = i_0 > 0$ are the initial conditions. In this model, birth and death rates are not considered or assumed to be equal, meaning that the total population remains constant.

The analytical solution of the ODEs is given in Eq. 3.

$$\begin{cases} I(t) &= \frac{i_0}{i_0+(1-i_0)e^{-\beta t}} \\ S(t) &= N(t) - I(t) \end{cases} \tag{3}$$

This model demonstrates how, over time, all susceptible individuals will become infected with the disease, assuming birth and death rates are constant.

3.2 SIS (Susceptible - Infected - Susceptible) Model

The model takes into account the possibility of recovery, where infected individuals return to a susceptible state. The birth and death rates are assumed to be equal, resulting in a constant total population in the SIS model. The total population, N, in this model is represented by the sum of the susceptible and infected individuals, $N(t) = S(t) + I(t)$.

The differential equation system for the SIS model, as proposed by Kermack and Mckendrick (Brauer, 2005), is given in Eq. 4:

$$\begin{cases} \frac{dS(t)}{dt} &= -\beta S(t)I(t) + \gamma I(t) \\ \frac{dI(t)}{dt} &= \beta S(t)I(t) - \gamma I(t) \end{cases} \tag{4}$$

where β is the spread rate of the disease and γ is the recovery rate. The initial conditions are given by $S(0) = s_0$ and $I(0) = i_0$, with $\beta > 0$, $i_0 > 0$, and $s_0 > 0$. In contrast to the SIR model, recovered individuals can be re-infected and return to a susceptible state at a rate of γI.

The analytical solution for this model is expressed as given in Eq. 5

$$\begin{cases} I(t) &= \frac{\alpha}{\beta+\alpha Ce^{-\alpha t}} \\ S(t) &= N(t) - \frac{\alpha}{\beta+\alpha Ce^{-\alpha t}} \end{cases} \tag{5}$$

where $\alpha = \beta N - \gamma$ and $C = \frac{\alpha - i_0\beta}{\alpha i_0}$. For the proof of this solution we refer to (Ahmad, 2021).

This study uses the SIS model, along with a neural network model Net, to predict the course of an outbreak. The Net is trained using the Extreme Learning Machine algorithm, which will be further described in a later section. These models are considered basic models, but there are also more advanced models that can estimate the number of deaths, the number of people recovering after vaccination, and the spread rate of the outbreak.

4 The proposed approach for solving compartmental models in epidemiology

The basic idea is to use two-stage neural networks to predict disease transmission in an efficient and more accurate way, in this study. The first neural network is designed as a feed-forward neural network, which processes data by passing it through a series of layers. Each layer contains a set of neurons, which are interconnected with the neurons in the adjacent layers. The input layer receives the raw data and each subsequent layer processes the data and passes it to the next layer until the final output layer produces a result.

The neurons in the feed-forward neural network are typically organized into layers, with each layer having a specific function. The first layer is called the input layer, and it receives the raw data. The last layer is called the output layer, and it produces the network's final output. In between the input and output layers, there can be one or more hidden layers, each of which performs some intermediate processing on the data.

As an example, consider a feed-forward neural network with one inner/hidden layer shown in Figure 1. ω_k and Ω_k values represent the weights of the connection between the input layer and the hidden layer, and α_k values represent the weights of the connection between the hidden layer and the output layer for $k = 1, 2, \ldots, m$. Similarly, $\eta_{1,k}$ values are the bias values of the neurons in the hidden layer and η_2 is the bias for the output of the network whereas σ represents the activation function. The output of this neural network can be given as:

$$Net(t_j, s_j, i_j, \vec{p}) = \sum_{k=1}^{m} \alpha_k \sigma(\omega_k s_j + \Omega_k i_j \eta_{1,k}) + \eta_2 \tag{6}$$

where $\vec{p} = (\vec{\alpha}, \vec{\omega}, \vec{\Omega}, \vec{\eta_1}, \eta_2) \in \mathbb{R}^{4m+1}$ such that $\vec{\alpha} = (\alpha_1, \alpha_2, \ldots, \alpha_m)$, $\vec{\omega} = (\omega_1, \omega_2, \ldots, \omega_m)$, $\vec{\Omega} = (\Omega_1, \Omega_2, \ldots, \Omega_m)$, $\vec{\eta_1} = (\eta_{1,1}, \eta_{1,2}, \ldots, \eta_{1,m}) \in \mathbb{R}^m$ and, $\eta_2 \in \mathbb{R}$ are the unknown weights of the network.

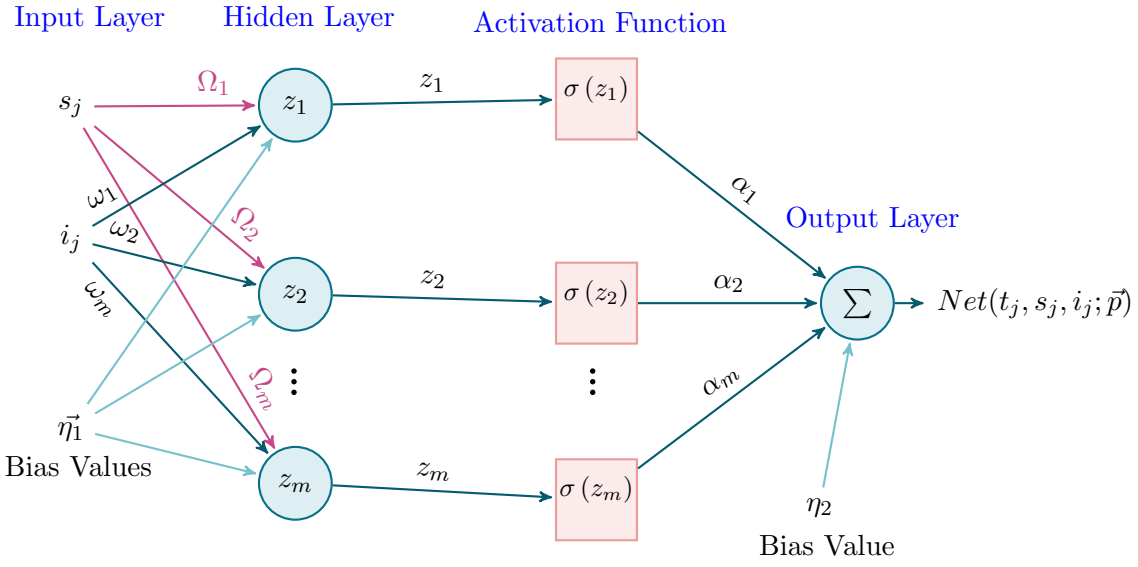


Figure 1: Structure of the feed-forward neural network for solving SI and SIS epidemic model.

In this study, the mentioned feed-forward neural network is defined as a part of trial solution to define a compartmental model in mathematical epidemiology. To find the solution set for the compartmental model described in Eqs. 2 and 4 over the interval $[a, b]$, trial functions that depend on the approximate solution generated by an artificial neural network and satisfy the initial conditions are used (Meade & Fernandez, 1994).

These trial functions are given Eq. 7 for predicting the rate of Susceptible and Infected person in a population respectively.

$$\begin{cases} S_T(t_j, s_j, i_j) &= s_0 + (t_j - t_0) \cdot Net(t_j, s_j, i_j, \vec{p_s}) \\ I_T(t_j, s_j, i_j) &= i_0 + (t_j - t_0) \cdot Net(t_j, s_j, i_j, \vec{p_i}) \end{cases} \tag{7}$$

where the points obtained from the partition of the interval $[t_0, t_n]$ are given by $t_j = t_0 + j$, with a constant step size of $h = 1$, whereas $j = 0, 1, \ldots n$. These t_j are used for the training of the network. Furthermore, s_j and i_j are the real observed susceptible and infected people ratios respectively at time t_j. Moreover, n represents the total number of inputs whereas $\vec{p_s}$ and $\vec{p_i}$ are the unknown parameters of the network. Which include the connection weights and threshold values between the neurons in the network. The size of these vectors depends on the number of neurons in the hidden layers of the network.

Now, let us assume that the network has an input layer, a hidden layer and an output layer. Then, the output of the neural network Net is given in Eq. 8 for the inputs $s, i \in \mathbb{R}$ at iteration $t \in \mathbb{Z}^+$.

$$Net(t_j, s_j, i_j, \vec{p}) = \sum_{k=1}^{m} \alpha_k . \sigma(z_k) + \eta_2 \tag{8}$$

where $z_k = \omega_k . s_j + \Omega_k . i_j + \eta_{1,k}$ such that ω_k and Ω_k represent the connection weights between the input layers and the hidden layer, α_k values represent the connection weights between the hidden layer and the output layer, and $\eta_{1,k}$ are the bias values of the hidden layer whereas η_2 is the bias value of the output layer. At this point, it should be emphasized that the inputs in Eq. 8 are assumed to be time-varying functions as $s_j = s(t_j)$ and $i_j = i(t_j)$. Furthermore, the function $\sigma(.)$ represents the activation function as the sigmoid function defined in Eq. 9

$$\sigma(x) = \frac{1}{1 + e^{-x}} \tag{9}$$

where x is the input to the function.

After constructing the feed-forward network model, the weights of this network are tuned by an Extreme Learning Machine (ELM) to obtain more robust result. The main idea of the training phase of the model is based on the thought that the trial functions given in Eq. 7 satisfy the epidemiology model defined with the system of the differential equations given in Eq. 2. At this point, we will use the notation $\hat{S}_j = S_T(t_j, s_j, i_j)$, $\hat{I}_j = I_T(t_j, s_j, i_j)$ and $\mathcal{N}_j(\vec{p}) = Net(t_j, s_j, i_j, \vec{p})$ for simplicity throughout the remainder of the article. So, the derivatives of trial functions in Eq. 7 as given in the Eq. 10.

$$\begin{cases} \frac{\partial S_T}{\partial t_j} &= \mathcal{N}_j(\vec{p_s}) + (t_j - t_0) \frac{\partial \mathcal{N}_j(\vec{p_s})}{\partial t_j} \\ \frac{\partial I_T}{\partial t_j} &= \mathcal{N}_j(\vec{p_i}) + (t_j - t_0) \frac{\partial \mathcal{N}_j(\vec{p_i})}{\partial t_j} \end{cases} \tag{10}$$

where

$$\frac{\partial \mathcal{N}_j(\vec{p})}{\partial t_j} = \sum_{k=1}^{m} \alpha_k \left(\omega_k \frac{d\hat{S}_j}{dt_j} + \Omega_k \frac{d\hat{I}_j}{dt_j} \right) \sigma(z_k)(1 - \sigma(z_k)) \tag{11}$$

for $j = 1, \ldots, n$.

If the derivatives of $\frac{d\hat{S}_j}{dt_j}$ and $\frac{d\hat{I}_j}{dt_j}$ in Eq. 11 are calculated numerically as following

$$\frac{d\hat{S}_j}{dt_j} = \frac{\hat{S}_{j+1} - \hat{S}_{j-1}}{2}$$

and

$$\frac{d\hat{I}_j}{dt_j} = \frac{\hat{I}_{j+1} - \hat{I}_{j-1}}{2},$$

and if the Eqs. 7 and 10 are substituted in Eqs. 2 for $j = 2, 3, \ldots, n-1$, we obtain a system of equations depending on the unknown weights of Net as $\vec{p}_s$ and $\vec{p}_i$ after some arrangements. Firstly, these weights are initialized randomly except for the weights α_k coming to the output layer. Then, the problem turns to finding the optimal values of α_k as shown in Eq. 12.

$$\sum_{k=1}^{m} \alpha_k . \left\{ 1 + (j+1) \left(\frac{\hat{S}_{j+1} - \hat{S}_{j-1}}{2} \omega_k + \frac{\hat{I}_{j+1} - \hat{I}_{j-1}}{2} \Omega_k \right) \sigma(z_k)(1 - \sigma(z_k)) \right\} = -\frac{\beta}{N} \hat{S}_j \hat{I}_j \quad (12)$$

The system is equivalent to the following system in matrix notation shown in Eq. 13,

$$\mathbf{H}.\mathbf{X} = -\frac{\beta}{N}\mathbf{F} \quad (13)$$

Since $\mathbf{H}$ is not a square matrix, the connection weights between the hidden layer and the output layer can be calculated via the Moore-Penrose generalized inverse of matrix $\mathbf{H}$ using the Eq. 14.

$$\mathbf{X} = -\frac{\beta}{N} pinv(\mathbf{H}).\mathbf{F} \quad (14)$$

where $\mathbf{H}$ is the matrix of order $(n-1) \times m$, $\mathbf{X}$ is order of $m \times 1$ and $\mathbf{F}$ is the matrix of order $(n-1) \times 1$ defined as follows.

$$\mathbf{X} = \begin{pmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_m \end{pmatrix}, \ \mathbf{F} = \begin{pmatrix} \hat{S}_1 \hat{I}_1 \\ \hat{S}_2 \hat{I}_2 \\ \vdots \\ \hat{S}_{n-1} \hat{I}_{n-1} \end{pmatrix},$$

and $\mathbf{H}$ is defined in Eq. 15 for $j = 1, 2, \ldots, n-1$.

$$\mathbf{H} = \begin{bmatrix} \sigma(z_1)\left(1 + 2(1-\sigma(z_1))\left(\frac{\hat{S}_2 - \hat{S}_0}{2}\omega_1 + \frac{\hat{I}_2 - \hat{I}_0}{2}\Omega_1\right)\right) & \cdots & \sigma(z_m)\left(1 + 2(1-\sigma(z_m))\left(\frac{\hat{S}_2 - \hat{S}_0}{2}\omega_m + \frac{\hat{I}_2 - \hat{I}_0}{2}\Omega_m\right)\right) \\ \sigma(z_1)\left(1 + 3(1-\sigma(z_1))\left(\frac{\hat{S}_3 - \hat{S}_1}{2}\omega_1 + \frac{\hat{I}_3 - \hat{I}_1}{2}\Omega_1\right)\right) & \cdots & \sigma(z_m)\left(1 + 3(1-\sigma(z_m))\left(\frac{\hat{S}_3 - \hat{S}_1}{2}\omega_m + \frac{\hat{I}_3 - \hat{I}_1}{2}\Omega_m\right)\right) \\ \vdots & \ddots & \vdots \\ \sigma(z_1)\left(1 + n(1-\sigma(z_1))\left(\frac{\hat{S}_n - \hat{S}_{n-2}}{2}\omega_1 + \frac{\hat{I}_n - \hat{I}_{n-2}}{2}\Omega_1\right)\right) & \cdots & \sigma(z_m)\left(1 + n(1-\sigma(z_m))\left(\frac{\hat{S}_n - \hat{S}_{n-2}}{2}\omega_m + \frac{\hat{I}_n - \hat{I}_{n-2}}{2}\Omega_m\right)\right) \end{bmatrix} \quad (15)$$

In this paper, the theory of the proposed method is given only for the SI model. One can easily adopt the proposed process by substituting the Eqs. 7 and 10 in Eq. 4 for SIS model.

5 Numerical demonstration

In this section, the epidemiological models mentioned in the study have been adapted to COVID-19 dynamics. To achieve this goal, data published by the Turkish Ministry of Health on their website has been used. A web crawling script is created to obtain the data from the website. Data collected between November 27, 2020 and April 24, 2021 has been considered in the study.

During the experimental studies, the S value represents the daily number of cases, the I value represents the daily number of patients. The numerical solutions of the SI and SIS models have been obtained using the proposed approach in the study.

In the proposed model, the first day is specified as November 27, 2020, and the daily data is accepted as input to the network. The other days are numbered in increasing order and presented as input to the network. Therefore, given that the input to the network is the t-th

day, the network provides one or more outputs according to the model. Since different amounts of data are obtained every day, the population count is a value that changes over time.

In this study, to ensure the healthy functioning of the models, the daily positive case numbers, the numbers of infected and recovered individuals are normalized by dividing them by the total population count. Therefore, in all experimental studies, the population count is taken as 1. The normalized positive case counts indicate the rate of individuals who tested positive for Covid-19 in the total population. Similarly, normalized numbers of infected is also indicated as ratios.

Unlike most studies in the literature, the values for the transmission coefficient β and the recovery coefficient γ, which are defined in the models, have not been determined as constants. In this study, these values have been obtained using the Least Squares curve fitting method as a function of time.

In this study, the proposed model is first trained using daily cases that are officially announced by the Turkish Ministry of Health for 120 consecutive days. In the test phase, in order to measure the performance of the proposed model, the rates of daily cases observed during the four weeks following the 120th day were compared with the results produced by the proposed model. In Table 1a and Table 1b, S_k and I_k represent the normalized number of susceptible and infected on $t_k - th$ day respectively. These are numerical solutions obtained by the model proposed in the study. Also, the absolute error between these numerical solutions and the actual solutions are given in Table 1a and Table 1b. Figure 2a and Figure 2b give the prediction for 4 weeks (28 days) using SI and SIS model respectively.

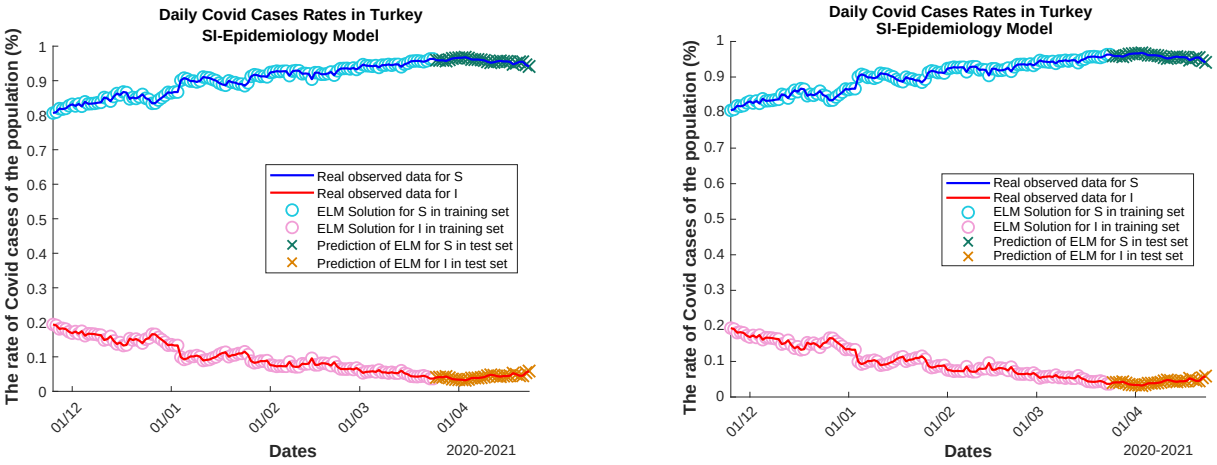
Table 1: The numerical solution of epidemic models via ELM for test set

(a) SI model

Day(k)	t_k	S_k	I_k	**Absolute Errors**
1	121	0.960	0.040	9.243×10^{-11}
2	122	0.959	0.041	9.232×10^{-11}
3	123	0.959	0.041	9.237×10^{-11}
4	124	0.957	0.043	9.212×10^{-11}
5	125	0.961	0.039	9.257×10^{-11}
6	126	0.964	0.036	9.301×10^{-11}
7	127	0.966	0.034	9.315×10^{-11}
8	128	0.966	0.034	9.324×10^{-11}
9	129	0.966	0.034	9.325×10^{-11}
10	130	0.968	0.032	9.344×10^{-11}
11	131	0.965	0.035	9.312×10^{-11}
12	132	0.961	0.039	9.265×10^{-11}
13	133	0.961	0.039	9.262×10^{-11}
14	134	0.961	0.039	9.264×10^{-11}
15	135	0.960	0.040	9.251×10^{-11}
16	136	0.959	0.041	9.231×10^{-11}
17	137	0.955	0.045	9.184×10^{-11}
18	138	0.952	0.048	9.153×10^{-11}
19	139	0.953	0.047	9.167×10^{-11}
20	140	0.956	0.044	9.200×10^{-11}
21	141	0.957	0.043	9.215×10^{-11}
22	142	0.956	0.044	9.196×10^{-11}
23	143	0.956	0.044	9.198×10^{-11}
24	144	0.955	0.045	9.184×10^{-11}
25	145	0.947	0.053	9.095×10^{-11}
26	146	0.951	0.049	9.135×10^{-11}
27	147	0.955	0.045	9.184×10^{-11}
28	148	0.955	0.045	9.185×10^{-11}
Mean Squared Error for S : 8.500×10^{-21}				
Mean Squared Error for I: 8.500×10^{-21}				

(b) SIS model

Day(k)	t_k	S_k	I_k	**Absolute Errors**
1	121	0.960	0.040	1.098×10^{-8}
2	122	0.959	0.041	1.096×10^{-8}
3	123	0.959	0.041	1.097×10^{-8}
4	124	0.957	0.043	1.094×10^{-8}
5	125	0.961	0.039	1.099×10^{-8}
6	126	0.964	0.036	1.105×10^{-8}
7	127	0.966	0.034	1.106×10^{-8}
8	128	0.966	0.034	1.107×10^{-8}
9	129	0.966	0.034	1.107×10^{-8}
10	130	0.968	0.032	1.110×10^{-8}
11	131	0.965	0.035	1.106×10^{-8}
12	132	0.961	0.039	1.100×10^{-8}
13	133	0.961	0.039	1.100×10^{-8}
14	134	0.961	0.039	1.100×10^{-8}
15	135	0.960	0.040	1.099×10^{-8}
16	136	0.959	0.041	1.096×10^{-8}
17	137	0.955	0.045	1.091×10^{-8}
18	138	0.952	0.048	1.087×10^{-8}
19	139	0.953	0.047	1.089×10^{-8}
20	140	0.956	0.044	1.093×10^{-8}
21	141	0.957	0.043	1.094×10^{-8}
22	142	0.956	0.044	1.092×10^{-8}
23	143	0.956	0.044	1.092×10^{-8}
24	144	0.955	0.045	1.091×10^{-8}
25	145	0.947	0.053	1.080×10^{-8}
26	146	0.951	0.049	1.085×10^{-8}
27	147	0.955	0.045	1.091×10^{-8}
28	148	0.955	0.045	1.091×10^{-8}
Mean Squared Error for S : 1.199×10^{-16}				
Mean Squared Error for I: 1.199×10^{-16}				



(a) SI model **(b)** SIS model

Figure 2: Prediction of Susceptible and Infected People ratios using Net

6 Conclusion

In this study, Feed forward neural network based model is proposed to predict the course of the COVID-19 pandemic. A multi-layer perceptron is used, and the data published by the Ministry of Health of the Republic of Turkey is used for training the network by Extreme Learning Machine. Thus, models that are compatible with the SI and SIS models and dependent on real observed values were attempted to be created. All approaches that attempt to predict COVID-19 data using artificial neural networks in the literature produce solutions independent of epidemic models. In other words, the cost function of the network is only expressed in terms of the squares of the output generated by the network and the observed data. This is the most fundamental difference that distinguishes our study from others.

From the results, we can conclude that the proposed model has successfully provided an accurate prediction for the course of the pandemic. Our proposed model is flexible enough to incorporate the effect of containment policies, such as lockdowns or the use of protective masks, and can be easily adapted to future epidemics. Therefore, it should be adapted to more realistic Susceptible-Infected-Recovered SIR and $SEIR$ Susceptible-Exposed-Infected-Recovered models as future works.

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Author Contributions

M.J. Ahmad collected and verified the data. K. Günel conceived of the proposed idea and supervised the project. M.J. Ahmad and K. Günel developed the theory and implemented the related codes together. M.J. Ahmad performed the numerical simulations. Both of the authors carried out the results of the experiments and writing to this manuscript.

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