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Original Article

Artificial intelligence-enabled rapid and symptom-based medication recommendation system (COV-MED) for the COVID-19 patients

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Abstract

In a general COVID-19 population in Cox's Bazar, Bangladesh, we developed a medication recommendation system based on clinical information from the electronic medical record (EMR). Our goal was also to enable deep learning (DL) strategies to quickly assist physicians and COVID-19 patients by recommending necessary medications. The general demographic data, clinical symptoms, basic clinical tests, and drug information of 8953 patients were used to create a dataset. The learning model in this COVID-MED model was created using Keras (an open-source artificial neural network library) to solve regression problems. In this study, a sequential model was adopted. In order to improve the prediction capability and achieve global minima quickly and smoothly, the COVID-MED model incorporates an adaptive optimizer dubbed Adam. The model calculated a mean absolute error of 0.0037, a mean squared error of 0.000035, and a root mean squared error of 0.0059. The model predicts the output medications, such as injections or other oral medications, with around 99% accuracy. These findings show that medication can be predicted using information from the EMR. Similar models allow for patient-specific decision support to help prevent medication errors in diseases other than COVID-19.

Keywords: COVID-19, Electronic Medical Records, Artificial Neural Networks, Machine Learning, Deep Learning, Artificial Intelligence, Bangladesh

Background

Global healthcare and biomedical research are progressively changing with artificial intelligence (AI) advancement. In fact, medicine was identified before as one of the most potential and promising AI application domains. The application of AI is being extensively used in areas previously regarded as solely the domain of human expertise [1]. Recently, the AI revolution has been fueled largely by the successful application of deep learning systems, which entails training an artificial neural network (ANN) with many layers on massive datasets to large sources of labeled data [1]. AI systems outperform physicians in numerous diagnostic tasks, can estimate patient prognosis better than clinicians and can aid in surgical treatments as well. As machine learning (ML) models improve, there is a growing belief that AI will change medical practice, redefining clinicians' responsibilities in the process [1,2,3]. The pandemic coronavirus disease (COVID-19) started affecting the global population in 2020 and is continuing to rise at a rapid pace with constantly changing variants. Though a handful of vaccines have come as of today, there is no permanent remedy yet. People are being hospitalized daily, and many are joining the death rally as a result of COVID-19. Due to the difficulties and sufferings of this novel disease, health professionals, patients, and their families have been compelled to make challenging and crucial decisions quickly and with minimal information. Given the priority of these situations, followed by the growing number of cases, an accurate and reliable tool based on existing healthcare resources is greatly warranted [4]. Advanced technologies such as ML and AI could better understand patient subgroups, drive clinical decision-making, and improve operational and patient-centered outcomes [4]. In consequence, ML algorithms could combine and analyze large-scale data

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from COVID-19 patients to better comprehend more successful therapeutic approaches and potentially identify the most vulnerable groups based on personalized, genetic, and physiological traits. The substantial amount of COVID-19 treatment data in hospitals worldwide requires the use of advanced ML and DL methods to analyze it to discover and predict new therapeutic options that could provide better care for each patient and contribute to local hospital arrangements and operations [5]. In addition, AI can answer different queries of the patient in the absence of doctors [6]. Aiding the appropriate medications in emergency conditions is critical in fighting this global battle [7]. Projecting the proper medications for the desired patients might alleviate the enormous strain placed on doctors and nurses. In contrast, ML and AI will save time and also provide patients with accurate medication administration instructions. Besides, it is also helpful if lockdowns were implemented and people were required to stay at home and want to take essential precautions and medications against coronavirus symptoms. Electronic medical records (EMRs), which store information about health conditions, diagnoses, and treatment methods, are excellent resources for optimizing clinical care through alerts, reminders, recommendations, and other forms of clinical decision support [8]. Patients with the same disease always have inter-individual symptoms, medications, treatments, and health conditions in common [8]. In this present work, we used EMRs to attain the objectives. Though the system requires supervisory confirmation, the model's amazing accuracy ensures dependence on the system and can get essential approvals to be introduced in practical sectors. The significance of this initiative demonstrates AI advancements in medical sciences as well as humanitarian relief. Considering all the aforementioned issues, the current research work was aimed:

a) To develop an AI-based model for the prediction and recommendation of medications for COVID-19 patients based on the input data using the ANN, and

b) To build a robust prediction model (COVID-MED), enabling deep learning (DL) strategies that can help the physicians as well as the COVID-19 patients quickly by recommending necessary medications.

Methods

Study design

A structured dataset including necessary features connected to the article objectives is required to materialize the idea of suggesting the necessary medications based on the symptoms of COVID-19-affected individuals. Following that, the ANN architecture, ML & DL approach will take over the responsibility for developing a model that will be supervised by the available dataset and predict the required output feature, which is nothing more than the drugs for the affected patients. A basic ML perceptron is illustrated in Figure 1.

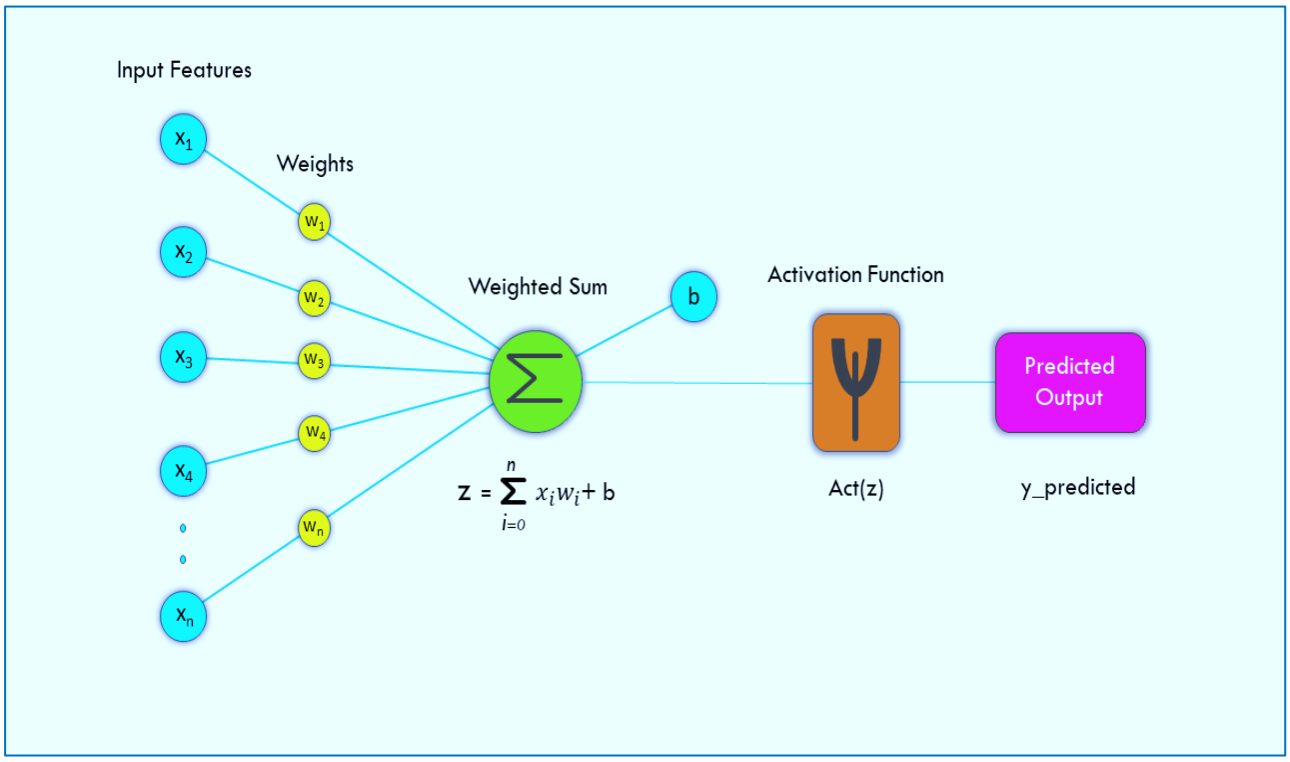

Figure 1: Basic ML Perceptron

Data Collection and Preparation Techniques for COVID-MED Model

Data are the characteristics or information, usually numerical, that are collected through observation [9]. The first and most important stage in constructing a machine learning or deep learning model is to preprocess data, which starts the process. The data used in this COVID-MED model has undergone several significant steps known as preprocessing in machine learning and neural networks. Figure 2 illustrates the data preprocessing stages, beginning with data acquisition and ending with processed and extracted features that are ready to be input into the model. Detailed information about the preprocessing steps that have been carried out in this proposed model is provided below.

Data Collection and Preparation Techniques for COVID-MED Model

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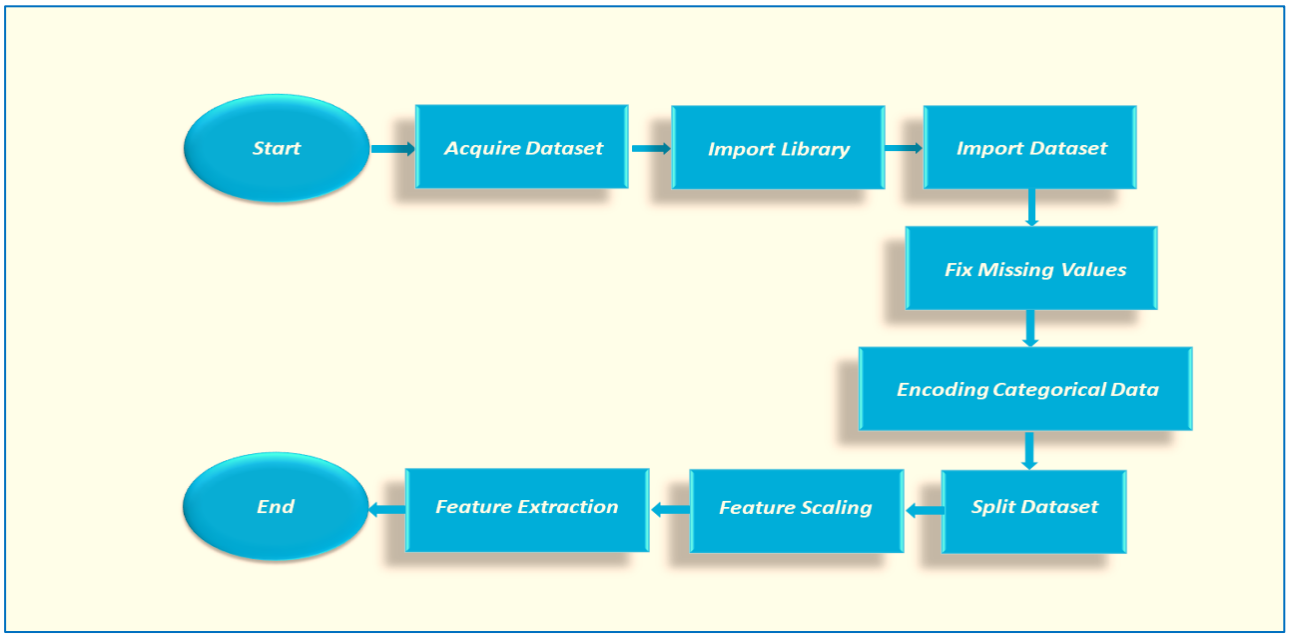

Figure 2: Flowchart for data preprocessing

Dataset Acquisition

To keep up with the ever-improving deep learning models, a suitable dataset needs to obtain initially. In this article, a dataset was obtained from the previous record of 8953 patients who were admitted to the 1) specialized COVID unit in the Cox's Bazar Medical College and Hospital, Bangladesh, 2) Sadar Isolation Center, Cox's Bazar, Bangladesh, and 3) Ramu Isolation Center, Cox's Bazar, Bangladesh. The data was collected between October 2020 and October 2021. This dataset included general demographic data, different symptoms before and after the hospitalization, a variety of basic clinical tests, as well as therapies and drugs used throughout their hospital stay. A questionnaire and clinical records were used to gather and organize data. Figure 3 represents the COVID-MED dataset that is comprised of various features. From the criteria mentioned above, medication ('injection and oral') is supposed to be predicted by the model using the other features as the supervisory input features. On the other hand, Table 1 shows the variables that were used in the analysis.

Age	Gender	Weight	Height (cm)	Smoker	Vaccination	Associated diseases	Suffered (Days)	Symptometic/A symptometic	Severity	Symptoms	Highest Temp (°F)	Complications after admission	Clinical tests							Treatment (medicine & injection)
													Hb	ESR	TC	N	L	PLT	Lowest O2 level	
25	M	71	172.72	No	No	No	3	Symptometic	Moderate	O	101	No	16.5	32	5700	71	25	230000	0.95	A
40	M	76	170.18	No	No	No	7	Symptometic	Moderate	I	104	No	16	33	5500	70	25	430000	0.95	A
52	M	68	170.18	Yes	No	Diabetic	7	Symptometic	Moderate	L	101	No	13.2	101	4220	62	32	185000	0.95	A
52	M	71	165.1	Yes	No	No	7	Symptometic	Moderate	N	101	No	15.2	35	5100	68	30	220000	0.96	A
57	M	74	170.18	No	No	Diabetic	7	Symptometic	Moderate	A	101	No	10.01	118	7000	65	62	288000	0.95	B
65	M	76	170.18	Yes	Yes	Hbs/Ag (+ve)	5	Symptometic	Mild	A	100	Yes	13	47	5500	67	26	206000	0.97	C
30	F	56	157.48	No	No	No	10	Symptometic	Moderate	A	104	No	11.8	80	13000	80	16	250000	0.96	A
35	F	50	157.48	No	No	No	14	Symptometic	Moderate	A	102	No	12.4	78	13500	85	15	220000	0.97	D
50	F	64	157.48	No	1st dose	No	10	Symptometic	Moderate	A	104	Yes	12.1	43	5300	68	18	185000	0.95	D
35	F	51	160.02	No	No	No	5	Symptometic	Moderate	A	102	No	12.1	60	4700	60	18	386000	0.90	C
56	F	52	154.94	No	Yes	HTN	7	Symptometic	Moderate	I	102	No	10.8	83	4000	54	38	300000	0.93	B
59	F	73	160.02	No	No	HTN, Asthma	3	Symptometic	Severe	S	104	Yes	12.1	43	5300	68	18	185000	0.94	A
55	F	69	160.02	No	No	HTN	3	Symptometic	Moderate	C	101	No	12	22	5600	58	30	180000	0.90	E
56	F	57	157.48	No	No	Asthma	7	Symptometic	Moderate	B	102	No	13.4	17	5600	55	37	180000	0.90	A
65	F	68	157.48	No	Yes	Asthma	8	Symptometic	Moderate	A	102	No	13	47	1300	78	19	298000	0.96	F
60	M	63	170.18	No	No	No	8	Symptometic	Moderate	C	102	No	13.5	88	4500	66	30	245000	0.95	G
62	M	64	167.64	No	No	No	6	Symptometic	Moderate	L	102	No	11	81	11800	80	16	223500	0.98	A
32	M	50	170.18	No	No	Hbs/Ag (+ve)	2	Symptometic	Mild	S	102	No	12.6	78	5800	64	32	400000	0.99	H
54	M	66	170.18	No	Yes	HTN	7	Symptometic	Moderate	A	102	No	12	83	4800	72	28	400000	0.95	D
31	M	58	162.56	No	No	No	7	Symptometic	Moderate	B	102	No	15.1	10	7500	76	20	300000	0.98	A

Figure 3: COVID-MED Dataset

Table 1. Characteristics of the acquired baseline and clinical data

Variable	All (n=8953)
Age	47.2 ± 11.4
Gender	Male=5211, Female=3742
Weight (kg)	66.5 ± 6.8
Height (cm)	163.8 ± 5.6
Smoker	Male=4123, Female=22, Non-smoker=4808
Vaccination status	Yes=2711, No=6242
Suffered with symptoms before admitting into the hospital (days)	6.8 ± 2.8
Symptomatic/ Asymptomatic	Symptomatic= 8112, Asymptomatic=841
Severity	Severe=328, Mild=2547, Not severe=6078
Highest body temperature (F)	101.6 ± 1.6
Hemoglobin (Hb), g/dL	12.4 ± 2.2
Erythrocyte sedimentation rate (ESR), mm/hr	59.5 ± 24.5
Total count (TC), wbc/mcL	7065 ± 2057
Neutrophils (N), cells/mcL	66.5 ± 10.2
Lymphocytes, %	27.9 ± 9.2
Platelet count (PLT)	248700 ± 55920
Lowest oxygen level during hospital staying.	0.94 ± 0.04
Clinical symptoms included (symptoms were classified as shown in Figure 3)	Fever, cough, cough with sputum, weakness, sore throat, diarrhea, and shortness of breath (SOB)
Associated diseases included	Diabetes, asthma, hypertension, hypotension, cardiovascular diseases (CVD), arthritis, anemia, chronic obstructive pulmonary disease (COPD), hypothyroidism, GOUT, pulmonary tuberculosis, acute kidney injury (AKI), benign prostatic hyperplasia (BPH), hepatitis B, and acute pyelonephritis.
Injections used for treatment	Low molecular weight heparins, steroids, antivirals, antibiotics, insulin, loop diuretics, and anti-emetics.
Medication (oral) used for treatment	Leukotriene receptor antagonists (LTRAs), antiulcerants, non-steroidal anti-inflammatory drugs (NSAIDs), antihistamines, antivirals, antibiotics, anxiolytic, vitamin supplements, cough suppracents, relaxants, antihypertensives, calcium antagonists, and anti-diabetic.

Importing Crucial Libraries

Python now offers a framework that provides the most comprehensive collection of chosen libraries by prominent data scientists. As a result, the platform has served as the foundation for this evolutionary effort, and numerous library functions have been built to enable the COVID-MED model to be executed.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

The three core predetermined libraries used for the preprocessing tasks are NumPy, Pandas, and Matplotlib.

Importing the Dataset

At this step, the obtained dataset is imported for the deep learning model to be constructed. Data is typically saved in a csv or excel file format that is easily imported by python libraries.

```
From Google. colab import drive
drive.mount('/content/drive')
data=pd.readexcel('drive/My
Drive/Injections_Manipulated.xlsx')
```

These lines of commands were implemented to import the dataset through the python library using Google Colaboratory notebook.

Identifying and Handling the Missing Values

After importing the dataset, it is pivotal to identify and correctly handle the missing values to make the model output efficient because missing values hampers the model's efficiency by creating a void in the calculations. As the data-obtaining process from the hospitals was successive in nature, there were hardly any missing values in the whole dataset. However, the dataset was handled and scrutinized for these kinds of error detection. Finally, to cross-check the null values following commands were run, which provided the satisfactory statement that the dataset was continuous.

```
data.isnull().sum()
```

Encoding the Categorical Data

Neural network and deep learning models are fundamentally based on mathematical equations. In the dataset cited above, there are several categorical variables such as 'Associated Diseases', 'Symptoms', 'Severity', 'Medications' and so on. So, the categorical features need to be encoded in a numerical format for being able to be analyzed by the COVID-MED model [10]. Here is how some categorical data have been encoded in the COVID-MED model. 'x' is represented as categorical input features.

```
From sklearn.preprocessing import LabelEncoder
lbl = LabelEncoder()
data['x'] = lbl.fit_transform(data['x'])
```

Here, the categorical features were encoded in corresponding numerical formats by the aforementioned lines of codes. It simply converted the data into a numerical form which is easily detectable by the neural network model.

Dataset Splitting

ML & DL models must split datasets into two separate sections, such as training and test sets, to ensure the dataset's relevant training and testing phase. The suggested model maintains a 70:30 ratio to train and test the data. The proposed model incorporated the train_test_split library to execute the task.

Feature Scaling

Feature scaling allows for comparison on common ground in order to narrow the range of variables. Deep learning makes it possible to apply a variety of scaling approaches. The 'Normalization' technique to scale the imported dataset has been used in this research work.

$$X' = \frac{X - \min(X)}{\max(\ ) - \min(X)} \quad (1)$$

Where,

X^'=New Value,

X=Old Value [11]

By normalizing the dataset, all the data points were renovated to a format that ranges from 0 to 1. It is much more convenient and efficient to deal with the numbers for a model which ranges in a minimalistic scale. Dealing with large digits was cumbersome and might make the model slow to perform. As far as it does not change the original information, it is logical to scale the dataset to obtain maximum efficiency.

Feature Selection

The process of automatically or manually picking characteristics that contribute the most to forecasting the variable or output the model is interested in is known as feature selection. Prominent techniques which have been incorporated for selecting features in this COVID-MED model are univariate selection and correlation with heatmap. Univariate selection measures the compatibility rank of the input features compared with the output feature. As a regression problem is being analyzed in this model, therefore "f_regression" score function is introduced to determine the best features. It works on selecting the best features according to the data points that fit the best line among all the features. Among the total 21 features, 19 prominent features are chosen using univariate selection, which ranks the features based on their importance to the output. On the other hand, correlation measures the relation among the features. Correlation states how the features are related to each other or the target variable. Correlation can be positive (an increase in one value of a feature increases the value of the target variable) or negative (an increase in one value of the feature decreases the value of the target variable). There are various correlation techniques, such as Pearson, Kendall, Spearman, etc. In this problem, the Pearson correlation technique is being used. The least correlated features among the inputs and the highly correlated features with the target output are chosen to be fed into the model. Heatmap easily identifies which features are most related to the target variable. Following that, the correlations between the features were determined, and lastly, the selection criteria chose 15 unique and essential features to train the model. A heatmap of correlated features using the seaborn library is represented in Figure 4.

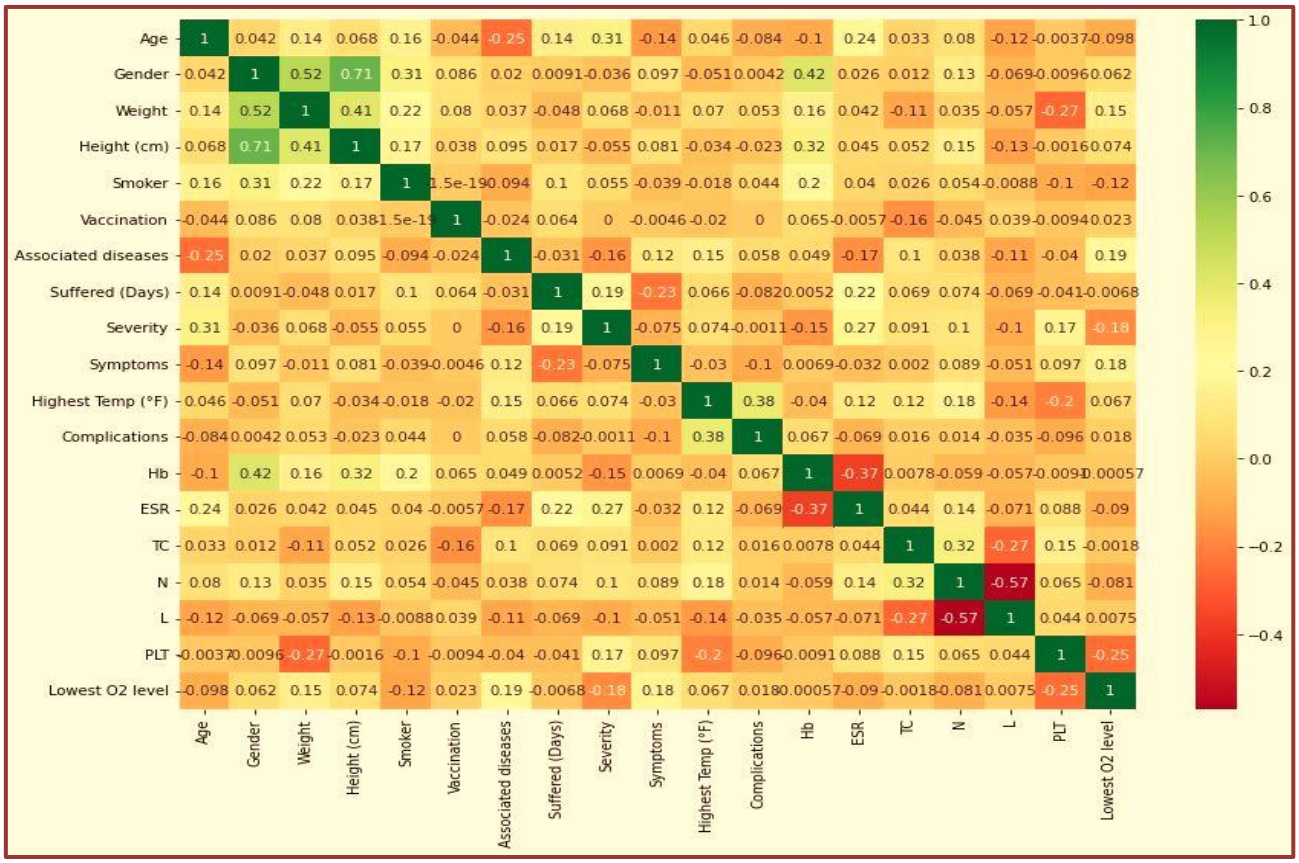

Figure 4: Correlation heat map between Input Features

Proposed COVID-MED Model

Deep Learning models are based on neural networks, whereas Keras is one of the most popular and user-friendly neural network libraries written in Python. In this proposed COVID-MED model, the learning model has been developed by using Keras to solve a regression problem. Two renowned ways to build and develop Keras models are sequential and functional. The sequential API consists of creating a model layer-by-layer for the majority of problems. On the contrary, the functional API enables the creation of models with significantly greater flexibility, allowing models to readily decide where layers relate to more than only the previous and next levels [12]. In this study, a Sequential model was adopted. It is made up of a single dense input layer with 64 neurons. The input layer is followed by three hidden layers with 32, 16, and 8 neurons, respectively, with multiple neural connections. Finally, they all deducted in predicting the outputs in a single neuron.

Notably, the activation function utilized in each neural connection in this model is referred to as the rectified linear unit (ReLu). The ReLu activation function has been incorporated into this SDL model to commence the learning behavior. The main rationale for utilizing it is that it eliminates problems such as vanishing gradients and exploding gradients produced by sigmoid or hyperbolic activation functions. The defining curve concludes that ReLu ranges between 0 and the maximum value of inputs. That is, if the input value is negative, it returns 0; otherwise, if it is positive, it returns the same positive integer. As a result, in this COVID-MED model, the derivative for this range will always be 1. Negatives, on the other hand, will yield a zero derivative. The derivatives in this method do not vary between 0 and 0.25, thus rescuing from the difficulties of vanishing gradients and exploding gradients [13]. Furthermore, the COVID-MED model has integrated an adaptive optimizer dubbed Adam in order to improve the prediction capability and attain global minima quickly and smoothly. It gradually improves competence by lowering losses and estimating the change in weights and learning rates with gradient position, resulting in accurate output forecasts.

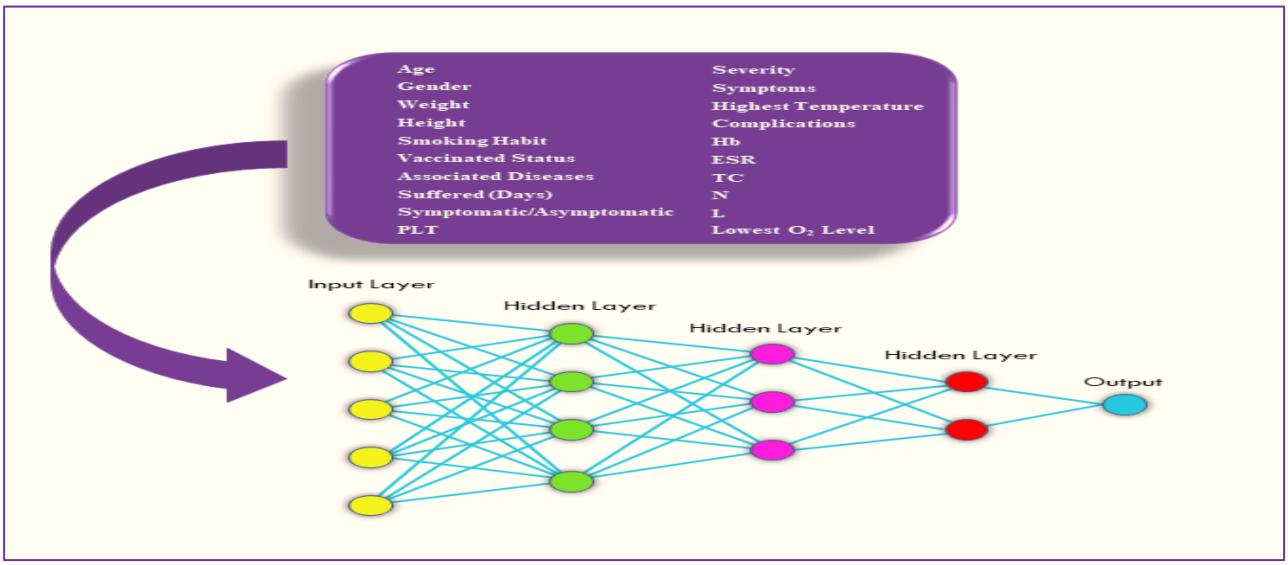

Figure 5: Neural Network Architecture for COVID-MED model

Algorithm for proposed COVID-MED model

Preprocess input features as 2.1

- number of samples: 1896, 70% for Training and 30% for Test;
- Training Set: train_x;
- Label of training data: train_y;

Architectural network of COVID-MED

- 64 input neurons, 3 hidden layers of 32, 16, and 8 neurons
- 1 output layer

Train neural network:

for i=1: numofepochs

kk-randperm(m);

% Introduces the ReLu activation function and Adam Optimizer

% Performs a feedforward pass

% Returns a net structure with updated weights

% Performs backpropagation pass

% Returns a net structure with the updated delta of weights

% Updates weights and biases with calculated gradients

% Returns a net structure with updated weights and biases

nn = nnapplygrads(nn);

end

end

Evaluate and test the neural network

Predict outputs and calculate errors

To delve deep into the characteristics and architecture of the proposed model, the following few lines illustrate the whole scenario of what has been implemented and how. The lines describe the model formulation and glimpse its possible outcomes.

```
import TensorFlow as tf
import DateTime, os
#from tensorflow.keras.callbacks import TensorBoard
#tensorboard = TensorBoard(log_dir='logs/ {}')
model = keras.models.Sequential()
model.add(keras.layers.Dense(64, activation='relu',
input_shape=(16,)))
model.add(keras.layers.Dense(32, activation='relu'))
model.add(keras.layers.Dense(16, activation='relu'))
model.add(keras.layers.Dense(8, activation='relu'))
model.add(keras.layers.Dense(1))
model.compile(optimizer= 'Adam', loss='mean_squared_error')
```

Results

To summarize what has been done so far, it can be said that the data was collected from 8953 patients across three hospitals where the mean age of subjects was 47.2 ± 11.4 years. The majority of the patients were male, and the majority of them did smoke. About 30% received the first or both doses of the COVID-19 vaccine. When they arrived at the hospital, most patients (about 90%) had some symptoms (Table 1). The clinical conditions of 328 patients have deteriorated during their hospital stay. Most of the patients have one or multiple associated diseases. Table 1 also includes a list of the medications used to treat these patients during their stays at these three hospitals. To validate the proposed COVID-MED model, a dataset comprising the affected patients' age, gender, height, weight, smoking habits, prevalent symptoms, associated diseases, different clinical test reports, medications used for treatments during the hospital stay, and so on was employed (Figure 3, Table 1). After the data was imported and fed into the suggested ML & DL-based model, it went through a series of preprocessing processes to help the prediction technique be more precise. Additionally, The COVID-MED model chooses the most significant features based on their relevance to the output feature, correlation with other features, and within the feature itself to produce a reliable forecast of the output medications. Soon after the data was prepared, a neural network model consisting of a single dense input layer with 64 neurons, followed by three distinct hidden layers with varying combinations of neural connections, was set up to predict the medications given to COVID-19 patients. Finally, the architecture deducts in predicting the output medication in a single neuron. Some outstanding results were discovered when the COVID-MED model was tested after it had been successfully implemented and trained. Parameters chosen for assessing the results are Mean Absolute Error (MAE), Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and R2 Score, where they resemble their usual expressions. A detailed elaboration of their executive computations can be found in Table 2.

Table 2. Accuracy & Error Measuring Parameters used in COV-MED

$MAE = \sum_{i=1}^{n} \frac{\lvert y_i - y_{pred} \rvert}{n}$	(1)
$MSE = \sum_{i=1}^{n} \frac{(y_i - y_{pred})^2}{n}$	(2)
$RMSE = \sqrt{\sum_{i=1}^{n} \frac{(y_i - y_{pred})^2}{n}}$	(3)
$R^2 = 1 - \frac{\sum(y_i - y_{pred})^2}{\sum(y_i - y_{mean})^2}$	(4)

Finally, it has provided a value for mean absolute error (MAE) of 0.0037, means squared error (MSE) of 0.000035, and 0.0059 roots mean squared error (RMSE).

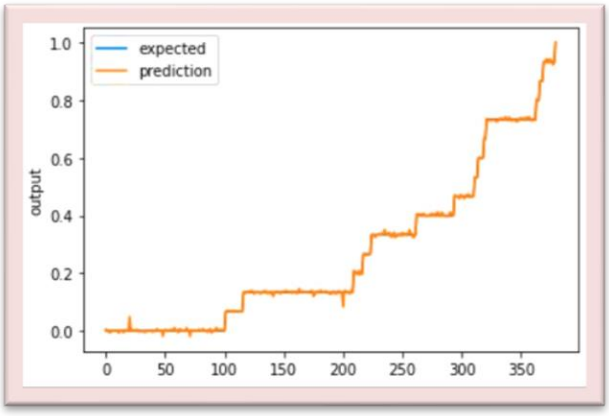

Figure 7: Expected vs predicted plot for COVID-MED

The model accuracy can be judged by plotting the actual values and the model-predicted values in a similar graph. As illustrated in Figure 7, the proposed COVID-MED model returned a 0.99 R2 score while offering the best fit curve of predicted data covering more than 99% of the actual data. That means the COVID-MED model anticipates the output medications, such as injections or other oral meds, with around 99% accuracy.

Table 3: Error & accuracy output from COVID-MED model

MAE	MSE	RMSE	R2 Score
0.0037	0.000035	0.0059	99.995

Table 3 summarizes the errors and the accuracy outcomes of the COVID-MED model that has been developed. Here, standard statistical formulations have been introduced to calculate the error functions like MAE, MSE, and RMSE. Similarly, the R2 score represents the relevance of the output medications with the originally fitted curve [11]. On the other hand, Figure 8 represents the epoch vs. loss curve, where the mitigation of the loss function can be visualized with the increasing number of epochs. Once the training phase is complete, the model begins to predict the output neuron by neuron. The neurons and the loss function assess the error in their initial prediction. The adaptive nature of the NN architecture optimization eventually reduces it. The image below depicts the gradual process of locating the global minima, or target output.

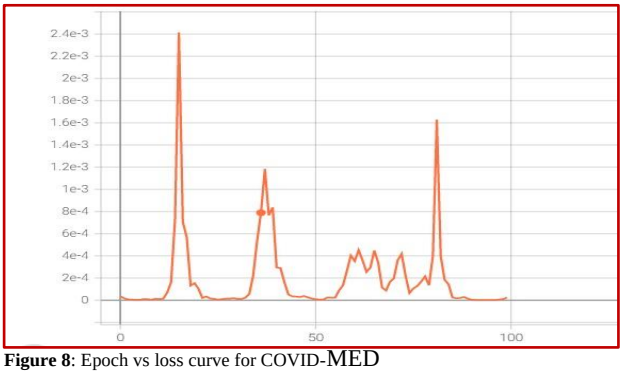

Figure 8: Epoch vs loss curve for COVID-MED

The curve depicted in Figure 8 shows that, despite some slight unusual rises, the loss function is settled very close to zero (0.000035). This also demonstrates how accurately the model can anticipate or generate outputs.

Discussion

According to the best of our knowledge, this is the first study to use ANN to recommend appropriate medications for COVID-19 patients. The model will recommend a medication after the user enters the necessary information. Although this model was developed for COVID-19 patients, physicians and other relevant stakeholders can apply it to any disease. It could be a significant advantage of this model. The critical situation of COVID-19 requires mobilization and the saving of medical, logistical, and human resources, and AI can not only facilitate this but also save time at a time when even one hour saved could result in the saving of lives in all locations where people are dying in COVID-19 [14]. According to the findings of a recent study, AI can answer various patient queries without the presence of doctors [6]. Following the emergence of COVID-19, various AI-based techniques are being used for drug repurposing and repositioning [15], designing novel anti-COVID compounds [16], vaccine design [17], and designing associated protein structures [18]. Many researchers believe that using AI in healthcare will result in error-free decisions once the input is provided [19].

A recent study used a computational methodology to calculate the global impact on the number of fatalities [20], and others used the SEIR method to forecast illness burden with a focus on South Asian countries (Bangladesh, India, and Pakistan) [21]. Furthermore, several researchers concentrated on the deep neural network (DNN) and convolutional neural network (CNN) models for behavioral analysis based on heterogeneous health data gathered in social media [22]. Notably, some research has employed various mathematical models to anticipate disease transmission, predict the number of incidents, deal with healthcare lacking data, and healthcare facilities in combating COVID-19 spread. As a result, choosing the right model and parameter values is critical for the forecasting model. However, a few models have been employed exclusively for countries with a high number of instances, such as China, Italy, Spain, the United Kingdom, Germany, and the United States. Motivated by the theories, this research proposes a DL-based regression model for predicting the prescriptions of COVID-19 patients. Patient's age, exposure to SARS-CoV-2, fever, cough, and cough with sputum, and white blood cell counts were significant features associated with SARS-CoV-2 status [23]. In this current study, these features are being used from acquired EMRs to develop the COVID-MED model. To the best of our knowledge, this is the first study to use an AI system to recommend appropriate medicine for COVID-19 patients. This model will hopefully be helpful in three possible ways: 1) doctors will be able to use this in an emergency situation where quick medication is required; 2) physicians will also be able to double-check the medications they have prescribed; 3) In some cases if this model is applied to other diseases, patients will be able to choose their own medication. The best part is that this will also be useful for any specific disease with an approved list of medicines. This technology will increase healthcare professionals' efficiency and improve healthcare quality at a lower cost. According to some research findings, AI may help doctors make more accurate diagnoses [24]. Machine-learning (ML) models can be trained using EHR data to predict medication orders for hospitalized patients in a patient-specific and time-specific manner [25]. We found a similar work has been done on the medication prediction model using the local–global memory neural network (LGMNN) and EMRs [8]. According to Song et al. [8], the developed model can improve prediction performance for any given disease in an unsupervised manner. In another study, a model was developed that could eventually help with patient-specific decision support to reduce the time spent placing orders or detecting unusual orders to prevent medication errors [25]. Inpatient medication predictions may have clinical decision support applications, despite the fact that they are outcome-agnostic. Recent studies have also used AI to ensure medication safety, particularly device-based administration, with minimal potential overhead for patients and healthcare professionals [26]. With so much diversity in modern medical research, we believe our system could have significant clinical implications. We hope that this system will be able to provide clinicians with continuous feedback. Based on the feedback from our system, health professionals can then make a clinical decision and cross-check the medication to avoid unintended consequences.

Our proposed model does have some limitations. One major limitation of this study is the small sample size. Despite the promising results of using the AI model to screen patients for COVID-19, more data is needed to test the AI model's generalizability to other patient populations. Moreover, this study only used data from one city, limiting its generalizability. Our research focused on the prediction of medication compounds rather than dosages. Due to differences in patient populations, prescribing practices, and health information storage in EHRs, the model, would most likely need to be retrained for use in different settings. The model was evaluated using only retrospective data. Models are likely to need to be retrained with new data regularly to prevent model performance degradation due to temporal changes in prescribing practices, such as adding new medications to formularies.

Conclusion

Finally, this paper summarizes the implementation of a Deep Learning-based Sequential Model (COV-MED) for recommending medications to COVID-19 patients using specific clinical input features. It represents a logical sequence of data preprocessing and feature selection steps that lead to the prediction of medication outputs. The results of this exploratory work are promising and highly accurate, as the medications were predicted so fluently and accurately. As a result, it can be implemented in practical field applications, which should aid in making important decisions and making necessary arrangements in times of emergency to save people from this deadly virus and help humanity. Furthermore, the model can be used for other types of prediction strategies, such as predicting medications for other diseases, forecasting load variables, solar radiations, and so on. Therefore, the significance of this model and research work extends beyond the medical sector and into the energy, health, and communication sectors, respectively. In future research, we hope to see if our model can help with better real-time detection and alerting for medication errors.

Abbreviation

EMR: Electronic Medical Record; DL: Deep Learning; COVID-19: Coronavirus Disease of 2019; AI: Artificial Intelligence; ANN: Artificial Neural Network; ML: Machine

Learning; API: Application Programming Interface; ReLu: Rectified Linear Unit; SDL: Specification and Description Language; MAE: Mean Absolute Error; MSE: Mean Squared Error; RMSE: Root Mean Squared Error; DNN: Deep Neural Network; CNN: Convolutional Neural Network; SEIR: Susceptible-Exposed-Infectious-Recovered; SARS-CoV-2: Severe Acute Respiratory Syndrome Coronavirus 2; LGMNN: Local–Global Memory Neural Network; EHR: Electronic Health Record.

Declaration

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Availability of data and materials

De-identified data supporting the study's findings are available from the authors upon reasonable request and with a signed data use agreement. By signing the agreement, the requester agrees that the data 1) will be used only for research purposes and will not be used for any product-related effort and 2) will not be shared with a third party. You can use the corresponding author email for further contact (fahadbau21@hotmail.com)

Authors' contributions

Md. Fahad Jubayer was the principal investigator of this manuscript and approved the final manuscript. Amit Shaha Surja, Md. Tariqul Islam Limon, Md. Janibul Alam Soeb, and Md. Fahad Jubayer was involved in conceptualization, data analysis, model development, writing, reviewing, and editing. Md. Shoaib Arifin, Md. Meftaul Islam, Md. Shahidullah Kayshar, Md. Amirul Islam and Md. Mizanur Rahman performed the data analysis, writing, reviewing, and editing. Md Abdul Malek, Faroque Md Mohsin, Mohammed Shah Jahan, Anupam Barua, Tanjima Binte Topaz, and Irin Sultana were involved in data collection, field study, and writing.

Ethical approval and consent to participate

We conducted the research following the Declaration of Helsinki. The study was checked and approved by the institutional review board of [Cox's Bazar Medical College and Hospital, Bangladesh] (2022). For this study, which evaluated de-identified data and involved no potential risk to patients, the institutional review boards waived the requirement to obtain written informed consent. No link between the patients and the researchers was made available to avoid any potential breach of confidentiality.

Consent for publication

Not applicable

Competing interest

The authors declare that they have no competing interests.

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