Shallow Net for COVID-19 Classification based on Biomarkers

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Abstract—**In many cases, especially at the beginning of epidemic disaster, it is very important to be able to determine the severity of illness of a given patient. Picking up the severe status will help in directing the effort in a proper way. At the beginning, the number of classified status and the available data are limited, so, in such situation, one needs a system that can be trained based on limited data to give a trusted result. The current work focuses on the importance of the bioscience in differentiation between recovered patients and mortalities. Even with limited data, the decision trees (DT) was able to distinguish between recovered patients and mortalities with accuracy of 94%. Shallow dense network achieved accuracy of 75%. However, when a 10-fold technique was followed with the same data, the net achieved 99% of accuracy. The used data in this work was collected from King Faisal hospital in Taif city under a formal permission from the health ministry. PCA analysis confirmed that there are two parameters that have the greatest ability to differentiate between recovered patients and mortalities. ROC curve reveals that the parameters that can differentiate between recovered patients and mortalities are calcium and hemoglobin. The shallow net gives an accuracy of 92% when trained using calcium and hemoglobin only. This paper shows that with a suitable choosing of the parameters a small decision tree or shallow net can be trained quickly to decide which patient needs more attention so as to use the hospitals resources in a more reasonable way during the pandemic. All codes and data can be accessed from the following link "codes and data".**

Keywords—*COVID-19; pandemic; shallow net; deep learning; decision trees; ROC curve; PCA analysis; biomarkers*

I. INTRODUCTION

During the early days of any pandemic, it is very important to provide a quick and sheep tool to detect infected people [1]. Also, it is very important to provide a tool to differentiate between the degrees of infection [2]. Moderate infections can be treated at home [4] but severe cases need to be under intensive care [3]. Intensive care needs huge resources that might not be available especially in areas that suffer from the low quality of health services [5]. Also, providing a service to differentiate between moderate cases and intensive cases should be with low cost for developing and especially for use [6].

This work will explore developing a cheap tool based on few data that can be collected at the early days of the pandemic. COVID-19 is an example of pandemic related to respiratory system but affects all body systems [7].

Many studies concentrated on detecting and clustering the cases based on images of lunges [8, 9, 10, 11]. Few papers give some interest to the levels of essential body parameters like hemoglobin, vitamins, and mineral levels as a tool to differentiate between categories of severe and light infections [2, 12, 13]. Most of these papers consider only one aspect to analyze and use as a tool of detection. Few papers discussed or proposed an intelligent tool to classify the infection degree [2, 14, 15]. No work discussed the computation cost of such tools and its validity to be applied in poor areas where health services might not be available.

In this work, the proposed solution can be applied based on the available resources, (Resources here means the availability of data and the availability of computing resources). Decision trees can be used in the case of availability of few cases with a good number of parameters, but it needs a suitable computing resource to be distributed over cloud or edge environments [16]. Another alternative is the shallow nets. Shallow nets do not need a big number of parameters and in many cases, it can achieve an accepted accuracy [17]. Based on experienced works in the pandemic domain, a suitable and limited number of parameters can be proposed to be used as the classification parameters. Providing such limited number of parameters might be expensive and cannot be provided in a suitable time [18]. So, getting a good sample of complete data to be analyzed using "reduction dimensionality tools" will help to reduce the number of parameters [19].

In this work, PCA and ROC curves will be used to determine the most important parameters. Also, the work will check the validity of training a shallow net on these limited set of parameters. The results ensure that training a shallow net on carefully reduced set of parameters will produce a light model that can differentiate between the patients' classes with a high suitable accuracy.

The remaining of this paper will continue as follows. Section II provides information regarding related works. The methods are explored in Section III. Detailed experiments and results are explored in Section IV. Finally, the whole paper is concluded in Section V.

II. RELATED WORK

This part will explore studies made to detect COVID-19 using AI approaches and different studies based on the type of data. Some studies depended on X-Ray images, then studies that use a mix of X-Rays and other symptoms. Also, it will explore studies that either used an AI for purpose different from detecting COVID-19 or used a different type of data.

Finally, studies that tried to review works related to AI and COVID-19 will be reviewed.

Based on images for X-Rays, some papers proposed a method to predict and detect COVID-19. For example, Qayyum et al. proposed a new depth-wise dense network to compete the ordinary convolutional layers in detecting COVID-19 based on analyzing image of lungs x-rays for suspected cases [7]. Sharma et al. proposed a deep learning model for quick identification of COVID-19 infected patients based on chest X-ray images. They implemented a variety of methods for data augmentations [8]. Jin et al. proposed a deep convolutional neural network for quick COVID-19 detection [9]. Vaid et al. developed a deep learning model that consists mainly of convolutional neural networks to improve the accuracy of detecting and predicting COVID-19 cases based on chest X-ray scans [10]. Based on Chest CT, Harmon et al. applied a series of deep learning algorithms to classify patients with COVID-19 [11].

Since the X-Rays images do not provide a quick tool to detect COVID-19 early enough, some works tried to combine X-Rays images with additional data in one model for more efficient system. For example, Ming et al. developed a method to separate between patients with COVID-19 and healthy individuals depending on clinical and laboratory testing data and imagining data. They developed a deep learning model for feature extraction then fed these data to three machine learning models for the classification process [2]. Attaullah et al. proposed a method that depends on X-Rays images and labeled patients' symptoms for early detection of COVID-19. All features are fed to a deep learning model that can benefit from the characteristics of patients' symptoms in early detection of COVID-19 and X-rays images that can define the type of infection [12]. Depending on a combination of chest CT and clinical symptoms, exposure history and laboratory testing, Mei et al proposed an AI algorithm for quick and accurate diagnosis of cases with COVID-19.[13]. Mario et al. proposed a machine learning method to detect risk COVID-19. They used historical data that include medical history, demographic data, as well as COVID-19-related information. The aim of their work is to differentiate between recovered patients and mortalities [14].

Some works tried to explore problems other than detecting or classifying COVID-19 patients. Also, some works implemented non-ordinary data for classifying or detecting COVID-19 patients. For example, JAMSHIDI et al. proposed intelligent framework to help physicians and researchers in detecting and treating COVID-19. The framework depends on unstructured and structured data that are fed to three types of deep learning net to implement each different data type [20]. Laguarta et al. proposed a method that depends on Cough Recordings only. Based on cough recordings of biomarkers can be extracted and used to monitor the patient in real time mode to detect COVID-19 in low cost [21]. Nawaz et al. used artificial intelligence methods to analyze hidden pattern in COVID-19 genome and then used these patterns to evaluate the ability of predicting nucleotide base(s) from historical data. Also, they used AI to analyze the mutation possibilities in the structure of COVID-19 genome [22]. Based on patients' self-reported symptoms, Obeid et al. proposed convolutional neural network for predicting COVID-19. The algorithm was fed by unstructured patient data collected through telehealth visits to predict COVID-19 possible infection [23].

Since there are a plenty of works related to AI and COVID-19, many works presented a review for these works to define the main trends in these works and try to define the main factors that direct these studies and affect their results. For example, Ahmad et al. compared between methods for predication COVID-19 depending on decision tree properties, the method can predict COVID-19 cases although there is imbalance in data availability [24]. Vaishya et al. reviewed possible application of AI in COVID-19. The study aimed to define the important application and their possible usages in the future to deal with pandemic like COVID-19 more effectively. The study results show that there is a proper application for screening, analyzing, prediction and tracking of current patients and future patients [25]. Shi et al. focused on reviewing works done during COVID-19 pandemic focusing on the integration of AI with X-ray and CT. They reported COVID-19 research works in enhancing the available technologies in the field of image acquisition scanning and image protection methods. Some works provide means to increase the accuracy of segmentation diagnosis, and follow-up methods [26]. Swapnarekha et al. reviewed methods proposed on decision trees, SVM and neural networks as well as statistical and mathematical models for COVID-19 detection. The work analyzed the factors that affect the efficiency of the classification method like the classification method and the impact of COVID-19 on the nature of data. Also, they discussed important research directions on COVID-19 research [27]. Ilyas et al reviewed many works that tried to classify patients with COVID-19 based on chest x-rays. Basically, all studies tried to develop a method for automatic detection of COVID-19. Varieties of deep learning models were built to overcome the difficulty to decide if the pneumonia was caused by COVID-19 or another cause [28]. Albahri et al. performed a study to review the proper AI studies in the field of detecting and predicting COVID-19 infections. The study tried to propose a systematic model to evaluate AI techniques for COVID-19. The work revealed the importance of combining between multi approach in the classification process [29]. Murphy et al. evaluated AI system for detection of COVID-19 based on chest X-Raya images. Six experts evaluated each testing image and their evaluation compared to the results of the AI system. AI system could outperform the experts and achieved an area 0.8 under ROC curve [30]. Piccialli et al. discussed the role of AI in facing COVID-19 pandemic. The work shows that AI alone cannot be enough without human clinical skills to detect or predict COVID-19. However, AI approved that it could play a significant role in health emergency and complex scenario of such pandemic. [31].

Recently, algorithms based on the intelligent behavior of animals and insects have been adopted in research and classification methods, such as the behavior of bees in swarm optimization techniques for medical diseases detection [32, 33], which aims to predict and classify diseases.

Also, depending on the characteristics of cooperative birds, hawks, methods for searching for preys by field detection have been developed [34]. The bat's radar feature was also relied

upon to develop research methods that depend on the concept of echo as a basis for the research process [35].

Despite huge amount of works presented to tackle the COVID-19 pandemic, few works concentrated on studying the importance of reasonable use of resources in hospitals especially in poor areas in the world. This work presents a cheap and quick approach that can be built quickly on a well-chosen data set to develop a light model that consumes a little computation power and less data to differentiate between severe and light cases during pandemic. The proposed model enables the decision-maker stationed in the place of receiving infected cases to identify severely infected cases that need intensive care inside the hospital from those that can be sent home to complete treatment safely.

III. METHOD

Fig. 1 explains the steps followed in this work. A shallow net consists of three dense layers was used to classify a number of samples. Also, a decision tree was built for the same purpose. The results reflect a huge gap between the accuracy of decision tree and shallow net. A cleaning and investigation process based on PCA and ROC curve determine which parameters have the main role in discrimination between recovered patients and mortalities. The shallow net was retrained using the principal components to show that a shallow net with suitable and carefully chosen parameters can

help effectively to separate early between patients who have light conditions and can easily recover with normal care and the severe patients' instances who need a special care.

A sample of 1000 recovered patients and 900 mortalities during 2020 from the records of patients in King Fasial hospital was retrieved to distill the data related to COVID-19. 53 parameters were collected according to data availability and doctors' recommendation for analysis. These data include information related to age, nationality, gender, blood analysis, minerals and vitamins levels. The main hypothesis in this study is to be able to differentiate between recover patients and mortalities based on a few numbers of samples. Also, with the aid of principal component analysis (PCA) and Receiver Operating Characteristic (ROC) curve a simple weak learner can be built to differentiate between recovered patients and mortalities. To this end a shallow net was designed as appears in Fig. 1. Also, a decision tree was built to support the shallow net. The decision tree was trained using only 10% of data to explore the validity of the data to be used in the case of availability of few samples especially in the beginning of the pandemic and the number of levels was tuned to be three.

All codes were written using python 3.10; however, ROC curve was implemented using SPSS. A specific code was written for the decision tree, PCA and the shallow net. All codes were run on a machine "11th Gen Intel(R) Core (TM) i7-1165G7 @ 2.80GHz 2.80 GHz" and 16.0 GB for RAM.
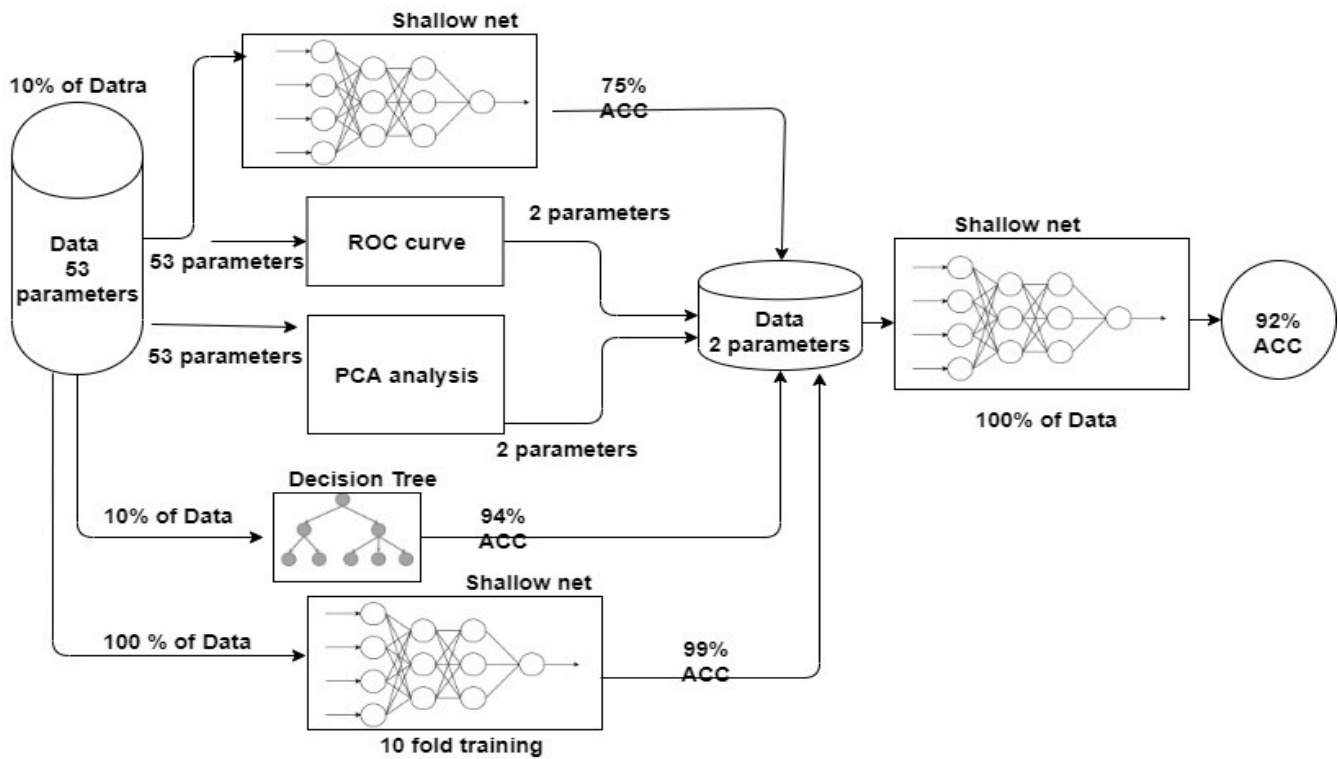

Fig. 1. Method Steps and Stages.

IV. RESULT AND DISCUSSION

The 53 parameters are divided into sets. Demographic parameters include (sex, age and nationality), vitamin sets, minerals set, extra. ROC curve was produced for each group and any parameter with area curve under the reference line was excluded. This gradual process leads to filter all the 53 parameters into two parameters, namely, calcium and hemoglobin (HEMO).

Table I says that hemoglobin and Calcium has at least one tie between the positive actual state group and the negative actual state group. Also, the area under the curve of calcium is 0.963 and the area under the curve of hemoglobin is 0.938. This means that both calcium and hemoglobin have a high ability to discriminate between recovered patients and mortalities with Bayes to the calcium ability.

Fig. 2 shows the structure of the used shallow nets used in the experiments. The first net used the whole 53 parameters as inputs while the next net used only two parameters. Fig. 3 represents final ROC curve. ROC curve expects that based on only two parameters; the shallow net can achieve a compete performance using the whole parameters. This assumption has been proved in the following sections.

A piece of code was written using python 3.10 to perform the PCA analysis to explore the nature of the data classes and determine the number of principal components. Fig. 4 gives the simulated graph of PCA results. The results ensure that there is a separable two classes and the fact that there are two principal components. This ensures the conclusion that was expected in Fig. 2 through gradual manual reduction of parameters using ROC curve. A 10% of the shuffled data using NumPy shuffle function was kept for training a decision tree and a shallow dense net. The decision was tuned to three levels. The final accuracy of the decision tree is 94% on test data. This result was expected since it is known that decision tree gives the optimal results if it is used with separable classes as given based on the PCA analysis. The shallow dense net failed to give a near result. Fig. 5 gives a comparison between the decision tree and the shallow dense net based on 10% of Data.

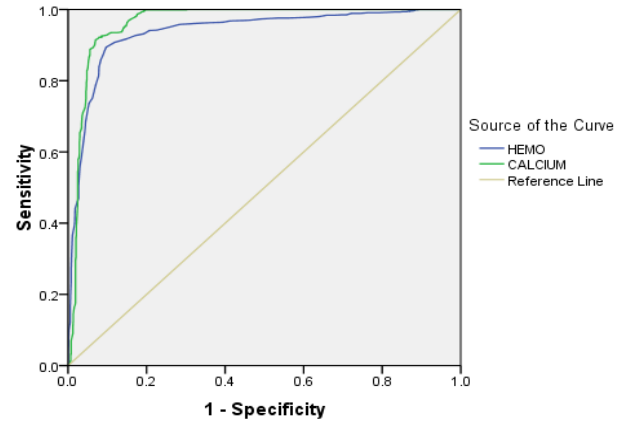Fig. 2. Shallow Net Model in the Case of 53 and 2 Parameters.

Fig. 3. Final ROC Curve.

TABLE I. AREA UNDER THE CURVE FOR HEMO, CALCIUM

Test Result Variable(s)	Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
				Lower Bound	Upper Bound
HEMO	.938	.006	.000	.927	.949
CALCIUM	.963	.005	.000	.953	.972

Fig. 4. PCA Results.

Accuracy and loss results of the shallow net using 10 % of data without folding
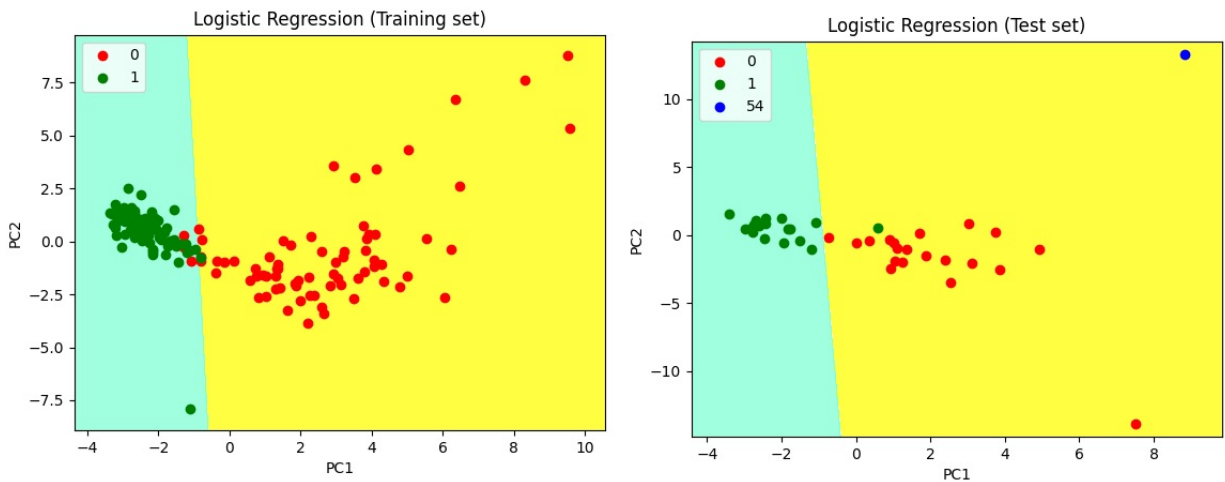

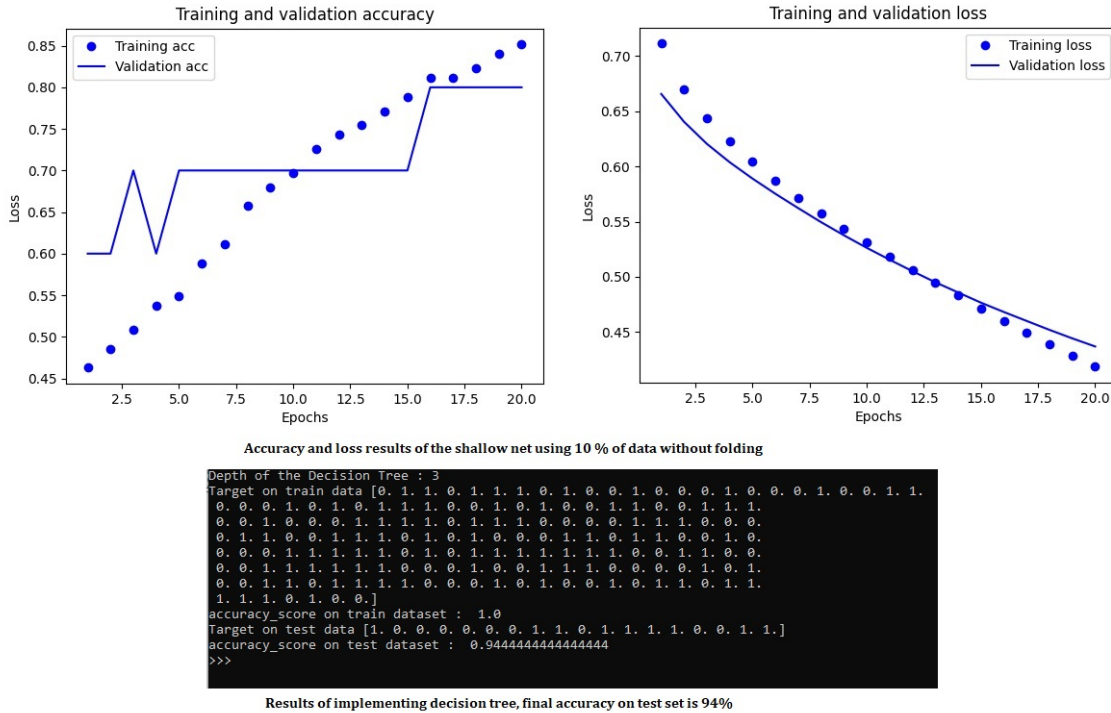Results of implementing decision tree, final accuracy on test set is 94%

Fig. 5. Implementation of Decision Tree and Shallow Net using 10% of Data.

The whole data was divided into 10 % for final testing and 90% for training. Using 90% of the data, a 10-fold training for the shallow net was done. In each fold the training data were divided into 10 % for validating and 90 % for training as appear in Fig. 6. Then re-trained the resulting model using the whole training data (90 % of the whole data). Following this technique, a 99% of accuracy was achieved. Fig. 7 shows the loss and accuracy when applying 10-fold method. Usually during the early pandemic days, it is not easy to provide such huge number of parameters to be tested. The results show that we can get a close result under suitable choosing of the parameters (two parameters in the case under consideration), which might be done based on the advice of doctors responsible for monitoring the pandemic and will lead to optimal trained model or under quick analysis of carefully selected sample data. Fig. 8 shows the 'accuracy and loss of the resulting model using only two parameters.
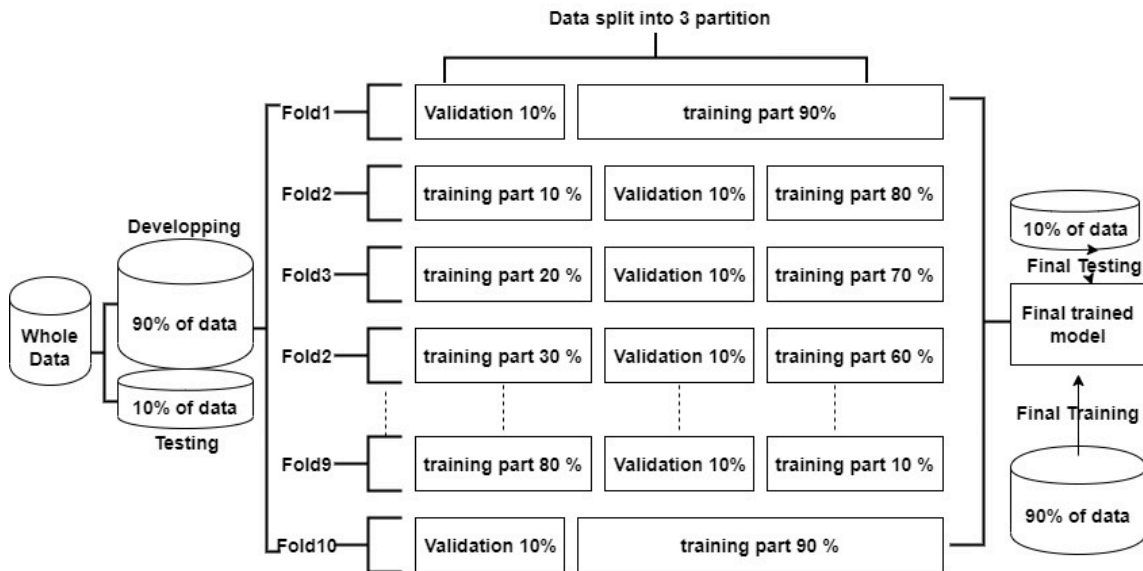

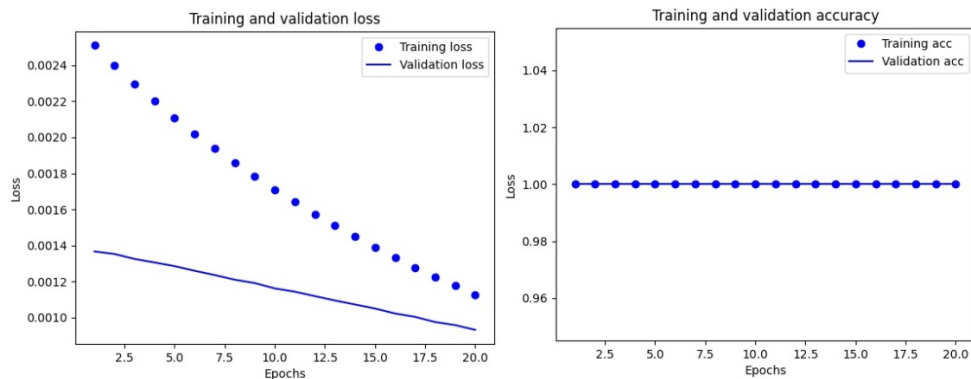Fig. 6. 10-fold Training Data for the Shallow Net.

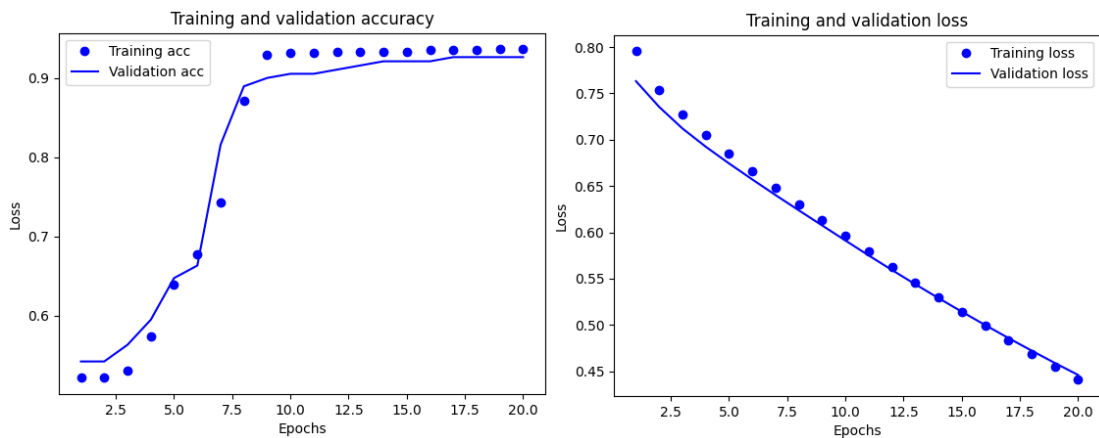Fig. 7.   Loss and Accuracy of Final 10-fold Model.

Fig. 8.   Loss and Accuracy Training Results of Shallow Net using 2 Parameters.

V.   CONCLUSION

This paper addressed the need of a light model with fewer data to differentiate between moderate patients and severe cases so as to use the hospitals resources more reasonably. The work begins using a real, officially collected and reviewed data under the supervision of expert doctors to determine which are the most suitable set of parameters that can be used to differentiate between recovered patients and mortalities. The number of parameters were 53. This number is not huge for ordinary computation available on any prepared machine for deep learning training and the results that achieved using decision trees (94% of accuracy) or 10-fold training (99% of accuracy) ensures that the used parameters can effectively differentiate between recovered patients and mortalities. However, it is better to get a light model with very few parameters (two parameters in this work) and achieve a reasonable result. Using the results of ROC and PCA analysis, the shallow net trained using two parameters achieved 92% accuracy on testing data. So, using a few carefully chosen parameters and a light architecture of shallow net, a light model that needs a very limited computation resources can be built to differentiate between moderate and sever patients during the early days of pandemic like COVID-19.

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