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Detection of Tuberculosis Disease with Convolutional Neural Networks

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Abstract— Tuberculosis is an infectious disease caused by bacteria called Mycobacterium tuberculosis. Tuberculosis is still an important public health problem worldwide and is common especially in developing countries. This respiratory disease can cause serious symptoms, especially affecting the lungs. Symptoms of tuberculosis include prolonged coughing, shortness of breath, chest pain, weakness, fever, night sweats, and malaise. The diagnosis of the disease is made by clinical signs as well as biomedical imaging methods and laboratory tests. These imaging modalities include techniques such as x-rays, computed tomography (CT), and magnetic resonance imaging (MRI). Early diagnosis of tuberculosis disease is of great importance in terms of treatment and prevention of the spread of the disease. The use of deep learning methods to classify biomedical images of tuberculosis disease can accelerate the diagnosis process, increase accuracy and guide treatment more effectively. In this study, it aims to be an important step in the classification of tuberculosis disease with deep learning. The generated CNN network, parameter values, layers used, complexity matrices obtained for verification data, accuracy and loss graphs are shown in detail. In our study, the success rate was increased by using a different network structure than the neural networks used in the literature. Approximately 98% success was achieved with the proposed CNN model.

Keywords— tuberculosis, CNN, deep learning, artificial intelligence, biomedical images

I. INTRODUCTION

Today, biomedical imaging methods play an important role in the diagnosis and treatment of diseases in the field of medicine [1]. Biomedical images can be examined with computer-based analysis methods and can provide valuable information in the classification and diagnosis of diseases. Deep learning methods have been an approach that is rapidly developing and attracting great attention in this field. The use of deep learning methods in the analysis of biomedical images in the diagnosis and classification of an infectious and fatal disease such as tuberculosis has great potential in the early diagnosis and treatment of the disease. Today, decision support systems have an important place among the powerful tools that help doctors diagnose diseases and make decisions [2]. Decision support systems have focused on many studies that will help physicians diagnose more easily. In this context, expert systems, deep learning and artificial intelligence techniques are used successfully in solving different problems in various medical branches. These systems assist physicians in analyzing clinical data, providing support in the diagnosis process, and evaluating treatment options. The use of decision support systems contributes to faster and more accurate diagnosis of patients, improving treatment processes and increasing the efficiency of health services [3].

Many diseases can affect human health in different ways by threatening the continuity and quality of life. Among these diseases, chest diseases such as tuberculosis (TB), chronic obstructive pulmonary disease (COPD - COPD), pneumonia, asthma and lung cancer are among the serious health complications and causes of death both in developing countries and developed countries.

Chest diseases are diseases that affect the respiratory system and negatively affect respiratory functions [4,5]. Infectious diseases such as tuberculosis are common especially in low-income countries and constitute an important public health problem. Diseases such as chronic obstructive pulmonary disease (COPD), pneumonia, asthma and lung cancer are also serious health problems and are among the important causes of death worldwide.

The aim of our study is to investigate the usability of biomedical images in the classification of tuberculosis disease using deep learning methods. Deep learning is a machine learning approach inspired by artificial neural networks and is very effective in detecting complex patterns in large data sets. In diagnosing tuberculosis disease, the use of deep learning algorithms that can detect and classify disease-specific changes can improve accuracy and reduce the risk of misdiagnosis.

In our study, various datasets will be used to evaluate the usability of deep learning methods in the classification of tuberculosis disease of biomedical images. Deep learning algorithms will gain the ability to accurately classify different stages of the disease by training and learning these datasets. The results will be statistically analyzed to evaluate the effectiveness of deep learning methods in diagnosing tuberculosis and to guide further studies in this area.

II. RELATED WORKS

Today, COVID-19 has adversely affected health and economy all over the world. COVID-19 contains symptoms similar to many chest diseases such as lung cancer, tuberculosis and pneumonia and causes these diseases in the future. Malik et al. developed a model using a convolutional neural network called CDC Net in order to minimize the devastating effects of Covid-19 on lung diseases [6]. With this model, it is aimed to diagnose COVID-19 at an early stage. COVID-19 data from chest X-ray images have been classified. Precision, recall, F1 Score metrics are used for classification accuracy. However, many problems arise for the improvement of the model at the stage of integration, maintenance, quality and usability of the X-ray films taken.

According to the World Health Organization, tuberculosis and COVID-19 are very serious lung diseases that cause the death of many people. Symptoms of these diseases include sneezing, coughing and shortness of breath. In order to identify these symptoms, Karaddi et al. carried out a study using the CNN network [7]. They used a chest X-ray image dataset to describe and categorize these lung diseases. In the study, it is recommended to use networks such as Alexnet, Darknet-19, Darknet-53, Densenet-201, Googlenet, InceptionResnetV2, MobilenetV2 and Resnet-18. They used 30 epochs and adam optimizers during the training phase. More data are needed for faster and more accurate classification and detection of lung diseases.

Lestari et al. tried to detect tuberculosis disease with Backpropagation Artificial Neural Network [8]. The back propagation algorithm uses supervised learning and has negative aspects in reaching the level of convergence. They conducted a study on the last 2 years data obtained from the North Sumatra Provincial Health Directorate. They achieved success with an accuracy rate of 81.82%. They observed the effect of the Mean Square Error value on the learning rate.

Gichuhi used Logistic regression (LR), artificial neural networks (ANN), support vector machines (SVM), Random Forest (RF) and AdaBoost model in the treatment of tuberculosis [9]. These five models showed AdaBoost (91.05%), RF (89.97%), LR (88.30%) and ANN (88.30%) and SVM 91.28% accuracy. With their work, machine learning techniques have enabled to determine the disease factors in the treatment of tuberculosis.

Lubis et al. performed feature extraction of tuberculosis images with the HOG (Histogram OF Oriented Gradients) method [10]. KNN (K-Nearest Neighbor) and SVM (Support Vector Machine) methods were used to detect tuberculosis images. While detecting tuberculosis with HOG features and detecting image-like data with KNN, 77.95% accuracy and negative ones 77.95% accuracy; In the results of SVM and Tuberculosis X-ray, HOG detection results were 65.75% in positive images and 79.39% in negative ones. Shakya et al. performed the detection of tuberculosis disease from chest CT scan images consisting of 1000 images [11]. They used SVM and KNN classifier in their work. During the test, 10 iterations were applied for the proposed methods. The SVM method gave more successful results than the kNN method. However, the study was applied for small data.

Tuberculosis disease is known as a malignant infectious disease in many parts of the world. For this reason, accurate and rapid classification of chest X-ray data is very important in the early diagnosis and treatment of the disease. For this purpose, Nafisah et al. used a method based on deep learning on Chest X-Rays (CXR) images [12]. In order to obtain detection of tuberculosis from CXR images, the original and segmented images were given as input to the proposed model. Attributes were extracted from each image with ResNet, Inception, Xception, MobileNet and EfficientNet. The performance of the models was evaluated according to different attribute criteria.

Ammar et al used a hybrid optimal deep learning-based model for tuberculosis disease recognition using MRI images [13]. With this study, they aimed to increase the classification accuracy with Vision Transformer (ViTs) and Efficient-Net models. They performed the success of the proposed model on the shenzhen and montgomery datasets. In this study, the success of hybrid deep learning models was evaluated. However, it is not easy to automatically determine the parameters of deep learning methods on different datasets.

Deep learning methods are frequently used, especially in the field of health, for the accurate and rapid detection of the disease. Convolutional neural network is a deep learning method widely used in many fields such as radiology and tomography. Venkataramana et al. enhanced X-ray or CT scan images with the SMOTE (Synthetic Minority Oversampling Technique) algorithm [14]. Thus, they have increased the success of deep learning methods by evenly distributing the distribution of the classes. However, different data augmentation methods should be applied for the detection of different chest diseases.

Asakawa et al. performed analysis of chest CT images for lesion detection for tuberculosis [15]. They proposed a CNN model to detect lung cavernous regions associated with lung cavern features in lung CT images with ImageCLEF 2022 data and to predict three binary features of caverns suggested by experienced radiologists. They used inputs from more than one CNN feature and tried to identify lesions in the lungs with a three-label median-based estimation algorithm.

Rahman and colleagues used various methods and techniques for the detection of SARS-CoV-2 virus using different images and data to reliably and quickly identify COVID-19, prevent the rapid spread of the disease, ease quarantine restrictions and reduce pressure on public health infrastructures. [16]. In this study, ECG data consisting of 1937 images with six different deep learning models (ResNet18, ResNet50, ResNet101, InceptionV3, DenseNet201 and MobileNetv2) and two classes (normal, COVID-19) were used. The aim of the study is to detect COVID-19 and other cardiovascular diseases from ECG data.

III. PROPOSED MODEL

Convolutional Neural Network is a very effective artificial neural network model in the field of deep learning. It has achieved significant success in areas such as image processing and image recognition. CNNs are designed to process visual information and identify complex patterns as perceived by the brain. The main purpose of CNNs is to learn features in a dataset and build a model that represents these features. These models consist of successive layers such as convolutional, pooling, and fully connected layers [17].

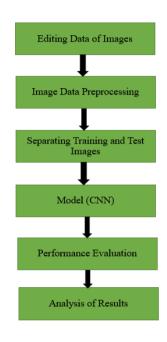


Fig. 1 Proposed model

The workflow diagram of our proposed model is given in Figure 1. We created a CNN model that will automatically detect disease from tuberculosis images. The layers of our proposed model are shown in Figure 2. It is a fundamental component of the Convolutional Neural Network structure and is of great importance in the field of image processing. The convolution layer applies a set of filters that generate feature maps by applying the convolution operation on an image data. The convolution layer performs a dot product at each location by moving a filter or kernel matrix over the input data. This dot product operation involves an element-wise multiplication and addition between the input data and the filter. As a result of each convolution operation, a specific feature detected by a filter is obtained. This property represents local patterns of image data. For example, features such as straight lines, edges, lines or corners can be detected by the convolution operation. The size and number of filters used in the convolution layer determines the variety of features the model can learn. Filters are usually 3x3 or 5x5 in size and their weights are learned automatically during the training process. By using multiple

filters, the convolution layer can detect different features and generate various feature maps. The pooling layer is used to shrink the feature maps in the input data and highlight important information. The pooling layer reduces the input data to smaller sizes while increasing the resilience of features to changes in scale, translation, and displacement. It also reduces computational complexity by reducing the number of parameters and improves the generalization of the network. Fully connected layers are one of the components of a neural network and are usually the last layers that move towards the output layer of the network. In these layers, each neuron is connected to all neurons in the previous layer. It takes all the outputs of the previous layer and associates these outputs with its neurons. Each neuron takes as input a sum of the outputs of the previous layer multiplied by a weight matrix. Then this sum is activated by an activation function and the output of the neuron is obtained. This process is repeated for each neuron of the fully connected layer.

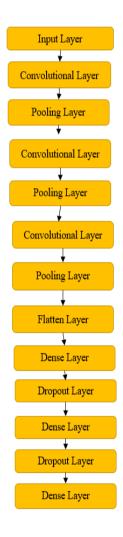


Fig. 2 Layers of the proposed model

IV. EXPERIMENTAL STUDY

The dataset we used for tuberculosis (TB disease) is shown in Figure 3. The layers and parameters we use in our proposed CNN networks are shown in Figure 4. In Figure 5, classification results of tuberculosis images of the proposed CNN model in education and thesis data are given. While it provides about 99% success for training, it has about 98% success for testing. The evaluation results according to accuracy, precision, precision and F1-Score for training and test data, respectively, are shown in Table 1 and Table 2.

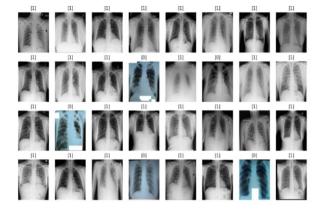


Fig. 3 Tuberculosis data

Layer (type)	Output Shape	Param #
Conv1 (Conv2D)	(None, 510, 510, 30)	840
MaxPool1 (MaxPooling2D)	(None, 255, 255, 30)	0
Conv2 (Conv2D)	(None, 253, 253, 40)	10840
MaxPool2 (MaxPooling2D)	(None, 126, 126, 40)	0
Conv3 (Conv2D)	(None, 124, 124, 50)	18050
MaxPool3 (MaxPooling2D)	(None, 62, 62, 50)	0
Flatten1 (Flatten)	(None, 192200)	0
Dense1 (Dense)	(None, 50)	9610050
dropout (Dropout)	(None, 50)	0
Dense2 (Dense)	(None, 30)	1530
dropout_1 (Dropout)	(None, 30)	0
Dense3 (Dense)	(None, 2)	62

Fig. 4 Parameters of the proposed model

Loss, Acc = Model.evaluate(xTrain, yTrain, verbose=0)
print(f"Train Loss : {Loss}")
print(f"Train Accuracy : {Acc}")

```
Train Loss : 0.018262911587953568
Train Accuracy : 0.9944499731063843
```

Loss, Acc = Model.evaluate(xTest, yTest, verbose=0)
print(f"Test Loss : {Loss}")
print(f"Test Accuracy : {Acc}")

```
Test Loss : 0.0340612530708313
Test Accuracy : 0.9891999959945679
```

Fig. 5 Layers of the proposed model

TABLE I Evaluation results for training data

Train Data	Precision	Recall	F1-Score
0	0.993	0.9973	0.9983
1	0.9939	0.9970	0.9955
2	0.9935	0.9970	0.9952
3	0.9954	0.9977	0.9966
4	0.9910	0.9957	0.9933
5	0.9921	0.9983	0.9952
6	0.9988	0.9921	0.9954
7	0.9979	0.9808	0.9893
8	0.9940	0.9954	0.9947
9	0.9883	0.9938	0.9910
Accuracy	-	-	0.9944
Max Avg	0.9944	0.9945	0.9945
Weighted Avg	0.9945	0.9944	0.9944

 TABLE III

 EVALUATION RESULTS FOR TEST DATA

Test Data	Precision	Recall	F1-Score
0	0.9969	0.9949	0.9959
1	0.9913	0.9982	0.9947
2	0.9808	0.9922	0.9865
3	0.9863	0.9960	0.9911
4	0.9809	0.9949	0.9879
5	0.9833	0.9910	0.9872
6	0.9968	0.9802	0.9884
7	0.9970	0.9708	0.9837
8	0.9877	0.9928	0.9903
9	0.9910	0.9802	0.9856
Accuracy	-	-	0.9892
Max Avg	0.9892	0.9891	0.9891
Weighted Avg	0.9893	0.9892	0.9892

The variation of the cross entropy error values for the tuberculosis dataset is shown in Figure 6 according to the epoch values. As can be seen in the graph, the error is the highest in the 7th epoch. In the epoch, the error is the lowest.

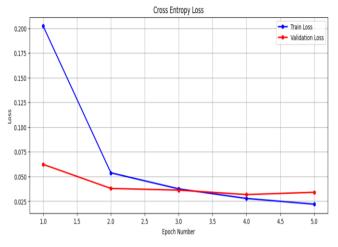


Fig. 6 Cross entropy error

The weights are constantly being updated and it is shown in Figure 7 that the best learning occurs at the 6th Epoch. In Figure 7, complexity matrix according to different evaluation metrics is given for training and test data, respectively.

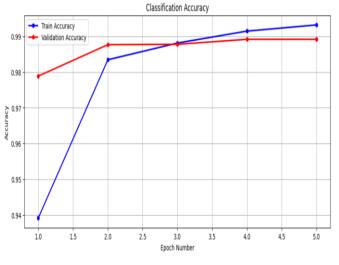


Fig. 7 Classification accuracy

V. CONCLUSION

In this study, the use of decision support systems that use some artificial intelligence techniques to help doctors diagnose tuberculosis (TB) disease through x-ray images has been studied. Classification has been made using the convolutional neural network (CNN), one of these techniques. Creating two different deep convolutional neural network models for disease classification, performing the training of these models, after model training, the disease classification performance criteria of the models created using the test fundus image set, the kappa value, F1 score, Area Under the Curve-AUC) and the final score, which is the average of these three criteria, to evaluate the classification performance of the models according to these criteria, and to use the model with the best score in the classification of ocular diseases.

The methods used were evaluated using a dataset from the Kaggle database. The proposed methods were compared with the machine learning methods used in previous studies.

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