iJRASET
International Journal For Research in Applied Science and Engineering Technology



INTERNATIONAL JOURNAL FOR RESEARCH

IN APPLIED SCIENCE & ENGINEERING TECHNOLOGY

Volume: 11 **Issue:** V **Month of publication:** May 2023

DOI: https://doi.org/10.22214/ijraset.2023.53278

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International Journal for Research in Applied Science & Engineering Technology (IJRASET)
ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 7.538
Volume 11 Issue V May 2023- Available at www.ijraset.com

Multiple Deep Learning Approaches to Detect Pneumonia with Chest X-Ray

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Abstract: ***Pneumonia is one of the top 10 causes of death worldwide and the leading cause of death in young children. Chest X-ray radiographs are often examined by highly qualified experts to look for pneumonia. Radiologists commonly disagree because of this laborious process. Computer-aided diagnostics systems have shown the ability to improve diagnosis accuracy. In this paper, we have given a computational technique for finding pneumonia regions using single-shot detectors, squeeze, and extinction deep convolution neural network (CNN) augmentations, and multi-task learning. One of the challenge's best results was obtained by a modified CNN model with the recommended procedure and got an accuracy of 96%, which was evaluated as part of the radiological society of North America's pneumonia detection challenge.***
Keywords: Pneumonia, radiographs, single-shot detectors, CNN, multi-task learning

I. INTRODUCTION

According to UNICEF's data, a child dies of pneumonia every 43 seconds in the world. More children than any other infectious disease pass away from pneumonia each year, killing about 700,000 kids under the age of five, or over 2,000 people each day. More than 200,000 infants are included too. Pneumonia affects more than 1,400 children worldwide per 100,000, or 1 kid in 71, with the highest incidence rates seen in South Asia (2,500 cases per 100,000 children) and Africa's West and Central region (1,620 cases per 100,000 kids). Pneumonia is an interstitial lung disease bacteria, fungi, or viruses. It killed about 880,000 kids in 2016, making up about 16% of the 5.6 million fatalities of children under five. Each year, it results in more than 50,000 fatalities and one million hospital admissions. In South Asia and Sub-Saharan Africa, pneumonia affects children most often. Even Western countries are suffering from the problem of pneumonia too. In the US, around 1.5 million people (about the population of West Virginia) receive a pneumonia diagnosis each year. Pneumonia caused the deaths of 131 450 persons in the European Union (EU) in 2016. 3% of all fatalities in 2016 were caused by pneumonia. The number of deaths among the elderly escalated, even though the mortality rate for those over the age of 70 marginally decreased. This age group accounted for 1.13 million pneumonia-related deaths. The prognosis for pneumonia in the elderly is poor, and they are more likely to develop severe pneumonia. Up to 20% of those who have severe pneumonia die [1]. The study by Kitamoto et al. found that 83% of pneumonia-related deaths were caused by organic problems with the respiratory system and alveoli, 48% of deaths were caused by respiratory failure brought on by the progression of pneumonia, and 35% were caused by prolonged respiratory failure despite the suppression of the development of pneumonic lesions [2].

II. LITERATURE SURVEY

Rajpurkar et al. [11] proposed CheXNet based on DenseNet and Grad-CAM. Four experienced radiologists evaluated CheXNet's performance using the F1 score method, which produced an F1 score of 0.435, which was higher than the radiologist average of 0.387. Despite low contrast surrounding structures on computed tomography, Roth et al.'s [12] presentation of a deep convolutional neural networks (CNN) capability to recognize lymph nodes in a clinical diagnostic test generated impressive results. CNN was developed by Ronneburger et al. [13] via data augmentation. The model captured outstanding accuracy even when trained on small samples of picture data using transmitted light microscopy, according to the scientists. Histogram equalization and thresholding were employed by Sharma and Raju [14] to find the pneumonia haze in chest X-rays. We must pre-process the image and occasionally crop it by a specific percentage to figure out that the lungs are the biggest form. SymText, an NLP-based technique for predicting pneumonia from a description of an X-Ray picture, was introduced by Fiszman [15]. To make this work, however, the system needs access to image interpretation. A sample of the 1.4 million images in the collection was taken in 2017 by Hsu et al. using 5000 images from the CXR-14 dataset [16]. They employed the ResNet50 model with information to train their model. An image analysis probabilistic neural network (PNN) model was introduced by Wozniak et al. [17]. To find abnormalities in chest x-rays, a tiny network model is used.

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For deep feature detection, Ho and Gwak [18] employed the DenseNet121 pre-trained deep learning model with four features. They classified 14 distinct chest disorders using local binary patterns (LBP), scale-invariant feature transform (SFT), histogram generated gradient (HoG), and GIST with CNN features. Gue et al.'s 3 D CNN and multi-scale forecasting technique with cube clustering detection and multiscale model for cube prediction as well as lung area detection and segmentation was proposed in Gue et al.'s [19] study.

III. METHODOLOGY

A. Dataset Description

A chest X-ray database was used to experiment with this study of Pneumonia discovery. This database contains around 4000 viral pneumonia images and around 10,000 healthy images. As a result, the dataset includes studies of Pneumonia and healthy individualities with a matrix resolution of 299 × 299. EnsNet can automatically remove all the text or comment from an image without any former knowledge. Data addition and image enhancement ways are performed to enhance the volume and variety of images given to the classifier for classification Image augmentations used to consist of vertical flip, spin, width shift, and peak shift on all the extracted records from the unique dataset. A perpendicular flip was not applied because chest X-ray images are not vertically leveled.

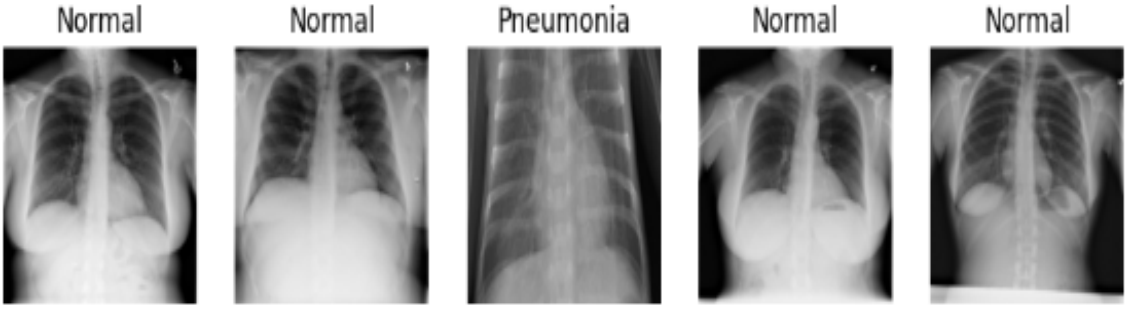


Fig. 1 Chest X-ray Dataset Sample

B. Model Selection

One of the main aims of this research is to acquire appropriate classification results utilizing freely available data with the common transfer learning models. The primary goal is to propose a modified novel deep-learning-based CNN model to gain the topmost accuracy on a large volume of chest X-ray data with the lowest compilation time and compare the modified novel approach like accuracy, effectiveness, and compilation time with existing deep-learning models on the same dataset. Fig. 1 shows the system figure of the trial.

C. Different Types of Models

1) VGG16

The Visual Geometry Group is shortened as VGG. VGG16 is constructed consecutively using many 33 kernel-sized clarifiers (11 and 5 in the first and different convolutional layers, individually).

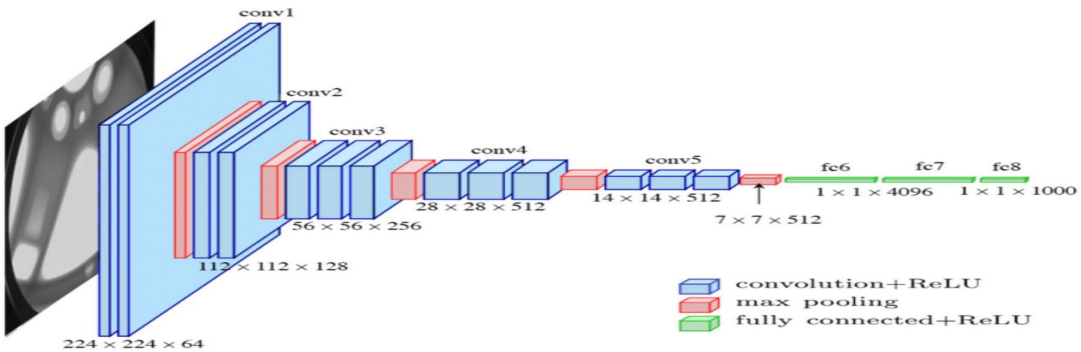


Fig. 2 VGG16 Architecture

2) ResNet50

ResNet50's structure is divided into 4 stages. The network may assume an input image with a height, dimension of multiples of 32, and channel dimension. The network may accept an input image with a height, reach of multiples of 32, and channel range Each ResNet architecture conducts original complication and max- pooling, individually. Each 2- position block is replaced with this 3- position tailback block in the 34- position net, performing in a 50- position ResNet.

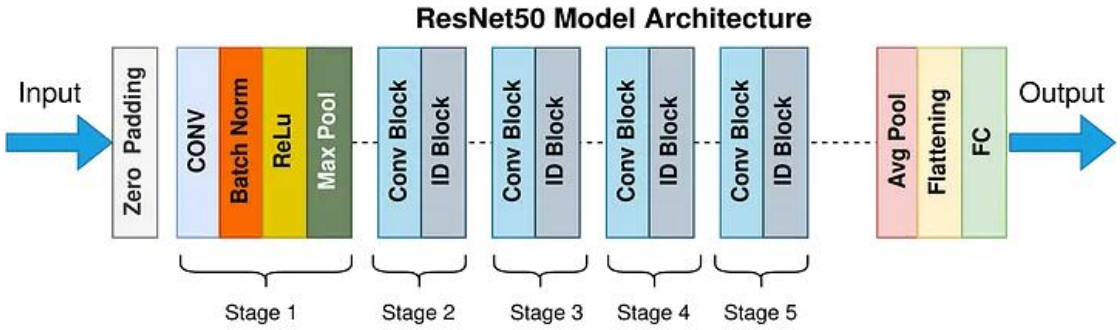


Fig. 3 ResNet50 Architecture

3) AlexNet

In order to create AlexNet, five convolutional layers, three max-pooling layers, two normalization layers, two totally linked layers, and one SoftMax layer were used. Each convolutional layer is composed of convolutional filters and a ReLU function. Max pooling is achieved using the pooling layers.

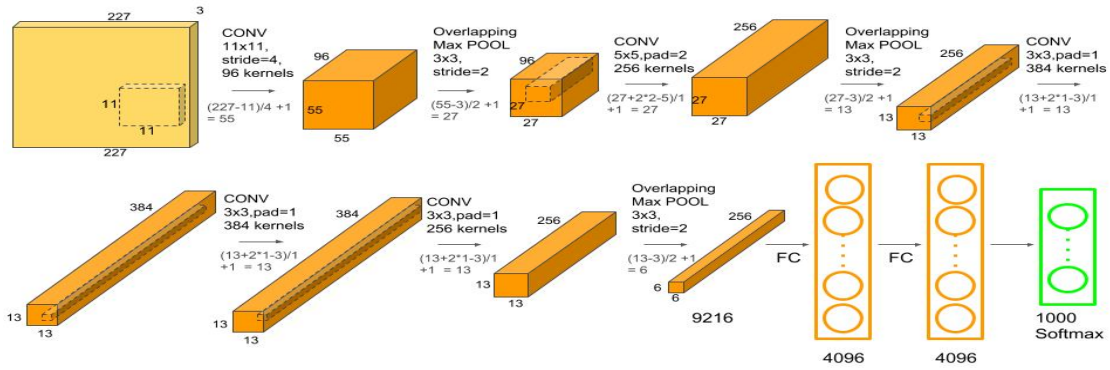


Fig. 4 AlexNet Architecture

4) CNN

CNNs are aimed to automatically learn and extract applicable features from input data through a series of layers.

a) Convolutional Layer

- The convolutional layer is the main structure block of a CNN.
- It applies a set of learnable filters (likewise understood as kernels) to the input data.

b) Activation Layer

- The network becomes non-linear due to the activation layer.
- It applies an activation function like ReLU, sigmoid, and tanh elementwise to the product of the convolutional layer.

c) Pooling Layer

- The pooling layer reduces the spatial range (range and height) of the point maps produced by the convolutional layers.
- It helps to make the learned features steadier to small paraphrases and deformations in the input data.

d) Fully Connected Layer

- The fully connected layer connects every neuron in the former layer to every neuron in the current layer.
- It performs a direct conversion on the input, followed by an activation function.

e) Dropout Layer

- The dropout layer is utilized to prevent overfitting in the network.
- It irregularly sets a bit of the output activations of the former layer to zero during training.

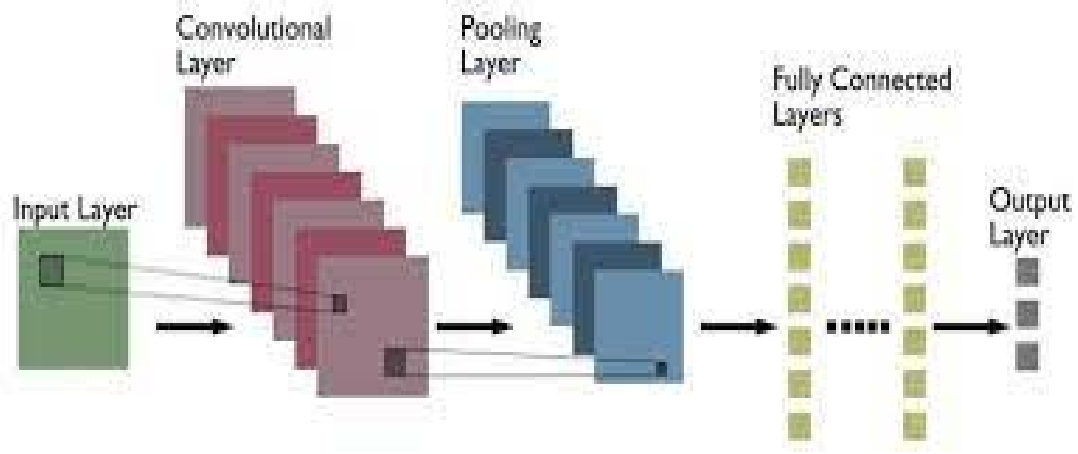


Fig. 5 Modified CNN Architecture

D. Modified CNN Model Architecture

The CNN that has been suggested is not just compact in size but also computationally effective, showing to improved performance on both large and small data sets.

First it applies a standard normalization to comfort zero mean and unit variance, and it performs a scaling by a term and shifting by another term. This result is again passed to the activation function, which provides the input for the coming convolutional layer. These terms are learned during network training via backpropagation to find the best values for the given task.

Pooling layers follow convolutional layers to reduce the number of parameters and range of the point maps. This is achieved so that the algorithm could learn quickly and become more productive by down-sample features it has detected. Overall, the main concept behind pooling layers is that they encapsulate the crucial points of the feature chart, by referring some kind of pooling to it. In our case, max pooling was applied, with both the strides and filter size equalling the output of the convolutional layers is data that represents the features learned from the layer. This data is stored in a matrix which at this point gets leveled out so neurons could have full connections to all activations in the former layer. This allows the network to learn the combinations of these features (in a non-linear way) to make the most stylish prediction.

The suggested network model's structure:

Table I
Proposed model

Layer (type)	Output Shape	Parameters
conv2d (Conv2D)	(None, 148, 148, 32)	896
max_pooling2d (MaxPooling2D)	(None, 74, 74, 32)	0
conv2d_1 (Conv2D)	(None, 72, 72, 64)	18,496
max_pooling2d_1 (MaxPooling2D)	(None, 36, 36, 64)	0

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conv2d_2 (Conv2D)	(None, 34, 34, 128)	73,856
max_pooling2d_2 (MaxPooling2D)	(None, 33, 33, 128)	0
dropout (Dropout)	(None, 33, 33, 128)	0
flatten (Flatten)	(None, 139392)	0
dense (Dense)	(None, 64)	8,921,152

Trainable params: 9,014,595
Non-trainable params: 0

E. Result Analysis

During the evaluation procedure, predictions are framed for the testing data, and the conclusions are collected in the confusion matrix, which reflects the number of true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN). These are stated below:

True-positive (TP): refers to instances of pneumonia that have been correctly classified.
False-positive (FP): refers to instances of pneumonia that were erroneously classed as healthy.
True-negative (TN): refers to instances that are correctly classified as healthy.
False-negative (FN): refers to instances of pneumonia that were erroneously categorized as healthy.
Using all elements we can classify model accuracy, precision, recall, F1 score, negative predicted values, and specificity.

1) Accuracy: It is the ratio of correctly identified pneumonia and healthy cases from all samples.

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad \text{.....1)}$$

2) Precision: Precision, also known as positive predicted value (PPV), is the proportion of pneumonia cases accurately recognized from all samples that were categorized as pneumonia.

$$\text{Precision} = \frac{TP}{TP+FP} \quad \text{.....2)}$$

3) Recall: Sensitivity or recall is the ratio of correctly identified pneumonia cases from the sum of correctly identified pneumonia and incorrectly classified pneumonia cases as healthy, i.e., all the original pneumonia samples.

$$\text{Recall} = \frac{TP}{TP+FN} \quad \text{.....3)}$$

4) F1 – Score: F1 score is the overall measure of the accuracy of the model using precision and recall.

$$\text{F1 – Score} = 2\left(\frac{Precision * Recall}{Precision + Recall}\right) \quad \text{.....4)}$$

5) Negative Predicted Value: Negative predicted value (NPV) is the ratio of correctly identified healthy cases from all samples classified as healthy.

$$\text{NPV} = \frac{TN}{TN + FN} \quad \text{.....5)}$$

6) Specificity: Specificity is the ratio of correctly identified healthy cases from the sum of correctly identified healthy and incorrectly classified healthy cases as pneumonia, i.e., all the original healthy samples.

$$\text{Specificity} = \frac{TN}{TN + FP} \quad \text{.....6)}$$

F. Experiment Outcome

The suggested study used pre-trained CNN models and compared their performance to a new modified CNN technique to get the highest performance for pneumonia identification from 14,000 (4,000 pneumonia and 10,000 healthy) chest X-ray images. Along with the proposed modified CNN, the VGG16, ResNet50, and AlexNet deep models were assessed in terms of performance and compilation time since the purpose of the study is to find the most optimal model.

Prior to being fed into the neural network, pictures were down-sampled to the 256×256 resolution that was best for the models. While 80% of the data was set apart for training, the remaining 20% was set apart for testing. In Figure 6, a sample of pneumonia and healthy chest X-ray image data are presented. To improve classification accuracy, the CNN models were fed with these improved data.

The performance of the models was assessed using the classification training and validation accuracy scores, and Figure 7 displays the resulting accuracy values for the 20 recorded epochs.

The modified CNN model proposed in the research achieved the topmost accuracy for training and validation at 99% and 96%. The AlexNet model accuracy, when applied to the dataset, is 95% for the training set and 91% for the validation set. The VGG16 and ResNet50 models both achieved an identical test accuracy of 93%.

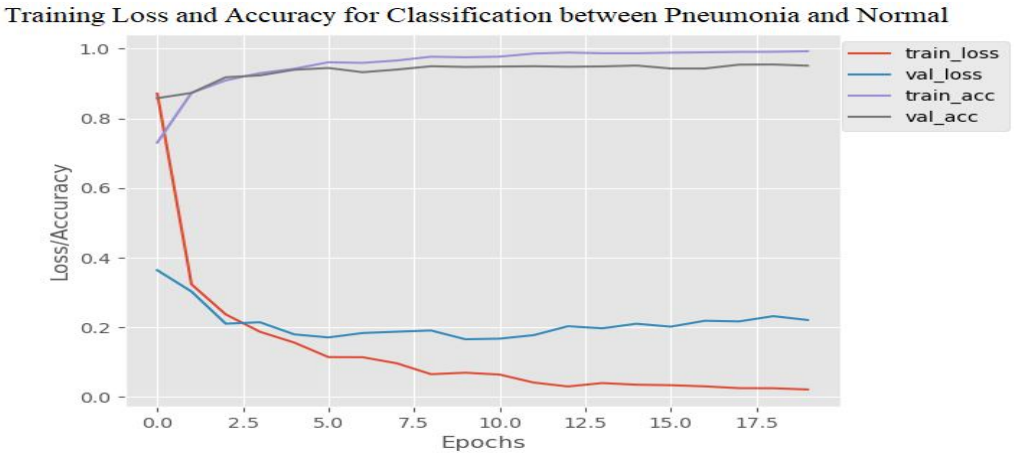


Fig. 6 Modified CNN

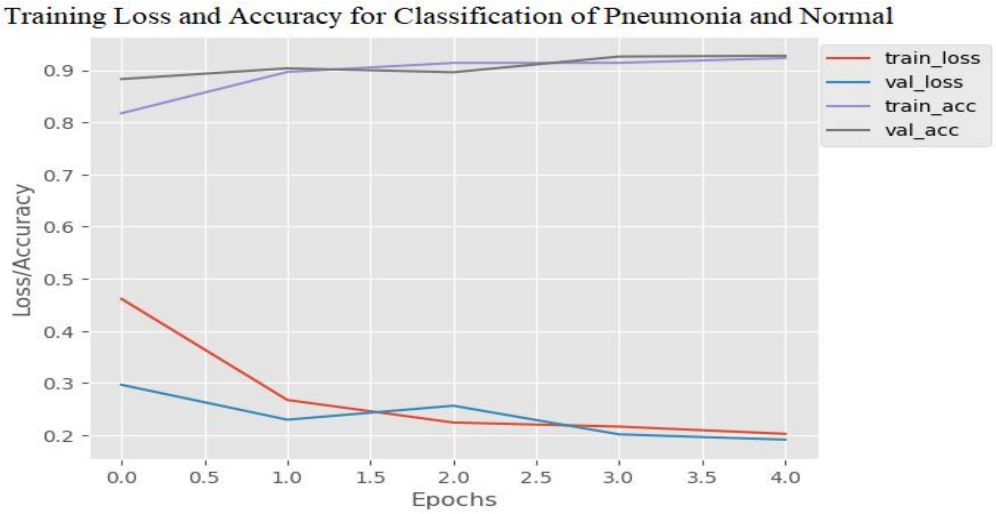


Fig. 7 VGG-16

G. Confusion matrix

Figures display the models' confusion matrix. The test dataset contains 14,000 data samples, 4000 of which are Pneumonia samples and 10,000 of which are healthy samples. Pneumonia and healthy cases are marked by the labels '1' and '0', respectively. From the matrix, modified CNN can successfully identify 9600 healthy samples and 3840 Pneumonia samples. In total, the model could accurately identify a total of 13,440 (96%) data samples from the test set. Similar to this, 93% accuracy was achieved by VGG16 models in identifying 3720 samples of pneumonitis and 9300 healthy patients.

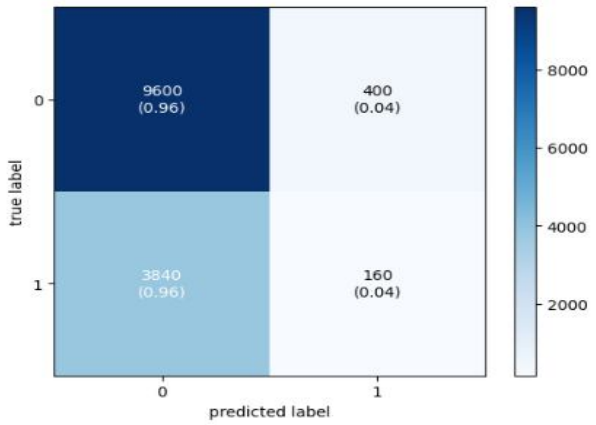


Fig. 8 Modified CNN

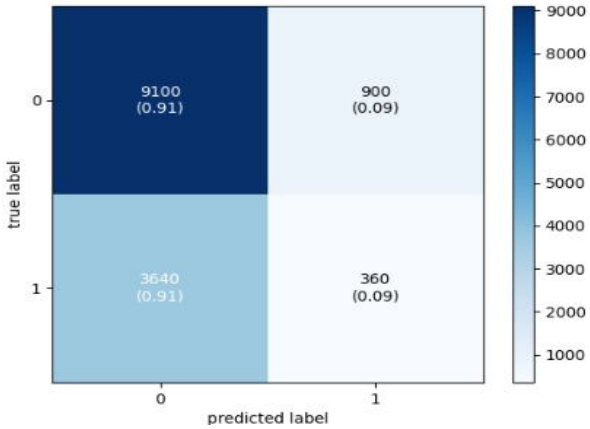


Fig. 9 AlexNet

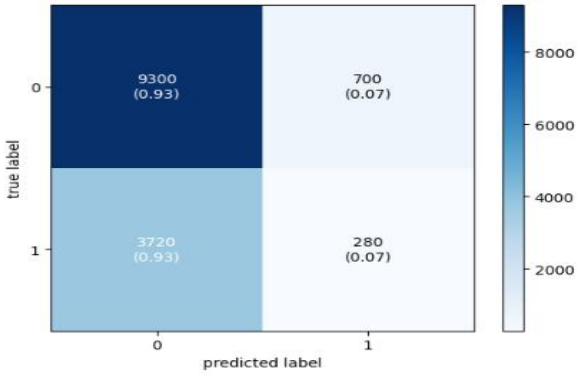


Fig. 10 VGG-16

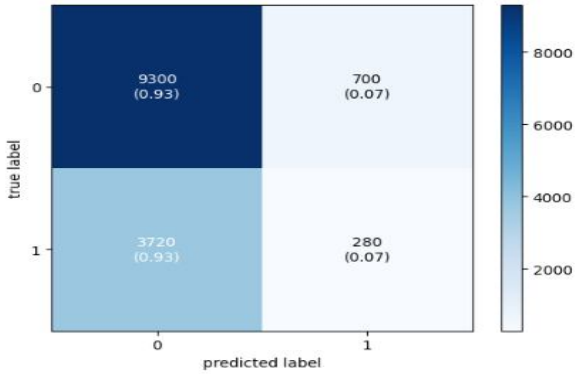


Fig. 11 ResNet50

The confusion matrix in Figure 8 was used to calculate the values of the tags TP, TN, FP, and FN. The values in Equations were used to calculate the models' accuracy, recall, precision, and F1 score. Table II displays the derived values for the performance measures. As shown in the table, the modified CNN has the best overall performance with a precision score of 95%, a recall score of 94%, a specificity score of 96%, NPV score of 95% and an F1 score of 96%, and Final Accuracy is 96%.

Table II
All model accuracy table

Model	Accuracy	Precision	Recall	NPV	Specificity	F1-Score
AlexNet	91%	87%	89%	88%	89%	90%
Modified CNN	96%	95%	94%	95%	96%	96%
VGG16	93%	91%	89%	87%	88%	86%
ResNet50	93%	89%	91%	93%	97%	90%

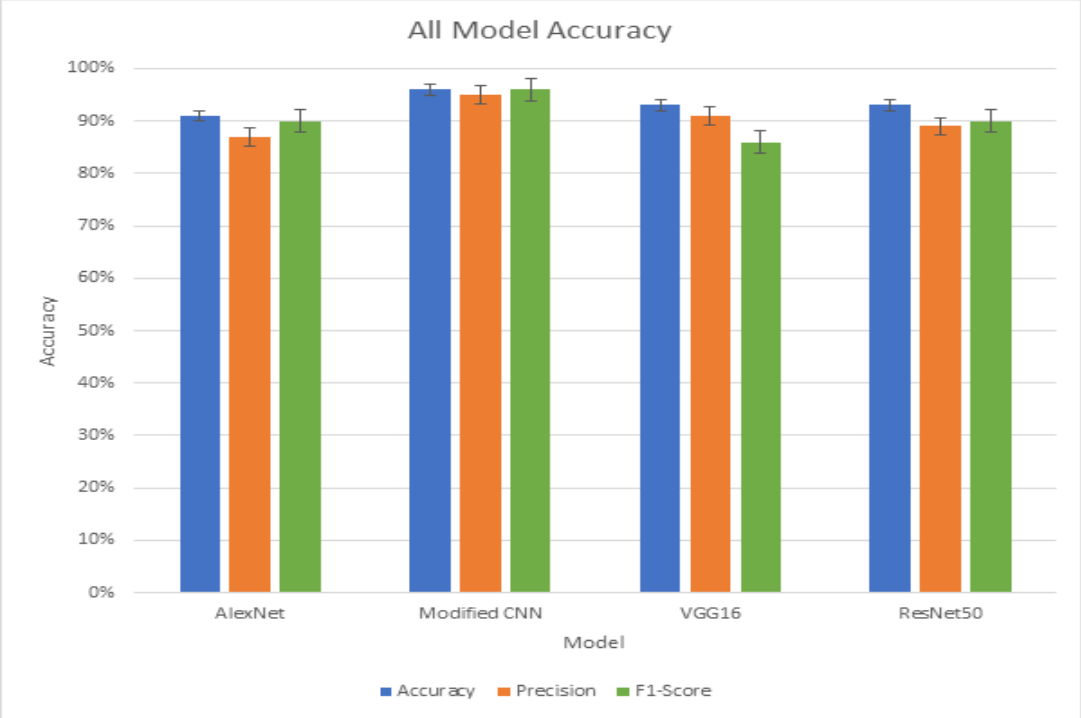


Fig. 12 Different Model Accuracy

Table III
Compilation Time of Model

Model	Compilation Time
VGG16	2 h 27 min 7 s
ResNet50	3 h 1 min 22 s
AlexNet	2 h 54 min 3 s
Modified CNN	1 h 45 min 25 s

Table IV
Modified CNN model performance on training and validation set.

Modified CNN	Recall	Precision	Accuracy	NPV	Specificity	F1-Score
Train	97%	98%	99%	97%	96%	97%
Validation	94%	95%	96%	95%	96%	96%

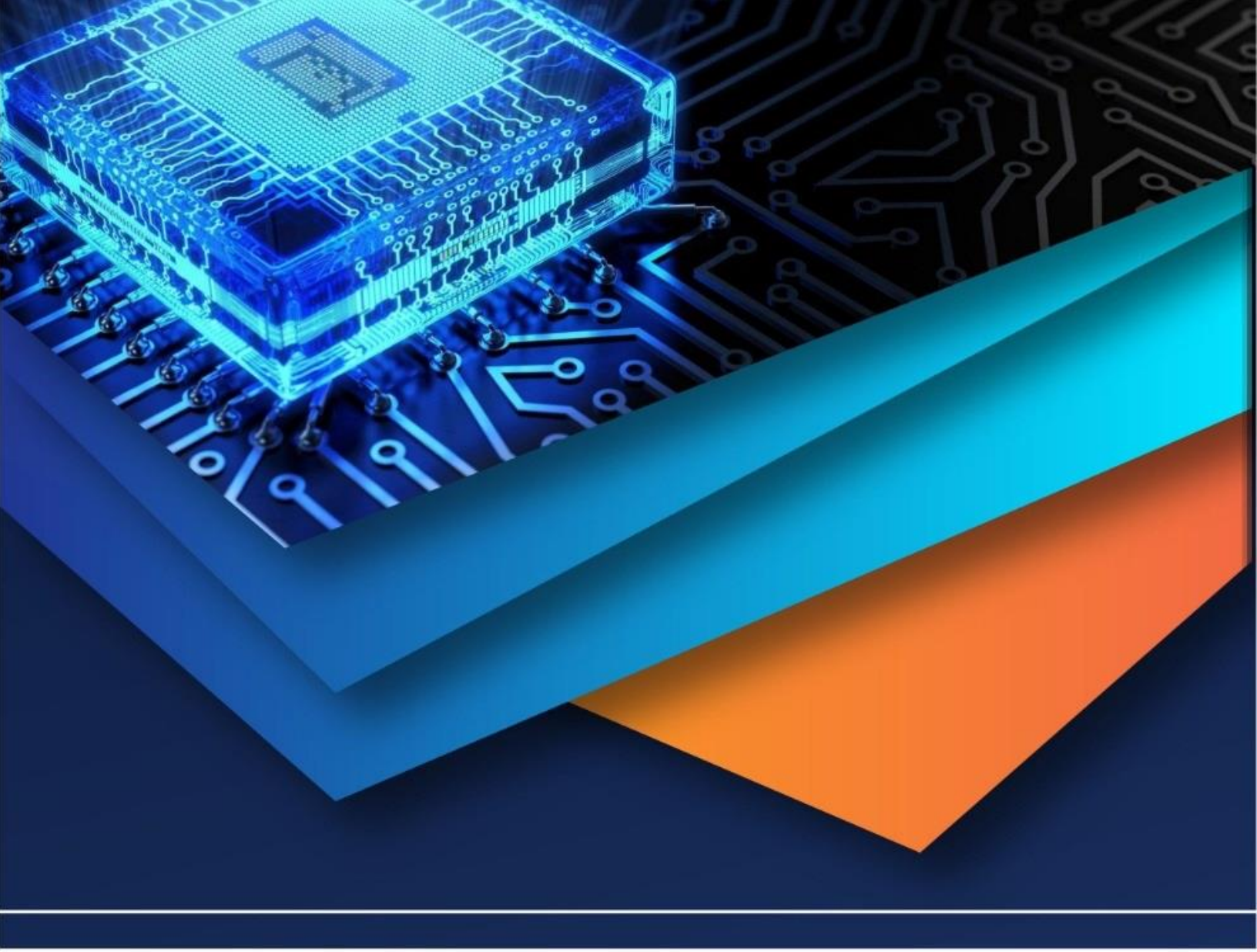
IV. CONCLUSION

The chest X-ray images (Pneumonia, healthy) were applied to dissect lung problems. This study was done to understand the specific strengths and weaknesses of deep-learning models to identify Pneumonia with high accuracy. This is critical for a doctor's decision-making since each has benefits and downsides. Similarly, a physician can be obliged to select only one modality when time, resources, and the patient's health are constrained.

In this work, deep learning techniques were used for automatic Pneumonia detection from chest X-ray images. For this, four different models were implemented. Among them, three models are existing CNN models while the last one is modified CNN, a novel approach suggested in the study for more accurate classification with the least compilation time. The classification accuracy of the modified CNN model is 96% in 1 h 45 min 25 s. The precision, recall, sensitivity, and F1 score of the model are 95%, 94%, 96% and 96%, respectively. This is the best accuracy among these four models. This will be more efficient for doctors to detect disease in a short span of time. In future work, the proposed method could be implemented on a dataset with more classes of diseases such as asthma, and lung cancer, and with more images on the dataset.

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