PREDICTION OF PNEUMONIA DISEASE FROM X-RAY IMAGES USING A MODIFIED RESNET152V2 DEEP LEARNING MODEL

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ABSTRACT

The lungs play a crucial role as the primary components of the human respiratory system, making them susceptible to inflammation and impact lesions in our daily lives. Among all infections, pneumonia holds the distinction of being the most widespread worldwide, with the lungs serving as the gateway for its spread throughout the body. In hospital settings, chest X-rays emerge as the most prevalent diagnostic tool employed to accurately identify pneumonia. Physicians heavily rely on these X-ray images to make precise diagnoses and monitor the progress of pneumonia treatment. Moreover, this type of chest X-ray facilitates the detection of other conditions like emphysema, lung cancer, the positioning of lines and tubes, and tuberculosis. The challenges faced by the existing deep learning models for pneumonia prediction include high computational complexity, prolonged model training times, and a lack of efficient preprocessing techniques. These issues contribute to misdiagnosis and inaccurate predictions of pneumonia. Moreover, the lack of interpretability in many of these models further hinders their acceptance and understanding in clinical applications. This research aims to tackle the challenges presented by current techniques by proposing a customized ResNet152v2 deep learning model. The primary objective is to design and deploy this modified ResNet152v2 model for pneumonia prediction from chest X-rays, achieving high accuracy while minimizing computational complexity and reducing computation time. This model outperformed well when compared with the existing methods and produced accuracy of 99.77%, Sensitivity of 99.86%, specificity of 95.4%, and precision of 99.86%.

Keywords: *Pneumonia, Resnet152v2, X-Ray, Deep Learning, Prediction.*

1. INTRODUCTION

One of the most common illnesses that kill infants, children, and the elderly is pneumonia. Since the lungs are naturally segmented into five lobes, each of which is further divided into segments, physicians can use chest radiographs to determine which lobe a lesion is localized in, despite the availability of simple, safe, effective, and affordable treatments to reduce the likelihood of death from pneumonia in young children [1].A person breathes in a lot of air each day, which is frequently contaminated with bacteria, dust, and other pests. The lungs, which resemble two spongy air sacs in the chest, suck the inhaled air deep inside, where oxygen from the air is transported to

the blood. The lungs are naturally free of germs and are kept sterile by a variety of natural defenses that shield the vital organ from infection. A person's lungs can become infected with pneumonia, a fatal condition. Breathing becomes difficult when an illness is present because the lung fills with water-like substances termed "spectrum". This is a widespread illness that primarily affects young children under the age of five. There is a considerable risk of death when this infection becomes serious[2]. A thorough X-ray examination helps the doctor establish a precise diagnosis and offers useful information about a patient's health. X-rays are occasionally utilized to help with therapeutic treatments or the implantation of tubes or other devices in the body. The most basic type of imaging is done with X-rays, which use ionizing radiation. It records the image using a cassette and an X-Ray tube[3].The risks associated with X-ray examinations vary depending on the individual. The hazards associated with each examination are simply added together to calculate the consequences of having numerous tests. The need for each additional examination should still be determined on its own merits if a person has already had a significant number of X-rays and the cumulative risk is of concern[4]. CNN is widely used in efficient feature extraction and prediction of various diseases[5][6][7]. Around the world, pneumonia is a leading cause of death for those over the age of 65 and young children under the age of 5. If not treated in a timely manner, this infection, which is brought on by a virus, bacterium, or other germ, can be fatal.

In the CXR, pneumonia appears as an area or areas of increased opacity. However, it is never easy for doctors and radiologists to correctly read chest x-rays for the diagnosis of pneumonia. This is mostly due to the fact that a number of different medical problems, including lung cancer, an excess of fluid, etc., can generate opacities in the imager the diagnosis of pneumonia. Interpretation is further complicated by the overlap of tissue features. Because of all these factors, interpreting pneumonia from chest x-rays is difficult and less precise. Additionally, it is necessary to have a procedure for correctly interpreting chest x-ray images. No architecture has ever been successful at classifying diseases from chest x-rays, despite numerous attempts. For instance, the VGG16 network is a smaller network overall. It can be difficult to identify the crucial characteristics required for pathology classification and prediction. This might be the cause of its weak performance. Full Densenet-121 network training required more time, but the results were comparable to those of VGG16. This might result from utilizing such a deep network design. A model's accuracy becomes saturated and starts to deteriorate when too many layers are added.

In this paper, we consider the following research gaps in deep learning models for pneumonia prediction from X-ray images: Firstly, the computational demands of some existing models limit their practical implementation in resource-constrained settings. The main focus is to develop efficient and lightweight models while maintaining high accuracy. Secondly, the negative impact of poor-quality X-ray images, variations in imaging protocols, and data inconsistency on model performance necessitates the resolution of data quality issues and the implementation of standardized preprocessing techniques to achieve reliable and accurate predictions. Lastly, the lack of interpretability in many existing models hinders their acceptance in clinical settings. Understanding the specific features and regions influencing predictions is vital to gaining healthcare practitioners' trust and ensuring seamless integration into clinical practice. Addressing these research gaps promises the development of more reliable, interpretable, and clinically applicable deep learning models, ultimately enhancing patient care and diagnostic accuracy in pneumonia cases. The objectives of this research are (i) to develop a deep learning model for the accurate prediction of pneumonia disease. (ii) To reduce the complexity of the deep learning model (iii) To provide high accuracy in pneumonia disease prediction. (iv) To use chest X-ray images because they are less expensive than CT and ultrasound images.

Section 1 gives an overview of the subject in light of its surroundings. The research challenge and specific objectives are covered. Finally, the topics of research scopes and methodology are covered. Section 2 gives the conceptual perspective needed to grasp the deep learning concepts and the broad literature review addressing the usage of deep neural networks in the diagnosis of diseases through chest radiography images. Section 3 discusses the proposed methodology. Section 4 discusses the results, along with the findings and comparison of the proposed model with different existing techniques. Section 5 is dedicated to the conclusions drawn from the research work and the introduction to the future recommendations.

2. RELATED WORK

Recently, a lot of researchers have explored using deep learning and machine learning models to

largely diagnose diseases. Convolutional neural network (CNN) models are widely used today for machine-generated image data such as CT scans, X-rays, and many other reports that investigate machines[8].Another system uses a tiny network model to look for abnormalities in chest x-rays for deep feature detection; it makes use of four features using the DenseNet121 pre-trained deep learning model[9]. They employed local binary patterns (LBP), scale-invariant feature transform (SIFT), histogram generated gradient (HoG), and GIST with CNN features to classify 14 different chest diseases using these four types of features. A 3D CNN and multi-scale forecasting approach with cube cluster detection and a multi-scale model for cube prediction and lung region detection and segmentation is suggested[10].A system utilized a deep learning Mask R-CNN model for segmentation and detection that made use of both global and local features. Here, it is utilized to segment and diagnose pneumonia using x-ray images that have undergone image processing, augmentation, dropout, and L2 regularization. They accurately identify and segment pneumonia in x-ray pictures; however, they do not discuss various forms of loss. Depending on the issue and the caliber of the supplied images, these user-defined attributes may change. In this manner, model performance can be influenced by human intervention. Prior to human involvement, several techniques were employed[11][12]. On the other hand, Jonathan Long et al. [13] proposed deep learning segmentation methods, and the input images will determine which features must be chosen in these fully machine learning models. The manual feature extractor has been replaced by a fully automatic version. The semantic segmentation deep learning model makes use of a fully convolutional network (FCN). Lihua Li et al.[14] employed the unique texture data to divide up x-ray images. They created models with excellent specificity, sensitivity, and accuracy for their dataset using Markov random fields (MRF).

N. Navab et al. [15] improved the FCN and created a U-Net model using encoder and de coder pathways and accounting for context changes. Additionally, our U-net model per forms well and needs less training time than FCN. U-net models have a proven track record of successfully segmenting biological pictures, but they are being used across all disciplines to get better segmentation outcomes. Yadavendra & Rajpurkar et al. [16][17] suggested a structure-correcting adversarial network (SCAN) model be used to create an accurate semantic segmentation model to separate the lungs and heart disease in chest x-ray images. When the CNN models are applied to these data, the researchers are able to successfully identify the target medical condition, such as cancer and other illnesses. These machine learning models are used to categorize, detect, and segment data accordingly.

Kumar et al.[18] used a COCO dataset to mask R-CNN transfer learning. This R-CNN model is expanded for lung segments and opacity detection in pneumonia-affected patients. The ResNet101 backbone is used for classification, and the configuration class is implemented in accordance with the dataset and requirements. With the classification CNN backbone resnet101 with strides of 4, 8, 16, 32, and 64, we used a single GPU arrangement in this case. Shuai Wang et al.[19] used a framework for a deep learning algorithm and fed this framework with radiographs of pneumonia patients and CT images of patients who tested positive for COVID-19. The aforementioned outcome validates the categorization accuracy of 82.9%. Additionally, a sensitivity of 84% and a specificity of 80.5% were recorded. CNN has also been used to accurately auto mate and diagnose pneumonia using chest X-ray images, to identify the nature of pulmonary nodules via CT scans, and to extract cystoscopy image identification from video[20].

Zhang et al.[21] suggested that deep learning techniques have shown comparable performances to those of humans on a variety of image classification tasks. A rapid and accurate deep learning-based LUS image classification system may help clinicians and reduce their workload. Because LUS is a quick, practical, precise, radiation-free, and straightforward to implement bedside method for the visualization of pulmonary diseases, this model used three CNN-based deep learning models - VGG, ResNet, and Efficient Net - for the detection and classification of pneumonia on a self-made lung ultrasound image dataset. Lichtenstein et al.[22] proposed a model in comparison to CXR and CT using lung ultrasound (LUS), which is a flexible, affordable, radiation-free, and practical imaging modality that is extensively used in most contemporary healthcare systems. Due to the fact that ultrasound imaging is related to the pulse-echo principle of sound waves, doctors in the past frequently undervalued the potential of LUS in the diagnosis of pneumonia. Due to the limited acceptability of LUS devices in clinical practice for the diagnosis of pneumonia and the capabilities of CT and CXR to identify pneumonia, together they could adequately meet the daily examination needs.

Zelin Meng et al.[23] designed a cheXNet, a 121-layer convolutional neural network proposed by researchers at Stanford. It was trained on the ChestX-ray14 dataset. In this study, deep learning algorithms were utilized to identify pneumonia and other chest disorders from chest x-rays with better accuracy than the typical radiologist. Pintelas [24] proposed a new framework for feature extraction and prediction of pneumonia from CT 3D images and used a 3D approach with explainability/interpretability properties. This framework achieved the specificity of 88.5% and sensitivity of 76.5%. Table 1 provides an examination of the approaches currently in use for detecting pneumonia disease.

3.   PROPOSED MODEL

Pneumonia, lung cancer, and most recently COVID-19 are just a few of the illnesses that can affect the human respiratory system. Chest CT or X-ray images are required for the diagnosis of various disorders as they play a vital and important function. Deep learning based systems are just one example of the medical diagnostic tools made possible by computer science. To achieve the objectives of this paper, we have created a deep learning model known as the "modified ResNet152v2" deep learning model. The necessary preprocessing steps are carried out to improve the quality of the dataset.

The following are the specific steps used to complete the tasks:

i) Dataset: In order to achieve the fourth objective of this paper, we used the dataset of the RSNA Pneumonia Detection Challenge from Kaggle, which consists of 1485 numbers of x-ray.

ii) Pre-processing: In this stage, we have concentrated on the activities taken in the previous step to use dataset samples as input for the classification models being trained and predicted. The three methods of pre-processing the data that are taken into consideration are adding, removing, and changing properties. For the purposes of classification and validation, the dataset is further divided into training, validation, and test sets.

iii) Transfer Learning: This step involves training the model. The model transfer learning technique is applied during training.

iv) Classification: For the classification task, the ResNet 152V2 model is employed.

v) Prediction: This phase involves loading a random chest x-ray image into the prediction model and checking it for pneumonia. The output is the accuracy of the prediction.

As shown in Figure 1, this proposed modified Restnet152v2 has the layers input (None, 224, 224, 3), zero padding (None, 114, 114, 64), convolutional1_pad (None, 224, 224, 3), Layer with batch normalization (None, 56, 56, 64), max pool (None, 1L4, 114, 64), activation layer (None, 56, 56, 64), and post_bn (Batch Normalization). This model has a total of 58,532,354 parameters, of which 200,706 are trainable and the other 58,331,648 are non-trainable. The parameters 9472, 256, 36864, 16640, 1024, 512, 131584, 66048, 65536, and 200706 are for the layers Conv2D, conv2_block1_2_conv, conv2_block1_0_conv, conv2_block2_preact_bn, conv3_block1_0_conv, conv3_block1,and dense (Dense), as shown in figures 2 and 3. The model's learning rate is increased through the use of batch normalization. The input is normalized by this layer. After each convolutional layer, batch normalization was applied to all models. The convolutional layer's feature map is down sampled using the pooling approach. Max pooling and average pooling are the two commonly used pooling strategies. In the straightforward CNN model, max-pooling with a pooling filter of size 2x2 was used after each convolutional layer. The inputs are transformed nonlinearly at the end of a layer using the activation function. Rectified Linear Unit, or ReLU, is now the activation function most frequently employed in convolutional neural networks. ReLU was applied at the conclusion of each layer, and the final layer, which had two nodes, was activated using a sigmoid function. The method called dropout is used to lessen the model's overfitting. Dropout allows a few nodes in the layer to be spontaneously selected to remain inactive for a portion of the time. This makes it impossible to use the model with the data. For this classification, dense layers with a dropout of 0.5 were utilized. The dense layer receives the output of the convolutional layer after further flattening it. Convolutional layers' function is to extricate features, and dense layers' function is to classify images. Transfer learning is the practice of applying a model that has already been trained for one specific task to another task, regardless of how similar the two tasks are. The transfer learning method is primarily and most frequently used in computer vision applications. A few advantages of transfer learning are as follows: i) It cut down on a model's training period. ii) The cost of computation decreased. iii) It lessens or prevents model overfitting. iv) It enables massive CNNs to be trained with only a modest quantity of data. v) It

also improves or worsens a model's performance.

3.1 Various stages of the proposed model

The model block diagram is shown in Figure 4. The model is divided into three primary steps, as can be seen from the diagram: data pre-processing, deep learning models for feature extraction, disease detection, and disease prediction, which are detailed step by step.

1. Import all the keras layers, input, and lambda, dense and flatten.

2. In order to preprocess our input, it is important to import Keras, which has a pre- processing library. The image data generator is used to make data augmentation, which means it tries to create some new images like zooming in, zooming out, doing a horizontalslip, and doing a vertical slip that are based on the specific type of parameters that we specified in the image data generator.

3. The image size of 224 x 224 was chosen for training and testing.

4. The include top = false specifies whether the last layer needs to be added or not, and here the last layer is getting removed. The existing weights of the VGG16 layers are not trained using this code for layer inresnet152V2.layers: layer. Trainable = False because the weights have already been trained and fixed. If we did not do this, the model would have to be trained again and again, and good accuracy would not be produced.

5. The number of outputs Classes will be decided based on the number of output classes available in the dataset using folders= glob ('/path /*'). The prediction will have two categories as per the dataset. Our model is combined with VGG input and prediction as output. In the summary of the model, we have two outputs. Categorical cross-entropy is the loss in model compilation, Adam is the optimizer, and accuracy is the metric. The augmentation will be performed with the help of data generation. The ResNet from the Keras library will be imported. The last layer of the VGG16 is removed. Because pneumonia images are black and white, ResNet152V2 (input shape=IMAGE_SIZE + [1]) is used to set the image size as 224 x 224 with a single channel for training and testing. Weight is given as an ImageNet, which is already available in a Keras.

For the new model created from a pre-trained model to perform successfully, transfer learning does not require it to train on a sizable dataset. Since the pre-trained model already contains all of the fundamental characteristics, training will take less time and require fewer memory and compute resources than if the model were trained from scratch. Training from scratch requires learning all of the fundamental features from scratch.

4. RESULTS AND DISCUSSION

To achieve the second objective of the paper, our model achieved better accuracy over 12 epochs; hence, this model uses less time to achieve high accuracy. Evaluation metrics are used to measure the performance of machine learning or deep learning models. There are different types of evaluation metrics that can be used to evaluate models. We have used the confusion matrix; accuracy, recall, precision, and F1 score performance measures for evaluating our proposed model. An analysis of the efficiency of classification methods makes use of a confusion matrix. Binary or multiple class classifications are used in the classification problems.
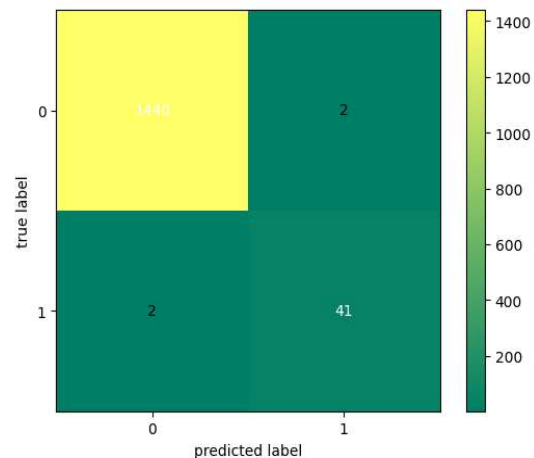

Figure 5: Confusion matrix of the performance of modified Resnet152v2 model

The confusion matrix calculates the precise number of false positive classes, true positive classes, false negative classes, and true negative classes by comparing the actual classes from the source data with a predicted label from the classification technique. Our proposed model predicted 1440 numbers of true positive classes, 2 numbers of falsepositive classes, 2 numbers of false negative classes, and 41 numbers of true negative classes, as shown in figure 5.Accuracy is a parameter that will assess the effectiveness of classification algorithms. Accuracy when used to evaluate a model trained on uneven data will be difficult to achieve or will display a misleading performance matrix.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \qquad (1)$$

Recall is a specific assessment metric that is used to measure the efficiency of the classifier. A correct classification obtained using the classification model is called a recall.

$$Recall = \frac{TP}{TP + FN} \qquad (2)$$

The true positive class is divided by the total of the true positive and false positive classes to determine precision, as written below.

$$Precision = \frac{TP}{TP + FP} \qquad (3)$$

The F1 score evaluation matrix is created by multiplying the precision and recall assessment matrices by two and calculating the sum of the results. The computation of the F1 score evaluation matrices is displayed below.

$$F1\ Score = \frac{(2\ x\ precision\ x\ recall)}{(precision + recall)} \qquad (4)$$

Our proposed model produced 99.77% of accuracy, 99.86 % of sensitivity, and 95.4 % of specificity, 99.86 % of precision, 0.14 % of negative predicted value, 4.65% of false positive rate value and 99.86 % of F1 score as shown in figure 6.
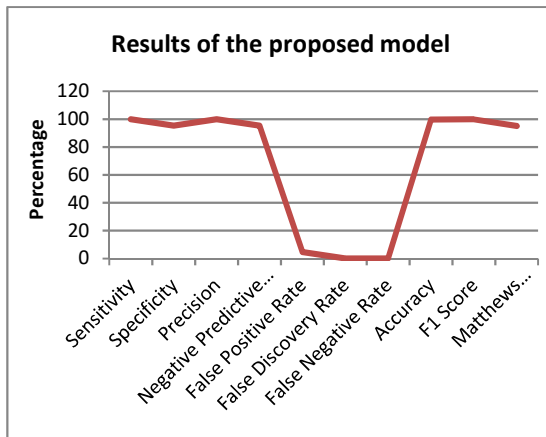

Figure 6: Results of the modified Resnet152v2 model in terms of its various performance measures

As shown in the figure 7, our model produced loss values of 2.4230, 0.3970, 0.4804, 0.3477, 0.4786, 0.2979, 0.1123, 0.3248, 0.1678, 0.1218 and accuracy values of 0.9527, 0.9767, 0.9752, 0.9850, 0.9940, 0.9895, 0.9932 and validation loss of 0.2695, 0.3246, 0.4031, 0.5537, 0.1213, 0.0933, 0.1391, 0.0539, 0.0546, 0.2047 and validation

accuracy of 0.9865, 0.9872, 0.9797, 0.9647, 0.9925, 0.9895 and 0.9955 for 10 epoch. The train loss starts at 0.1123 and ends with the highest value of 2.4230. Validation starts at 0.0539 and ends at 0.5537. Our model produced loss values of 0.2356, 0.1055, 0.0430, 0.2718, 0.0815, 0.1073, 0.0328, 0.1008, 0.2889, 0.2028, 0.1014 and 0.1268 as shown in Figure 8, and accuracy values of 0.9872, 0.9932, 0.9955, 0.9887, 0.9940, 0.9895, 0.9917 and 0.9925. The train loss starts at 0.0328 and ends with the highest value of 0.2889. Validation loss starts at 0.0182 and ends at 1.1205.
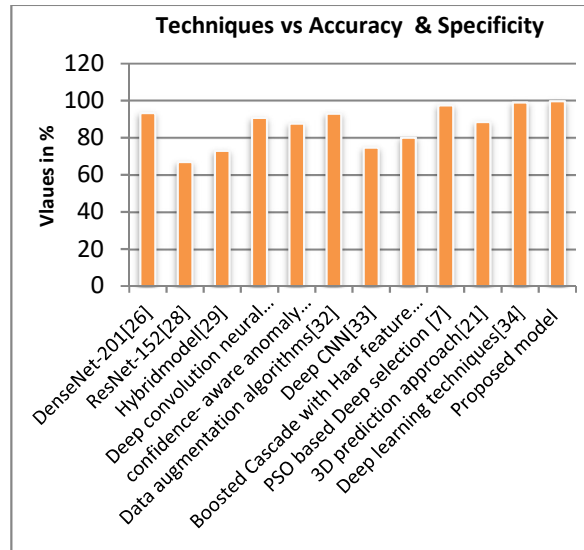

Figure 9: Comparison of the proposed model for Pneumonia disease prediction with existing methods

Our proposed deep learning model is compared with the existing methods as shown in figure 9. When compared to existing methods such as DenseNet-201, ResNet-152, the hybrid model, the deep convolution neural network, the confidence-aware anomaly detection model, the data augmentation algorithms, and the boosted cascade with the Haar feature, Our proposed deep learning model outperformed well on the pneumonia image sets with a size of 224 x 224 pixels and produced 99.55% accuracy and 99.77% accuracy for both the 10 and 12 epochs, respectively. The research paper effectively addressed the identified research gaps by developing a highly interpretable model. This was achieved by incorporating additional changes to the layers, setting appropriate weights in the networks, and implementing effective preprocessing techniques to improve the dataset's quality. The proposed ResNet152v2 deep learning model demonstrated remarkable accuracy while requiring

less computation and training time. In comparison to all existing methods, the proposed model showcased superior performance, achieving significant differences in accuracy of 5.22%, 31.52%, 25.52%, 7.84%, 10.95%, 5.49%, 23.82%, 18.52%, and 0.22%.

5. CONCLUSION AND FUTURE WORK

This research paper proposed a modified ResNet-152v2 model for predicting pneumonia diseases, by developing a highly interpretable model. This was achieved by incorporating additional changes to the layers, setting appropriate weights in the networks, and implementing effective preprocessing techniques to improve the dataset's quality. The pneumonia dataset with 1485 pneumonia images is preprocessed and converted into two different image sizes. The proposed model outperformed well on a pneumonia dataset with 224 x 224 pixels of image size, and 99.55% of accuracy was produced for 10 epochs. A result of 99.77% accuracy on a 224 x 224 pixel image data set for 12 epochs was produced. The proposed model produced better accuracy, precision, recall, sensitivity, and specificity values as results on both datasets when compared with existing methods for less computation time. In our future research, we aim to integrate our proposed model with deep learning models and ensemble techniques. By employing these ensemble techniques, we expect to achieve even better results in various scenarios. We plan to evaluate the model's performance on diverse datasets, seeking to improve its overall accuracy, particularly on different disease datasets. We will evaluate its performance on datasets related to lung diseases and other respiratory conditions. This cross-disease validation will enable us to assess the model's potential for detecting similar radiological patterns and its capability to distinguish between different lung abnormalities. Such an investigation will provide valuable insights into the broader applicability of our model and its effectiveness in diagnosing a wide range of lung-related health issues.

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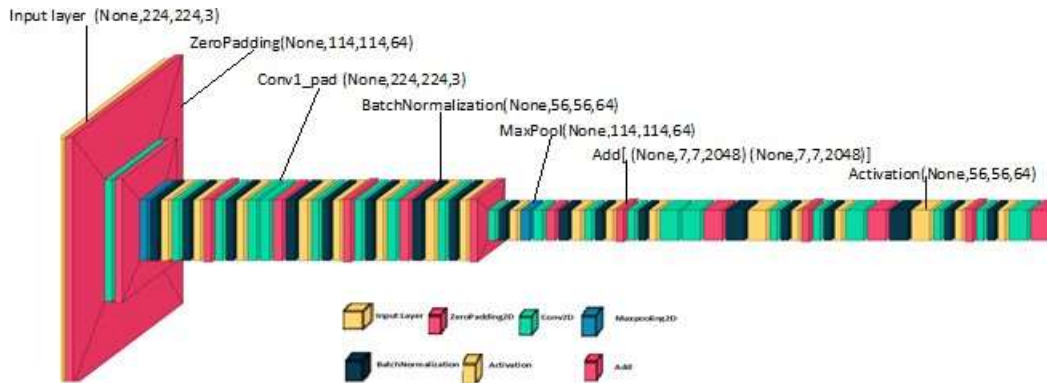[34] N. H. Singh, "Deep Learning Techniques for Prediction of Pneumonia from Lung CT images," pp. 1–19, 2023.

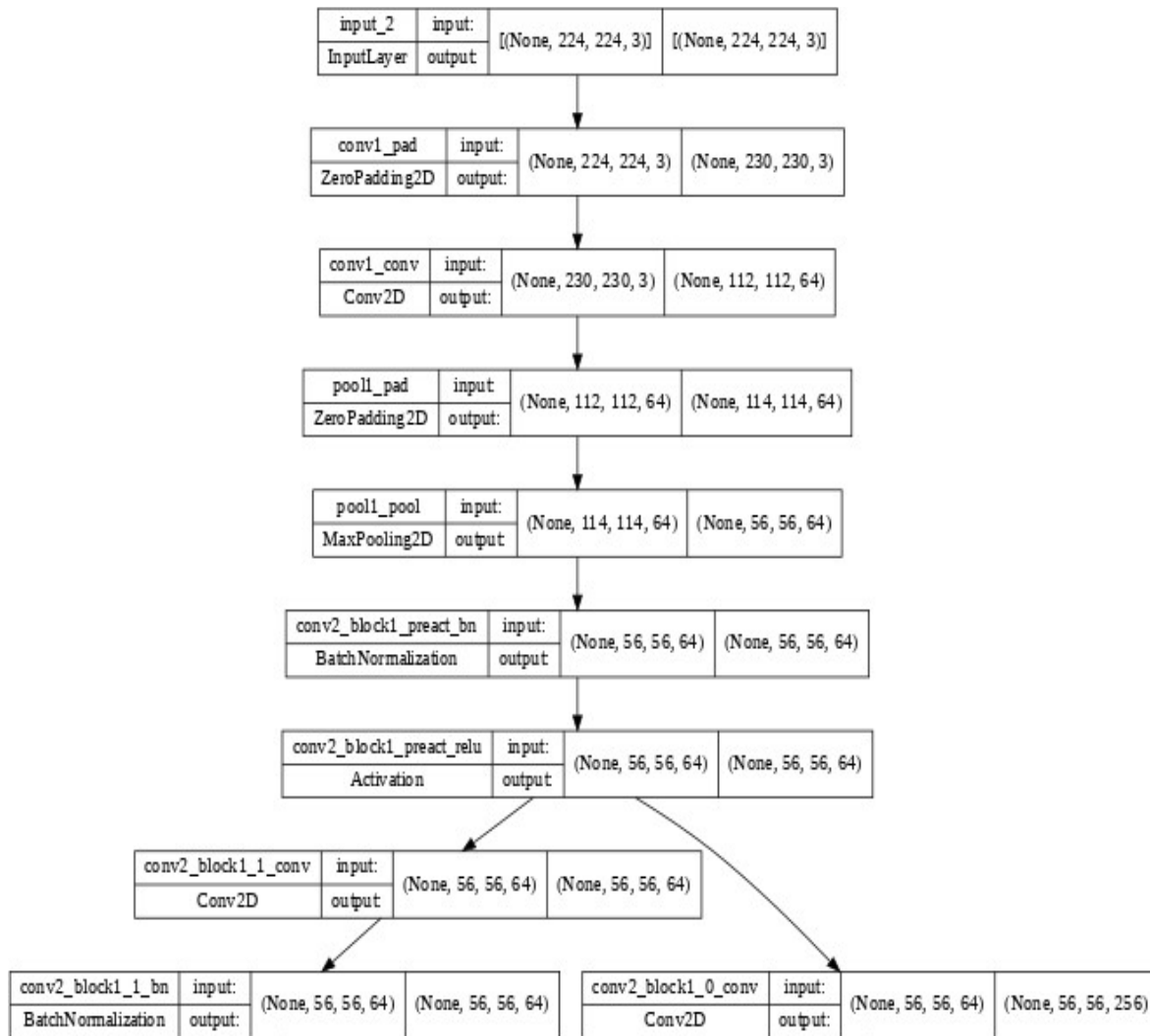*Figure 1: Overall architecture of the proposed modified ResNet152v2*

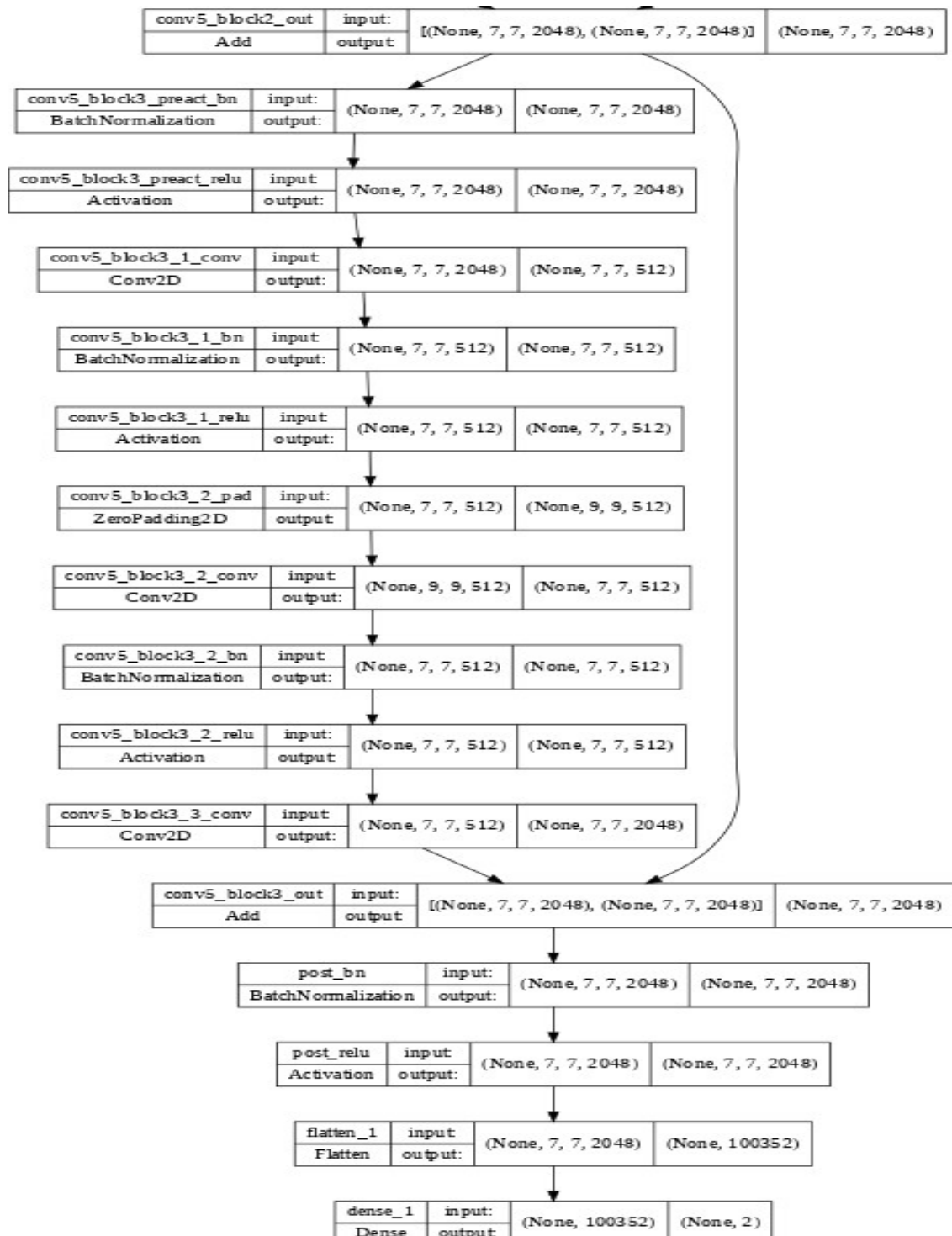*Figure 2: First page of the modified Resnet-152v2 model that was constructed*

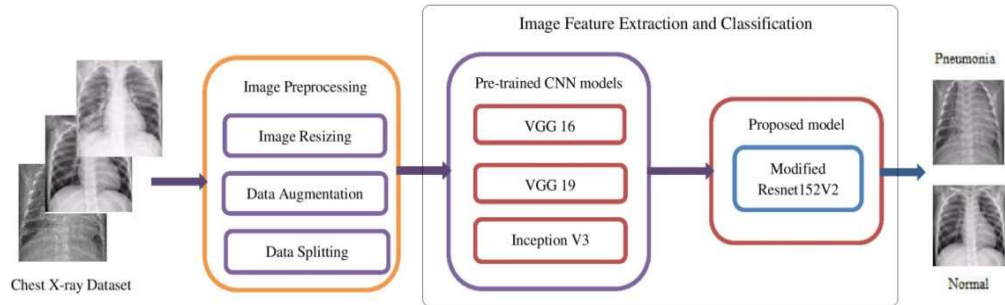*Figure 3: Last page of the modified Resnet-152v2 model that was constructed*

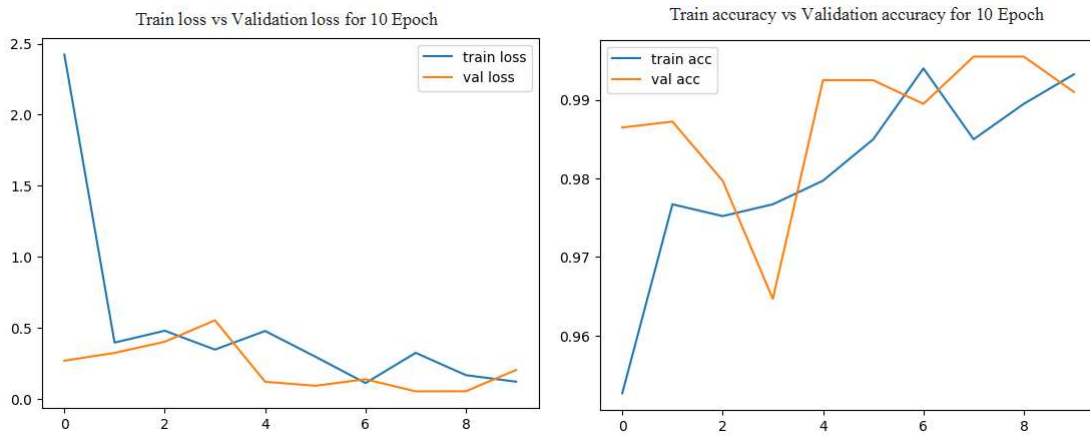*Figure 4: Block diagram of the proposed pneumonia disease prediction model.*

Figure 7: The proposed model's training, valid accuracy, and loss results on the Pneumonia image dataset for 10 epochs
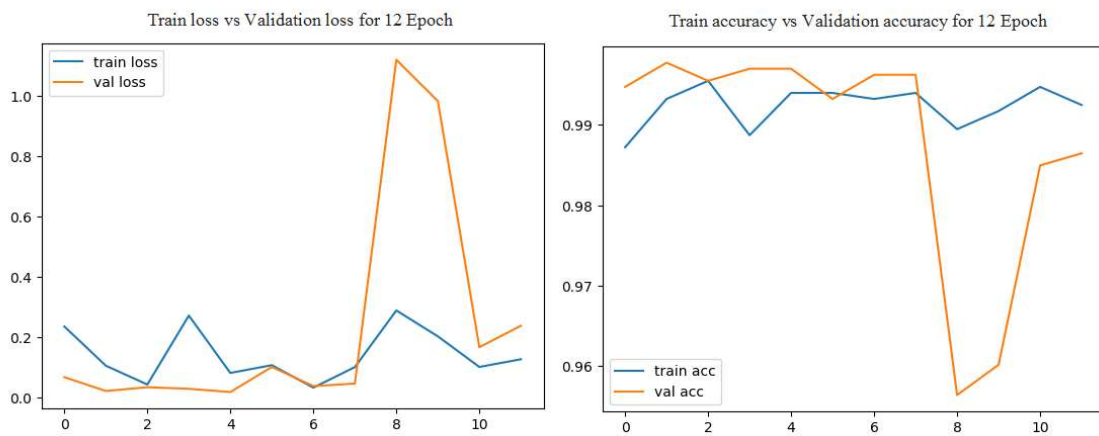

Figure 8: The proposed model's training, valid accuracy, and loss results on the Pneumonia image dataset for 12 epochs

Table 1: Literature review on Pneumonia disease detection and classification

S.No	Methods	Performance metrics(Accuracy)	Advantages	Gap identified
1	InceptionResNet-V2[25]	98.81%	Reusing previously trained models on a huge dataset.	Misrepresented as having complicated and difficult pattern recognition problems, low performance, and being unsuitable for use in real world applications.
2	DenseNet-201[26]	93.3%	Reusing models that have been trained on a huge dataset.	There will be 5% performance degradation be- tween fold 1 and fold 2.
3	ResNet-50 pre-trained on ChestX-ray14 dataset [27]	99.82%	Reusing models that have been trained on a huge dataset.	Misrepresented in a complicated and difficult pattern recognition problem.
4	ResNet-152[28]	67%	Creation of synthetic data to balance the data classes because there are few medical data	The classification results (67% accuracy rate) are not suitable for applicationin real-world situations.
5	Hybrid model[29]	73% to 83%	When diagnosing and treating patients with schizophrenia, psychiatrists canreceive a timely warning about the potential onset of pneumonia.	Patient data are frequently not publicly accessible and are kept private while being used to construct classification models.
6	Deep convolution neural network (CNN)[30]	90.68%	For difficult patterns, learning features are automatically enabled.	Simple, linearly advancing CNN models cost more to compute without significantly improving performance.
7	Confidence-aware anomaly detection model[31]	87.57%	The model's performance was enhanced by presenting the detection problem as asingle-class issue.	The dataset's sensitivity was too low (71.70%) for practical usage.
8	Data augmentation algorithms [32]	93.03%	Sort data on pneumonia from a set of X-ray pictures into positive and negative categories.	Additionally, larger images needed more training and computation time.

9	Boosted Cascade with Haar feature[3]	80%	When it comes to sparse form refinement, this model requires more time.	Reduce the number of true positives
10	Deep CNN[33]	74.7%	When evaluated in cutting-edge healthcare systems, this model performs better in terms of generalization.	Patient sex is not predicted well by this approach, which performs considerably better at predicting radiograph view than sex.
11	Deep Learning techniques[34]	98-99%	Few deep learning techniques were used for predicting pneumonia disease.	LSTM took more time to extract the features.