Classification of Medical Images Through Convolutional Neural Network Modification Method

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The COVID-19 positive, tuberculosis and pneumonia, share the trait of being able to be identified using radiological investigations, such as Chest X-ray (CXR) images. This paper aims to distinguish between four classes, including tuberculosis (TB), COVID-19 positive, healthy, and pneumonia using CXR images. Many deep-learning models such as a Convolutional Neural Network (CNN) have been developed for the Classification of CXR images. Deep learning-based models such as CNN offer significant advantages over traditional methods in the classification of diseases like TB, COVID-19, pneumonia, and healthy states. They provide higher accuracy, automation, early detection, reduced subjectivity, and resource efficiency, ultimately leading to improved patient care and outcomes. However, well-liked CNNs are massive models that require a lot of data to achieve optimal accuracy. In this paper, we propose a new CNN model that can be used to distinguish between different classes of CXR images. This model proves to be effective in classifying different diseases such as pneumonia, COVID-19, and tuberculosis. This study has used 6326 CXR images dataset containing COVID-19 positive, tuberculosis, and pneumonia and has normal images. In this dataset, 80% of the CXR images are taken for the training purpose and 20% are taken for the validation purpose, of the proposed CNN model. The proposed CNN modified model with parameter adjustment as well as using categorical cross-entropy as a loss function obtains the highest classification accuracy of 98.51% with a precision, recall, and F1 score of 0.98, 0.985, and 0.98 respectively.

Keywords: Image Classification; Fuzzy Membership; VGG-19 Modified Model

Introduction:

COVID-19 has set historical records on a global scale. More than 116 million confirmed cases and more than 2.5 million fatalities had been recorded by the World Health Organization (WHO) as of 8 March 2021. The SARS-CoV2 virus, which causes the infectious disease COVID-19, is easily spread by contact and the air and has a serious impact on the lungs of those who contract it. The COVID-19 virus can develop consequences, including pneumonia, as well as other symptoms that may be mistaken for those of other infections [1].

In contrast, the infectious disease tuberculosis, which is caused by Mycobacterium tuberculosis, also results in antibiotic resistance and the death of tissue in various sections of the body, primarily the lungs. The WHO estimates that tuberculosis kills over 1.5 million people worldwide each year, making it the most lethal infectious disease. An estimated 10 million people contracted TB in 2019 alone [1].

As a result, COVID-19, pneumonia, and tuberculosis all have the ability to be identified by radiological procedures like CXR images. Prior to the development of deep learning (DL) frameworks, feature extraction and classification methods were used to classify medical images. Medical image classification through Convolutional Neural Networks (CNNs) is an application of deep learning that has revolutionized the field of medical imaging. With the increase in availability and quality of medical imaging data, there has been a growing demand for automated and accurate image classification tools that can assist clinicians in their diagnoses and treatment decisions. CNN is a neural network that is designed specifically for image analysis tasks. They are made up of several layers of interlinked nodes able to recognize and extract features from pictures. In medical image classification, CNN is typically trained on large datasets of labeled images, where the labels represent the different diagnostic categories or pathologies of interest. The process of medical image classification through CNN involves several steps. First, the input medical images are preprocessed to ensure that they are in a suitable format for analysis. Next, the CNN is trained on a dataset of labeled medical images, using a process called backpropagation to adjust the weights of the network to optimize its performance on the training data. Once the CNN has been trained, it can be used to classify new medical images by passing them through the network and observing the output of the final layer, which represents the predicted class label.

CNN-based models have been successfully applied and used to create dependable, quick, and accurate detection methods against COVID-19 and other respiratory diseases, demonstrating their potential for transforming medical diagnostic procedures. This is due to the models' deep learning capabilities and intricate architectures [2][3][4][5][6][7]. This is why the current study's objective is to determine whether it is possible to distinguish between healthy patients and those with COVID-19 positive, pneumonia, and TB using early automated classification of CXR images. To determine if a patient is normal or has a lung illness, we have built a deep transfer learning pipeline called the VGG-19 modified model. The VGG-l9 is ideally modified in the suggested network. Transfer learning techniques are implemented using pre-trained networks on the VGG-19 model. We put our suggested network to the test for four ICTIS 2024 class classification problems (TB, pneumonia, healthy, and COVID-19 positive).

To the best of our current understanding, this work is an important attempt to investigate the viability and effectiveness of using early automatic identification and differentiation methods with a particular focus on differentiating between people who are COVID-19 positive, suffering from pneumonia or tuberculosis, and those who are considered healthy using only CXR images as the primary diagnostic modality. The suggested model has demonstrated robust and enhanced performance over the state-of-the-art methods for the classification of 1ung disorders in all of our datasets and has been able to perform optimally in a variety of multi-class tasks. Moreover, it has demonstrated its versatility and efficacy in intricate diagnostic circumstances by continuously outperforming a wide range of multi-class tasks. This work represents a major step forward in using computational approaches to support early and precise identification of respiratory diseases, especially when it comes to using CXR imaging to differentiate COVID-19 from other related disorders. The following are this paper's major contributions:

- The building of a new convolutional neural network, named VGG-19 modified model, for robustness and more precise classification.
- Evaluating the VGG-19 modified model's precision and robustness on CXR image datasets with many classes of labels (TB, pneumonia, COVID-19 positive, and healthy).
- The comparison of the VGG-19 modified model with the other state-of-the-art architectures such as VGG-16, DenseNet-121, and ResNet-50.

The pattern of the paper is organized as follows:

- Section I introduces the specified title.
- The associated works are briefly summarized in Section II.
- The preprocessing approach and the suggested methodology are presented in Sections III and IV respectively.
- The numerical outcomes of our methodology on the CXR dataset are shown in Section V.
- Section VI presents the final conclusion.

Literature Review:

The classification of CXR images has been the subject of extensive research in recent years. A brief summary of these research initiatives is provided below: Jaiswal et al. [8] introduced a Mask-Region-based CNN model, aimed at automating the classification process of pneumonia cases utilizing CXR images. Bharati et al. [9] concentrated on making use of a hybrid deep learning system that blends several modern techniques, such as data augmentation approaches, spatial transformer networks (STNs), and Convolutional Neural Networks (CNNs) with VGG architecture. Bharati et al. sought to create a complete framework that may improve the resilience and accuracy of classification tasks by combining these disparate components, especially when it came to the diagnosis of medical disorders from CXR pictures.

CNNs are well known for their ability to extract features and recognize patterns; this helped to provide the groundwork for the proposed system's learning capabilities. Additionally, the utilization of VGG architecture, known for its depth and effectiveness in image classification tasks, further bolstered the model's performance. To address potential spatial variations and distortions within the CXR images, Bharati et al. integrated a spatial transformer network (STN), enabling the network to dynamically adapt and rectify spatial transformations to enhance its adaptability and resilience to image variations. Furthermore, to augment the training dataset and mitigate overfitting, data augmentation techniques were employed, facilitating the generation of diverse training samples by applying transformations such as rotations, translations, and scaling. Through extensive experimentation and training on the National Institutes of Health (NIH) CXR dataset, Bharati et al. reported notable results, achieving an accuracy rate of 73%. They trained their network in the NIH CXR dataset and achieved 73% accuracy.

Pereira et al. [10] introduced the RYDLS-20 network model, representing a significant advancement in the field of medical image analysis. The primary focus of their study was on the diagnosis of COVID-19 utilizing deep learning techniques. The RYDLS-20 model, meticulously designed and optimized by Pereira et al., achieved an impressive F1 value of 89%, underscoring its efficacy and reliability in accurately identifying COVID-19 cases. Notably, the dataset utilized in their study exhibited a considerable imbalance, consisting of 2000 healthy cases compared with only 180 patients afflicted by COVID-19. Without using any cross-validation steps, the RYDLS-20 model's classification performance was shown, demonstrating the model's capacity to attain high accuracy even in the absence of such validation processes. This omission may cause questions about how well the model generalizes to new data, but the stated F1 value indicates that there is a good chance that it will be useful in everyday life.

Song et al. [2] built a COVID-19 patient identification system for computed tomography (CT) scans called deep pneumonia that is based on deep learning. After manually segmenting the lung area using a DL network, they classified healthy or COVID-19 patients. They combined ResNet50 with a feature pyramid network (FPN) and an attention model to create their own network, which they called DRE-Net. The investigation's primary strengths were highlighted by the study, which used multi-vendor datasets from three different hospitals and showed impressive sensitivity (95%) and specificity (96%), as well as a quick diagnostic time of only 30 seconds per patient. Several drawbacks can be identified in this study. Firstly, the reliance on semi-automatic lung segmentation raises concerns about the consistency and accuracy of the segmentation process, potentially introducing variability in the analysis. Secondly, the classification of datasets solely based on CT images without stratification according to factors such as advanced age, underlying diseases, or the presence of pleural effusions could lead to biased results.

Chen et al. [7] applied 46, 095 anonymized images of 106 hospitalized patients at Renmin Hospital of the University of Wuhan to train their deep network. Of them, 51 patients had COVID-19 pneumonia confirmed by a laboratory, and the remaining 55 patients had various illnesses. The lungs were divided into sections, and any scar tissue was located using a U-net++ network. The time difference between the radiologist and the model was compared using a two-tailed paired Student's t-test with a significance level of 0.05. The main strengths of this work are the huge and equally distributed training dataset, the good classification accuracy (above 95%), and the use of three experienced radiologists who considered inter-observer variability to obtain the ground truth.

Ozturk et al. [11] leveraged the Dark Covid Net model as a tool to assist radiologists and medical professionals in diagnosing COVID-19. This model demonstrated a remarkable accuracy in binary classification, achieving an impressive 98.08% accuracy rate in distinguishing between COVID-19 cases and healthy individuals. Additionally, in more complex multi-class classification scenarios where the model had to differentiate between pneumonia, COVID-19, and healthy cases, it maintained a respectable accuracy of 87.02%.

A brand-new transfer learning-based model for the categorization and detection of pneumonia (both viral and bacterial) was put out by Rahman et al. [12]. To determine which pre-designed CNN architecture had the greatest performance, they suggested comparing the various ones. The results demonstrated that, of all the utilized architectures, DenseNet201 demonstrated remarkable accuracy rates, with a noteworthy 98% accuracy in differentiating between chest X-rays that showed no symptoms and those that showed indicators of pneumonia (bacterial or viral). In addition, when the model was required to distinguish between cases of bacterial, viral, and normal pneumonia, it performed admirably, scoring 93.3%. In this particular subset, the model had a robust accuracy rate of 95% when it came to differentiating between pneumonia caused by bacteria and viruses.

Michail et al. [13] presented the DenResCov-19 deep transfer learning model to identify patients with Pneumonia, TB, COVID-19, or health based on the CXR images dataset. Their method combines the previous ResNet-50 and DenseNet-121 architectures with an extra layer of convolutional neural network (CNN) building blocks to improve the model's functionality. They were able to leverage the advantages of both networks by combining these topologies, using ResNet's residual connections to mitigate vanishing gradient problems and DenseNet's dense connections for feature reuse. Their network was tested on the CXR image dataset, which included several classifications such as COVID-19, pneumonia, TB, and normal cases. With careful tweaking and training, the network demonstrated an amazing accuracy rate of 96.40%. This significant accuracy highlights the potential of deep transfer learning approaches in the field of medica1 image analysis, providing promising paths for the early and accurate diagnosis of a variety of respiratory conditions, including COVID-19, and enabling prompt intervention and treatment plans.

Dataset Description:

We have collected a large set of CXR images and applied data augmentation techniques to increase data diversity in an attempt to improve classification accuracy. The study employed a dataset consisting of 6326 CXR images that were obtained from the free software platform Kaggle. This dataset contains pictures of a variety of diseases, such as pneumonia, tuberculosis, and COVID-19-positive patients, in addition to typical cases.

Preprocessing:

Fuzzy set theory and Gaussian kernel-based enhancement are used to improve the performance of CNN-based image classification. Fuzzy set theory is a mathematical framework that deals with uncertainty and imprecision. It allows for the representation of a concept with degrees of membership instead of a binary yes/no value. In the context of image classification, this means that instead of assigning a single label to an image, we can assign multiple labels with different degrees of certainty. This approach can be particularly useful when dealing with images that contain ambiguous or overlapping features.

Fuzzy set theory involves the use of membership functions to assign degrees of membership to elements of a set. Let X be the set of possible image features, and let A be a fuzzy subset of X. The membership function for A is denoted by $\mu A(x)$, where x is an element of X, and $\mu A(x)$ is a value between 0 and 1 that represents the degree to which x belongs to A. For each image feature x, we compute the membership function values $\mu A_1(x)$, $\mu A_2(x)$, ..., $\mu A_n(x)$ for each of the fuzzy subsets A_1, A_2, ..., A_n. Then we apply the Gaussian kernel function to the image to smooth it and reduce noise.

To improve the quality of the images, we experimented with a range of image enhancement methods, such as Histogram Equalization (HE), Contrast Limited Adaptive Histogram Equalization (CLAHE), and Fuzzy Contrast Enhance (FCE). Each of these methods was applied to a single dataset image. Figure 1 displays the outcomes of various methods. HE and CLAHE have demonstrated impressive results in denoising and improving the images, as illustrated in Figure 1. But it may also be possible to see that using CLAHE intensifies the color of the bones, which could have an impact on how well the classification model performs because the rib and sternum bones may be identified by the neural network as the main X-ray detection features [14].

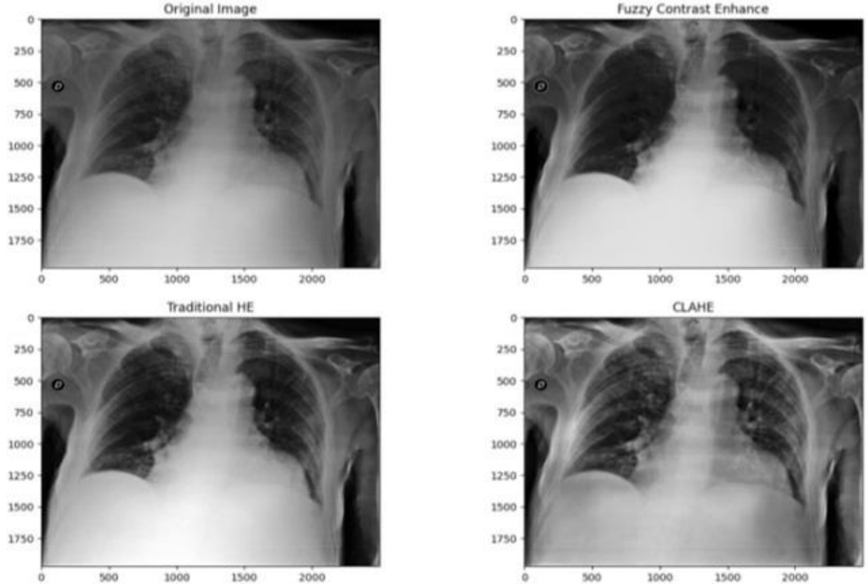


Figure 1: Comparison of different image enhancement techniques

Thus in our suggested framework, histogram equalization was chosen as the image-enhancing method. Our second step is to split the dataset. The dataset of CXR images is divided into two groups. 80% of the CXR images (5061 images) are used for training the proposed model, and 20% (1265 images) are reserved for validating the model. The images in the dataset originally had different sizes (512 × 512) pixels. To make them uniform and suitable for deep learning, they are resized to a smaller size of 112 × 112 pixels. This resizing step ensures that all images are in the same format and size, making it easier for the model to analyze them. Resizing techniques' underlying theory is covered in [15].

Methodology:

In this section, we will discuss the methodology of the proposed network. We started with the VGG-19 model, which is CNN architecture, designed for image classification. VGG-19 is a well-known CNN architecture with 19 layers, consisting of 16 convolutional layers followed by 3 fully connected layers. The model VGG-19 is known for its effective feature extraction. It uses 16 convolutional layers organized into 5 groups. After each group of convolutional layers, there is a max-pooling layer. These convolutional layers are designed to capture the important features from the input images. They use (3, 3) filters with Rectified Linear Units (ReLUs) as activation function. Max-pooling is employed with a (2, 2) kernel and a stride of 2 pixels for downscaling.

We have changed some layers in VGG-19 architecture to adapt it to our X-ray image classification task. One of the convolutional layers in the VGG-19 was replaced with a dropout layer and also skipped one or more than one convolutional layer in each group. Dropout is a regularization technique that helps to prevent overfitting by randomly deactivating a fraction of neurons during training. We added one more group for feature extraction, making a total of six groups, each one followed by a max-pooling layer. These layers are responsible for extracting important features from the input images. In the first layer of our modified model, we used a 2D convolution operation with a (5, 5) kernel size, applying the same padding, followed by max-pooling with a (2, 2) kernel for reducing the spatial dimensions. ReLU activation function and dropout are applied in this layer. We continued to build the model with similar convolutional layers for feature extraction. The final layer in the features extraction process uses a 2D convolution with a (3, 3) kernel size, (2, 2) stride, and additional (2, 2) max-pooling which is shown in Figure 2.

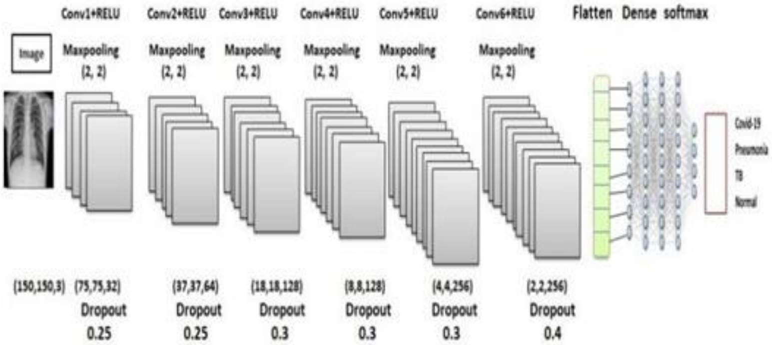
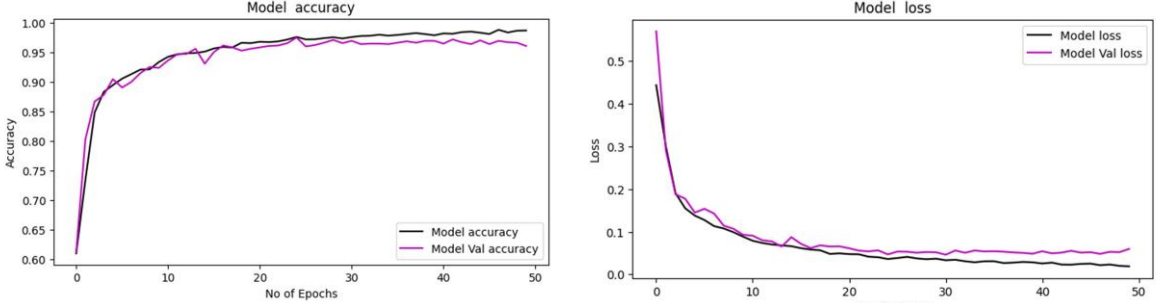


Figure 2: Architecture of the proposed model

After these convolutional and max-pooling layers, we used a flattened layer to convert the extracted features into a one-dimensional vector. Following the flattened layer, we added dense (fully connected) layers for the classification task. The first dense layer has 1024 features and the final dense layer has only 4 features, indicating the number of classes in our X-ray image classification. Following the last dense layer, there is a softmax layer with the same number of outputs as the classes. The softmax layer computes class probabilities. In this work, categorical cross-entropy is used as the loss function, which is common for multi-class classification problems. We specified a learning rate of 0.00150 for the optimizer. The learning rate controls how quickly the model adjusts its weights during training. Hyperparameter tuning was performed to optimize parameters like step size, kernel size, number of dropouts, and number of channels. We obtained results as output in the output layer and achieved optimal accuracy in CXR image classification.

Experimental Results:

In this study, we classified CXR images using a CNN-modified model. Adamax optimizer is used to compile the CNN model after it has been constructed. The experimental results of the proposed model are compared with the existing model [13] and also with other state-of-the-art architectures. It is a very potent optimization method for deep learning networks. The suggested model, which utilized the Adamax optimizer with a learning rate of 0.00150, successfully classified CXR images and obtained 98.51% accuracy.



(A). Training and validation accuracy vs epochs

(B). Training and validation loss vs epochs

Figure 3: Training and validation loss and accuracy

Our study's main training goal is to reduce the average probability error between each pixel's anticipated and the actual values for CXR images. This was accomplished by using categorical cross-entropy as the loss function [16]. This method works well for multi-class classification problems such as our CXR image classification, as it penalizes discrepancies between predicted and true class labels, making it easier to optimize the CNN model's parameters. With the help of this loss function, which efficiently measures the difference between the ground truth labels and the projected probability distributions, the network can iteratively modify its weights and biases in order to reduce this difference over the course of subsequent training epochs. This progression across the 50 epochs is graphically depicted in Figure 3, which provides insights into the convergence behavior and generalizability of the model to new data. We can evaluate the learning dynamics of the proposed CNN model, to spot any overfitting or underfitting scenarios and adjust hyperparameters to maximize performance by examining the trends shown in the graphical output of the model.

Confusion Matrix:

A confusion matrix is used as a fundamental tool in classification algorithms. In essence, it's a square matrix that can handle several classes; normally, it's 2 × 2 in size for binary classification issues. The results of a classification task are concisely summarized in this matrix, where the rows represent the actua1 class 1abels and the columns represent the anticipated class 1abes. Figure 4 shows the Confusion Matrix of the proposed network. The four fundamental values within the confusion matrix are as follows:

True Positive (TP): This describes situations in which both the expected class and the actual class are positive. For example, in the medical domain, this might mean accurately diagnosing patients with a certain illness.

True Negative (TN): In these cases, the predicted and actual classes are both negative. In the context of medical diagnostics, this could mean accurately identifying people who do not have a specific illness.

False Positive (FP): This is also referred to as a Type I error and happens when the actual class is negative but the projected class is positive.

False Negative (FN): When the expected class is negative but the actua1 class is positive, this results in a false negative (Type II mistake). This could indicate, in the context of healthcare applications, that a patient was not correctly diagnosed with a condition.

Researchers can assess the accuracy, precision, recall, and other performance parameters of the classification algorithm by examining these four variables, which offer crucial insights into the algorithm's operation. The distribution of examples inside the confusion matrix can be analyzed to spot misclassification trends and gauge how well the algorithm performs generally in differentiating between classes. As a result, the confusion matrix is an essential analytical tool for evaluating the advantages and disadvantages of classification algorithms, which helps to improve and optimize them for a range of practical uses.

Precision:

In the context of classification, precision is a metric that calculates the proportion of all cases that were correctly anticipated to be positive, that a classifier predicts as positive. It is calculated as using Eq. (1)

$$\text{Precision} = \frac{TP}{TP+} \qquad (1)$$

Recal1 (Sensitivity or true positive rate): In the context of classification, Recall is a performance metric that measures how well the classifier identified and retrieved all instances in the dataset that belong to a particular class. It is calculated as using Eq. (2):

$$\text{Recall or true positive rate} = \frac{TP}{TP+FN} \qquad (2)$$

F1-Score: The Fl-score is the harmonic mean of precision and recal1. This provides a fair evaluation of a classifier's performance by taking into account both precision and recall. It is calculated as using Eq. (3):

$$\text{F1-score} = \frac{2\,(Precision\ x\ Recall)}{Precision + Recall} = \frac{2TP}{2TP + Fp + FN} \qquad (3)$$

The overall training performance of the proposed model derived from the confusion matrix is presented in Table. 1 while the validation performance is shown in Table. 2. Table. 3 shows the comparative Analysis of the proposed network with the other deep learning networks performing classification of TB, pneumonia, COVID-19, and healthy.

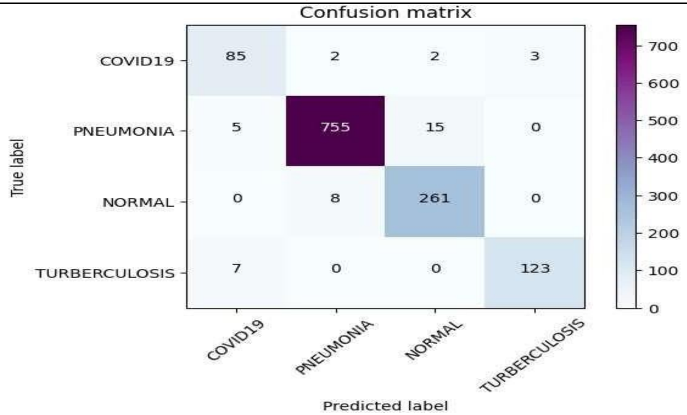


Figure 4: Confusion matrix

Table 1. Training results of the proposed CNN modification method

Class Name	Precision	Recall	F1-Score	Support
Covid-19	0.98	0.98	0.98	368
Pneumonia	1.00	0.98	0.99	3100
Normal	0.94	1.00	0.97	1072
Tuberculosis	1.00	0.98	0.99	520

Table 2. Validation results of proposed CNN modification method.

Class Name	Precision	Recall	F1-Score	Support
Covid-19	0.88	0.92	0.90	92
Pneumonia	0.99	0.95	0.97	775
Normal	0.88	1.00	0.94	269
Tuberculosis	0.98	0.92	0.95	130

Table 3. Comparative analysis of the proposed network with other deep learning networks performing classification of pneumonia, TB, COVID-19, and health.

Model	Precision (%)	Recall (%)	AUC-ROC(%)	F1(%)
Proposed Model	98	98.5	98.51	98.25
DenResCov-19	82.90	69.7	95.00	75.75
Dense Net-121	79.35	62.70	91.00	70.07
Res Net-50	78.60	62.00	93.21	69.51

Conclusion:

In the field of medical science, classifying CXR images is crucial. This research project aims to create a new type of computer algorithm called a Convolutional Neural Network (CNN) that can distinguish between four different categories of CXR images: Pneumonia, Covid-19, TB, and Normal. The process starts with preparing the images by making them a consistent size and reducing noise. Then, the dataset is divided into two parts: one part for training the algorithm and another part for validating its performance. After that, the CNN is used to automatically categorize the CXR images. Impressively, the model achieved a high accuracy rate of 98.51% in experimental tests using the CXR image dataset. Looking ahead, future research should aim to find new and innovative ways to classify CXR images in the medical field. This work will contribute to efforts to investigate the potential of artificial intelligence (AI) in the future. Additionally, it contains a number of research avenues that could be pursued in the future that are pertinent to the study of medical sciences.

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