IEEE Access
Multidisciplinary | Rapid Review | Open Access Journal

Date of publication xxxx 00, 0000, date of current version xxxx 00, 0000.

Digital Object Identifier 10.1109/ACCESS.2017.Doi Number

Ensembling of Efficient Deep Convolutional Networks and Machine Learning Algorithms for Resource Effective Detection of Tuberculosis using Thoracic (Chest) Radiography (June 2022)

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ABSTRACT Tuberculosis (TB) is a communicable pulmonary disorder and countries with low and middle-income share a higher TB burden as compared to others. The year 2020-2021 universally saw a brutal pandemic in the form of COVID-19, that crushed various lives, health infrastructures, programs, and economies worldwide at an unprecedented speed. The gravity of this estimation gets intensified in systems with limited technological advancements. To assist in the identification of tuberculosis, we propose the ensembling of efficient deep convolutional networks and machine learning algorithms that do not entail heavy computational resources. In this paper, the three of the most efficient deep convolutional networks and machine learning algorithms are employed for resource-effective (low computational and basic Imaging requirements) detection of Tuberculosis. The pivotal features extracted from the deep networks are ensembled and subsequently, the machine learning algorithms are used to identify the images based on the extracted features. The said model underwent k-fold cross-validation and achieved an accuracy of 87.90% and 99.10% with an AUC of 0.94 and 1 respectively in identifying TB infected images from Normal and COVID infected images. Also, the model's error rate, F-score, and youden's index values of 0.0093, 0.9901, and 0.9812 for TB versus COVID identification along with the model's accuracy claim that its use can be beneficial in identifying TB infections amid this COVID-19 pandemic, predominantly in countries with limited resources.

INDEX TERMS COVID-19, Chest X-Ray, Deep Convolutional Networks, Ensemble Learning, Machine Learning, Tuberculosis.

I. INTRODUCTION

Tuberculosis (TB), a deadly disease and a communicable pulmonary disorder is a result of Mycobacterium tuberculosis. As per World Health Organization, Worldwide, approximately 10 million individuals fell prey to TB in the year 2019 which includes a projected 1.2 million deaths due to TB amongst non-HIV infected individuals, with an added over 0.2 million deaths in HIV infected people. 56 % of males with age above 15 years, 32% of females, and 12% of children below 15 years of age suffered from TB in the year 2019 [1]. Tuberculosis together with HIV is the most lethal disease combination prevailing currently[2]. TB being a

communicable disease disseminates its bacteria via coughing, speaking, sneezing, etc. Africa and Southeast Asian countries are the most overburdened with TB chiefly because of inadequate medical infrastructure and a comparatively higher rate of poverty. China, India, Bangladesh, and Pakistan are the nations with a higher TB burden as compared to others [3]. Around two-thirds of total cases of TB are reported in countries with low and middle income like India which shares the major burden of the total TB cases, trailed by Indonesia and China. Well-in-time detection is pivotal in battling TB efficiently and in curbing the mortality rate. However, the absence of sufficient health infrastructures in countries that are not economically developed and which are still in developing mode makes the process of in-time disease detection very problematic. Despite the reality, that tuberculosis can be efficiently cured using antibiotics the rate of mortality is still very high and it reciprocates that the in-time detection rate of TB is very poor. Chest radiography and Sputum Smear Microscopy are two of the most widely recognized methods for detecting TB [4]. Although chest radiography despite being efficient suffers from a few difficulties, it needs a medical expert for interpreting the radiography images. There are various manifestations of TB on the lungs like solidification, infiltrates, and cavitation [5]. A competent radiologist is expected to interpret the radiographic images precisely for the in-time detection of any serious diseases. However, in low-income countries, there is a scarcity of competent medical practitioners who can diagnose the disease accurately [6]. Digital diagnosis through chest radiography is the first step in the early detection of tuberculosis. It may aid in diminishing the rate of mortality particularly in the regions with inadequate resources by easing the work of competent medical practitioners [7]. Looking into the present scenario of the COVID-19 pandemic, TB is a major health issue. Tuberculosis and COVID-19 both disseminate among individuals via close social contact and the manifestations are more or less like COVID-19, like high temperature, fatigue, and, difficulty in breathing [8]. Consequently, economically weak nations where TB is intensified by the presence of COVID are at a major risk. In these situations, quick tuberculosis and COVID identification are the utmost priority. This pandemic of COVID-19 may result in diminishing the detection rate of TB by a quarter percent which may turn up the deaths because of TB by 13% [9]. As per the data of the government of India, there is a dip of almost 25% in the reported TB cases due to this pandemic from the year 2019 to the year 2020 as indicated by figure 1 which itself shows the severity of this issue [10]. Ever since the development of algorithms for deep learning (DL) along with the accuracy of results they gave in a variety of clinical usage, deep learning networks have seen a huge advancement [11-20] in detecting chronic pulmonary disorders like tuberculosis, etc. Amid different deep learning techniques, a deep convolutional network (DCN) has come out as a fascinating method for the detection and identification of tuberculosis [17]. In such deep convolutional networks, there is a mutually sharing of weights inside every layer so as to lessen the intricacy and calculation of the network. Such networks utilize a huge set of data to study new parameters as well as extract pivotal features of an image both local and global. Conventional machine learning algorithms (MLA) depend on customized features, which limits the capability of the network. While the DL methods do the extraction of reliable and essential features by themselves, they present altogether a much better result. Besides, DL algorithms need a lot of labeled sets of information for the purpose of training, and securing such a large set of information is a difficult task.

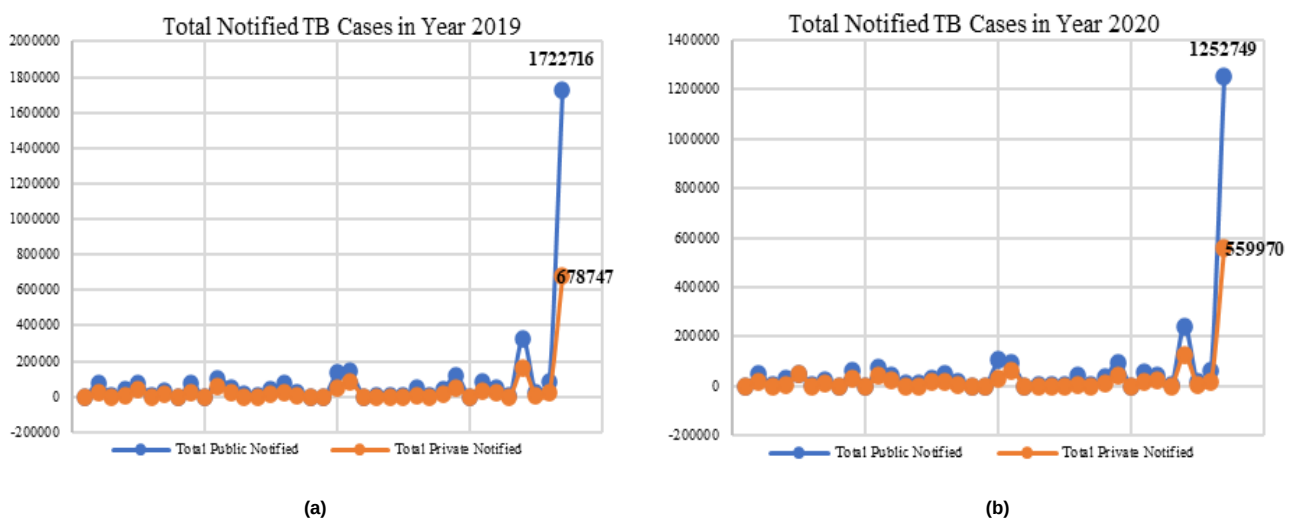


FIGURE 1. Year-wise reported TB cases in India in (a) year 2019, (b) year 2020

To suppress such intricacies, we in this article propose the ensembling of efficient deep convolutional networks and machine learning algorithms. In this paper, three of the most efficient deep convolutional networks and machine learning algorithms are employed for resource-effective detection of Tuberculosis. The pivotal features extracted from the deep networks are grouped together and subsequently, the MLAs are implemented to identify the images based on the extricated features. In the proposed model, we grouped the pivotal features extracted from the three efficient deep networks to create simulated features. The process of grouping the key features is to combine the bottleneck features extracted through 3 deep convolutional networks to form a new set of enhanced features that are more distinctive than the features extracted from an individual convolutional network. The grouped features are then given as an input to three machine learning classifiers for final predictions contrary to most of the past research works [21].

The research done in the presented paper reveals that the ensembling of features extracted through deep convolutional networks and using ML algorithms for classification can enhance the performance of the model substantially. Through this paper, our major contributions are listed below:

1. Here an effective and completely automated (involving low computational and basic imaging requirements) TB detection system is developed that makes use of efficient deep convolutional pretrained networks for extracting significant bottleneck features from radiographic X-ray images and, MLAs are implemented to identify TB infected images from the COVID-19 and Normal images hence can be utilized for speeding up medical procedures as per the type of disease.

2. We put forward a novel technique that includes three stages:

(a) The model will first extract the region of interest (ROI) from the input images and preprocess it for improving the quality so that better image features may be extracted for subsequent processing.
(b) Further, from the extracted ROI, pivotal bottleneck features will be extricated through deep convolutional pretrained networks for significant data and a better impression of the image.
(c) Thereafter the selected significant bottleneck features from the three deep convolutional pretrained networks will be grouped which will then be given to three different machine learning classifiers for accomplishing best in a class detection system for TB identification.

3. This work also evaluates the efficacy of three deep convolutional networks, used as feature extractors, in identifying the infected lung features from the normal ones and subsequently in detecting the TB infected lung features from other infected lung X-ray images. Further, it also analyses the efficiency of machine learning algorithms in classifying the lung image classes.

4. This work investigates the performance of every deep convolutional pretrained network individually and in all possible pairs along with different classification models in classifying TB-infected CXR images from normal and COVID-infected images. Also, a comprehensive study of several substantial parameters obtained through experiments is done to additionally approve the superiority of this research model.

The remaining of the paper is segmented as: section 2 gives details about the past work done in this field, section 3 talks about the methodology employed for conducting the presented research, and section 4 gives the comprehensive results of the investigation conducted in this research and lastly section 5 will give the concluding remark.

II. RELATED WORK

In this section, we will do an analysis of the earlier work done in this area and the gaps that inspired us to do this research. Extracting features using pretrained deep convolutional networks and then tunning them precisely so that they could be used over a diversified set of data is what transfer learning is. Using the parameters trained over a larger set of data is an efficient approach in contrast to developing a new system and training it over a small set of data [22]. In [23] put forward an automated identification framework for detecting the cavity signs in CT scans of lungs using a combination of deep convolutional and handmade features. The combination of multiple features showed enhanced performance and accomplished higher sensitivity than others. In [24] design a pediatric TB classification system that better represents the variety and grimness of this disease than existing techniques. They provided a paradigm for categorizing the inclemency of TB in children and every single infection was thoroughly examined. Each infectious entity was then classed as "severe" or "non-severe" based on the amount and occurrence of problems. They equated the suggested categorization to the conventional (PTB, E-PTB) in an ally of HIV- infected and HIV- uninfected newborns with culture-confirmed TB as a first application. In [25] worked out the identification of normal disorders in lung CT images using a multistep similarity method. This measurement of similarity is then categorized into scales of low, mid-level, and high-level. The weighted summation of every level provided the finalized similarity scores. Authors in [26] presented a classification system for thoracic illnesses utilizing deep convolutional networks (DCN). The authors named their model Thorax-Net which gave results by averaging two different branches. Their proposed model accomplished an AUC which is better when contrasted with other deep models. Authors [27] presented a tuberculosis detection framework dependent on distorted edges of thoracic maps keeping in view that the infected tuberculosis X-ray displays distorted edges in thoracic maps. The authors executed five different ROI detection techniques for finding

the model with the best performance. In [28] authors put forward a classification system for tuberculosis utilizing techniques called 'Speeded Up Robust Feature' (SURF) descriptor along with another approach called 'Bag of Features'. For segmenting the lung region distance regularized technique was utilized and a multiple layer perceptron model was utilized for the purpose of TB classification. Paper [29] presented a method of selecting the best features from an extensive range of lung features. Segmentation of the lung was done in order to concentrate on features the of lung area only forming three distinct subsets of the preliminary feature pool. Each feature pool is comprised of various features such as edge, sharpness, shape, gradient, and intensity. They found that feature descriptors like texture, edge, and shape gave the best results in the classification of normal and infected TB x-ray images. In [30] deployed a pretrained model like VggNet, ResNet, and GoogleNet using fine tunned transfer learning technique at the last layers. The experiment was conducted in three steps, in the primary step, images were directly given to the above-mentioned pretrained models as input by reducing the image size to acceptable to individual models. As reducing the image size may cause some information loss, therefore the images were partitioned into small segments called bags of features in the next step. Lastly, the results of all the models were grouped together. As a deep convolutional network requires large computational expenses hence it is challenging to use them in portable equipment. The author in [31] presented an effective convolutional neural network that has only five layers of convolution succeeded by average-pooling layers as well as a softmax layer. The proposed model preserved the accuracy while reducing the computational complexity and size of the model. Usually, deep convolutional models use the same set of data for testing and training, therefore it is very likely that the convolutional model might get biased over a particular set of data. To acknowledge this issue, [32] put forward a cross-population model for both testing and training where both testing and training data will be from varied sources so as to measure the system performance. The summary of the work discussed in this section is given in table 1. In brief, various hard work has been put into creating a completely automated TB detection system. In the past, studies were restricted only to features that were too hand-made but now the power of deep convolutional models is recognized. Nonetheless, the lower precision of the said models is as yet an unsettled problem. One of the essential reasons for the low precision varied manifestations of TB in X-ray images creates a challenge for automated TB detection systems. To deal with such challenges, a strong framework is required which can genuinely detect TB and normal images.

III. MATERIALS AND METHODOLOGY

In the current section, we will discuss the methodology employed for carrying out the proposed research work. The proposed model for tuberculosis detection is presented in figure 2. To begin with, the model will first extract the region of interest (ROI) from the input chest X-ray images and preprocess it for improving the quality so that better image features may be extracted for subsequent processing. Subsequently, from the extracted ROI, pivotal features will be extricated using three deep convolutional pretrained networks namely DenseNet201, XceptionNet, and InceptionResNetv2, for significant data and a better impression of the image. The features extricated from the above-mentioned pretrained networks are then grouped together to form a simulated feature pool which is then fed into three machine learning tools: SVM, KNN, and Ensemble, for the purpose of disease identification. Each of the three machine learning tools undergoes a cross-validation process of 5-fold and 10-fold to validate the model performance. A detailed description of the proposed model is given below.

TABLE I
OVERVIEW OF THE RELATED WORK

Literature	Dataset Used	Method of Evaluation	Technique	Maximum Accuracy	AUC
Lopes et al. [30]	406 Normal; 394 Tuberculosis	Deep feature extraction	SVM	84.70%	0.926
Santosh et al. [27]	420 Normal; 400 Tuberculosis	Thoracic edge map encoding	Neural Network	86.36%	0.930
Pasa et al. [31]	406 Normal; 394 Tuberculosis	------	Conventional CNN	86.20%	0.925
Vajda et al. [29]	422 Normal; 392 Tuberculosis	Textural & Statistical Features	Neural Network	95.57%	0.990
Govindarajan et al. [28]	80 Normal; 58 Tuberculosis	Bag of features; speeded-up Robust feature	Multilayer perceptron	87.80%	0.940
Ma et al. [25]	511 Lung CT images	Precision-Recall Graph	Multi-level similarity	80% precision	------
Das et al. [32]	420 Normal; 400 Tuberculosis	------	Transfer learning with InceptionV3	76.05%	0.840

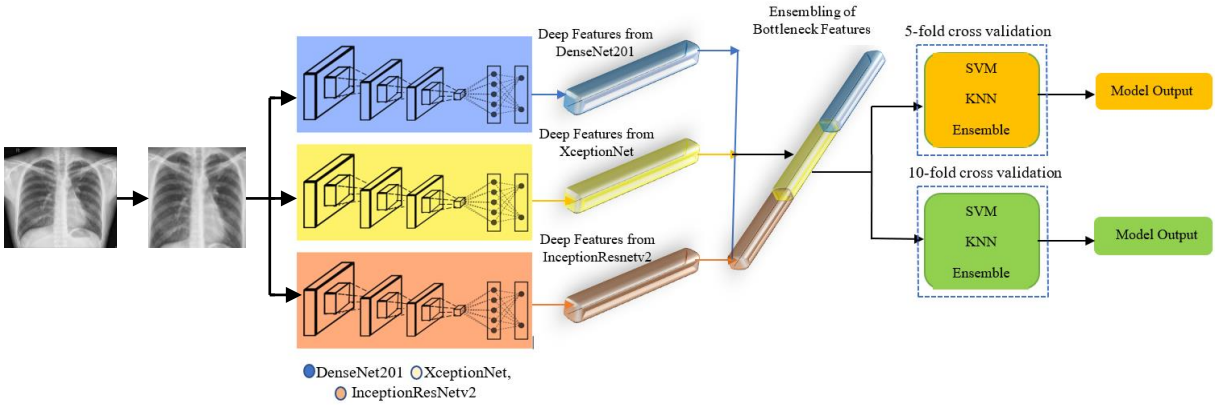
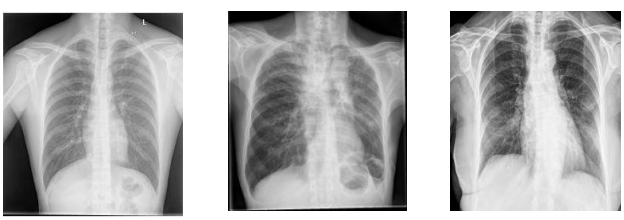


FIGURE 2. **Proposed ensembled model for tuberculosis detection using DCN and machine learning algorithms**

A. DATASET DESCRIPTION

The use of deep convolutional techniques (DCT) in the computer-assisted diagnosis of TB gives promising results in tuberculosis detection. But the inadequate data for training the system obstructs the development of the computer-assisted diagnosis of TB. Chest radiography is a highly popular and inexpensive medical imaging technique even though on several occasions it does not provide as accurate results as a chest CT scan. A resourceful and comprehensive openly accessible dataset is missing and consequently, it is very trying to concede the clinically significant analysis and computer-assisted diagnosis in various clinical endpoints using X-ray images. This presented research work uses three openly accessible resources namely Tuberculosis X-Ray (TBX11K) dataset [33] (Y. Liu et al. 2020), the Augmented COVID-19 x-ray Image dataset [34], and the Shenzhen dataset [35]. TBX11K imageset consists of 11200 radiographic x-ray images in total of size $512x512$, which includes 1200 TB images, 5000 images of non-TB but sick, and the rest 5000 normal x-ray images out of these 800 TB infected images are used for the proposed work. TBX11K imageset is approximately seventeen times bigger as compared to the prevailing biggest imageset, i.e., the Shenzhen dataset that contains 326 normal and 336 TB infected images. Images in the TBX11K dataset are verified through diagnostic microbiology, a golden standard, and thereafter marked by qualified medical experts. This dataset has been made openly accessible in order to encourage forthcoming research on Tuberculosis detection. Whereas the augmented COVID-19 x-ray dataset comprises 912 radiographic x-rays augmented images of COVID-19 having a size of 1024x1024 out of which 878 images are employed for the research work. The employed imageset is separated into test and training data in the ratio of 20:80. The detailed description of the dataset used for the presented research work is tabulated below in table 2. The image dimensions in the employed datasets are altered in JPG/JPEG setup to suit the input of the model, as displayed in figure 3, for enhancing the deep convolutional network performance.



(a) (b) (c)

FIGURE 3. **Resized images (a) Normal (b) Tuberculosis (c) COVID-19 affected X-ray**

B. PRE-PROCESSING AND ROI EXTRACTION

Radiographic lung images are primarily set through the pre-processing step for improving the image quality. Firstly, the dimensionality of the images in the employed dataset is reduced to a suitable value fit for the deployed deep convolutional network so that the presented model takes fundamentally lesser time in reaching the best outcomes. The model then extracts the region of interest (ROI) from the input images and preprocesses it for improving the quality so that better image features may be extracted for subsequent processing [36]. Firstly, all the images are resized into the dimensions suitable for input to the respective DCNs, thereafter a rectangular window of appropriate size is defined that crops the images as per the dimensions and area determined in the rectangular window which comprises the pixels of images indicating the ROI that is bounded by the rectangular window. Fast Local Laplacian (FLL) filtering is utilized in this work for image upgradation along with the amputation of noise from the image. It is a technique that is computationally rigorous and increases the processing speed by discretizing the intensities into a different sample balancing both quality and speed. Figure 4 below shows the original image, ROI extracted image, and the improved ROI through Fast Local Laplacian filtering. Apart from this, other common filtering techniques like median filtering and Gaussian filtering are also tried to compare the quality of the enhanced image with the FLL filtering on various image quality parameters as shown in a comparative graph in figure 5. From the figure, it is evident that FLL filtering gave better results on both referenced and non-referenced image quality parameters as compared to the median and Gaussian filtering

for the three types of images. In the presented work, we have zeroed in just on the segment containing the lung region in x-ray and rejected the encompassing parts from the image [37,38]. In this way, the chest radiographic images are boosted to develop an enhanced ROI as represented below.

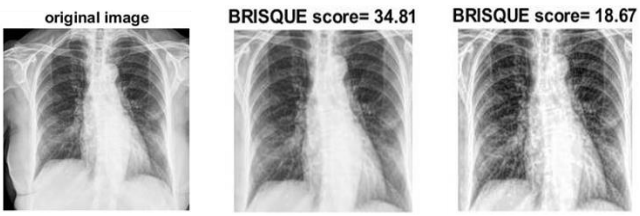
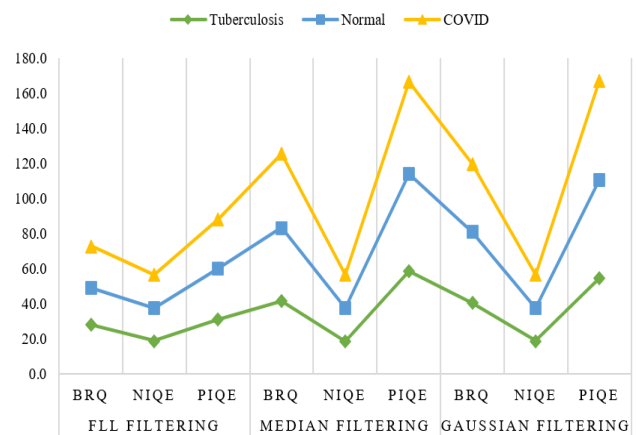


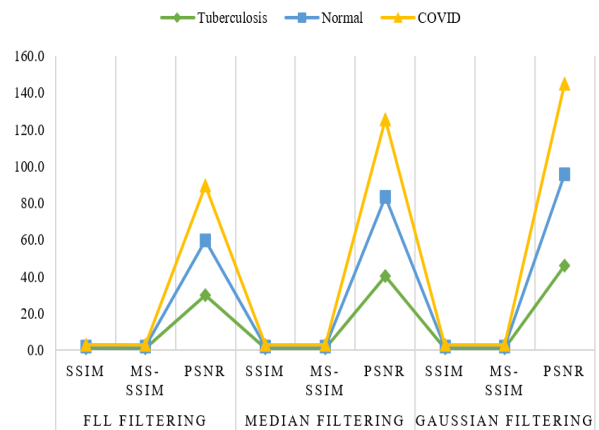
FIGURE 4. (a) Original Image (b) ROI extracted from (a), and (c) Enhanced ROI using FLL filtering

C. EXTRACTION OF DEEP FEATURES

DCNs are a type of deep network that primarily utilizes convolutional filters to filter out significant statistics. These filters are applied to the input of the layer for calculating the neuron's output which is associated with the surrounding area of the input and assist in extracting the sequential as well as spatial features from the input image. The technique of mutual sharing of weights is utilized by the convolutional layers to lessen the overall network parameters [39,40]. Any DCN is normally composed of a layer with convolutional filters to assist in extracting the sequential as well as spatial features along with a layer called max-pooling for image dimensionality reduction, and lastly, a layer named fully connected classification layer for image classification [41]. The work presented here utilizes a DCN for extracting deep features as it can detect significant features with no manual intervention. To extract features, we are here utilizing an approach based on transfer learning as the dataset used in this work is not sufficiently large to train a deep network from scratch. Therefore, we utilize pretrained DCNs with a set weight. values for extracting deep pivotal features from the chest X-ray images. Three pretrained DCN models are utilized in this research work which are DenseNet [42], Inception-ResNet-v2 [43], and Xception [44]. These DCNs are used without any modification as they may result in increasing the complexity of the system. The features extricated from these DCNs are grouped and put into machine learning models for prediction. The detailed information of the three pretrained DCNs described here for extracting features is listed in Table 2.



(a) Non-Reference Image Quality Parameters



(b) Referenced Image Quality Parameters

FIGURE 5 (a, b). A comparative representation for FLL filtering on various image quality parameters

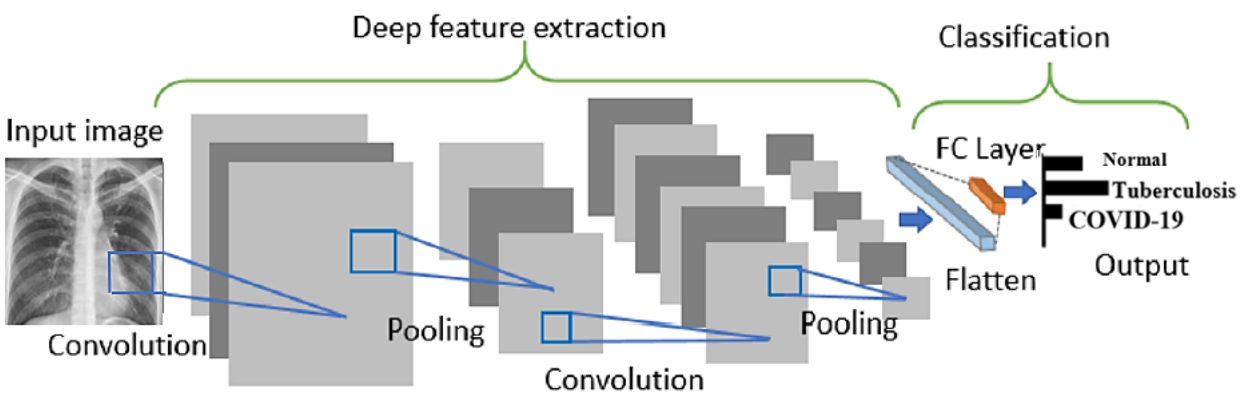


FIGURE 6. A general working structure of a deep convolutional network (DCN)

TABLE II
DETAILED INFORMATION ON THE THREE PRETRAINED DCNS USED IN THE PROPOSED WORK

Network Name	References	Input image size	FC layer	Layers	Parameters in Million
DenseNet-201	Huang *et al.* [39]	224x224x3	fc1000	709	20
Inception-ResNet-v2	Szegedy *et al.* [40]	299x299x3	predictions	825	55.9
Xception	Chollet *et al.* [41]	299x299x3	predictions	171	22.9

D. ENSEMBLING OF DEEP EXTRACTED FEATURES

Ensembling of deep extracted features is done with an objective to enhance the system performance and avert the possibility of underperformance by utilizing a lone extracted feature and merging it with several different features extracted from various DCNs. Classifier ensembling and feature ensembling are the two important parts of ensembling based on the level of integration. Classifier ensembling is the integration of classifier output groups and the outcome is decided by the method of voting whereas feature ensembling integrates feature groups which are then given as an input to the classifier to get the final results. As the ensembling of deep features encompasses richer and refined data regarding the images of chest X-rays as compared to the features extracted from the individual classifier improved results are anticipated by the combination of features at this stage. Thus, in the presented work, the deep extracted features derived from three efficient DCNs: *DenseNet201*, *InceptionResNetv2*, and *Xception* are ensembled, to form a pool of significant bottleneck features, as presented in Figure 2. These grouped features are then given to three machine learning classifiers for classification. Additionally, all likely feature combinations are also investigated using machine learning classification techniques for comparison with the ensembling of the three deep features.

E. IMAGE CLASSIFICATION USING MACHINE LEARNING ALGORITHMS

The deep extracted features from pretrained DCN models are given to three machine learning classifiers, for classifying the features. Matlab-2020a was utilized for the purpose of classification. In this work, the cross-validation process of 5-fold and 10-fold is used to avert the problem of overfitting [45-48]. The most efficient classifiers like Support Vector Machine (SVM), k-Nearest Neighbors (KNN), and Ensemble classifier are used here for the classification of the dataset. The description of the machine learning classifiers used in the proposed work for TB classification is described below.

1) Support Vector Machine (SVM): SVM [49] is an extremely effective supervised machine learning tool for binary classification. It makes use of the kernel functions, $K(y_m, y_i)$, to convert the data into another space with an advanced dimension. The function used for data separation also known as hyper-plan may be expressed as:

$$f(y_i) = \sum_{m=1}^{M} \beta_m x_m K(y_m, y_i) + c \qquad (1)$$

Here represents the support feature vector, β_m represents the Lagrange multiplier, and x_m denotes the target class of the employed dataset$m = 1, 2, 3, \ldots, M$. In the presented research work linear, medium gaussian, and cubic kernels are employed for the purpose of classification.

2) K-Nearest Neighbors (K-NN): K-Nearest Neighbors is the least complex technique for classification. In this, the prediction is done straight from the training data. As an example, for the classification of a new instance of data like a significant image feature from an X-ray, K-Nearest Neighbors selects a group of k articles from the training cases which are nearest to this new case by measuring the distance and assigning the class labels with them and select the best label going by the votes of its K-Nearest Neighbors. Euclidean, as well as Manhattan distance, are mostly utilized to calculate the familiarity of the new instances with the data used for training. Here, we have utilized the Euclidean distance for our work, and is expressed as:

$$d(p, q) = \sqrt{\left(\sum_{m=1}^{M} (p_i - q_i)^2\right)} \qquad (2)$$

In the k-NN classification technique firstly an appropriate matrix of distance is selected and then all the set of data X used for training is stored in the training stage:

$$X = (q_i, s_i); i = 1, \ldots\ldots, m \qquad (3)$$

Here, q_i is the pattern of training, m is the volume of patterns, and s_i is the equivalent class in the set of training data. During the phase of testing, the distances amid the new feature vectors and the features stored as training data are computed, and the classification of the new class is done by its k-neighbors majority votes. The correct test classification is utilized to assess the algorithm accuracy and if it does not show satisfactory results, the value of k can then be attuned until an acceptable accuracy is attained.

3) Ensemble Learning: Ensemble learning techniques are the ones that develop a bunch of classifiers and thereafter take their weighted sum for classification. Bayesian averaging is the first ensemble technique however many new algorithms like Boosting and Bagging are recently developed. Ensemble learning gives a spontaneous, sophisticated, and powerful method of machine learning classification. Initially created to enhance the accuracy of classification by variance reduction in classification, ensemble learning techniques have demonstrated their efficiency in various domains that are hard to acknowledge through a single framework. A common ensemble learning technique comprises three segments: a method to select features, that augments the ensemble variety; a system to train the ensemble components for classification; and a method for classifier consolidation [50]. The feature selection can be done either randomly, like in bagging, or else by using a system executed by a dynamic updation of the distribution as done in boosting algorithms. Normally, ensemble learning systems are mostly self-governing and do not depend on the base classifier utilized for ensembling, a critical benefit that permits utilizing a particular classifier type that might be known to be most appropriate for a specific task. Three types of ensembles learning namely bagging, boosting, and subspace K-NN are utilized in this research work.

IV. MATHEMATICAL EVALUATIONS AND RESULTS

A. CLASSIFICATION RESULTS

In this work, evaluation of the proposed model based on deep feature extraction with machine learning classification is done using various parameters derived from the matrix of confusion which includes True Positive Rate (TPR), True Negative Rate (TNR), Positive Predictive Value (PPV), F-score, Error Rate, Accuracy, Youden's Index and Area Under Curve (AUC). The prime objective here is to develop an effective and completely automated TB detection system that makes use of efficient deep convolutional pretrained networks for extracting significant features from radiographic X-ray images and, machine learning algorithms to identify TB infected images from the normal and COVID-19 infected images and hence can be utilized for speeding up medical procedures as per the type of disease. The outcomes acquired from the proposed model can either be positive or negative. Likewise, the outcomes may perhaps synchronize with the actual class. Consequently, here TP implies the positive expected results that are positive. TN means the predicted negative results that are negative. FN signifies the anticipated classes that are negative but are positive in reality. FP addresses the positive assessed cases however were negative in reality. For doing the validation the model proposed subsequent parameters are evaluated.

(i) True Positive Rate (TPR): It represents the fraction of true (positive) classes which are appropriately recognized and is expressed as:

$$True\ Positive\ Rate = \frac{TP}{TP + FN} \tag{4}$$

(ii) True Negative Rate (TNR): It represents the fraction of false (negative) classes which are appropriately recognized and is expressed as:

$$True\ Negative\ Rate = \frac{TN}{TN + FP} \tag{5}$$

(iii) Positive Predictive Value (PPV): represents the fraction of true (positive) and false (negative) classes that are actually true and false respectively and is expressed as:

$$Positive\ Predictive\ Value = \frac{TP}{TP + FP} \tag{6}$$

(iv) F1-Score: It is an evaluation of diagnostic correctness and is represented by the harmonic mean of TPR and PPV. It is expressed as:

$$F1_{score} = \frac{2 * (PPV * TPR)}{(PPV + TPR)} \tag{7}$$

(v) Accuracy: It is the competency of a model to appropriately identify the true and false class cases respectively. It is expressed as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{8}$$

(vi) Error Rate: It is the ratio of all the false estimations to the complete data and is expressed as:

$$Error = \frac{FP + FN}{TP + TN + FP + FN} = 1 - Accuracy \tag{9}$$

(vii) Youden's Index: It evaluates the competency of a classifier in evading misclassifications and is given by:

$$Youden's\ Index = TPR - (1 - TNR) \tag{10}$$

The investigational outcomes were acquired for the identification of normal, tuberculosis, and COVID infected images from the lung X-rays. Firstly, all the three DCNs are individually employed for extracting features and these features are then given for classification to three machine learning classifiers. Thereafter feature ensembling of different combinations of two DCNs is done to evaluate the model performance using the three machine learning classifiers. And finally, the deep bottleneck features extracted from the three DCNs are ensembled for classification. Each of the above steps is evaluated using 5-fold and 10-fold cross-validation. Table 3 presents the time taken by each of the deep

convolutional networks to extract features from the normal and TB infected 1651 images and from TB and COVID infected 1678 images. Table 4,5,6,7 shows the results of the presented model with 5-fold and 10-fold cross-validation. The comparison of these evaluations is graphically depicted in Figures 7 and 8. From the given data it can be realized that ensembling of the deep extracted features of the three convolutional networks as in Feature model 3 gives more prominent and distinguishable features and employing the machine learning classifiers on these features gives the best classification output. An error or confusion matrix is a detailed tabular representation that helps us to visualize how the particular model has performed. Figure 9(a-b) and figure 10(a-b) presents a confusion or error matrix that shows results for the best performing SVM Cubic and Quadratic classifier in model 3 among all the other models both for 5-fold and 10-fold cross-validation. The vertical and horizontal axis represents the predicted output and target in the error matrix. The measured value for True Positive Rate (TPR), True Negative Rate (TNR), Positive Predictive Value (PPV), F-score, Error Rate, Accuracy, Youden's Index for best-performing feature model 3 as obtained from the confusion(error) matrix for 5-fold and 10-fold is presented in Table 8 and 9 for TB and COVID identification, while table 10 & 11 presents the values obtained for TB and Normal identification from confusion (error) matrix using 5-fold and 10-fold cross-validation. Receiver Operating Characteristics (ROC) and Area Under Curve (AUC) represent the problem of evaluating the classification at numerous thresholds. It represents a curve that addresses the extent of distinguishability along with the probability. It also elaborates on the classification capability of the model. The closer the value of AUC to unity, the better is the model in identifying different classes. The AUC of the best performing model 3 with all the three classifiers is shown in figure 11(a-b) where class 1 represents TB. Also, the minimum classification error plot for the best performing model for both TB versus Normal and TB versus COVID identification using 5-fold and 10-fold cross-validation is presented in figure 12 and figure 13.

TABLE III
TIME TAKEN TO EXTRACT FEATURES USING DIFFERENT IMPLEMENTED DEEP CONVOLUTIONAL NETWORKS

Models	Deep Convolutional Networks	Time to Extract Features for Normal+TB (1651 Images) in Minutes	Time to Extract Features for TB+COVID (1678 Images) in Minutes
Model 1	DenseNet201	18.13	21.41
	InceptionResNetv2	22.15	35.33
	XceptionNet	11.40	13.57
Model 2	DenseNet201+XceptionNet	28.42	29.44
	DenseNet201+InceptionResNetv2	41.20	50.20
	XceptionNet+InceptionResNetv2	42.15	32.40
Model 3	DenseNet201+InceptionResNetv2 +XceptionNet	53.23	61.47

TABLE IV
THE EVALUATION RESULTS OF DEEP CONVOLUTIONAL MODELS WITH 5-FOLD CROSS-VALIDATION FOR NORMAL AND TB IDENTIFICATION

Models 1	SVM (%Accuracy)			KNN (%Accuracy)			Ensemble (%Accuracy)		
	Quadratic	Medium Gaussian	Cubic	Cosine	Weighted	Cubic	Sub Discrim.	Boosted	Bagged
DenseNet201	**87.7%**	87.0%	86.4%	80.0%	**80.5%**	79.8%	**85.6%**	81.5%	77.7%
InceptionResNetv2	**85.6%**	84.4%	84.6%	**77.3%**	77.1%	76.7%	**82.8%**	79.8%	75.0%
XceptionNet	**83.7%**	83.4%	83.0%	**74.7%**	72.9%	72.0%	**82.3%**	76.9%	72.7%
Models 2									
DenseNet201+XceptionNet	**87.9%**	86.0%	87.8%	77.5%	**78.7%**	77.7%	**86.1%**	79.0%	76.1%
DenseNet201+InceptionResNetv2	**87.8%**	86.1%	87.0%	**79.0%**	78.9%	78.7%	**87.3%**	80.4%	76.8%
XceptionNet+InceptionResNetv2	**86.3%**	85.3%	85.8%	76.4%	**76.8%**	75.9%	**85.2%**	78.0%	74.6%
Models 3									
DenseNet201+InceptionResNetv2 +XceptionNet	**87.8%**	85.7%	86.8%	77.4%	**80.7%**	77.3%	**87.7%**	78.8%	75.6%

TABLE V
THE EVALUATION RESULT OF DEEP CONVOLUTIONAL MODELS WITH 10-FOLD CROSS-VALIDATION FOR NORMAL AND TB IDENTIFICATION

Models 1	SVM (%Accuracy)			KNN (%Accuracy)			Ensemble (%Accuracy)		
	Quadratic	Medium Gaussian	Cubic	Cosine	Weighted	Cubic	Sub Discrimi.	Boosted	Bagged
DenseNet201	**87.8%**	87.0%	86.1%	80.1%	**80.8%**	80.3%	**86.3%**	81.8%	78.4%
InceptionResNetv2	**85.5%**	84.1%	84.9%	76.9%	**77.8%**	76.3%	**83.4%**	79.1%	75.4%
XceptionNet	**84.6%**	84.3%	82.7%	**75.6%**	72.9%	73.1%	**82.7%**	77.3%	72.0%
Models 2									
DenseNet201+XceptionNet	**87.9%**	86.3%	87.8%	77.9%	79.4%	78.2%	**86.7%**	78.4%	76.4%
DenseNet201+InceptionResNetv 2	**87.9%**	86.6%	87.5%	79.7%	**79.8%**	78.5%	**87.2%**	80.5%	77.3%
XceptionNet+InceptionResNetv2	**87.0%**	85.6%	86.6%	77.7%	77.0%	76.3%	**85.5%**	78.2%	75.7%

Models 3									
DenseNet201+InceptionResNetv2 +XceptionNet	**87.9%**	86.2%	87.4%	78.4%	**80.8%**	78.7	**87.7%**	79.1%	75.6%

TABLE VI

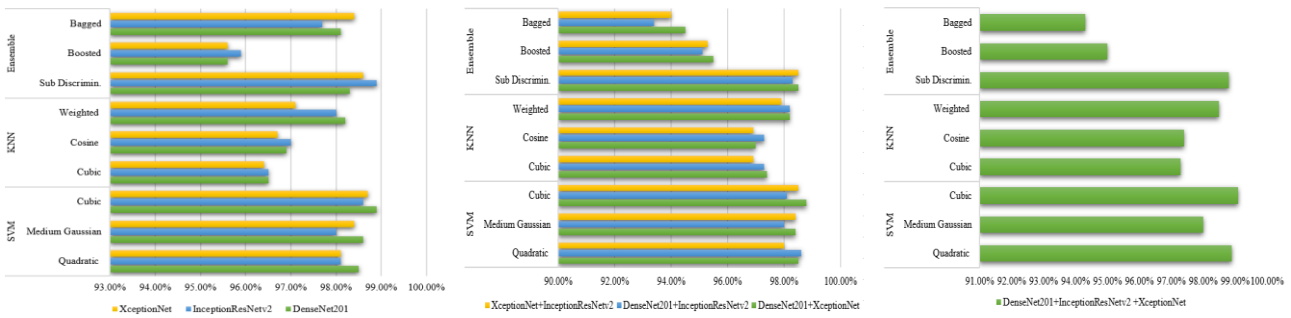
THE EVALUATION RESULT OF DEEP CONVOLUTIONAL MODELS WITH 5-FOLD CROSS-VALIDATION FOR TB AND COVID-19 IDENTIFICATION

Model 1	**SVM** (%Accuracy)			**KNN** (%Accuracy)			**Ensemble** (%Accuracy)		
	Quadratic	**Medium Gaussian**	**Cubic**	**Cubic**	**Medium**	**Weighted**	**Sub Discrimin.**	**Boosted**	**Bagged**
DenseNet201	98.3%	98.0%	**98.9%**	98.4%	98.5%	**98.6%**	**98.8%**	95.6%	98.7%
InceptionResNetv2	98.0%	98.3%	**98.6%**	97.6%	97.7%	**98.3%**	**98.8%**	94.7%	98.0%
XceptionNet	98.2%	98.7%	**98.8%**	97.4%	97.1%	**97.7%**	**98.7%**	97.2%	98.5%
Model 2									
DenseNet201+XceptionNet	98.7%	98.6%	**98.8%**	97.9%	97.7%	**98.4%**	**98.7%**	95.9%	94.2%
DenseNet201+InceptionResNetv2	**98.6%**	98.3%	98.1%	97.9%	97.5%	**98.5%**	**98.5%**	95.0%	93.6%
XceptionNet+InceptionResNetv2	98.2%	98.6%	**98.5%**	97.3%	97.4%	**98.2%**	**98.5%**	96.0%	94.2%
Model 3									
DenseNet201+InceptionResNetv2 +XceptionNet	98.9%	98.3%	**99.1%**	97.8%	97.8%	**98.5%**	**98.8%**	95.2%	94.5%

TABLE VII

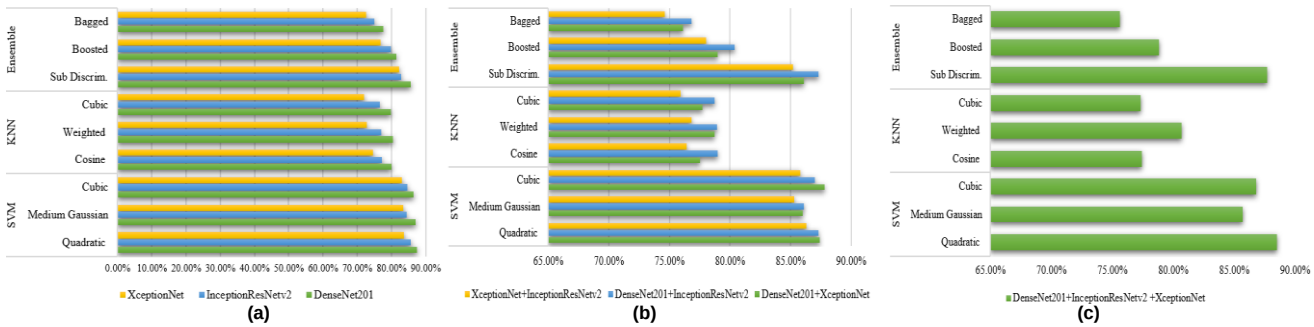
THE EVALUATION RESULT OF DEEP CONVOLUTIONAL MODELS WITH 5-FOLD CROSS-VALIDATION FOR TB AND COVID-19 IDENTIFICATION

Model 1	**SVM** (%Accuracy)			**KNN** (%Accuracy)			**Ensemble** (%Accuracy)		
	Quadratic	**Medium Gaussian**	**Cubic**	**Cubic**	**Cosine**	**Weighted**	**Sub Discrimin.**	**Boosted**	**Bagged**
DenseNet201	98.5%	98.6%	**98.9%**	96.5%	96.9%	**98.2%**	**98.3%**	95.6%	98.1%
InceptionResNetv2	98.1%	98.0%	**98.6%**	96.5%	97.0%	**98.0%**	**98.9%**	95.9%	97.7%
XceptionNet	98.1%	98.4%	**98.7%**	96.4%	96.7%	**97.1%**	**98.6%**	95.6%	98.4%
Model 2									
DenseNet201+XceptionNet	98.5%	98.4%	**98.8%**	97.4%	97.0%	**98.2%**	**98.5%**	95.5%	94.5%
DenseNet201+InceptionResNetv2	**98.6%**	98.0%	98.1%	97.3%	97.3%	**98.2%**	**98.3%**	95.1%	93.4%
XceptionNet+InceptionResNetv2	98.0%	98.4%	**98.5%**	96.9%	96.9%	**97.9%**	**98.5%**	95.3%	94.0%
Model 3									
DenseNet201+InceptionResNetv2 +XceptionNet	98.9%	98.0%	**99.1%**	97.3%	97.4%	**98.5%**	**98.8%**	95.0%	94.3%



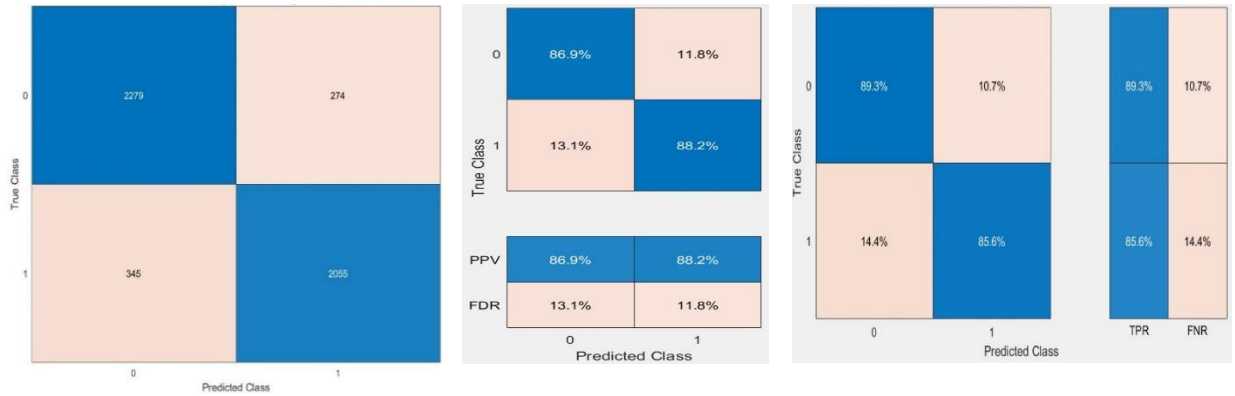
(a) (b) (c)

FIGURE 7. Classification results of (a) Individual DCN models (b) ensembling of different combinations of two DCN features (c) ensembling of three DCN features for TB and COVID identification



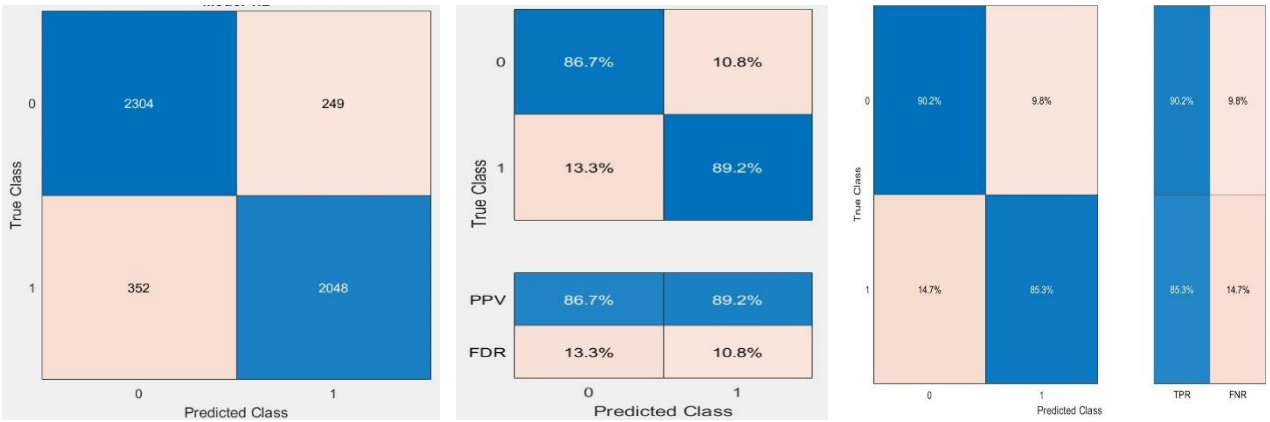
(a) (b) (c)

FIGURE 8. Classification results of (a) Individual deep models (b) ensembling of different combinations of two DCN features (c) ensembling of three DCN features for TB and Normal CXR identification



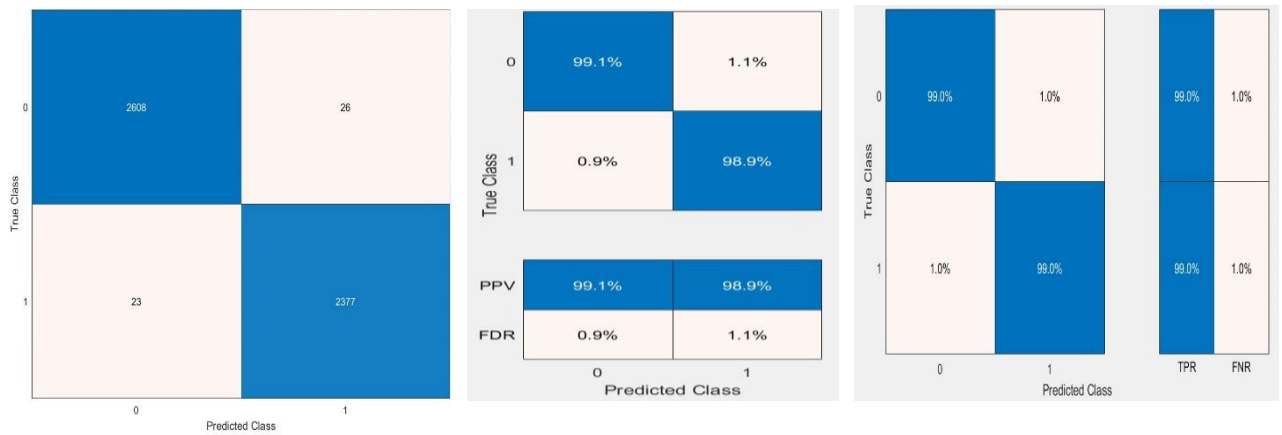
(i) (ii) (iii)

FIGURE. 9a. (i) Confusion matrix with (ii) PPV and FDR, (iii) TPR and FNR for the best performing SVM Quadratic classifier, 0 is for Normal, and 1 for TB for 5-Fold cross-validation



(i) (ii) (iii)

FIGURE. 9b. (i) Confusion matrix with (ii) PPV and FDR, (iii) TPR and FNR for the best-performing SVM Quadratic classifier, 0 is for Normal, and 1 for TB for 10-Fold cross-validation

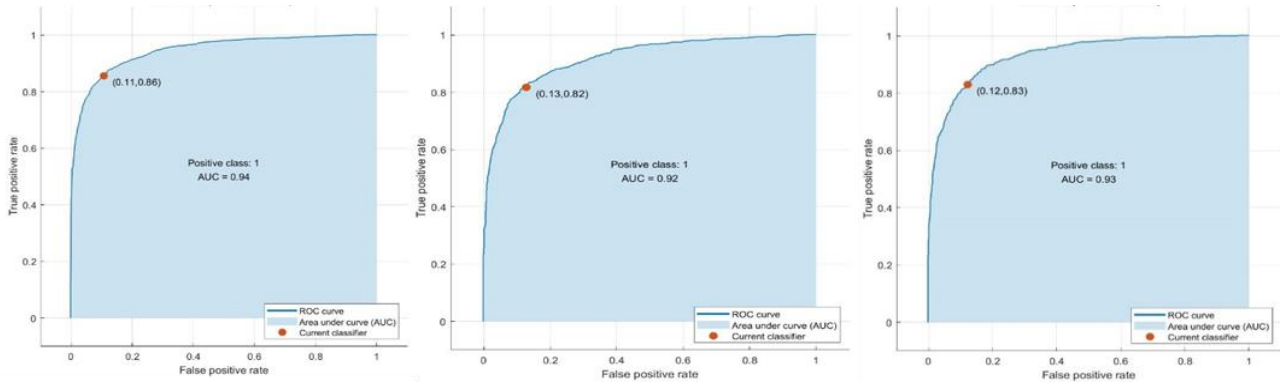


(i) (ii) (iii)

FIGURE 10a. (i) Confusion matrix with (ii) PPV and FDR, (iii) TPR and FNR for the best performing SVM Cubic classifier, 0 is for COVID-19 and 1 for TB for 5-Fold cross-validation

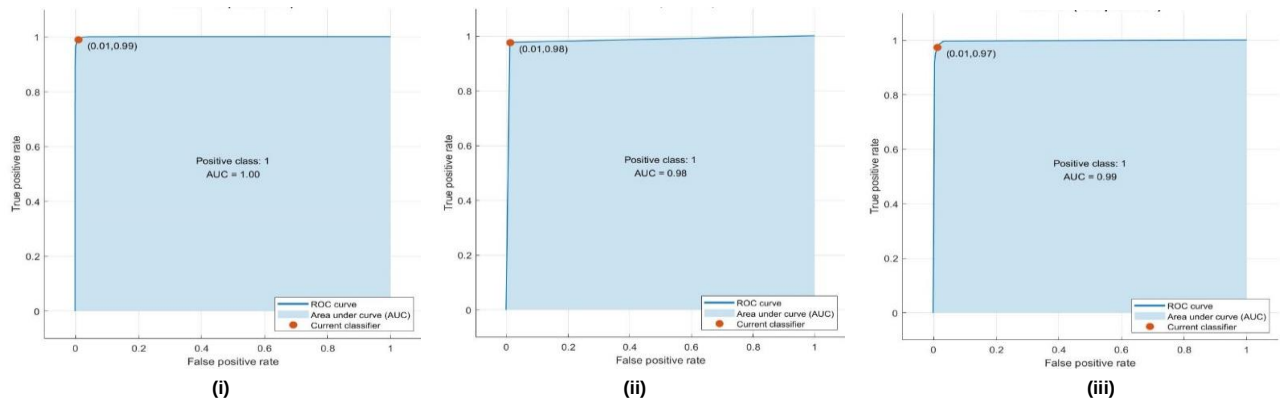
(i) (ii) (iii)

FIGURE 10b. (i) Confusion matrix with (ii) PPV and FDR, (iii) TPR and FNR for the best performing SVM Cubic classifier, 0 is for COVID-19 and 1 for TB for 10-Fold cross-validation



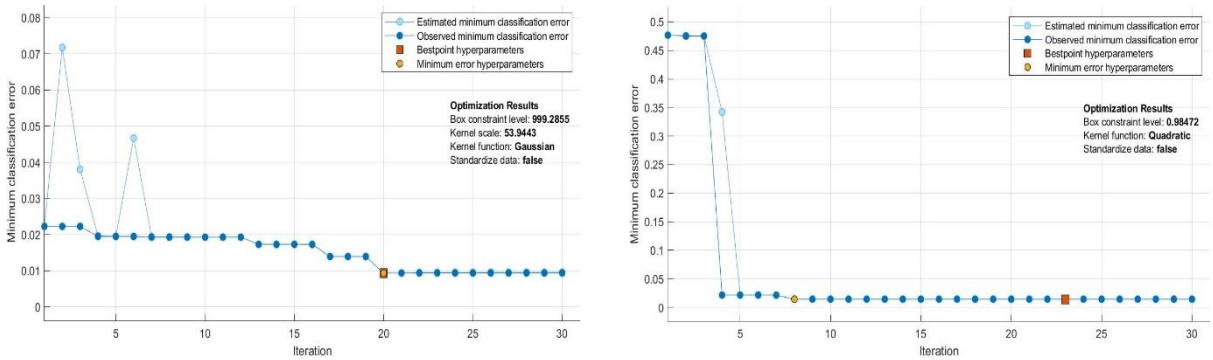
(i) (ii) (iii)

FIGURE 11a. (i) AUC of SVM Cubic (ii) AUC of K-NN Weighted, (iii) AUC of Ensemble Subspace Discriminant for COVID Vs. TB



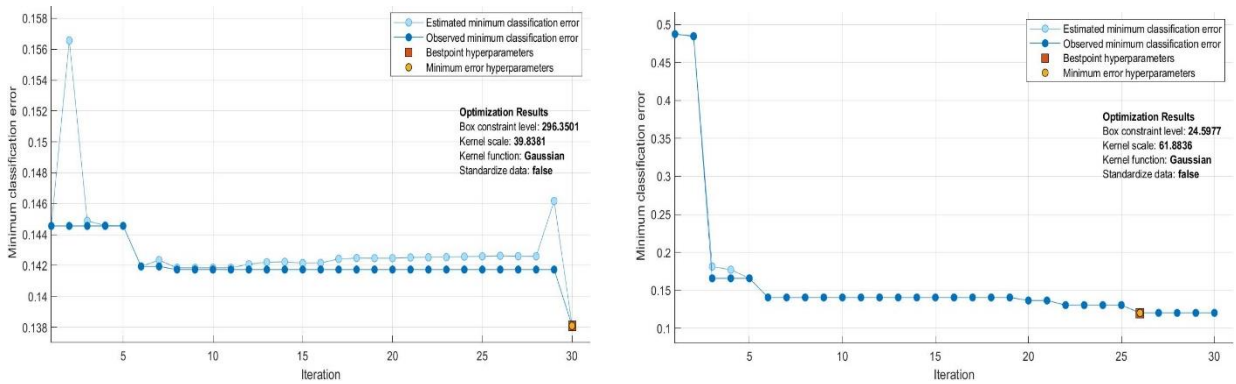
(i) (ii) (iii)

FIGURE 11b. (i) AUC of SVM Quadratic (ii) AUC of K-NN Weighted, (iii) AUC of Ensemble Subspace Discriminant for Normal Vs. TB



(i) (ii)

FIGURE 12. Minimum Classification Error Plot for COVID Vs. TB identification using (i) 5-Fold (ii) 10-Fold cross-validation



(i) (ii)

FIGURE 13. Minimum Classification Error Plot for Normal Vs. TB identification using (i) 5-Fold (ii) 10-Fold cross-validation

TABLE VIII

CONFUSION (ERROR) MATRIX EVALUATION WITH 5-FOLD CROSS VALIDATION FOR TB AND COVID IDENTIFICATION (DENSENET201+ INCEPTIONRESNETV2 + XCEPTION) WITH SVM (CUBIC)

Classes	TP	TN	FP	FN	TPR	TNR	PPV	Error rate	F1-Score	Youden's Index	AUC	Accuracy
Tuberculosis	2377	2608	23	26	0.9891	0.9912	0.9904	0.0097	0.9897	0.9804	1	0.9902
COVID	2610	2377	24	23	0.9912	0.9891	0.9901	0.0097	0.9906	0.9804	1	0.9902
Overall Accuracy							**99.1%**					

TABLE IX

CONFUSION (ERROR) MATRIX EVALUATION WITH 10-FOLD CROSS VALIDATION FOR TB AND COVID IDENTIFICATION (DENSENET201+ INCEPTIONRESNETV2 + XCEPTION) WITH SVM (CUBIC)

Classes	TP	TN	FP	FN	TPR	TNR	PPV	Error rate	F1-Score	Youden's Index	AUC	Accuracy
Tuberculosis	2377	2610	23	24	0.99	0.9912	0.9904	0.0093	0.9901	0.9812	1	0.9906
COVID	2610	2377	24	23	0.9912	0.99	0.9908	0.0093	0.9923	0.9812	1	0.9906
Overall Accuracy							**99.1%**					

TABLE X

CONFUSION (ERROR) MATRIX EVALUATION WITH 5-FOLD FOR TB AND NORMAL CXR IDENTIFICATION (DENSENET201+ INCEPTIONRESNETV2 + XCEPTION) WITH SVM (QUADRATIC)

Classes	TP	TN	FP	FN	TPR	TNR	PPV	Error rate	F1-Score	Youden's Index	AUC	Accuracy
Tuberculosis	2055	2279	345	274	0.8823	0.8685	0.8562	0.1210	0.8690	0.7508	0.94	0.8790
Normal	2279	2055	274	345	0.8685	0.8823	0.8926	0.1210	0.8803	0.7508	0.94	0.8790
Overall Accuracy							**87.9%**					

TABLE XI
CONFUSION (ERROR) MATRIX EVALUATION WITH 10-FOLD FOR TB AND NORMAL CXR IDENTIFICATION (DENSENET201+ INCEPTIONRESNETV2 + XCEPTION) WITH SVM (QUADRATIC)

Classes	TP	TN	FP	FN	TPR	TNR	PPV	Error rate	F1-Score	Youden's Index	AUC	Accuracy
Tuberculosis	2048	2304	352	249	0.8915	0.8674	0.8533	0.1213	0.8720	0.7590	0.95	0.8786
Normal	2304	2048	249	352	0.8674	0.8915	0.9024	0.1213	0.8846	0.7590	0.95	0.8786
Overall Accuracy							**87.9%**					

B. OBSERVATION AND DISCUSSION

Up till now all the important investigative results related to various experiments done in this research work from extracting deep features from the three efficient DCNs and grouping them to form a feature pool for classification of the desired classes using the three most effective machine learning classifiers are presented in the above section. From the results as presented in table 7 to table 10, it is very much evident that out of the three DCNs, the features extracted by DenseNet201 and InceptionResNetv2 models are much more discernibly distinguishable and effective as compared to Xception. The capabilities of these networks in extracting deep features may also be linked to the depth of the layers in each of these deep networks. From table 5 we can see that the DenseNet201 and InceptionResNetv2 are much deeper networks as compared to Xception. Another observation made in this work is that the support vector machine (SVM) has outpaced almost every other machine learning classifier both in 5-fold and 10-fold cross-validation. This is due to the fact that SVM can discover much more complex and effective decision margins as compared to any other machine learning classifiers. SVM also performs effectively on the set of data having multifaceted features providing a clear and distinct boundary.

C. EVALUATION WITH THE STATE-OF-THE-ART TECHNIQUES

In the proposed work an effective and completely automated TB detection system is developed that makes use of efficient deep convolutional pretrained networks for extracting significant features from radiographic X-ray images and, MLAs are implemented to identify TB infected images from the Normal as well as COVID-19 infected images and hence can be utilized for speeding up medical procedures as per the type of disease. At this point, we have evaluated the performance capability of our model that executes the ensembling of efficient deep convolutional networks and machine learning algorithms for the purpose of the desired classification. In this section, we have explored various state-of-the-art works done in the given field of research and evaluated our proposed work in their light as shown in table 12. From the table, it is clearly evident the ensembling of efficient deep convolutional networks and machine-learning algorithms presented here have completely outperformed the cutting-edge literature in this field and illustrate the competency of our proposed methodology.

TABLE XII
PERFORMANCE EVALUATION WITH THE STATE-OF-THE-ART TECHNIQUES

Literature	Dataset Used	Method of Evaluation	Classification Technique	Maximum Accuracy (%)	AUC
Lopes et al. [30]	406 Normal; 394 Tuberculosis	Deep feature extraction	SVM	84.70%	0.926
Santosh et al. [27]	420 Normal; 400 Tuberculosis	Thoracic edge map encoding	Neural Network	86.36%	0.930
Pasa et al. [31]	406 Normal; 394 Tuberculosis	------	Conventional CNN	86.20%	0.925
Vajda et al. [29]	422 Normal; 392 Tuberculosis	Textural & Statistical Features	Neural Network	95.57%	0.990
Govindarajan et al. [28]	80 Normal; 58 Tuberculosis	Bag of features; speeded-up Robust feature	Multilayer perceptron	87.80%	0.940
Narin *et al.* [47]	341 COVID; 2800 Normal	------	Transfer learning with Resnet50 and InceptionV3	96.1%	------
Ozturk *et al.* [45]	127 COVID; 500 Normal	------	DarkCovidNet	98.08%	------
Das et al. [32]	420 Normal; 400 Tuberculosis;	------	Transfer learning with InceptionV3	76.05%	0.840
Proposed Model	851 Normal; 800 Tuberculosis	Deep Feature Extraction	Machine Learning SVM	**87.90%**	**0.940**
	878 COVID; 800 Tuberculosis			**99.10%**	**1**

D. Applications and Limitations

To assist in the identification of tuberculosis amid the pandemic of COVID-19, the ensembling of efficient deep convolutional networks and machine learning algorithms are proposed that do not entail heavy computational resources. The proposed algorithm will help in the following way:

i) As this algorithm requires a low computational and basic imaging facility it can be cost-effective and can be easily employed in underdeveloped nations and in many areas of developing nations that are susceptible because of the absence of appropriate healthcare facilities.
ii) It can also, up to a certain extent, help in reducing the disparity in healthcare services available in economically weak nations and some regions of developing nations due to a lack of sufficient medical resources and experts.
iii) There are countries in the world that have the worst doctor-to-patient ratio, with merely 10 doctors existing for every million people and this proposed framework can help in bridging this gap to some degree.

The suggested classification approach has a constraint in terms of medical datasets and their accessibility. As the datasets are often limited and do not capture all of the disease's symptoms, which is a major obstruction in the use of computer-assisted diagnosis in real-world scenarios. Hence, a larger dataset with complete disease manifestations is essential for improving the robustness of the classification.

V. CONCLUSION

Tuberculosis is a deadly disease that displays various manifestations on chest radiography. An efficient, highly effective, and accurate procedure that considers all of these manifestations is required for in-time treatment of the affected patients. Here we have presented an amalgamation of DCNs and machine learning techniques for classifying the chest radiographic images into three broad categories namely Tuberculosis, Normal, and COVID-19. The difficulties faced by TB patients in this pandemic era due to the limited availability of resources were the major inspiration behind this proposed work. In this work, the deep extracted features derived from three efficient DCNs: DenseNet201, InceptionResNetv2, and Xception are grouped together, to form a feature pool. These ensembled features are then given to three machine learning classifiers: SVM, K-NN, and Ensemble classifier for classification. Additionally, all likely feature combinations were also investigated using these machine learning classification techniques for comparison with the ensembling of the three deep features. The above model is evaluated using a 5-fold and 10-fold cross-validation technique giving an apex accuracy of 87.9% and 99.1% with an AUC of 0.94 and 1 respectively in identifying TB infected images from normal and COVID infected images. The model's accuracy claims that its use can be beneficial in identifying TB infections amid this COVID-19 pandemic, predominantly in countries with limited resources as this model can also be put to work effectively on a normal CPU with an i5 processor, 8GB RAM, and 2GB Nvidia card as well which is the pivotal feature of this work. Clinical datasets are mostly restricted and do not include the complete manifestations which act as a major blockage in the deployment of computer-assisted diagnosis in actual medical situations. The presented approach may be used over a bigger set of data for enhanced robustness of the system with improved accuracy. Furthermore, manually extracted features could be used to create a fine set of features that can enhance the model performance. A cross-population testing technique can be implemented for averting the biasness in classification. We would also like to apply the proposed approach to real-time applications in the future for the analysis of the competency of the proposed model as we were not able to do it due to COVID-19 restrictions.

ACKNOWLEDGMENT

The authors are grateful to the Deanship of Scientific Research, King Saud University for funding through the Vice Deanship of Scientific Research Chairs.

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