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Tuberculosis Classification using SVM and Modified CNN

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Abstract: Tuberculosis (TB) is a dangerous disease caused by mycobacterium leads to mortality. Early detection and identification of tuberculosis is crucial for managing tuberculosis infections. Recent technological improvements use a machine learning-based SVM and Modified CNN to identify specific diseases more accurately, as demonstrated in this research. The modified CNN's improved feature extraction and classification accuracy are maintained throughout construction. To obtain good performance a TBX11K publicly accessible dataset is used it consists of 11000 images of which 4600 chest x-ray (CXR) images are considered in this research, and the suggested model is verified. This approach significantly increases the accuracy of categorizing TB symptoms. The PCA in this system locates the elements and extracts a large amount of variance technique applied to the full chest radiograph for pulmonary tuberculosis identification accuracy using SVM is 93.14% and modified CNN 96.72% respectively. When it comes to helping radiologists diagnose patients and public health professionals screen for tuberculosis in places where the disease is endemic, the proposed system SVM and modified CNN perform better than existing methods.

Keywords: Tuberculosis, SVM, Modified CNN

1 Introduction

MYCOBACTERIUM tuberculosis (MTB), a bacterium that causes tuberculosis, is a deadly infectious disease that goes by the name TB [1]. Though it mostly affects the lungs, it also spreads to the spine, kidneys, and brain, among other body parts. Severe coughing, weight loss, fever, and sweats at night are some of the signs of tuberculosis. When someone who is infected coughs or sneezes, the bacteria are released into the air and can be ingested by those who are close. This is the major way that it is spread through respiratory droplets [2].

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A worldwide public health worry is tuberculosis (TB), which can be brought on by an infection with MTB. The World Health Organization Global TB Report 2021 claims that there were about 10 million new infections and a total of 1.5 million deaths in 2020 [3]. TB may be avoided and is typically treatable. However, TB accounted for nearly twice as many deaths as HIV/AIDS in 2022 and was the next most common infectious agent worldwide cause of death, following coronavirus disease (COVID-19).

To eliminate the worldwide tuberculosis epidemic by 2030, every member nation of the United Nations (UN) and the World Health Organization (WHO) have agreed that immediate action is necessary [4]. Since there are insufficient medical services, particularly in low and middle-income countries (LMIC), to enhance early identification, TB remains the most common infectious disease fatality [5]. To prevent the illness from spreading and drastically lower the death rate, early diagnosis is crucial [6].

Image processing for TB diagnosis uses sophisticated computational methods to examine chest X-rays (CXR) to spot anomalies linked to TB. To improve contrast and guarantee constant input quality, the program starts with image preprocessing, which includes scaling, noise

reduction, and histogram equalization. More sophisticated techniques like adaptive filtering and brightness adjustment enhance image clarity even more, which helps with feature extraction. Annotated datasets of CXRs with and without TB are used to train these models. Utilizing pre-trained models is made possible by the incorporation of transfer learning, which greatly increases accuracy in environments with restricted resources.

Rotation, flipping, and scaling are examples of augmentation procedures that make the models more robust. Post-processing entails using heatmaps (such as Grad-CAM) to visualize predictions to pinpoint particular areas that may be TB-indicative. Together with confidence scores, the system provides a categorization result (TB positive or negative). These applications, which provide quick, precise, and affordable TB screening, are revolutionary in areas with limited resources. Image processing applications in TB detection save lives and aid public health efforts by decreasing diagnostic delays and reliance on radiologists.

Medical imaging has greatly improved due to artificial intelligence (AI), and X-ray imaging technology is more widely available and less expensive than computed tomography (CT) scans. CXR constitutes one of the main instruments for evaluating and examining TB as a component of the WHO's preventative strategy for ensuring early and accurate diagnosis for all patients with TB because it is an extremely high sensitivity, relying upon how the result of the CXR is interpreted [7].

TB can be detected from medical images, especially CXR, using Convolutional Neural Networks (CNNs) [8]. Because CNNs are so good at extracting hierarchical characteristics, they may spot tiny patterns that would not be obvious to the human eye but are symptomatic of tuberculosis. To get CXRs ready for analysis, the program starts with preprocessing actions such as image scaling, normalization, and contrast enhancement. These photos are processed by CNNs, which are made up of convolutional, pooling, and fully connected layers, to extract useful features. These characteristics aid in differentiating between normal and TB-positive cases.

A labeled dataset of TB-positive and TB-negative CXRs is fed into CNNs during training, enabling the model to identify patterns such as TB-related lesions, cavities, or nodules. To improve resilience, data augmentation methods like flipping, rotation, and brightness modifications are used. Through transfer learning, sophisticated CNN architectures such as pre-trained networks like VGG, Inception, or ResNet—improve performance. TB-specific datasets are used to fine-tune these networks for improved accuracy and quicker convergence. A classification (TB-positive or negative) together with corresponding confidence values is the result. CNN-based TB detection systems are revolutionizing healthcare by providing quick, scalable, and precise solutions, especially in areas with low resources when prompt diagnosis is essential to life preservation.

The following is a summary of the primary contributions made by the suggested work:

(i) This research suggests using a support vector machine (SVM) and modified CNN to detect TB on CXR pictures, such as normal and abnormal.
(ii) When evaluated with medical radiology professionals, modified CNN algorithms clearly explain the model's results on CXR pictures without sacrificing the model's accuracy.
(iii) Additionally, this explains that our approach surpassed the current methods in classifying CXR images as TB and Normal by comparing its performance with previous methods.

Subsequent sections: Section 2 - Literature Review, Section 3 - Methodology, Section 4 - Results and Discussion, Section 5 – Conclusion.

2 Literature Review

An automated model for classifying CXR related to TB using a Deep Convolutional Neural Network (DCNN). In both the training and intramural test sets, the model demonstrated an AUC of 0.9845 and 0.8502 respectively strong diagnostic performance. However, the model's performance dramatically decreased (AUC = 0.7054) when tested with a CXR dataset that was not specific to TB in patients. The results highlight the significance of considering, before using deep learning algorithms in various contexts, the technical characteristics of CXR pictures, the degree of illness distribution, dataset dispersion shift, and an overdiagnosis [7].

Three main types of CXR can be distinguished based on the patient's posture and position to the Anteroposterior, lateral, and posteroanterior locations of the X-ray generator and detection panel. The X-ray source is placed in front of the patient in the anteroposterior (AP) view and the rear of the patient in the posteroanterior (PA) view, respectively, making both views frontal. Patients are generally supine when the AP image is obtained, but they are usually standing when the PA image is obtained. Typically, the lateral image is obtained in conjunction with a PA image [9].

In locations with limited resources, applying deep learning to radiological image analysis may make it easier to employ CXR as triage diagnostic for pulmonary TB. The goal was to find out if commercially available software for analyzing CXR complies with WHO

guidelines for the minimum levels of sensitivity and specificity needed for pulmonary TB triage tests. Two software programs, CAD4TB version 6.0 CAD4TBv6, and qXR version 2.0 qXRv2, were examined using two sputa mycobacterial cultures as a point of comparison. Using the manufacturer-specified threshold score for classifying TB or normal on CXR, qXRv2. The minimum accuracy for pulmonary TB triage testing that was advised by the WHO was met by this program. A higher prevalence of smear-negative pulmonary TB will result in decreased sensitivity [10].

For TB diagnosis on CXR images, transfer learning using VGG16 was used [11]. They built the model using 1324 CXR images and produced an accuracy of 80.0% when dividing CXR images in TB and healthy groups. The Inception-V3 model, which was trained using a DCNN with transfer learning, was used by [12]. 3532 CXR photos in all were improved and shrunk to 299 × 299 × 3 in the gathered dataset. The reliability of the model was 93%.

However, TB in CXR pictures was not categorized by the study. Three distinct pre-trained CNN models i.e., Alexnet, GoogleNet, and ResNet—on the identification of pulmonary TB were observed by [13]. When GoogleNet combined photos from the datasets of Montgomery, PadChest, and Shenzhen, totaling 1092 samples, the maximum accuracy it could attain was 75%.

[14,15] state that the spatial resolution of CXR varies in practical applications and that features based on the single-scale bags of deep visual words (BoDVW) are unable to adequately capture the intricate semantic details of the lung infection areas. For multiscale bags of deep visible words-based features, this performs the convolution with max pooling operations across the fourth pooling layer using three different kernels: 1 × 1, 2 × 2, and 3 × 3. After evaluating the proposed features using the SVM classification algorithm, their method produced notable classification accuracy respectively 84.37%, 88.88%, 90.29%, and 83.65% for 4 public CXR datasets.

3 Methodology

The CXR images of both TB and Normal were preprocessed using data collected from the TBX11K datasets [16], of which 4600 images were divided into train and test CXR images. Since the image sizes varied, they were cropped to 224 × 224. To increase the samples on the fly, a horizontal flip technique was carried out. Ultimately, the images were normalized by rescaling each pixel into the interval [0,1]. Fig. 1 (Figure) displays sample CXR images of normal and TB data that were taken from the CXR dataset, (a) represents the Normal (b) represents the TB (c) represents the after preprocessing i.e. brightened image.

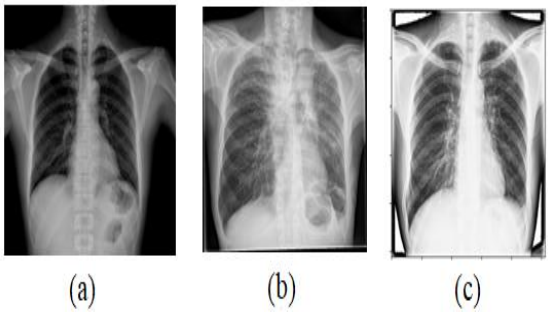


Fig. 1 Sample images are taken out of the CXR image dataset.

3.1 SVM Methodology

An SVM is a binary classification technique that establishes the ideal division between multiple classes.

$$Y = w * x + C \quad (1)$$

Where Eq. (1) w, x and c – weight vector, input feature vector, intercept.

Fig. 2 indicates the architecture of the SVM model for TB classification.

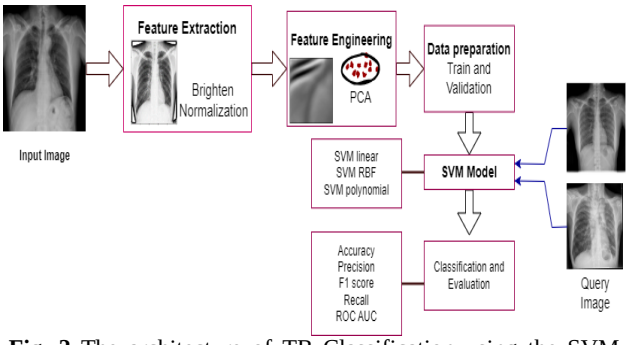


Fig. 2 The architecture of TB Classification using the SVM model.

Data Preprocessing

The input images accessed from the dataset and then resizing images to a 224 * 224 region of interest, each area of interest will contain disease areas while avoiding unnecessary information. Two ways to use a calculation are Lanczos filtering and resampling. It can smooth the interpolation of a digital signal's values between sampling or applied with a low-pass filter, and after that, adjust the backdrop brightness of the image and, usually, convert a variable that represents an image then normalized.

Feature Extraction

In this work, feature extraction is used to turn an image with two dimensions onto a feature vector, and can then be used as an input for the classifier's mining stage. When describing the pertinent qualities of the image into a feature vector, the features obtained should give the classifier the features of the input type. The main reason we flatten an Image Array before processing the data

in our system is that 1-D arrays require less memory than multi-dimensional arrays. Since we typically work with datasets that have a lot of images, flattening aids in both lowering memory usage shortening the training time of the model, and enlarging N-dimensional images by doing interpolation. that to prevent anti-aliasing, aliasing artifacts must be turned on while reducing the size of images.

Principal Component Analysis – (PCA)

PCA, typically referred to as the Karhunen-Loeve (KL) transform [17], is the projection-based method that makes it easier to reduce the dimension of the data by creating orthogonal principal components, that constitute weighted, linear combinations among the constituent variables. The PCA transform can be represented as follows, assuming that it is a linear transformation that maps the initial N-dimensional feature set into an M-dimensional set, where M < N.

$$Y_D = Y_V X_a \quad (2)$$

Where Eq. (2) the components we want to express the observation of the feature set rely on the length of the so-called eigenvector, or Y_V. The original data source is projected over the covariance matrix's eigenvectors to create the final feature space. In this research, PCA is used to examine whether a smaller collection of characteristics can still significantly differentiate the predicted data. First, a standard matrix was created by converting the original matrix. In other words, the characteristics had been normalized to have unit variances along with zero means. The weights of each attribute in the space of input were then computed to create the covariance matrix, the second step. Furthermore, the covariance matrix's eigenvalues and associated eigenvectors were calculated. Primarily, the eigenvector with its greatest eigenvalue represents the most significant knowledge and explains a greater proportion of the variation in the data.

The subsequent pre-processing techniques were used to modify the input data so that it complied with the SVM model requirements: Each image underwent resizing, normalization, and conversion into an array so that they could be used as input for the subsequent stage of the model. To verify that the picture variation satisfies the necessary criteria for training a proposed algorithm, the data were randomized into training and validation subsets at 80% and 20%, respectively. To comply with the framework's requirements, every image was resized to 224 * 224. Each image was first normalized within the interval [0,1], and then an array representing the data was created for each image.

This research suggests a machine learning-based SVM system that can detect and classify TB in radiography. Among the most effective machine learning methods for classification, regression, and outlier identification are SVM. An SVM classifier creates a model by classifying fresh data points into one of the predefined groups. It is hence comparable to an uncertain binary linear classifier, radial bias, and polynomial classifier.

$$f(x) = \text{sign}\,[\sum_{i=1}^{n} \propto_i y_i K(x_i, x) - b] \quad (3)$$

A hyperplane decision formula is represented by Eq. (3), where b is the classification threshold, $K(x_i, x)$ is a kernel function, and $\propto_i$ lagrangian multiplier.

3.2 Modified CNN methodology

The framework of the envisaged model is shown in Fig. 3.

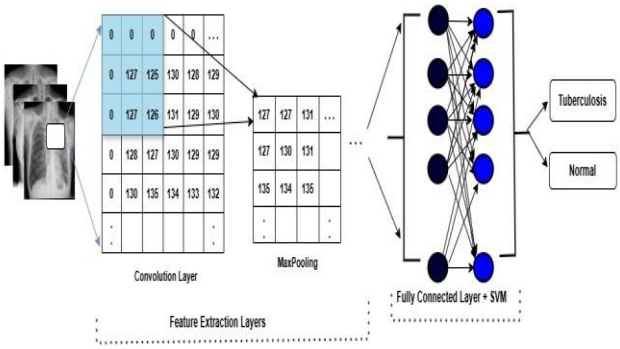


Fig. 3 The architecture of the proposed methodology

The input layer, composed of the primary layer of the approach has an input shape of (224, 224, 3) with a filter size of 96 and four strides. The convolution layer having 256 filters brings up the second layer. This layer has a 5 × 5 kernel size. The activation function ReLU with the 2 × 2 max pooling layer comes next. The convolution layer, with 384 filters, is the third layer.

This layer has a 3 × 3 filter size and is followed by a 2 x 2 max pooling layer, the activation function ReLU. This layer has a 3 × 3 filter size. It is followed by a 2 x 2 max pooling layer and the activation function ReLU. With 256 filters, the convolution layer is the fourth layer.

The activation function ReLU as the 2 x 2 max pooling layer comes after this layer, which has a 3 × 3 filter size. A convolution layer using 128 filters makes up the architecture's fifth layer. The activation function is ReLU and the 2 x 2 max pooling layer comes after this layer, which has a 3 × 3 filter size. The optimizer used here is RMSprop which will control the learning rate, epsilon, and decay rate. In the fully connected layer, the SVM algorithm is incorporated by calling the regularizer, flattened layers with a 50% or 0.5 dropout rate. The next two layers are dense, containing 1024 neurons each, with a 50% or 0.5 dropout rate. The loss function is considered as binary cross entropy is given by Eq. (4).

$$H_p(q) = -\frac{1}{N}\sum_{i=1}^{N} y_i, \log\big(p(y_i)\big) + (1 - y_i),\ \log\,(1 - p(y_i)) \quad (4)$$

With an i7 Intel Core 8th generation processor, a Quadro P4000 GPU 8 GB NVIDIA, and 16 GB of RAM, a workstation equipped with these specifications was used to conduct the experiments via Python 3.9.

Performance Evaluation Metrics

Analyzing the model's ability requires a thorough examination of performance. The performance of the network can be evaluated using a variety of metrics. We employed recall, accuracy, precision, and F1-score as measures in the current research, and we calculated them using Equations

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (5)$$

$$Precision = \frac{TP}{TP+FP} \quad (6)$$

$$Recall = \frac{TP}{TP+FN} \quad (7)$$

$$F1\ Score = \frac{2*Precision*Recall}{Precision+Recall} \quad (8)$$

Where *TP* and *TN*, the true positive and negative parameters, are indicated, respectively. The symbols *FN* and *FP* stand for false negative and positive values, respectively.

4 Results and Discussion

The approach previously presented is being assessed using a collection of CXR from TBX11K, the features were selected using PCA, and then the classification is done based on the SVM classifier using linear, radial, and polynomial methods. Using an SVM linear 10x10 paramgrid and grid search, the best values for gamma and C were 0.000977 and 70782, respectively, for SVM radial and SVM polynomial. The performance parameters used are accuracy, precision, recall, and F1 score are shown in Table 1.

(a) (b)

Fig. 4 Shows the Accuracy and Loss for training and validation

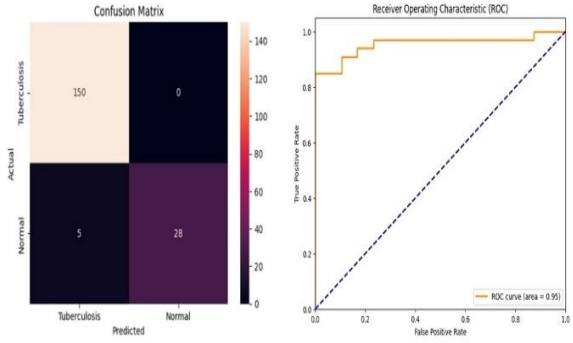
Table 1 gives the comparison results, as compared with the existing system our proposed SVM and modified CNN give better accuracy so this model can be implemented to classify the TB and Normal.

Table 1. The performance comparison of SVM and modified CNN

Methodology	Accuracy	Precision	Recall	F1 Score
K-Nears Neighbors Random forest (13)	69% 78%	0.65 0.75	0.81 0.83	0.72 0.79
BoDVW four public CXR datasets using SVM (15)	84.37%, 88.88%, 90.29%, and 83.65%	-	-	-
VGG model for chest X-ray (14)	87.49%	-	-	-
SVM Linear SVM Radial Bias SVM Polynomial for TBX11K	92.81% 92.38% 93.14%	0.93 0.93 0.93	0.93 0.92 0.93	0.92 0.92 0.93
Proposed method Modified CNN for TBX11K	96.72%	0.98	0.92	0.95

For the modified CNN algorithm using optimizer as RMSprop and the loss function as binary cross entropy the accuracy and loss for training and validation data are shown in Fig. 4.

Till 5 epoch the accuracy is approx. 90% as the number of epochs increases the accuracy increases slightly. Fig. 4(a) The accuracy achieved is 95.61% and 96.72% for train and validation respectively. Fig. 4(b) gives the loss.



(a) (b)

Fig. 5 Shows the Confusion matrix and ROC.

Fig. 5 (a) confusion matrix plotted actual vs predicted from the matrix precision, sensitivity, and F1 score is calculated. The ROC curve is shown in Fig. 5 (b), it occupies 0.95 of the ROC area for 20 epochs.

5 Conclusion

One of the most prevalent infectious diseases, tuberculosis (TB) claims many lives every year. It is often misdiagnosed, particularly in rural areas where resources are scarce and radiologists are few. This research assessed the effectiveness of an ensemble of chest disease classification based on SVM and modified CNN architecture for TB and normal categorization using CXR pictures. The results of SVM are 93.14% and the modified CNN model for tuberculosis classification is 96.72 % respectively.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Experiments were designed by Srinivas Babu N and Shashikiran S. Experiments performed by Srinivas Babu N, Shashikiran S, Ranjani N, Kushalatha M R. Results were analyzed by M Jayanthi and K M Palaniswamy. All authors were involved in the interpretation of data and paper writing and revision of the article.

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Informed Consent Statement

Patient consent was waived as this is the standard dataset that was taken from open source from the Kaggle.

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