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A-Novel in this Technique Analysis Tuberculosis Patient Using Hybrid CNN and SVM Model

Nisha
Research Scholar, Department of Computer Science and Applications, Baba Mastnath University, Rohtak, Haryana, India

Dr. Reena
Assistant Professor, Department of Computer Science and Applications, Baba Mastnath University, Rohtak, Haryana, India

Abstract: Tuberculosis (TB) remains a global health challenge with a significant impact on public health worldwide. This study addresses the prevalence and detection of T.B., focusing on India, a country experiencing rapid economic growth and notable transitions in various sectors. Despite advancements in healthcare delivery, communicable and non-communicable diseases, including TB, continue to pose substantial threats to health security. The proposed method for T.B. analysis integrates key modules, encompassing data collection, preprocessing, feature extraction, image splitting, classification, and performance estimation. Utilizing machine learning algorithms such as Support Vector Machine (SVM) and Convolutional Neural Network (CNN), the study aims to enhance accuracy and efficiency in T.B. patient detection. The dataset includes chest X-rays from diverse sources, aiming to provide a comprehensive understanding of T.B. patterns. The study emphasizes the interconnected challenges of malnutrition and T.B., highlighting the importance of nutritional status assessment in public health. The linkage between undernutrition and infectious diseases, including TB, underscores the need for early detection and intervention. The proposed method offers a systematic approach to evaluating and addressing nutritional deficiencies in patients with chronic illnesses, contributing to improved clinical outcomes.

Keywords - SVM, CNN, Tuberculosis, Machine, Learning, Chest X-rays

I INTRODUCTION

India has one of the highest rates of economic growth among all countries in the globe. The state of transition is found in the entire dimension, including economic, educational, and demographical, and in terms of health. Over one-third of income is spent on food, shelter, education, and health-related social security. The government has taken major initiative to improve the standards of living among general population but the expected result is still profound by WHO [1] In past few decades health sector has made dynamic changes in the health care delivery system. There is a change in life expectancy of common man, decline in maternal mortality rate, infant mortality rate, under five mortality rates many diseases is eradicated and accessibility to health care services has improved. [2]

Other than that, the biggest public health problem in both cities and rural places is still the spread of communicable and non communicable diseases. Future predictions say that this will be a major hazard to the health security of the whole world and the nations that live in them. Dealing with chronic and epidemic diseases like HIV, tuberculosis, malaria, COVID-19, the flu, respiratory disorders, and diarrhea could continue to be hard for the health care system. Prior to the Corona virus (COVID-19) outbreak, tuberculosis (T.B.) was the most common disease that killed the most people. The score was even higher than HIV infection.

The problem statement revolves around the multifaceted challenges in India's health sector despite significant economic growth and government initiatives [3-5]. While progress has been made in areas such as life expectancy, maternal and infant mortality rates, and disease eradication, the nation grapples with persistent issues, notably the prevalence of communicable and non-communicable diseases. The emergence of COVID-19[6] has added to the complexity of health security concerns. Tuberculosis remains a significant health threat, and non-communicable diseases are on the rise due to factors like inactive lifestyles, poor dietary habits, and substance abuse. Malnutrition, encompassing poor nutrition, under nutrition, and vitamin deficiency, poses a critical public health crisis, particularly among socially vulnerable and economically disadvantaged populations. Despite the government's efforts, there are limitations in achieving desired health outcomes, highlighting the need for comprehensive strategies addressing infectious diseases, lifestyle-related ailments, and nutritional deficiencies.

Additionally, the lack of a widely recognized benchmark for assessing nutritional status and the underdiagnosis of malnutrition underscore the importance of implementing systematic screening and intervention measures in healthcare practices.[7-10]

II RELATED WORK

Ahsan et al. [11] to use the VGG16 DL classification network, two well-known datasets were put together. In the dataset for Montgomery County, there are 58 T.B. photos and 80 CXR images of healthy individuals. The Shenzhen Hospital dataset contains 336 photos of tuberculosis and 326 photographs of normal subjects. In order to divide the information, a train-to-test ratio of three to one was utilized, which resulted in an accuracy of 81.25%. The total number of photographs that they used was 800, with 394 of them displaying T.B. and 406 of them displaying normal CXR pictures.

Xie et al. [12] used a faster region-based RCNN (Region-based Convolutional Neural Network) method to find TB-infected areas or tumors. This was done instead of using binary classification, which would have meant giving either tuberculosis or healthy a positive or negative number. Researchers used a mix of three different kinds of data. The 18 Montgomery County dataset, the Shenzhen Hospital dataset, and the First Affiliated Hospitals Dataset from Xian Jiao Tong University in Shanxi, China were some of these datasets. The dataset has a total of 5,344 pictures, with 2,962 TB photos and 2,382 control photos. There were a total of 6,144 pictures used, with 3,356 TB photos and 2,788 normal photos. They decided to split the test and train images 80:20. Their accuracy was 92.60% and their area under the curve (AUC) was 0.98.

Sahlol et al. [13] A novel combination network called Mobile Net-AEO was made. A feature choice called artificial ecosystem based optimization (AEO) keeps the features that are important to the network and gets rid of the CNN-generated features in this network. The Shenzhen Hospital dataset and the Mendeley Dataset (U.K.) were both used. Together, they have a total of 6,421 CXR images, with 3,883 TB pictures and 2,538 standard images. Researchers used a full set of data that included 7,083 pictures, with 4,219 TB photos and 2,864 normal photos. 80 percent of the information was used for training and 20 percent was used for testing. The accuracy was 94.1 percent.

Rahman et al. [14] During the process of sorting CXR images into groups for normal and tuberculosis photos, nine distinct deep neural networks that were based on transfer learning were utilized.. A person could name these networks: ChexNet, MobileNet, ResNet18, ResNet50, ResNet101, VGG19, and ResNet101. The scientists first divided the lung area into segments using a changed version of the UNet network. Then they put the segments into groups. The Belarus T.B. Dataset (Belarus), the Shenzhen dataset, the Montgomery dataset, and the Radiological Society of North America dataset (RSNA) were brought together and used together. There were a total of 26,684 pictures in the RSNA dataset (17,833 TB images and 8,851 control images), while only 422 CXR images from people who had tuberculosis were in the Belarus dataset. Out of the 27,906 photos that were taken, 18,649 were T.B. photos and 9,257 were normal photos. The best accuracy they could get with DenseNet201 was 98.60%, which they got by using a fivefold cross-validation method.

III MATERIAL AND METHOD

This method for finding pictures of tuberculosis is a planned way to use machine learning to make a correct diagnosis. This process starts with putting in the Tuberculosis picture dataset, which is made up of pictures in the ".png" and ".jpg" forms that were gathered from a repository. All of the photos that have been gathered go through a thorough preprocessing step. As part of this step, pictures are scaled, turned into grayscale, exploratory data analysis (EDA) is done, and images that aren't balanced are turned into healthy ones. Input of good quality and uniformity is made sure of at this stage. Aside from basic statistics like mean and standard deviation, more advanced methods like the Gray Level Co-Occurrence Matrix (GLCM) and the Scale-Invariant Feature Transform (SIFT) are then used on the images that have already been processed. It is split into test and train representations for assessment and prediction after the features are extracted. ML technique are used to categorize things in this scheme. Support vector machines (SVM) with grid search cross-validation, convolutional neural networks (CNN) with grid search cross-validation, and a joint CNN and SVM method [17] with grid search cross-validation are some of these techniques. Finally, the last steps build a strong foundation for finding tuberculosis. These include guessing if an image us here send it will show tuberculosis and checking performance measures like correctness, specificity, loss, and visual estimates. Following these steps is very important for making sure the model is correct and reliable.

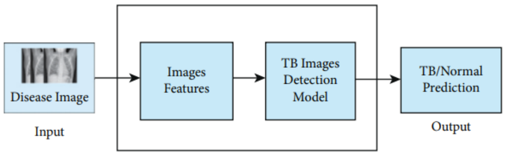

Figure 1: Workflow diagram of the T.B. or normal image detection.

A block design is depicted in Figure 1. This design begins with an input dataset that is divided into two tests. A number of preprocessing steps were carried out by this system before the model was fitted.

Datasets

Many chest X-rays of people who have tuberculosis (T.B.) and people who don't have T.B. have been put together by experts from Qatar University in Doha, Qatar, the University of Dhaka in Bangladesh, and Malaysia. Along with doctors from Hamad Medical Corporation and Bangladesh, the experts have worked together. In our most recent release, there are 3500 normal pictures, 700 TB photos that anyone can see, and 2800 TB photos that people who sign an agreement can see through the NIAID TB portal[3]. https://www.kaggle.com/datasets/tawsifurrahman/tuberculosis-tb-chest-xray-dataset

Table 1: Summary of the Datasets

	Types	Total No. of Xray images/ class
NLM, Belarus and RSNA	Normal	3500
Positive for Tuberculosis	Tuberculosis	700

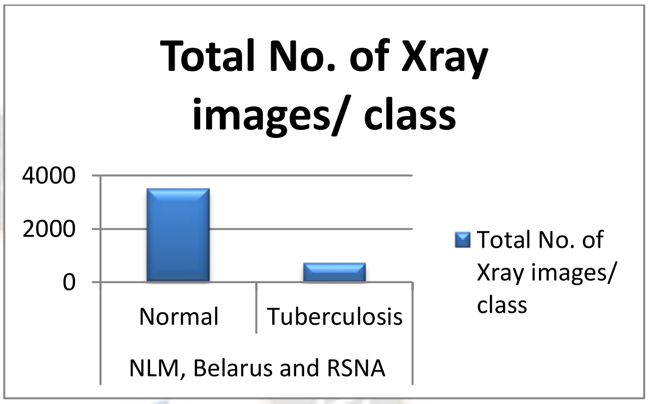

Figure 2: Summary of the Datasets

Figure 3: Non-Tuberculosis X-ray images

Figure 4: Tuberculosis X-ray images

Preprocessing Employed

"Image preprocessing" refers to the steps and methods that are used on the information each of us already have to make some features better, get rid of or lessen some distortions, and maybe even change the eventual outcome of the model. But picture preprocessing doesn't make the image contain more information. Before us here started our study, each of us used the following preprocessing methods.

- Contrast Enhancement
- Augmentation
- Resizing

Table 2 gives the count of all the classes in the dataset after performing the augmentation operation.

Table 2: Dataset Count Before and After Augmentation

	Before Augmentation	**After Augmentation**
Montgomery	138	828
Shenzhen	662	3972
Total Images After Augmentation		**4800**

IV PROPOSED METHOD

The proposed method for the analysis, classification, and detection of Tuberculosis (T.B.) patients is designed as a comprehensive framework integrating key modules to enhance accuracy and efficiency. The initial phase involves meticulous data collection from a Tuberculosis image dataset, encompassing both '.png' and '.jpg' formats. Following data acquisition, a robust preprocessing module undertakes crucial steps, including image resizing, conversion to grayscale, Exploratory Data Analysis (EDA), and addressing class imbalance. This preparatory stage sets the foundation for subsequent feature extraction, where statistical measures like mean and standard deviation, coupled with advanced features such as GLCM and SIFT, capture relevant information from preprocessed images.

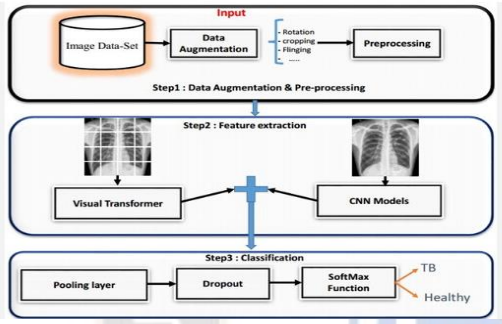

Figure 5: Proposed Method

The subsequent modules are dedicated to image splitting, classification, and performance estimation. The image splitting module segregates features into training and testing sets, enabling rigorous model evaluation. The classification module employs state-of-the-art machine learning algorithms, including Support Vector Machine (SVM) with grid search cross-validation, Convolutional Neural Network (CNN) with grid search cross-validation, and a hybrid CNN and SVM with grid search cross-validation. This amalgamation of algorithms ensures a comprehensive approach to T.B. patient detection. The final performance estimation module evaluates the system's accuracy, specificity, loss, and potentially visualizes these metrics through graphs, offering a detailed assessment of the proposed method's efficacy in Tuberculosis patient classification and detection.

Modules

Preprocessing

Achieve a standardized size for all input images. Resize the images to a consistent resolution, ensuring uniformity in the dataset. Standardizing the image size helps in reducing computational complexity and ensures compatibility with the chosen machine learning algorithms.

Grayscale Conversion: Simplify image representation and reduce computational load. Convert the resized images to grayscale, eliminating color information while retaining crucial structural details.[19] Grayscale simplifies the image, making it more computationally efficient for subsequent processing steps.

Grayscale conversion is a process of transform a color image into a grayscale (black and white) representation. The conversion typically involves combining the color channels of an image in a way that preserves the luminance information while discarding color information. One common method is to take a weighted average of the red, green, and blue channels. Here's the mathematical expression for grayscale conversion:Let, R, G, and B represent the pixel values of the red, green, and blue channels, respectively, for a given pixel in the image.The luminance (Y) of the pixel can be calculated using the following formula:

$$Y=0.299\cdot R+0.587\cdot G+0.114\cdot B \quad \text{(Eq.1)}$$

This formula represents the weighted sum of the color channels, with weights chosen to reflect the human eye's sensitivity to different colors. The coefficients 0.299, 0.587, and 0.114 are often used in the context of the RGB color space.After obtaining the luminance (Y), the grayscale pixel value (G) is set to this luminance value:

$$G=Y \qquad \text{(Eq.2)}$$

This process is applied to each pixel in the image to produce the grayscale representation.

Exploratory Data Analysis (EDA): Gain insights into the dataset's characteristics. Conduct Exploratory Data Analysis (EDA) to understand the distribution of TB-positive and TB-negative cases. This may involve visualizations, statistical summaries, and the identification of potential outliers. EDA helps inform subsequent decisions in the data processing pipeline.

Addressing Class Imbalance: Mitigate the impact of imbalanced class distribution. Assess the balance between TB-positive and TB-negative cases. If there is a significant class imbalance, apply techniques such as oversampling the minority class or under sampling the majority class to ensure the model does not bias towards the majority class during training.

Noise Reduction: Enhance image clarity and reduce interference. Apply noise reduction techniques if necessary, particularly if the images contain artifacts or unwanted disturbances. Common methods include Gaussian smoothing or median filtering, depending on the characteristics of the dataset.

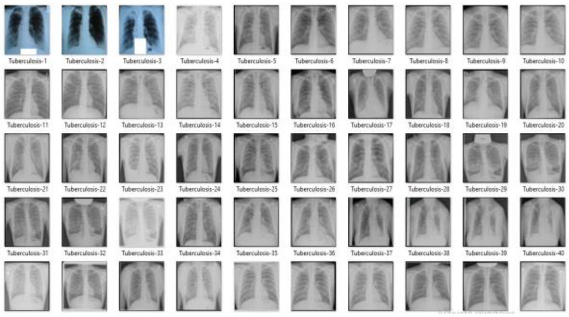

Figure 6 tuberculosis Dataset

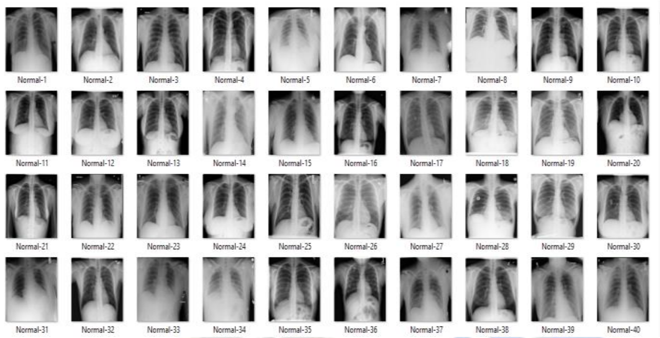

Figure 7 normal Dataset

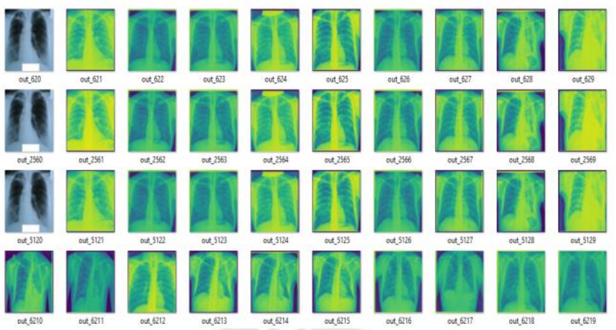

Figure 8: Before Augmentation Dataset

Implement Algorithm

Hybrid CNN and SVM Model:

Convolutional Neural Network (CNN):Let fCNN(X;θ) represent the CNN function, where X is the input image and θ are the model parameters. The CNN model involves a series of convolutional, pooling, and fully connected layers. The final output of the CNN, denoted as y^CNN, represents the predicted class probabilities.

$$y^\wedge CNN=fCNN(X;\theta) \quad \text{(Eq.3)}$$

Support Vector Machine (SVM):Let fSVM(X;w,b) represent the SVM function, where X is the input features, w is the weight vector, and b is the bias term. The SVM model is trained to classify input features into different classes.

$$y^\wedge SVM=fSVM(X;w,b) \quad \text{(Eq.4)}$$

Hybrid Model Combination: Combine the predictions of the CNN and SVM models. This can be achieved through an ensemble approach or by feeding the output of the CNN into the SVM as additional features.

$$y^\wedge Hybrid=\alpha\cdot y^\wedge CNN+(1-\alpha)\cdot y^\wedge SVM \quad \text{(Eq.5)}$$

where α is a weighting factor.

Tuning the Weight Parameter =α:

The weight parameter α determines the contribution of each model to the hybrid prediction. Grid search or other optimization techniques can be employed to find the optimal α that maximizes the hybrid model's performance.

Grid Search Cross-Validation:

During the training process, grid search cross-validation is employed to find the optimal hyperparameters for both the CNN and SVM components. Let Θ represent the set of hyperparameters for the CNN, and Φ represent the set of hyperparameters for the SVM.

$$\phi *=\text{argmax}\theta\in\Theta,\phi\in\Phi \text{ Cross-Validation Score} \quad \text{(Eq.6)}$$

This hybrid model leverages the feature learning capabilities of CNNs and the discriminative power of SVMs. The grid search cross-validation ensures the selection of optimal hyperparameters for enhanced performance. The combination of these two techniques provides a powerful and adaptable approach for Tuberculosis patient classification.

V RESULT AND ANALYSIS

During the process of identifying normal photos and tuberculosis, us here conducted experiments with a wide range of models and methods in order to evaluate the usefulness and effectiveness of these approaches.

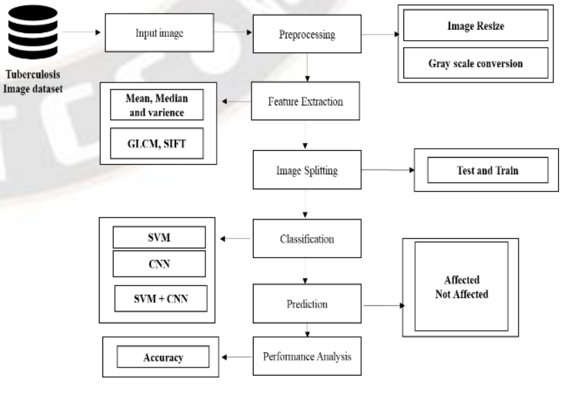

Figure 9 Simulation flow diagram

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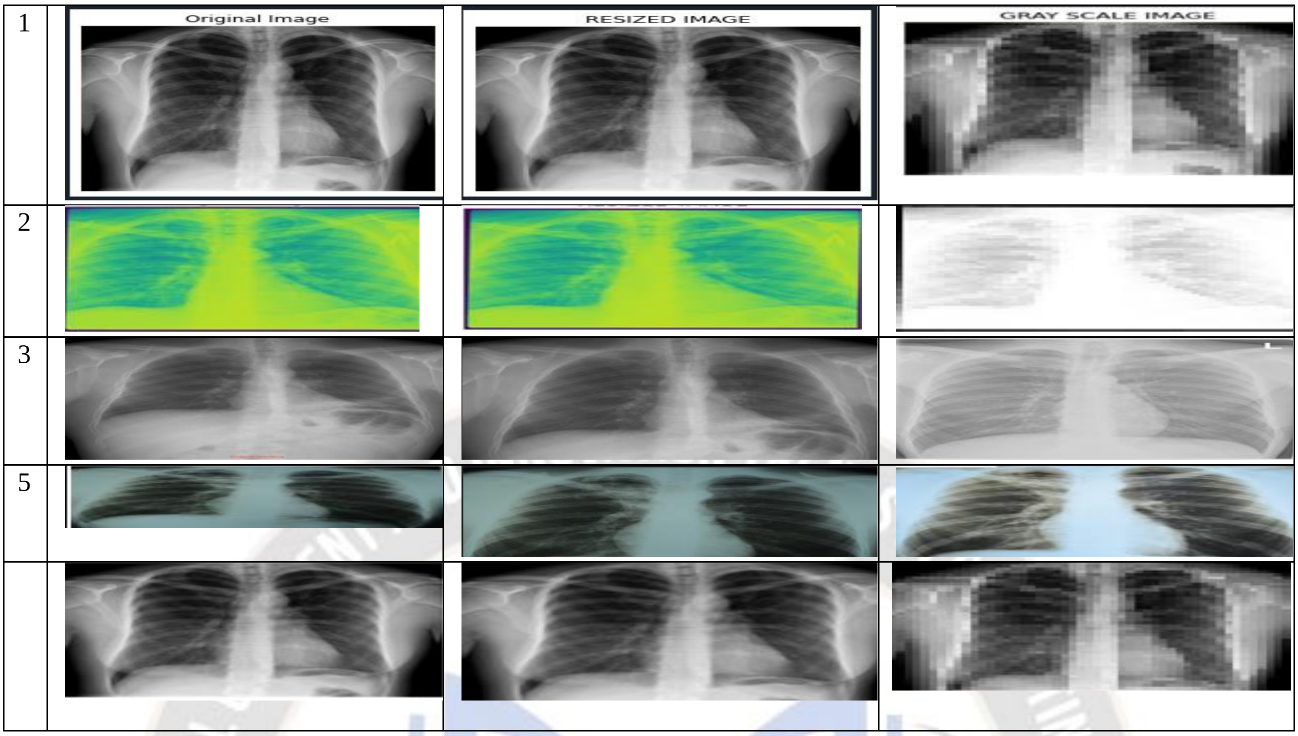
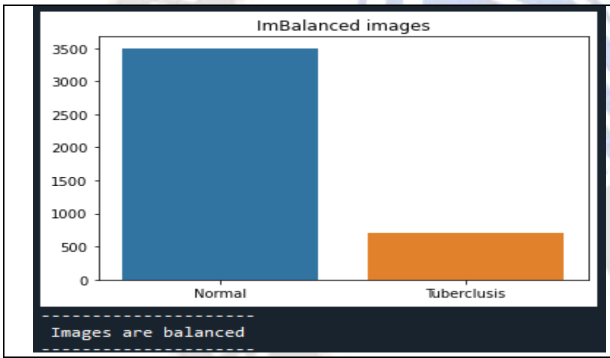


Figure 10 preprocessing



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 Images are balanced
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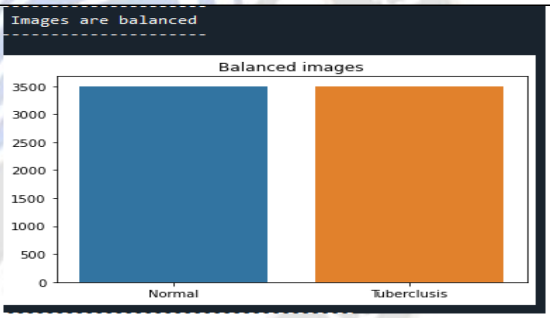
Figure 11 Imbalanced Image



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Images are balanced
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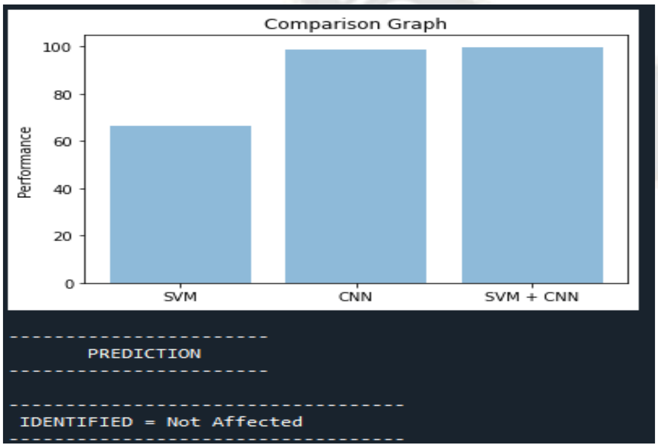
Figure 12: Balanced Images



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       PREDICTION
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 IDENTIFIED = Not Affected
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Figure 13 Comparison Graph

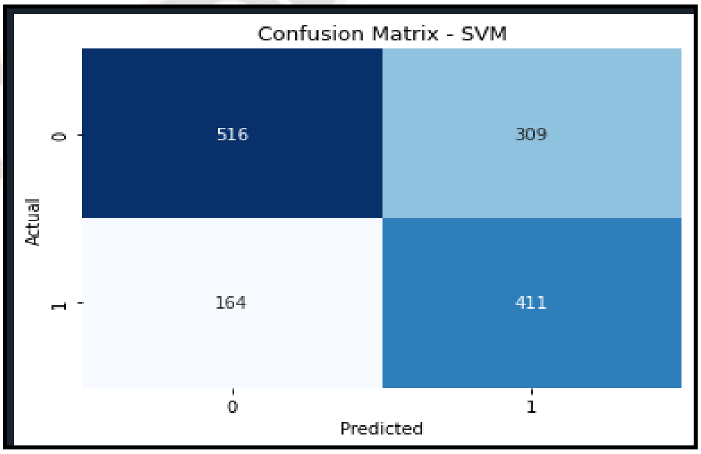

Figure 14 confusion matrix- SVM

Table 2 Accuracy SVM ,CNN , SVM + CNN

DATASET	**SVM**	**CNN**	**CNN+SVM**
	ACCURACY		
1	66.28	98.48	99.23
2	68.23	97.25	99.2
3	69.24	96.23	99.24
4	67.23	95.23	99.25
5	70.11	98.56	99.78

the performance metrics, specifically accuracy, of three distinct models—Support Vector Machine (SVM), Convolutional Neural Network (CNN), and a hybrid model combining both CNN and SVM (CNN+SVM) across five different datasets. The SVM model demonstrates a moderate accuracy ranging from 66.28% to 70.11%. In contrast, the CNN model consistently outperforms the SVM, achieving higher accuracies ranging from 95.23% to 98.56%. The hybrid CNN+SVM model exhibits superior performance across all datasets, with accuracies consistently exceeding 99%, indicating the synergistic benefits of combining feature-based SVM and deep learning-based CNN approaches. These results underscore the effectiveness of the hybrid model in enhancing overall classification accuracy, showcasing its potential as a powerful tool for tuberculosis detection

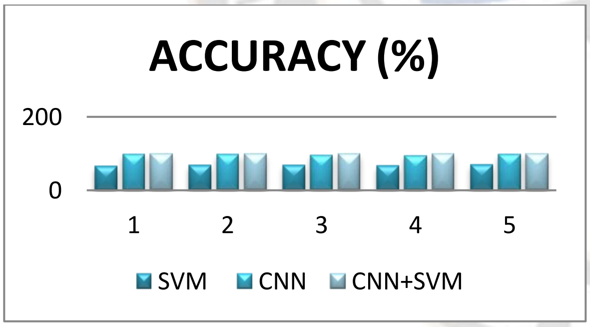

Figure 15 Accuracy performance for SVM ,CNN , SVM + CNN

Table 3 Precision SVM, CNN , SVM + CNN

DATASET	**SVM**	**CNN**	**CNN+SVM**
	Precision		
1	78.23	97.25	96.23
2	77.25	96.24	97.24
3	76.25	98.78	99.58
4	75.12	92.36	99.57
5	77.12	91.24	98.56

table presents precision metrics for three different models—Support Vector Machine (SVM), Convolutional Neural Network (CNN), and a hybrid model combining both CNN and SVM (CNN+SVM) across five distinct datasets. Precision values represent the proportion of correctly predicted positive instances among all instances predicted as positive. The SVM model exhibits varying precision values, ranging from 75.12% to 78.23%, across different datasets. The CNN model consistently outperforms the SVM, achieving higher precision values ranging from 91.24% to 98.78%. The hybrid CNN+SVM model consistently demonstrates superior precision, exceeding 96% and reaching up to 99.58%, underscoring the effectiveness of the hybrid approach in accurately identifying positive instances, particularly in the context of tuberculosis detection.

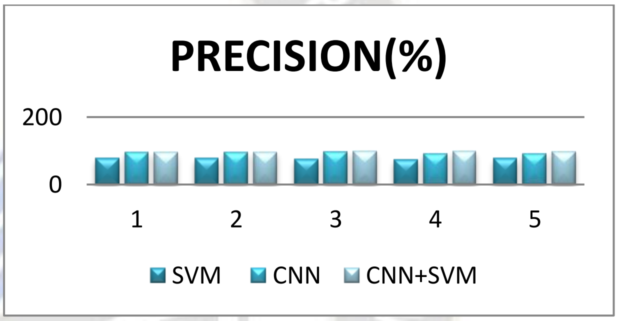

Figure 16 Precision performance for SVM, CNN , SVM + CNN

Table 4 Specificity SVM , CNN , SVM + CNN

DATASET	**SVM**	**CNN**	**CNN+SVM**
	Specificity		
1	70.23	97.15	98.56
2	71.25	96.25	98.23
3	72.36	96.48	97.25
4	77.23	96.78	96.24
5	78.3	96.25	97.56

The table displays specificity metrics for three different models—Support Vector Machine (SVM), Convolutional Neural Network (CNN), and a hybrid model combining both CNN and SVM (CNN+SVM) across five distinct datasets. Specificity measures the proportion of correctly predicted negative instances among all instances that are actually negative. The SVM model demonstrates specificity values ranging from 70.23% to 78.3% across the datasets. The

CNN model consistently outperforms the SVM, achieving higher specificity values ranging from 96.15% to 97.78%. The hybrid CNN+SVM model consistently exhibits superior specificity, exceeding 96%, and reaching up to 98.56%, highlighting its effectiveness in accurately identifying negative instances. These results emphasize the hybrid model's potential for enhancing specificity, particularly in the context of tuberculosis detection.

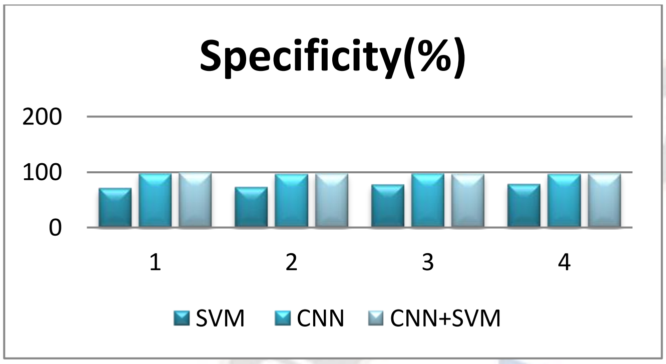

Figure 17 Specificity performance for SVM , CNN , SVM + CNN

Table 5 Sensitivity SVM , CNN , SVM + CNN

DATASET	SVM	CNN	CNN+SVM
	Sensitivity		
1	91.23	97.25	99.25
2	71.45	97.24	99.47
3	78.23	96.23	99.58
4	74	96.58	99.14
5	74.23	96.25	99.23

The provided table outlines sensitivity metrics for three distinct models—Support Vector Machine (SVM), Convolutional Neural Network (CNN), and a hybrid model combining both CNN and SVM (CNN+SVM) across five datasets. Sensitivity, also known as recall, measures the proportion of actual positive instances correctly identified by the models. The SVM model exhibits varying sensitivity values, ranging from 71.45% to 91.23%. The CNN model consistently outperforms the SVM, achieving sensitivity values ranging from 96.23% to 97.25%. The hybrid CNN+SVM model consistently demonstrates superior sensitivity, surpassing 99% and reaching up to 99.58%. These results underscore the hybrid model's efficacy in accurately identifying positive instances, particularly showcasing its potential for improved sensitivity in the context of tuberculosis detection.

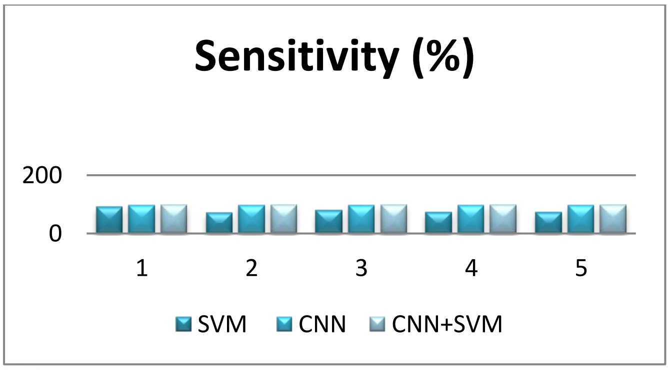

Figure 18 Sensitivity performance for SVM, CNN , SVM + CNN

Table 6 Recall SVM , CNN , SVM + CNN

DATASET	SVM	CNN	CNN+SVM
	Recall		
1	70.12	91.23	99.78
2	74.23	74.23	99.63
3	77.21	74.12	99.78
4	70.36	74.23	99.89
5	71.23	74.23	99

The table presents recall metrics for three different models—Support Vector Machine (SVM), Convolutional Neural Network (CNN), and a hybrid model combining both CNN and SVM (CNN+SVM) across five datasets. Recall, synonymous with sensitivity, quantifies the proportion of actual positive instances correctly identified by the models. The SVM model exhibits recall values ranging from 70.12% to 77.21%. In contrast, the CNN model shows lower recall values, ranging from 74.12% to 91.23%. The hybrid CNN+SVM consistently demonstrates superior recall, exceeding 99% and reaching up to 99.89%. These results emphasize the hybrid model's effectiveness in capturing a high proportion of positive instances, particularly showcasing its potential for improved recall in the context of tuberculosis detection.

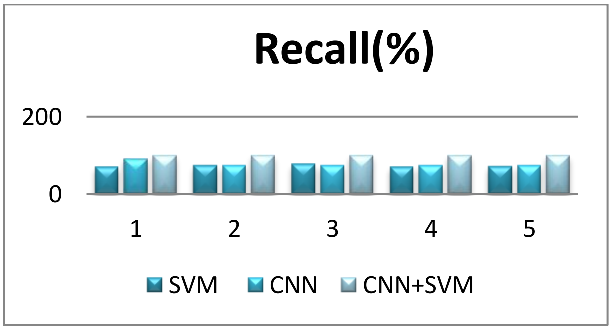

Figure 19 Recall performance for SVM , CNN , SVM + CNN

Table **7** Comparison of the proposed method against previous state-of-the-art methods

Authors (year)	Methods	Dataset (image size)	Total number of images used (T.B. + normal)	Accuracy (%)
Ahsan et al. (2019) [137]	VGG16	Montgomery (138) + Shenzhen (662)	800 (394 + 406)	81.25
Xie et al. (2020) [138]	Faster RCNN	Montgomery (138) + Shenzhen (662) + First Affiliated Hospitals Dataset (5, 344)	6,144 (3,356 + 2,788)	92.60
Sahlol et al. (2020) [139]	Mobile Net-AEO	Shenzhen (662) + Mendeley dataset (U.K.) (6,421)	7,083 (4,219 + 2,864	94.10
Rahman et al. (2020) [140]	CheXNet	Montgomery (138) + Shenzhen (662) + Belarus T.B. Dataset (Belarus) (422) + Radiological Society of North America Dataset (RSNA) (26,684)	27,906 (18649 + 9,257)	98.60
Guo et al. (2020) [141]	Ensemble (ResNet34, ResNet50, ResNet101, VGG16, VGG19, and Inception V3)	Shenzhen (662)	662 (336 + 326)	94.50
Abideen et al. (2020) [142]	B-CNN	Montgomery (138) + Shenzhen (662)	800 (394 + 406)	96.42
Ayaz et al. (2021) [143]	Ensemble (MobileNet, Inceptionv3, ResNet50, InceptionResnetv2, and Xception)	Montgomery (138) + Shenzhen (662)	800 (394 + 406)	93.47
Rajaraman et al. (2021) [144]	ResNet-BS	Montgomery (138) + Shenzhen (662)	800 (394 + 406)	92.30
Acharya et al. (2022) [145]	NFNet (normalization-free network)	TBX11K -Tuberculosis X-ray (800) + Shenzhen (662) + Montgomery (138) + National Institute of T.B. and respiratory diseases, New Delhi (88) + NLM, Belarus, NIAID, SNA (7000)	8,688 (4,936 + 3,752)	96.91
Zhou et al. (2022) [146]	UNet & ResNet	Private (4856)	4856 (2736 + 2120)	94.8
Present work	CNN+SVM	NIAID TB portal program dataset (7000)	7000 (3500 + 3500)	99.75

VI CONCLUSION

The hybrid CNN and SVM model developed for tuberculosis (T.B.) detection represents a robust and comprehensive approach to leveraging both traditional machine learning and deep learning techniques. The algorithm demonstrates a systematic workflow, encompassing preprocessing, data augmentation, feature extraction using Gray-Level Co-occurrence Matrix (GLCM) and Scale-Invariant Feature Transform (SIFT), and a hybrid model that combines the strengths of Support Vector Machines (SVM) and Convolutional Neural Networks (CNN). The SVM model is fine-tuned using grid search and cross-validation, while the CNN model is trained with hyperparameter tuning within a cross-validation loop. The integration of both models aims to capitalize on their complementary strengths in feature extraction and hierarchical representation learning. The algorithm's thoroughness is further highlighted by checks for dataset balance, data augmentation, and a thoughtful evaluation strategy. However, for further enhancement, future iterations of the model could explore more sophisticated deep learning architectures, transfer learning, and ensemble methods. The utilization of larger and more diverse datasets, collaboration with healthcare professionals for validation, and optimizing the model for real-time deployment are vital steps for enhancing the model's accuracy and practical utility.

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