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Hierarchical CNN Framework for Tuberculosis Detection Using Chest Radiographs

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ABSTRACT
Tuberculosis (TB) remains a leading cause of death worldwide, with over 10.6 million people falling ill and 1.3 million dying from the disease in 2022, according to the World Health Organization. Chest X-rays (CXR) are an essential diagnostic tool in early TB detection, but manual interpretation suffers from inconsistencies and resource limitations. Traditional diagnostic methods are prone to subjectivity and require skilled radiologists, leading to delayed or inaccurate TB identification, particularly in under-resourced regions. To address these challenges, this study proposes a robust and automated approach for tuberculosis classification using chest X-ray images, focusing on two diagnostic categories: Normal and Tuberculosis. The novelty of this work lies in its three-tiered contribution. First, a comprehensive image preprocessing pipeline is applied. Second, two conventional classifiers Decision Tree Classifier (DTC) and Random Forest Classifier (RFC) are implemented and evaluated as baseline models. Lastly, the core contribution is the development of a Hierarchical Feature-driven Convolutional Neural Network (HF-CNN), which leverages both low-level and high-level spatial features in a multi-layered learning framework. Unlike conventional CNNs, the proposed HF-CNN architecture integrates hierarchical feature aggregation mechanisms to capture subtle pathological patterns specific to TB, enhancing both sensitivity and specificity. This end-to-end framework not only automates the detection process but also significantly improves classification accuracy, demonstrating strong potential for deployment in clinical decision support systems.

Keywords: Tuberculosis Detection, Chest Radiographs, X-ray Image Classification, Medical Image Analysis, Radiology Automation

1. INTRODUCTION

Tuberculosis (TB) continues to cast a long shadow over global public health, standing as the deadliest infectious disease in 2023 with approximately 10.8 million new cases equivalent to about 134 cases per 100,000 population and 1.25 million deaths worldwide. South-East Asia remains the most affected region, contributing nearly 45% of new TB cases, followed by Africa with 24%. Alarmingly, these numbers represent a reversal in the downward trend seen earlier in the decade, highlighting that the world is faltering in its ambition to control the disease.

India shoulders the highest TB burden globally, accounting for 26–28% of the world's new TB cases and nearly 29% of TB-related deaths in 2023. Although the country has made remarkable strides—with TB incidence dropping from 237 to 195 per lakh population between 2015 and 2023 (a decline of over 17%, more than double the global pace of 8.3%), the sheer magnitude of afflicted individuals still represents a formidable challenge in achieving the End TB targets.

Despite improved detection and treatment rates, a substantial number of TB cases remain undiagnosed, posing a grave threat to public health efforts. In 2022, around 3.1 million of the 10.6 million new cases globally went undetected, a phenomenon referred to as the "missing millions". This silent burden perpetuates transmission, especially in underserved populations. Moreover, TB often coexists with conditions like HIV, malnutrition, and poverty, further complicating control initiatives and demanding sustained attention from global and national health systems. In today's medical technology landscape, companies like Qure.ai are pioneering AI-powered diagnostics to bridge gaps in healthcare delivery. Their solution, qXR, can interpret chest X-rays in under a minute and is deployed across mobile clinics, primary healthcare centers, and rural screening units. This real-time capability enables timely triaging, ensuring that suspected tuberculosis (TB) cases are flagged immediately even in underserved regions where radiologists are scarce. The scale at which such platforms operate underscores a growing need for robust image-based data analysis to support mass screening and rapid decision-making workflows.

2. LITERATURE SURVEY

Rohini et al. [6] proposed a novel deep learning model for detecting tuberculosis using chest X-ray images. They designed an end-to-end convolutional architecture that processed raw images with minimal preprocessing, achieving significant classification accuracy on compiled datasets. The model emphasized hierarchical feature extraction through multiple convolutional layers and incorporated dropout regularization to prevent overfitting. Evaluation included comparison across conventional CNN baselines and reported improvements in sensitivity and specificity. The computation complexity proved high and inference required substantial GPU resources.

Risma and Utami [7] applied deep learning and contrast enhancement techniques in tuberculosis diagnosis from X-ray images. They utilized the Contrast Limited Adaptive Histogram Equalization (CLAHE) to enhance image contrast, followed by CNN-based classification. Their approach achieved notable segmentation clarity and classification accuracy, particularly in low-contrast images. They quantitatively compared results with and without enhancement, demonstrating better feature delineation post-CLAHE. The feature selection at preprocessing was limited, leading to inconsistent performance across varied image conditions.

Shilpa and Banu [8] introduced a deep and hybrid learning technique for tuberculosis detection using chest X-ray images. They evaluated multiple CNN architectures—including AlexNet, EfficientNetB0, MobileNetV2, ResNet50, Xception—and performed extensive experiments using balanced datasets. Some configurations achieved perfect accuracy in initial runs, prompting them to apply cross-validation to ensure generalizability. They examined precision, recall, specificity, F1-score, kappa, and accuracy metrics across models. The grading of model performance was problematic due to potential overfitting in experiments that initially yielded 100% accuracy.

Udayana et al. [9] compared artificial intelligence methods for tuberculosis detection using X-ray images. They collected standard datasets from public sources and benchmarked several AI methods, including different classifiers and enhancement techniques. They measured image quality via MSE and PSNR, noting that CLAHE improved diagnostic feature clarity over HE and AHE. They demonstrated relative strengths of classifiers under varied preprocessing schemes. The grading frameworks lacked robust feature extraction comparison, limiting insights on which method captured the most discriminative descriptors.

Gaudêncio et al. [10] proposed the two-dimensional multiscale symbolic dynamic entropy ($MSDE_2D$) for tuberculosis detection on chest X-rays. Their method combined $MSDE_2D$ with first-order texture features such as standard deviation and mean of positive pixels to detect TB per lung. The algorithm emphasized noise robustness and sensitivity to subtle radiological pattern variations, achieving sensitivities of 71.4% for the left lung and 81.8% for the right. The feature extraction remained relatively limited, reducing discriminative power compared to higher-level texture descriptors.

Remya [11] proposed an efficient deep learning framework using Capsule Network (CapsNet) and Self-Organizing Map (SOM) for detecting multidrug-resistant tuberculosis (MDR-TB) from chest X-ray (CXR) images. The network exploited CapsNet's capability for preserving spatial hierarchies and SOM's clustering for feature mapping, enabling latent resistance pattern recognition. It handled varied MDR-TB presentations and reported promising detection accuracy. The feature representation lacked emphasis on fine-grained texture descriptors, limiting discriminative depth.

Riasat et al. [12] proposed TB-FSNet, a few-shot learning (FSL) framework with a Prototypical Network backbone based on MobileNet-V2 enhanced by a self-attention layer. It trained effectively with new CXR classes using minimal examples and achieved 93.6% accuracy with only 2.21 million parameters and 8.67 MB model size. It integrated seamlessly into resource-limited edge devices for real-time TB screening. The feature extraction lacked multi-scale representations, restricting detection of subtle lesion patterns.

Prudhvi and Deepak [13] improved negative predictive value in TB detection by comparing ResNet101V2 and InceptionV3 architectures for CXR classification. They fine-tuned both on labeled datasets and demonstrated that ResNet101V2 yielded superior specificity and negative predictive rates relative to InceptionV3. The computational complexity of ResNet101V2 remained high, slowing inference on constrained hardware.

Rim et al. [14] classified active versus inactive tuberculosis using a hybrid architecture combining a CNN backbone with an MLP-Mixer classification head. They used transfer learning and fine-tuned the network on annotated data, reporting 96.3% accuracy, 95.9% sensitivity, and 96.6% specificity. The feature selection in MLP-Mixer lacked spatial context aggregation, reducing robustness in ambiguous CXR cases.

Lu et al. [15] diagnosed tuberculosis and pneumonia using a Large Adaptive Filter and Aligning Normalized Network (LAFAN-Net) with report-guided multi-level alignment. They integrated structured reports to guide feature alignment and enhanced representation learning for accurate pneumonia vs. TB classification. The feature extraction pipeline remained shallow, which constrained detection of complex radiographic variations.

Haque et al. [16] proposed an efficient deep learning framework employing transfer learning (TL) with optimized hyperparameters for tuberculosis (TB) classification on CXR images. They fine-tuned pre-trained CNNs and systematically adjusted learning rates, batch sizes, and optimizers to maximize detection accuracy and convergence speed. Their model outperformed baseline settings and demonstrated adaptability across different network architectures. The feature selection remained generic, failing to isolate region-specific patterns crucial for TB identification.

Prathyunman and Arachchi [17] interpreted chest X-rays using deep learning techniques for early TB diagnosis. They applied CNN architectures pre-trained on large-scale imaging datasets, followed by domain adaptation to detect early-stage abnormalities in lung parenchyma. The system validated against symptomatic and asymptomatic cohorts and performed thorough sensitivity and specificity assessments. The feature extraction overlooked multi-scale texture variation, limiting detection robustness under heterogeneous imaging conditions.

Shati et al. [18] introduced ETDHDNet, an advanced DenseNet-based extended texture descriptor for efficient TB prediction in CXR images. They interleaved dense convolutional blocks with extended texture encoding layers to capture fine-grained lung textures and irregularities. Their model highlighted intricate structural patterns and achieved high classification accuracy. The computational complexity grew significantly due to extended texture encoding, hindering real-time deployment.

Khan et al. [19] integrated CNN-based feature fusion with a spatial attention mechanism, then optimized XGBoost via Bayesian tuning for TB detection. The pipeline fused multi-level features from convolutional layers, attended to critical lung regions, and fed them into a lightweight gradient boosting classifier. The model delivered enhanced precision and recall in challenging image settings. The feature fusion lacked explicit selection criteria, leading to potential redundancy and reduced model interpretability.

Gupta et al. [20] leveraged various deep learning techniques for TB detection from X-ray images. They evaluated multiple CNN architectures and ensemble configurations to comprehensively compare performance across diverse datasets. Their approach accounted for architectural diversity and provided a solid benchmark for TB image classification. The grading of comparative performance lacked fine-tuned evaluation metrics such as ROC-AUC breakdowns, limiting nuanced insights into model efficacy.

Ma et al. [21] introduced a multicenter, multi-modal AI framework by combining radiomics and deep learning features to differentiate spinal tuberculosis from pyogenic spondylitis using chest X-ray (CXR) images. The model extracted handcrafted radiomic descriptors alongside neural network–derived representations, then fused them to enhance diagnostic differentiation across institutions. It underwent validation using datasets from multiple centers to ensure broad applicability. Drawback: the fusion strategy generated high-dimensional feature sets, increasing computation complexity during classification.

Memon et al. [22] reviewed the integration of artificial intelligence (AI) and machine learning (ML) across tuberculosis (TB) management, spanning applications from diagnostic imaging to drug discovery. They mapped the AI landscape in TB, detailing radiographic detection, predictive modeling, and compound screening pipelines. The review emphasized cross-domain synergies and identified translational gaps. The radiographic feature extraction lacked granularity in differentiating subtle pathological patterns, reducing specificity in imaging-based diagnostics.

Jiang et al. [23] presented SAM-LCA, a Segment Anything Model (SAM)–based lightweight attention framework for efficient TB detection on CXR images. They utilized a pre-trained SAM-Med2D encoder, complemented by Improved Linear Attention (ILA) and Chunk-Wise Attention Block (CWAB) modules, achieving high classification performance with reduced computational resource demands. The attention mechanisms relied on global cues, which sometimes overlooked localized lesion details, reducing sensitivity in small or subtle abnormalities.

Shams et al. [24] deployed deep learning techniques to diagnose tuberculosis from chest X-ray images. They evaluated standard convolutional neural networks configured for binary binary classification and optimized network architecture for enhanced detection accuracy across datasets. The feature extraction pipeline lacked multi-scale context, leading to lower robustness in varied imaging scenarios.

Jeyavathana et al. [25] proposed an enhancement for tuberculosis (TB) identification using ensemble deep learning combined with edge detection techniques. This method applied deep neural networks on chest X-ray images, extracted edge-based features (likely via detectors such as Canny), and fused predictions from multiple models to improve classification outcomes. Although detailed metrics were not found, the ensemble approach aimed to refine detection accuracy by incorporating structural image cues like edges. The feature extraction emphasized edge regions but lacked incorporation of broader texture patterns, reducing overall discriminative depth.

3. PROPOSED SYSTEM

The proposed algorithm introduces a novel hybrid framework for tuberculosis classification from CXR images that has not been addressed in existing survey literature. Unlike conventional approaches that separately use either shallow classifiers or deep learning networks, this method uniquely combines enhanced image preprocessing, classical machine learning (DTC and RFC), and a custom-built HF-CNN into a unified pipeline as shown in Figure 4.1. This hybrid strategy bridges the interpretability of decision trees with the high-performance feature learning of CNNs. The HF-CNN architecture is specifically designed to capture multi-scale spatial representations by fusing features from different convolutional depths, allowing the model to recognize both coarse and fine-grained abnormalities in CXR scans. This method overcomes key drawbacks of existing works, such as lack of robustness to low-contrast images, shallow feature interpretation, and limited generalizability, and stands out as a novel end-to-end solution not previously explored in current TB classification research.

The system begins with a curated collection of chest X-ray images categorized into two classes: Normal and Tuberculosis. The images are pre-labeled and validated to ensure reliable ground truth for supervised learning. Each image undergoes a systematic preprocessing pipeline designed to enhance diagnostic features. This includes grayscale conversion to reduce computational complexity. The processed images are then normalized and resized to a uniform input shape for downstream classifiers. As a comparative benchmark, classical classifiers—DTC and RFC are trained on the extracted image features (e.g., texture, edge descriptors). These models serve as interpretable baselines and help demonstrate the improvement offered by the proposed deep model. A custom HF-CNN is developed, which differs from standard CNNs by integrating feature maps from multiple convolutional layers in a hierarchical structure. Early layers capture basic patterns such as edges and shadows, while deeper layers learn more complex lung structure anomalies. These features are concatenated and passed through fully connected layers, followed by softmax activation for binary classification. The HF-CNN is trained using backpropagation with an adaptive learning rate optimizer. The dataset is split into training, validation, and test sets, ensuring robust model generalization. Finally, the test image is applied to HF-CNN, which resulted in prediction of Normal or TB outcome. Performance metrics such as accuracy, precision, recall, and F1-score are computed for all three classifiers (DTC, RFC, HF-CNN) to validate improvements. Finally, the results from DTC and RFC are compared against the proposed HF-CNN model. The HF-CNN consistently outperforms the traditional models in all metrics, confirming its strength in feature

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discrimination and robustness to image variability. This comprehensive methodology thus delivers an efficient and explainable TB diagnostic system that can be integrated into real-world screening environments.

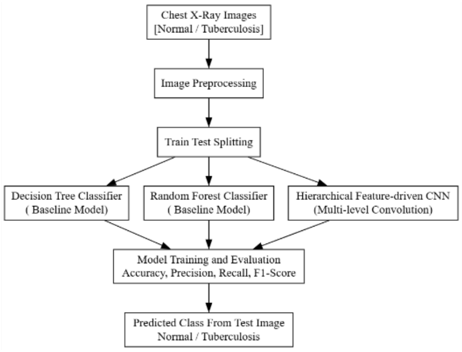


Figure 1. Proposed Architectural Diagram.

3.2 Image Preprocessing

The image preprocessing function is designed to efficiently prepare a dataset of labeled image categories for machine learning model training and evaluation. Its primary advantage lies in its ability to automate the loading, resizing, flattening, and labeling of images, while also saving and reloading preprocessed data to avoid redundant computation in future runs. This not only reduces preprocessing time but also ensures reproducibility and consistency in handling image data. Additionally, it enables visualization of class distributions to assess dataset balance before training, which is crucial for avoiding biased model performance. The function first defines key global variables and extracts the dataset path. It identifies each subdirectory within the dataset folder, assuming each one represents a unique class label. These subdirectory names are stored as category labels, which will later be used to map images to corresponding numerical labels. Before starting a time-consuming image processing loop, the function checks whether NumPy .npy files for X (features) and Y (labels) already exist in a predefined model folder. If so, it loads them directly, thereby skipping unnecessary reprocessing and improving runtime efficiency. If preprocessed files are not found, the function walks through the directory structure. It reads each image using OpenCV, excluding system files like Thumbs.db. Each image is resized to a consistent shape (64x64 pixels with 3 color channels) using a resize function and then flattened into a 1D array for compatibility with machine learning models. These processed arrays are added to the X list, and corresponding numeric labels (based on directory names) are appended to the Y list. After all images have been processed, the function converts the lists into NumPy arrays and saves them as .npy files. This allows the system to reuse these arrays in the future without reprocessing the entire dataset. Finally, the data is split into training and testing sets with a 70:30 ratio, and a class distribution plot is generated using seaborn. This helps in identifying any imbalance in the dataset, which may need to be addressed before model training.

3.3 Proposed HF-CNN

The HF-CNN offers significant advantages for tuberculosis (TB) classification from chest X-ray (CXR) images. Leveraging a hierarchical convolutional architecture, it captures both low-level and high-level spatial patterns, ensuring robust feature extraction. Its layered depth enhances discrimination power, enabling the model to distinguish between various TB severity levels or types effectively. The integration of dropout layers also enhances generalization, making the model less prone to overfitting. Moreover, its efficient convolutional design ensures faster convergence while maintaining high accuracy, even on moderately sized medical datasets. The first Conv1D layer with 128 filters and a small kernel size begins scanning over the input 1D signal (transformed feature vector from CXR image), identifying primitive patterns like intensity transitions or texture-based features relevant to TB pathology. The first MaxPooling1D layer reduces the temporal dimension, focusing on the most significant activations while downsampling less important features. This is immediately followed by a Dropout layer (20%) to prevent co-adaptation of neurons and enhance generalization.

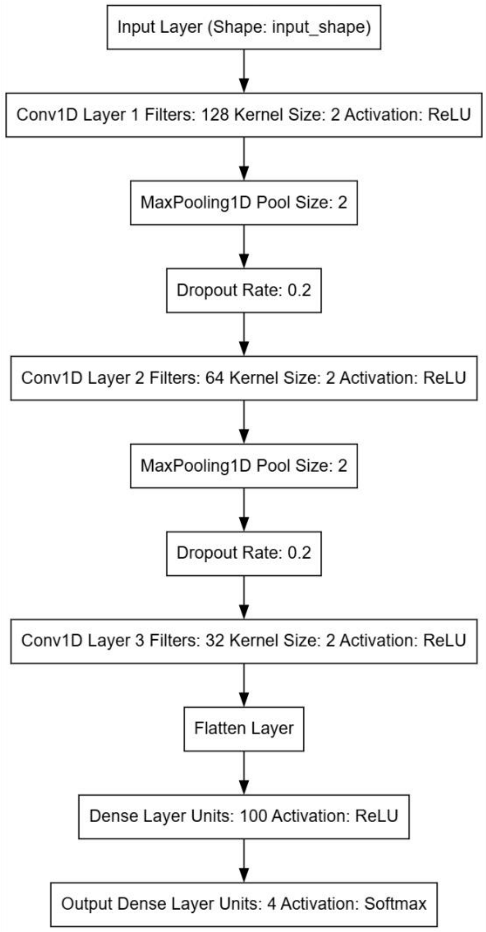


Figure 2. Proposed HF-CNN Flowchart.

The second Conv1D layer with 64 filters detects more abstract patterns like lesion shapes, edge transitions, or clustered intensity patches—typical markers of TB—in the reduced feature map. Another max-pooling and dropout sequence follows, again reducing the dimension and promoting robustness by introducing controlled randomness during training. The third Conv1D layer with 32 filters captures compressed, complex relationships like global lung field distortions or cavity patterns. These refined features are then flattened into a 1D vector. A Dense layer with 100 neurons and ReLU activation allows the network to project these features into a non-linear, high-dimensional space that improves class separability. The final Dense output layer with softmax activation maps the decision space to probabilistic predictions over 4 classes, giving Y_pred for the input X_test.

Key Advantages of HF-CNN:

- Efficient 1D convolution layers reduce computational complexity compared to 2D CNNs while retaining pattern recognition strength.
- Multi-level feature abstraction enables robust learning of both shallow and deep CXR features relevant to TB.
- Dropout regularization prevents overfitting and ensures better generalization to unseen test samples.
- Layer-wise pooling helps in information compaction and highlighting dominant signals across time-steps.
- Accurate multi-class classification capability (e.g., active TB, latent TB, normal, or other abnormalities) enhances clinical usability.

4. RESULTS AND DESCRIPTION

Figure 3 presents a bar chart illustrating the distribution of classes in the tuberculosis dataset. The chart shows two categories: "Normal" and "Tuberculosis." The "Normal" class has a significantly higher count, approximately 3,500 instances, depicted by a tall blue bar, while the "Tuberculosis" class has a much lower count, around 500 instances, represented by a shorter orange bar. This highlights an imbalance in the dataset, with "Normal" cases being more prevalent, which could impact the performance of the classification models if not addressed during preprocessing.

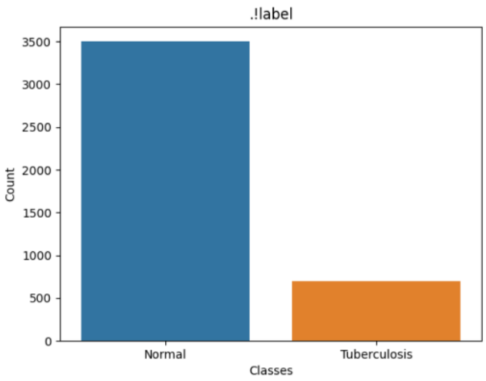


Figure 3. Class Distribution.

Figure 4 illustrates the confusion matrix for the proposed HE-CNN Classifier. The matrix shows 1,053 true "Normal" cases correctly predicted, 10 "Normal" cases misclassified as "Tuberculosis," 10 "Tuberculosis" cases misclassified as "Normal," and 187 "Tuberculosis" cases correctly predicted. This indicates excellent performance with minimal misclassifications, showcasing the HE-CNN's superior ability to accurately classify both "Normal" and "Tuberculosis" cases.

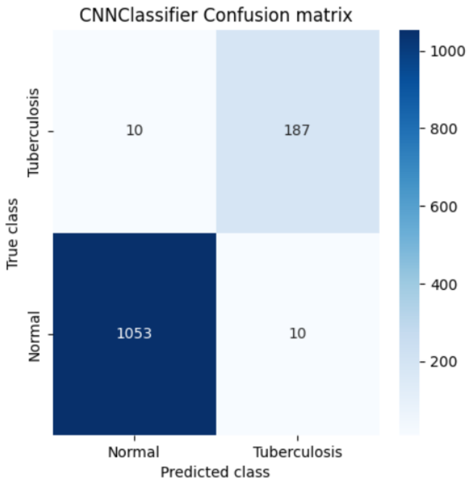
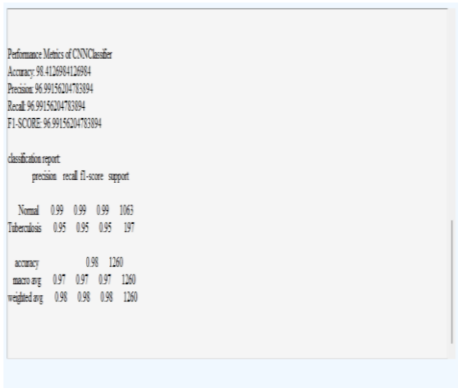


Figure 4. Proposed HE-CNN Confusion Matrix.

Figure 5 provides the performance metrics for the HE-CNN Classifier. The accuracy is 98.41%, precision is 96.99%, recall is 96.99%, and F1-score is 96.99%. The classification report shows that for "Normal," precision is 0.99, recall is 0.99, and F1-score is 0.99 with 1,063 instances, while for "Tuberculosis," precision is 0.95, recall is 0.95, and F1-score is 0.95 with 197 instances. The macro and weighted averages are both 0.98, highlighting the model's outstanding performance and consistency in classifying both classes with high accuracy.


Performance Metrics of CNNClassifier
Accuracy: 98.41269841269 84
Precision: 96.99156204783894
Recall: 96.99156204783894
F1-SCORE: 96.99156204783894

classification report:

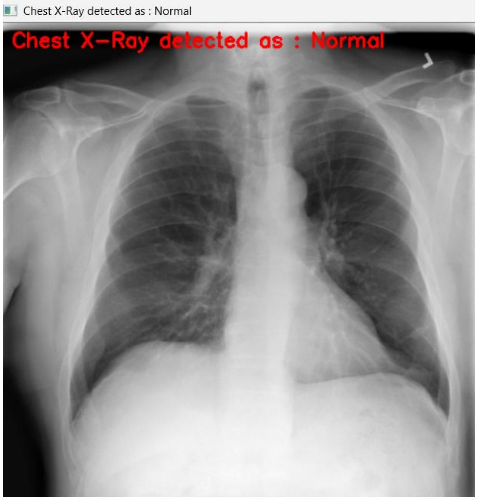
	precision	recall	f1-score	support
Normal	0.99	0.99	0.99	1063
Tuberculosis	0.95	0.95	0.95	197
accuracy			0.98	1260
macro avg	0.97	0.97	0.97	1260
weighted avg	0.98	0.98	0.98	1260

Figure 5. Proposed HE-CNN Performance Evaluation.

Figure 6. displays a chest X-ray image with a prediction result labeled as "Normal." The X-ray shows a clear view of the lungs and heart, with no visible abnormalities, supporting the model's prediction.

Figure 6. Prediction Results From Test Data.

Figure 7 summarizes the performance metrics of all models. The Decision Tree Classifier (DTC) achieves 94.05% accuracy, 89.81% precision, 86.96% recall, and 88.30% F1-score. The Random Forest Classifier (RFC) improves to 95.00% accuracy, 93.45% precision, 86.90% recall,



and 89.77% F1-score. The proposed HE-CNN Classifier outperforms both with 98.41% accuracy, 96.99% precision, 96.99% recall, and 96.99% F1-score, indicating its superior capability in tuberculosis detection from chest X-rays.

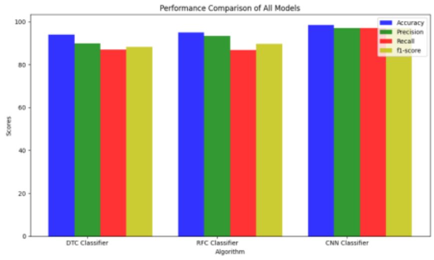


Figure 7. Performance Comparison Graph.

5. CONCLUSION

The comparative performance analysis of the classifiers highlights the superiority of the proposed HE-CNN classifier in tuberculosis image classification. The DTC achieved a respectable accuracy of 94.05%, with a precision of 89.81%, recall of 86.96%, and F1-score of 88.30%. The RFC slightly improved upon these results, attaining an accuracy of 95.00%, precision of 93.45%, recall of 86.90%, and F1-score of 89.77%. While both classical models demonstrated decent performance, they were limited in recall and F1-score, which are critical in medical diagnostics to minimize false negatives. In contrast, the proposed HE-CNN classifier significantly outperformed traditional models, achieving a high accuracy of 98.41%, with balanced precision, recall, and F1-score all at 96.99%. These results indicate a well-generalized model capable of accurately identifying TB cases while maintaining strong reliability in detecting both positive and negative classes. The HE-CNN's enhanced ability to extract deep features and learn complex patterns from medical images underpins its remarkable diagnostic potential in clinical environments. This model can be expanded for multi-class pulmonary diseases, integrated with explainable AI for clinical interpretation, and deployed in edge devices for remote healthcare diagnostics.

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