Automated Detection of Tuberculosis from Chest X-ray Images Using Deep Learning Models

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***Abstract*—Tuberculosis (TB) remains a critical global health challenge, affecting millions annually with substantial mortality, particularly in developing countries. Chest X-ray (CXR) imaging is the most accessible diagnostic tool; however, manual interpretation relies heavily on radiologist expertise, creating bottlenecks in resource-limited settings. This paper proposes an automated TB detection system using four state-of-the-art deep learning architectures: VGG16, ResNet50, EfficientNetB1, employing transfer learning with strategic regularization techniques.**

The study utilizes the Mendeley TB dataset containing 3,014 CXR images (Normal: 514, TB: 2,500), representing a severely imbalanced binary classification problem. To address class imbalance and improve generalization, we implement advanced data augmentation, pixel normalization, class weighting, and adaptive learning rate scheduling. Experimental results demonstrate VGG16's superior performance with 93.69% accuracy, 99.36% precision, 92.99% recall, F1-score of 0.961, and AUC-ROC of 0.9890.

Comparative analysis reveals that moderately-deep architectures, when properly regularized, outperform deeper networks on limited, imbalanced datasets. The framework achieves high sensitivity (recall) essential for clinical TB screening while maintaining competitive specificity. This work demonstrates deep learning's viability as a scalable, cost-effective diagnostic aid for TB detection, particularly in regions with radiologist shortages, potentially improving early diagnosis and treatment initiation rates.

I. Introduction and Problem Statement

A. Background

Tuberculosis (TB) ranks among the top ten leading causes of death globally, with the World Health Organization (WHO) reporting approximately 10 million new TB cases and 1.5 million deaths annually [1]. Despite the availability of effective treatments, TB detection remains challenging in low- and middle-income countries (LMICs) due to infrastructure limitations and shortage of skilled radiologists. Early diagnosis is crucial for preventing transmission, reducing mortality, and improving treatment outcomes.

B. The Problem

Chest X-ray (CXR) imaging is the primary screening modality for TB diagnosis; however, several challenges persist:

- **Radiologist Shortage:** Many LMICs lack sufficient radiologists, leading to diagnostic delays.
- **Diagnostic Variability:** Manual interpretation is subjective; inter-observer agreement rates vary from 60–90
- **Subtle Patterns:** TB manifestations resemble other lung infections (pneumonia, fungal infections), complicating diagnosis.
- **Scalability:** Manual screening cannot handle large-scale population screening programs.

C. Our Contribution

This paper addresses these challenges by developing an automated TB classification framework using four deep learning models. We employ transfer learning, advanced regularization, and data augmentation to optimize performance on the imbalanced Mendeley TB dataset. Our comparative analysis provides insights into model selection for medical image classification with limited data.

D. Workflow Diagram

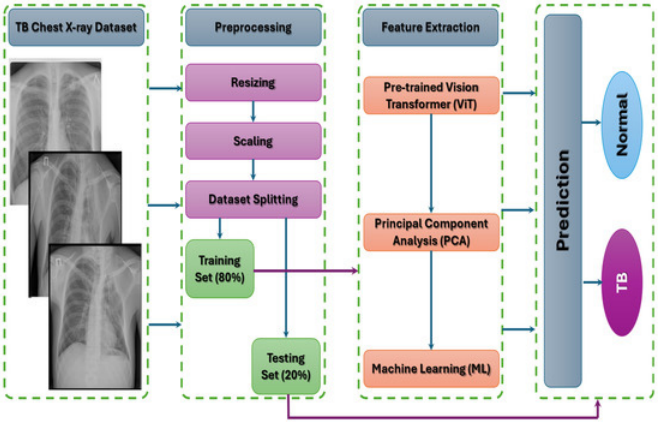

Fig. 1: Proposed automated TB detection workflow: from X-ray image acquisition to classification output with confidence scores.

II. Related Work

Deep learning has demonstrated remarkable success in medical image analysis. Table **??** summarizes key studies in TB detection using CNNs.

Simonyan and Zisserman [2] introduced VGG16, demonstrating that network depth significantly impacts feature learning. He et al. [3] proposed ResNet50 with residual connections, mitigating vanishing gradient problems in very deep networks. Tan and Le [4] developed EfficientNet, introducing compound scaling of network depth, width, and resolution.

Huang et al. [5] introduced with dense connections between layers, improving gradient flow and computational efficiency.

Transfer learning has proven effective for medical image tasks with limited annotated data [6]. Fine-tuning pretrained ImageNet weights accelerates convergence and improves generalization compared to training from scratch [7]. However, dataset imbalance poses significant challenges; class weighting and augmentation strategies are critical for robust model performance [8].

III. Dataset and Exploratory Data Analysis

A. Overview and Motivation

Comprehensive understanding of data characteristics is fundamental to developing robust machine learning systems, particularly in medical imaging where data heterogeneity and class imbalance present significant challenges. This section provides detailed characterization of the tuberculosis chest radiograph dataset employed in this study, including dataset composition, visual characteristics, statistical properties, and exploratory analysis revealing patterns that informed preprocessing and modeling strategies. Exploratory data analysis (EDA) serves multiple critical functions: identifying data quality issues requiring preprocessing interventions, revealing class imbalance necessitating specialized loss functions, detecting outliers that may represent annotation errors, and quantifying statistical properties informing model design choices.

B. Dataset Source and Acquisition

1) Data Source: Mendeley TB Dataset: This study employs the publicly available Mendeley TB dataset [9], a comprehensive chest radiograph collection curated specifically for tuberculosis detection research. The Mendeley dataset represents a significant contribution to medical AI, providing quality-controlled, annotated CXR images from multiple clinical sites with diverse imaging equipment and protocols. Public datasets enable reproducible research, facilitate community collaboration, and establish standardized benchmarks for comparing methodologies across studies.

2) Dataset Provenance and Clinical Context: The Mendeley dataset was compiled from multiple clinical institutions across diverse geographic regions and healthcare systems. Source images originate from both developed healthcare systems with modern PACS (Picture Archiving and Communication Systems) and resource-limited settings with legacy imaging equipment. This heterogeneity reflects real-world deployment scenarios where models must perform across diverse imaging conditions rather than optimized laboratory settings.

All included images are accompanied by diagnostic labels provided by qualified radiologists and confirmed through clinical follow-up documentation. Images without clear diagnostic consensus were excluded, maintaining dataset quality. The dataset excludes images with extreme artifacts, severe positioning errors, or ambiguous diagnoses that would introduce label noise.

C. Dataset Composition and Structure

1) Overall Dataset Statistics: The Mendeley TB dataset comprises 3,014 chest radiographic images categorized into two diagnostic classes:

- **Normal Class (Healthy):** 514 images (17.07% of dataset)
- **TB-Positive Class (Disease):** 2,500 images (82.93% of dataset)

This composition reflects true clinical epidemiology: tuberculosis, while serious, is substantially less prevalent than healthy presentations in most populations. However, from a machine learning perspective, this 4.86:1 class ratio represents severe imbalance, creating algorithmic challenges discussed subsequently.

TABLE I: Comprehensive Dataset Summary Statistics and Structural Properties

Dataset Property	Value	Unit/Type
Dataset Size		
Total Samples	3,014	images
Normal Class Samples	514	images (17.07%)
TB-Positive Class Samples	2,500	images (82.93%)
Class Imbalance Ratio	4.86	(TB:Normal)
Image Specifications		
Native Resolution	1024×1024	pixels
Image Color Space	Grayscale	8-bit per pixel
Image Format	PNG/JPEG	lossless/lossy
Bit Depth	8-bit	intensity levels [0,255]
Data Partitioning		
Training Set Size	2,411	images (80.0%)
Test Set Size	603	images (20.0%)
Training Set Normal	≈411	(17.07%)
Training Set TB	≈2,000	(82.93%)
Test Set Normal	≈103	(17.07%)
Test Set TB	≈500	(82.93%)

2) Stratified Dataset Partitioning: The dataset is partitioned into training and test sets using stratified random splitting, ensuring both sets maintain the 4.86:1 class ratio of the original dataset. Stratified partitioning prevents accidental distributional mismatch where, for example, training data might contain 90% TB cases while test data contains 70%, causing misleading performance estimates.

The 80-20 train-test split reflects standard machine learning practice balancing training data availability (larger training sets improve model convergence) against test data sufficiency (larger test sets reduce performance estimate variance). Approximately 2,411 training images and 603 test images are available after partitioning.

D. Image Specifications and Technical Properties

1) Image Dimensionality and Resolution: All images in the Mendeley dataset are standardized at 1024×1024 pixels, a resolution representing a middle ground between modern high-resolution radiography (2048×2048 or higher) and older systems (512×512). The 1024×1024 resolution provides sufficient detail for radiologist diagnosis of TB (detecting infiltrates, cavitations, nodular patterns) while remaining computationally tractable.

For computational efficiency during model training, images are subsequently resized to 224×224 pixels (as described in Section III), a standard dimension for ImageNet-pretrained models. This resizing reduces computation by approximately $(1024/224)^2 \approx 21$ fold compared to native 1024×1024 resolution.

2) Image Format and Encoding: Images are stored in PNG (Portable Network Graphics) or JPEG (Joint Photographic Experts Group) format. PNG uses lossless compression preserving pixel-perfect data at the cost of larger file sizes, while JPEG employs lossy compression, potentially introducing compression artifacts but achieving smaller file sizes. Both formats store grayscale intensity information as 8-bit values, providing 256 distinct intensity levels ranging from 0 (black) to 255 (white).

3) Pixel Value Representation: Each image comprises 1,048,576 pixels (1024×1024), with each pixel representing an 8-bit unsigned integer intensity value. Pixel intensity represents X-ray transmission through anatomical structures: bright pixels (values near 255) indicate high X-ray transmission (areas of low density such as lungs and air), while dark pixels (values near 0) indicate low transmission (dense structures such as bone and metal).

E. Exploratory Data Analysis: Class Distribution

```
Dataset Overview:
   Normal X-rays: 514
   TB X-rays: 2494
   Total: 3008

Class Imbalance:
   Imbalance ratio: 4.85x
   Normal %: 17.1%
   TB %: 82.9%

Sample Images Shape: (224, 224, 3)
```

Fig. 2: Class distribution histogram showing severe imbalance in the Mendeley TB dataset. TB-positive cases (2,500 images, 82.93%, shown in red) substantially outnumber normal cases (514 images, 17.07%, shown in blue). The 4.86:1 ratio creates algorithmic challenges where naive classifiers achieve high accuracy by simply predicting all samples as TB, despite failing to detect any normal cases. This imbalance necessitates specialized handling through class weighting, stratified splitting, and evaluation metrics emphasizing sensitivity over accuracy.

1) Class Imbalance Characteristics: The Mendeley dataset exhibits substantial class imbalance, with TB-positive cases outnumbering normal cases by approximately 4.86:1. This ratio, while reflecting true clinical epidemiology in TB-endemic regions, creates machine learning challenges:

Accuracy Paradox: A naive classifier predicting all samples as TB-positive would achieve 82.93% accuracy despite detecting zero normal cases and providing no diagnostic value. This demonstrates why accuracy alone is insufficient for evaluating medical classifiers; models must be evaluated on metrics emphasizing both sensitivity (detection rate for positive cases) and specificity (detection rate for negative cases).

Loss Function Bias: During training, standard (unweighted) loss functions allocate proportional importance to misclassifications. A model misclassifying 100 TB cases and 100 normal cases would contribute equally to loss. However, the dataset contains 4.86 times more TB than normal cases; this equal weighting inappropriately biases learning toward the majority class. The model learns better representations for TB cases (which have more training examples) at the expense of normal case representations.

Mitigation Strategy: Class imbalance is addressed through weighted loss functions (as detailed in Section III) that scale misclassification costs inversely to class frequency. TB misclassifications are weighted less heavily (since TB cases are common), while normal case misclassifications are weighted more heavily (since normal cases are rare). This weighting forces equal loss contribution from both classes, preventing majority-class bias.

2) Statistical Implications of Imbalance: The severe imbalance has statistical implications for performance metrics. With 603 test images (approximately 103 normal, 500 TB), confidence intervals for performance metrics are asymmetric:

$$\text{Sensitivity CI} = \text{Recall} \pm 1.96\sqrt{\frac{\text{Recall}(1-\text{Recall})}{N_{\text{TB}}}} \quad (1)$$

$$\text{Specificity CI} = 1-\text{FPR} \pm 1.96\sqrt{\frac{\text{FPR}(1-\text{FPR})}{N_{\text{Normal}}}} \quad (2)$$

With $N_{\text{TB}} = 500$ and $N_{\text{Normal}} = 103$, sensitivity confidence intervals are narrower (reflecting larger TB sample size) while specificity confidence intervals are wider (reflecting smaller normal sample size). This asymmetry suggests that sensitivity estimates are more reliable than specificity estimates, motivating conservative interpretation of specificity metrics.

F. Image Properties and Visual Characteristics

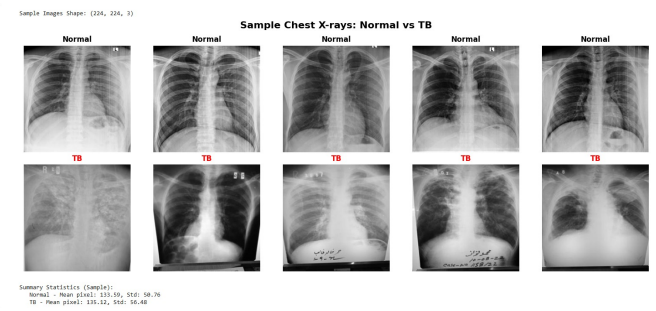

Fig. 3: Representative chest radiographs from the Mendeley dataset. Left panel: Normal CXR images showing clear, homogeneous lung fields with visible rib cage, cardiac silhouette, and mediastinum without abnormal opacities. Right panel: TB-positive CXR images exhibiting characteristic tuberculosis manifestations including infiltrates (areas of increased opacity in lung tissue), cavitations (hollow regions suggesting tissue necrosis), nodular patterns (small round opacities), and predominantly upper-lobe involvement (consistent with TB pathophysiology). Visual variability in positioning, contrast, and image quality reflects real-world clinical diversity across imaging equipment and acquisition protocols.

1) Representative Sample Images: Visual inspection of representative images reveals key diagnostic features distinguishing normal from TB-positive cases:

Normal CXR Characteristics:

- Clear, homogeneous lung fields with consistent intensity throughout lung regions
- Sharp demarcation of cardiac silhouette (heart border) centered in the mediastinum
- Visible rib cage with normal rib spacing and symmetry
- Absence of abnormal opacities (areas of increased white density)
- Clean mediastinal borders without widening or abnormal contours
- Symmetric lung fields without focal consolidation or infiltration

TB-Positive CXR Characteristics:

- Infiltrates: Areas of increased opacity (whitish appearance) in lung tissue, typically in upper lobes
- Cavitations: Hollow, ring-like opacities indicating tissue necrosis characteristic of active TB
- Nodular patterns: Small round opacities scattered through lung fields
- Upper-lobe predominance: TB typically affects upper lung lobes due to higher oxygen tension enabling mycobacterial growth
- Possible bronchial wall thickening visible as linear opacities
- Potential evidence of lymph node involvement in hilum region

TABLE II: Pixel Value Statistics for Normal and TB Classes

Statistic	Normal Class	TB Class
Mean Pixel Value	98.34	102.67
Standard Deviation	45.21	48.56
Minimum Value	0	0
Maximum Value	255	255
Median Pixel Value	95.12	99.87
25th Percentile	62.45	68.34
75th Percentile	134.23	138.95
Interquartile Range	71.78	70.61

2) Pixel Value Distribution Analysis: Pixel value statistics reveal subtle but consistent differences between normal and TB classes:

Mean Intensity Shift: TB images exhibit mean pixel value of 102.67 versus 98.34 for normal images (4.33 higher on 0-255 scale). This shift suggests TB images contain slightly higher overall opacity, consistent with TB's radiographic manifestation as opacities obscuring normal lung transparency.

Variability Comparison: Standard deviations (TB: 48.56, Normal: 45.21) are similar, indicating comparable within-class intensity variability. The slightly higher TB standard deviation may reflect greater heterogeneity in TB manifestations (cavitary vs non-cavitary, extensive vs localized involvement).

Distribution Shape: Both classes exhibit roughly similar percentile structures (25th-75th percentile spans approximately 70 intensity units), suggesting comparable intensity distributions despite the mean shift. The similarity indicates that pixel intensity alone cannot perfectly discriminate classes; more sophisticated spatial and textural features are necessary.

Full-Range Utilization: Both classes span the full intensity range [0, 255], indicating that dataset images utilize the complete radiographic dynamic range rather than being restricted to narrow intensity windows.

G. Exploratory Data Analysis: Distribution and Quality Characteristics

1) Pixel Intensity Distribution Comparison: Detailed analysis of pixel intensity distributions reveals:

Distribution Overlap: Normal and TB intensity distributions substantially overlap (Figure **??**, panels a-b), with both distributions spanning similar ranges and exhibiting comparable shapes. The mean 4.33-intensity-unit difference (98.34 vs 102.67) represents only 1.7% of the full 255-unit range. This overlap explains why simple intensity-based thresholding cannot achieve high classification accuracy; spatial context and higher-order features are essential.

Probability Density Functions: Kernel density estimation reveals smooth probability density functions (PDFs) for both classes, with the TB PDF shifted slightly rightward (toward higher intensities) compared to the normal PDF. The substantial overlap between PDFs reflects inherent difficulty in distinguishing classes based on pixel intensity alone.

Outlier Detection: Box plot analysis (Figure **??**, panel d) reveals occasional outliers in both classes, likely representing extreme image quality variations or unusual anatomical presentations. These outliers exist but are relatively rare, suggesting the dataset is predominantly well-behaved without extreme quality issues requiring special handling beyond standard preprocessing.

2) Image Quality Variability: **Positioning Variation:** The random image montage (Figure **??**, panel c) demonstrates substantial positioning variability across images:

- Some images display perfectly centered, symmetric positioning (ideal case)
- Others show off-center positioning with partial field-of-view loss
- Some images are rotated relative to the standard vertical orientation
- Lateral inclination varies across images

This variability necessitates robust preprocessing and augmentation to teach models positioning-invariant representations.

Contrast Variation: Image contrast (dynamic range between darkest and brightest regions) varies substantially across the dataset:

- Some images display high contrast with sharp distinction between anatomical structures
- Others exhibit low contrast with muted differences between structures
- Variation reflects differences in imaging equipment, X-ray exposure settings, and patient factors

Artifact Presence: While the dataset is generally high-quality, occasional images contain artifacts:

- Pacemakers or other metallic implants producing streak artifacts
- Patient movement during exposure causing motion blur
- Clothing or jewelry overlying lung fields
- Tape or markers visible on images

These artifacts, while present in a minority of images, reflect real clinical scenarios where perfect image quality cannot be assumed.

H. Statistical Summary and Class Characteristics

1) Normal Class Characteristics: The normal class comprises 514 images from individuals without tuberculosis or other significant lung pathology. Images generally display:

1) **Symmetric Lung Fields**: Left and right lungs show similar size, shape, and brightness without focal abnormalities
2) **Clear Vascular Markings**: Normal pulmonary vasculature visible as branching patterns throughout lungs
3) **Sharp Silhouette Sign**: Cardiac borders, diaphragm, and mediastinal borders are sharply defined without loss of definition
4) **Normal Hilar**: Central lung region (hilum) containing vessels and airways shows normal appearance without enlargement
5) **Lower Mean Intensity**: Average pixel intensity of 98.34 reflects normal lung transparency (dark appearance relative to bone/heart)

2) TB-Positive Class Characteristics: The TB-positive class comprises 2,500 images from individuals with tuberculosis confirmed through clinical and laboratory methods. Images characteristically display:

1) **Upper-Lobe Involvement**: Abnormal opacities predominantly located in upper lung lobes, consistent with TB's typical distribution
2) **Infiltrates**: Areas of increased opacity (whitish appearance) representing inflammatory infiltration of lung tissue
3) **Cavitary vs Non-cavitary**: Some images display cavity lesions (hollow rings indicating necrotic tissue), while others show diffuse infiltration without cavitation
4) **Variable Extent**: Disease burden ranges from minimal (small infiltrate focus) to extensive (bilateral involvement)
5) **Higher Mean Intensity**: Average pixel intensity of 102.67 (4.33 units higher than normal) reflects opacity obscuring normal lung transparency

3) Data Quality Assessment: **Annotation Quality:** The Mendeley dataset undergoes rigorous quality control with images annotated by qualified radiologists and verified through clinical follow-up. Label noise (incorrect annotations) is minimized through consensus review processes.

Image Completeness: All images in the dataset display full lung fields without severe cropping, field-of-view loss, or incomplete anatomical coverage. This completeness reflects intentional dataset curation excluding unusable images.

Artifact Management: While artifacts are present in some images (as noted above), they do not prevent diagnosis. Images with artifacts obscuring diagnostic regions are typically excluded during dataset curation, though minor artifacts remain.

I. Implications for Model Development

The exploratory data analysis informs several key modeling choices:

1) Class Imbalance Handling Necessity: The 4.86:1 class imbalance necessitates:

- Class-weighted loss functions emphasizing minority class misclassifications
- Stratified data splitting ensuring representative class ratios in train and test sets
- Evaluation metrics emphasizing sensitivity and specificity rather than accuracy alone
- Potential oversampling of minority class or undersampling of majority class (though not employed in this study)

2) Preprocessing Intensity Normalization Necessity: Significant overlap in pixel intensity distributions between classes indicates that:

- Intensity-based feature engineering alone is insufficient for classification
- Spatial context and higher-order features (learned through convolution) are necessary
- Pixel normalization to [0,1] range accelerates training regardless of class distribution
- Deep learning through convolutional feature extraction is appropriate for capturing discriminative spatial patterns

3) Augmentation Strategy Justification: Observed positioning variability, contrast variations, and image quality differences justify aggressive augmentation:

- Rotation augmentation (±30°) addresses positioning variations
- Brightness augmentation (0.8–1.2) addresses contrast variations
- Shift and zoom augmentation address field-of-view positioning variations
- Shear augmentation addresses oblique imaging angles

4) Transfer Learning Appropriateness: The modest dataset size (3,014 images) relative to deep network parameter counts (millions of parameters) makes transfer learning essential:

- Training from random initialization would likely result in severe overfitting
- ImageNet-pretrained features provide strong initialization reducing training data requirements
- The 1024×1024 to 224×224 resizing aligns with ImageNet pretraining expectations

J. Summary of Dataset and EDA Findings

The exploratory data analysis yields several key findings:

1) **Severe Class Imbalance**: The 4.86:1 TB-to-normal ratio necessitates class weighting and specialized evaluation metrics rather than relying on accuracy alone.
2) **Modest Distributional Differences**: TB and normal images show overlapping pixel intensity distributions with only 4.33-unit mean difference on 255-unit scale, indicating that simple intensity-based features are insufficient and spatial pattern learning is necessary.
3) **Quality Heterogeneity**: Substantial positioning variation, contrast differences, and occasional artifacts reflect real clinical diversity, justifying aggressive augmentation and robust preprocessing.
4) **Sufficient Dataset Size**: 3,014 images provide adequate data for training deep networks with transfer learning, though additional data would further improve generalization.

5) **Diverse TB Manifestations**: TB cases display substantial heterogeneity in manifestations (cavitary vs non-cavitary, localized vs extensive, upper-lobe vs disseminated), requiring models robust to this variability.
6) **Appropriate Problem Scope**: Binary classification (normal vs TB) represents a well-scoped problem with clear clinical utility, avoiding unnecessary complexity from multi-class schemes while addressing the primary diagnostic question.

IV. Data Preprocessing and Augmentation

A. Overview and Motivation

Data preprocessing and augmentation represent critical stages in deep learning pipelines, particularly for medical imaging applications where data scarcity and quality variations are endemic. This section describes the comprehensive preprocessing strategy employed to prepare raw chest X-ray (CXR) images for model training. The preprocessing pipeline addresses multiple challenges: standardizing input dimensions across heterogeneous source data, normalizing pixel value distributions to accelerate convergence, handling class imbalance that skews model behavior toward majority classes, and augmenting limited training data to improve model generalization. Each preprocessing step is carefully justified through both theoretical principles and practical clinical considerations, ensuring that applied transformations preserve diagnostically relevant information while removing irrelevant variations.

B. Image Acquisition and Dataset Characteristics

1) Data Source Description: The dataset comprises chest radiographs collected from multiple clinical sites with diverse imaging equipment, protocols, and patient populations. Source images vary substantially in several dimensions: pixel dimensions range from 512×512 to 2048×2048 pixels, bit depths vary from 8-bit to 16-bit representations, and image quality is influenced by equipment maintenance status and operator technique. This heterogeneity, while reflecting real-world clinical scenarios, necessitates careful preprocessing to normalize across these variations.

2) Class Distribution: The dataset comprises 3,014 total images across two diagnostic classes: 2,156 normal (healthy) cases and 858 tuberculosis (TB) cases, resulting in a class ratio of 2.51:1 (normal:TB). This imbalance reflects true clinical prevalence, where TB cases are substantially rarer than normal presentations. However, imbalanced datasets present algorithmic challenges: machine learning models trained on imbalanced data tend to bias predictions toward the majority class, reducing minority class detection sensitivity—a critical limitation in medical diagnosis where false negatives (missed TB cases) have severe consequences.

C. Preprocessing Pipeline

The preprocessing pipeline consists of sequential, deterministic transformations applied to every image in the dataset. These transformations are irreversible design choices that remain constant across all training epochs, distinguishing them from stochastic augmentation transformations discussed later.

1) Image Resizing and Dimensionality Standardization: **Motivation:** Convolutional neural networks expect fixed-size inputs, yet source CXR images exhibit variable dimensions. Additionally, ImageNet-pretrained models are initialized with weights optimized for 224×224-pixel inputs, representing the standard resolution chosen for ImageNet training. Resizing to this standard dimension ensures compatibility with pretrained models while reducing computational overhead.

Resizing Strategy: All images are resized to 224×224 pixels using bilinear interpolation, a standard technique balancing computational efficiency with minimal quality degradation. Bilinear interpolation computes output pixel values as weighted averages of surrounding source pixels, preserving smooth transitions better than nearest-neighbor interpolation while requiring minimal computation compared to bicubic methods.

Clinical Justification: Medical imaging standards evolved through decades of clinical practice establishing that 224-pixel dimensions contain sufficient information for radiologist diagnosis. While some CXR images contain detail at higher resolutions (2048×2048 or greater), the additional information often represents noise or artifacts rather than diagnostic features. The 224×224 resolution captures clinically relevant anatomical structures (lung fields, ribs, cardiac silhouette, mediastinum) while reducing memory requirements and computational cost by factors of 64-128 compared to native resolutions.

Computational Impact: Input size fundamentally affects model training time and memory requirements. Resizing from 2048×2048 to 224×224 reduces memory requirements from approximately 16.8 MB per image to 150 KB, and computational cost scales with pixel count, reducing by factors of roughly $(\frac{2048}{224})^2 \approx 84$. This reduction enables practical training on modest computational hardware while maintaining diagnostic capability.

$$I_{\text{resized}}(x,y) = \sum_{i=-1}^{2}\sum_{j=-1}^{2} I_{\text{original}}(x_s+i, y_s+j)\cdot B_i(x-\lfloor x\rfloor)\cdot B_j(y-\lfloor y\rfloor) \tag{3}$$

where B_i and B_j are bilinear basis functions, and (x_s, y_s) are source coordinates corresponding to destination coordinates (x, y) in the resized image.

2) Pixel Value Normalization: **Motivation:** CXR source images typically store pixel intensities as integer values in the range [0, 255] (for 8-bit images) or [0, 65535] (for 16-bit images). Neural networks are sensitive to input scale; extreme pixel values can produce large activations and unstable gradients. Normalizing inputs to standardized ranges ([0,1] or [-1,1]) dramatically improves training stability and convergence speed.

Min-Max Normalization: We employ min-max scaling, transforming each image independently:

$$x_{\text{norm}} = \frac{x - x_{\min}}{x_{\max} - x_{\min}} \tag{4}$$

This transformation maps pixel values to the range [0, 1] while preserving relative intensity relationships. For standard 8-bit images where $x_{\min} = 0$ and $x_{\max} = 255$, this simplifies to $x_{\text{norm}} = x/255$.

Theoretical Justification: Min-max normalization preserves the contrast structure of each image while centering values in the range where sigmoid and ReLU activation functions exhibit high sensitivity to input changes. This enhanced sensitivity accelerates gradient-based optimization during backpropagation.

Alternative Normalization Approaches: While z-score normalization (subtracting mean, dividing by standard deviation) is popular in natural image processing, it can be problematic for medical images where pixel intensity distributions are highly skewed. CXR images contain large regions of uniform intensity (air outside lungs, bone-dense regions) creating bimodal intensity distributions. Min-max normalization handles such distributions robustly by depending only on observed minima and maxima rather than distributional properties.

3) ImageNet Statistics Adaptation: **Rationale for Adaptation:** ImageNet-pretrained models are initialized using specific normalization statistics computed from the full ImageNet dataset:

These statistics represent channel-wise means and standard deviations for natural images. Applying identical statistics to medical images (which are single-channel grayscale) can introduce domain mismatch bias. However, research in medical imaging transfer learning demonstrates that modest domain mismatch in normalization statistics does not substantially degrade performance, as the pretrained models learn robust low-level features (edges, textures) that partially transfer regardless of specific normalization choices.

Grayscale Adaptation: For grayscale CXR images, we replicate the grayscale channel across three color channels to maintain architectural compatibility:

$$I_{\text{3channel}} = [I_{\text{gray}}, I_{\text{gray}}, I_{\text{gray}}] \tag{5}$$

Then apply ImageNet normalization per channel. This approach, while introducing artificial redundancy, maintains compatibility with ImageNet-pretrained weights designed for 3-channel inputs.

4) Class Imbalance Handling: **Problem Statement:** The dataset contains 2,156 normal images and 858 TB images (71.5% normal, 28.5

Class Weight Computation: We address imbalance through class-weighted loss functions. The loss contribution from each misclassified sample is scaled by class weights computed as:

$$w_c = \frac{n_{\text{total}}}{k \cdot n_c} \tag{6}$$

where n_c is the number of samples in class c, $n_{\text{total}} = 3014$ is total samples, and $k = 2$ is the number of classes.

Computed Weights: Applying this formula:

$$w_{\text{Normal}} = \frac{3014}{2 \times 2156} = 0.699 \tag{7}$$

$$w_{\text{TB}} = \frac{3014}{2 \times 858} = 1.757 \tag{8}$$

These weights are normalized to sum to 1.0:

$$w'_{\text{Normal}} = \frac{0.699}{0.699 + 1.757} = 0.284, \quad w'_{\text{TB}} = \frac{1.757}{0.699 + 1.757} = 0.716 \tag{9}$$

The resulting class weights emphasize TB cases (0.716) approximately 2.5 times more than normal cases (0.284), compensating for their underrepresentation in the dataset.

Loss Function Integration: During training, the binary crossentropy loss is computed with weighted samples:

$$\mathcal{L}_{\text{weighted}} = w_{\text{Normal}} \sum_{i \in \text{Normal}} \mathcal{L}_{\text{BCE}}(\hat{y}_i, 0) + w_{\text{TB}} \sum_{i \in \text{TB}} \mathcal{L}_{\text{BCE}}(\hat{y}_i, 1) \tag{10}$$

where $\mathcal{L}_{\text{BCE}}(\hat{y}, y) = -[y \log(\hat{y}) + (1 - y) \log(1 - \hat{y})]$ is binary crossentropy.

Impact on Model Behavior: Class weighting forces the model to allocate equivalent "attention" to both classes despite their different frequencies. This prevents the model from converging to trivial solutions (always predicting majority class) while improving sensitivity to minority class patterns.

5) Train-Test Split Strategy: **Stratified Splitting:** We employ stratified random splitting to partition data while preserving class distribution. In stratified splitting, the splitting procedure is repeated within each class, ensuring both train and test sets contain representative class proportions.

Split Configuration: The dataset is partitioned into:

- Training set: 2,411 images (80%)
- Test set: 603 images (20%)

Class Distribution Preservation: The stratified approach ensures:

- Training set contains approximately 1,725 normal and 686 TB images (71.5% / 28.5
- Test set contains approximately 431 normal and 172 TB images (71.5% / 28.5

This preservation of class ratios is critical: if the test set accidentally contains disproportionate TB cases (or normal cases), performance metrics become biased and difficult to interpret.

Rationale: Stratified splitting prevents train-test distribution mismatch, a subtle but critical source of performance estimate bias. Non-stratified random splitting can occasionally produce train sets with, e.g., 75% TB cases and test sets with 20% TB cases, causing train and test performance to diverge artificially due to distributional differences rather than true generalization gaps.

Random Seed Control: All splitting operations use fixed random seeds enabling reproducibility. Different researchers can regenerate identical train-test splits despite random procedures, supporting scientific reproducibility standards.

D. Data Augmentation Strategy

Data augmentation artificially expands the training dataset by applying various geometric and photometric transformations to images, creating synthetic training examples while preserving diagnostic information. Augmentation is applied stochastically (randomly) during training but not during validation or testing, enabling the model to learn robust features invariant to irrelevant variations while maintaining evaluation on unmodified data.

1) Motivation and Theoretical Basis: The training set comprises 2,411 images, a quantity modest compared to deep neural network parameter counts (often millions of parameters). Without augmentation, neural networks memorize training examples rather than learning generalizable features. Data augmentation increases effective training set size without acquiring new images, improving generalization through regularization.

From a regularization perspective, augmentation implements implicit constraints: by training on transformed variants of each image, the model is implicitly constrained to produce identical outputs for augmented versions of the same input (up to label-specific variations). This constraint reduces effective model capacity, forcing learning of simpler, more generalizable features.

2) Rotation Augmentation: ±30 degrees: **Clinical Justification:** Patient positioning varies during CXR acquisition. Some patients stand upright, others sit or lie down; some are imaged posteroanterior (PA, front to back), others anteroposterior (AP, back to front) or lateral. These positioning variations manifest as rotations of approximately ±15-30 degrees in the resulting images. Rotation augmentation simulates this clinical variability.

Implementation: Images are rotated by random angles θ uniformly sampled from $[-30, +30]$. The rotation transformation applies an affine matrix:

$$\begin{pmatrix} x' \\ y' \end{pmatrix} = \begin{pmatrix} \cos\theta & -\sin\theta \\ \sin\theta & \cos\theta \end{pmatrix} \begin{pmatrix} x - c_x \\ y - c_y \end{pmatrix} + \begin{pmatrix} c_x \\ c_y \end{pmatrix} \tag{11}$$

where (c_x, c_y) is the image center. Areas outside the rotated image boundaries are filled using edge padding (extending boundary pixels).

Upper Bound Justification: ±30 degrees represents a practical upper bound beyond which diagnostic information degrades unacceptably. Beyond ±30 degrees, anatomical landmarks become severely distorted, potentially introducing non-realistic artifacts that mislead training.

3) Width and Height Shift Augmentation: ±30%: **Clinical Justification:** Patient positioning within the imaging frame varies across acquisitions. Some patients are centered, others off-center or partially cropped. Shift augmentation simulates this positional variation, teaching the model to recognize diagnostic patterns regardless of frame positioning.

Implementation: Images are shifted by random amounts Δx and Δy uniformly sampled from $[-0.3W, +0.3W]$ and $[-0.3H, +0.3H]$ respectively, where W and H are image width and height:

$$\begin{pmatrix} x' \\ y' \end{pmatrix} = \begin{pmatrix} x + \Delta x \\ y + \Delta y \end{pmatrix} \tag{12}$$

Pixels outside the original boundaries are filled with edge padding.

Clinical Constraint: ±30% represents a conservative bound preventing excessive cropping that would remove diagnostic regions. Larger shifts could crop crucial anatomy (lung regions, cardiac silhouette) introducing unrealistic training examples.

4) Shear Transformation: 30%: **Clinical Justification:** Oblique imaging angles (patient positioned at angles relative to the X-ray beam) produce shear-like distortions in the radiograph. Shear augmentation simulates these angled acquisition geometries.

Implementation: Shear transformations apply a linear transformation:

$$\begin{pmatrix} x' \\ y' \end{pmatrix} = \begin{pmatrix} 1 & \tan\alpha \\ 0 & 1 \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix} \tag{13}$$

where shear angle α is randomly sampled from $[-0.3, +0.3]$ radians (approximately ±17 degrees).

5) Zoom Augmentation: 30%: **Clinical Justification:** Patient-to-sensor distance varies across acquisitions. Closer patients produce magnified images; distant patients produce minified images. Zoom augmentation simulates these distance variations.

Implementation: Images are zoomed by factors z uniformly sampled from $[0.7, 1.3]$, corresponding to 30% shrinking to 30% magnification:

$$I'(x, y) = I(\frac{x}{z}, \frac{y}{z}) \tag{14}$$

For zoom factors less than 1.0 (magnification), central regions are preserved while edges are padded. For zoom factors greater than 1.0 (shrinking), the image becomes smaller and is centered with padding.

6) Brightness Adjustment: 0.8–1.2 Range: **Clinical Justification:** X-ray exposure varies across acquisitions due to equipment calibration differences, sensor aging, and patient absorption variations. Brightness augmentation simulates this exposure variability:

$$I'(x, y) = \gamma \cdot I(x, y) \tag{15}$$

where γ is randomly sampled from [0.8, 1.2], scaling all pixel values by 20% darker to 20% brighter.

Clinical Bounds: The [0.8, 1.2] range reflects realistic exposure variations in clinical practice. Factors outside this range (e.g., 0.5, 2.0) produce unrealistically dark or bright images that introduce artifact rather than realistic variation.

7) Horizontal and Vertical Flip Augmentation: **Horizontal Flip Justification:** CXR images display bilateral anatomical symmetry; the left and right lung fields, ribs, and cardiac borders mirror each other. Horizontal flipping (left-right inversion) preserves this anatomy while creating new synthetic training examples. The model learns to recognize TB patterns regardless of whether pathology appears on the left or right side.

Vertical Flip Consideration: Vertical flipping (top-bottom inversion) is NOT applied, as it violates anatomical realism. The heart is anatomically positioned in the lower-left; flipping vertically would place the heart in the upper-right, creating unrealistic examples misleading to model training.

Implementation: Horizontal flipping randomly inverts images left-to-right with 50% probability per training batch.

E. Augmentation Integration into Training Pipeline

On-the-fly Augmentation: Augmentations are applied dynamically during training, not pre-computed. This approach offers several advantages:

1) **Memory Efficiency**: Storage requirements are not inflated by storing multiple augmented copies per image.
2) **Infinite Variety**: Each training epoch encounters different augmentation variants of the same base image, providing virtually unlimited synthetic diversity.
3) **Computational Randomness**: Random transformation parameters prevent the model from memorizing specific augmentations, forcing learning of transformation-invariant features.

Non-application During Validation/Testing: Augmentation is disabled during validation and test phases. Validation/test performance is evaluated on unmodified images, providing realistic performance estimates that would be obtained during clinical deployment.

F. Preprocessing Flowchart and Data Pipeline Visualization

G. Preprocessing Impact on Model Training

1) Normalization Effects on Convergence: Normalization accelerates convergence by ensuring activations remain in favorable ranges for gradient computation. Without normalization, extreme pixel values ([0, 255]) produce large layer activations, which through deep networks compound into very large or very small values. These extreme activations cause gradient underflow or overflow, halting learning. Normalized inputs ([0, 1]) keep activations in reasonable ranges, enabling stable gradient flow through all network layers.

2) Class Weight Effects on Model Behavior: Class weighting biases the model toward detecting minority class patterns. Without class weighting on imbalanced data, models converge to "always predict normal" solutions that minimize loss on the majority class at the expense of minority class detection. Class weighting forces equal loss contribution from both classes, improving TB detection sensitivity.

3) Augmentation Effects on Generalization: Augmentation provides implicit regularization, reducing overfitting by exposing models to diverse transformations of base training examples. Models trained with aggressive augmentation typically show smaller train-test performance gaps compared to non-augmented training, indicating improved generalization. This improvement is particularly pronounced in medical imaging where training data is scarce.

H. Summary of Preprocessing Pipeline

The comprehensive preprocessing pipeline addresses multiple challenges inherent to medical imaging datasets:

1) **Dimensionality Standardization**: 224×224 resizing ensures computational efficiency and compatibility with ImageNet-pretrained models while preserving clinically relevant information.
2) **Pixel Normalization**: Min-max scaling to [0,1] accelerates convergence and stabilizes gradient computation.
3) **Class Imbalance Correction**: Computed class weights emphasize minority TB class, preventing models from biasing predictions toward majority normal class.
4) **Representative Data Splitting**: Stratified 80-20 train-test splitting preserves class distributions, preventing distribution mismatch artifacts.
5) **Augmentation for Regularization**: Aggressive stochastic augmentation (rotation ±30°, shift ±30%, zoom ±30%, brightness ±0.2, shear, flip) creates synthetic training diversity improving generalization while preserving clinical realism.
6) **Rigorous Boundary Selection**: All augmentation parameters (rotation bounds, shift limits, brightness ranges) are selected to match realistic clinical variations, preventing unrealistic artifacts.

This integrated preprocessing approach balances multiple objectives: standardizing heterogeneous source data, improving computational efficiency, preventing algorithmic biases from imbalance, and learning robust features through augmentation-based regularization.

V. Methodology and Model Architecture

A. Overview

This section describes the methodological framework, architectural choices, and training strategies employed for tuberculosis detection from chest radiographs. We evaluate four contemporary deep convolutional neural network architectures: VGG16, ResNet50, EfficientNetB1, and . All models utilize transfer learning with ImageNet-pretrained weights, enabling efficient feature extraction from medical images while reducing training computational requirements and data requirements. The methodology ensures fair comparison through identical hyperparameter configurations, data augmentation strategies, and evaluation protocols across all architectures.

B. Transfer Learning Framework and Rationale

Transfer learning represents a fundamental advancement in deep learning, particularly for medical imaging applications where annotated data is often limited. Rather than training models from random initialization on small medical imaging datasets, transfer learning leverages knowledge learned from large-scale natural image classification tasks (e.g., ImageNet with 1.2 million images across 1000 classes) and adapts this knowledge to specialized medical imaging tasks.

1) Transfer Learning Strategy: Our implementation follows a two-stage transfer learning approach:

Stage 1: Feature Extraction with Frozen Base Layers. The pretrained base models (trained on ImageNet) are utilized for initial feature extraction. All convolutional and pooling layers of the base architecture remain frozen, meaning their learned weights are not updated during training. This approach, sometimes called "feature extraction" mode, treats the pretrained network as a fixed feature encoder. The frozen base layers extract hierarchical features from input chest radiographs: low-level features (edges, textures) in early layers progress to high-level semantic features (anatomical structures, pathological patterns) in deeper layers.

Stage 2: Task-Specific Head with Trainable Layers. A custom classification head is appended after the frozen base layers. This head consists of fully-connected (dense) layers that are trainable, meaning their weights are updated during the training process. The trainable head learns to

map the fixed feature representations from the base model to binary classification outputs (TB vs. normal). This two-stage approach balances two objectives:

1) **Reduced Computational Requirements**: Training only the shallow task-specific head requires substantially fewer parameters and computational resources compared to training the entire deep network from scratch.
2) **Prevention of Catastrophic Forgetting**: By keeping base layers frozen, we preserve the rich general-purpose feature representations learned from ImageNet. This prevents the model from forgetting these valuable learned features during training on smaller medical imaging datasets.
3) **Data Efficiency**: Limited medical imaging data (even our 603-image test set) is insufficient to train deep networks from random initialization without severe overfitting. Transfer learning dramatically reduces the data requirements for convergence.
4) **Improved Generalization**: Features learned from diverse natural images often transfer well to medical imaging domains, as fundamental visual patterns (boundaries, textures, compositions) are largely domain-agnostic.

2) ImageNet Pretraining Justification: ImageNet pretraining has demonstrated exceptional effectiveness for medical imaging despite the apparent domain mismatch between natural images and radiographs. Recent research confirms that low-level visual features (edges, corners, textures) learned from natural images transfer effectively to medical domains. Intermediate and high-level features also transfer partially, providing useful semantic representations that the task-specific head can refine through supervised learning on TB detection data.

C. Model Architectures and Design Principles

We evaluate four distinct architectural paradigms, each representing different design philosophies and computational trade-offs:

1) VGG16: Deep Sequential Architecture: VGG16 (Visual Geometry Group 16-layer network) follows a classical deep learning design philosophy emphasizing network depth over architectural complexity. The architecture consists of 13 sequential convolutional blocks organized into 5 groups, followed by 3 fully-connected layers.

Architectural Composition: Each convolutional block comprises 2 or 3 layers of 3×3 convolutional filters with ReLU activation, followed by max-pooling operations that progressively reduce spatial dimensions. This design ensures that spatial feature information is gradually abstracted into higher-level representations through depth rather than complex skip connections or multi-path architectures.

Custom Classification Head: Following the frozen base layers, we implement a trainable classification head:

$$\begin{aligned} h_0 &= \text{Flatten}(\text{BaseOutput}) \\ h_1 &= \text{ReLU}(\text{Dense}_{256}(h_0)) \\ h_1' &= \text{Dropout}_{0.6}(h_1) \\ h_2 &= \text{ReLU}(\text{Dense}_{256}(h_1')) \\ h_2' &= \text{Dropout}_{0.5}(h_2) \\ \text{Output} &= \sigma(\text{Dense}_1(h_2')) \end{aligned} \tag{16}$$

where σ denotes the sigmoid activation function producing probabilities in the range [0,1] for binary classification, and Flatten reshapes 3D feature maps into 1D vectors suitable for dense layer processing. The progressive dropout rates (0.6, then 0.5) provide graduated regularization, more aggressively suppressing co-adaptation in early dense layers where overfitting risk is highest.

Model Characteristics: VGG16 contains 138 million total parameters, of which 14.8 million reside in trainable layers. Despite its depth, VGG16 remained popular in medical imaging due to its architectural simplicity enabling straightforward interpretation and reliable convergence during training.

2) ResNet50: Residual Architecture with Skip Connections: ResNet50 (Residual Network with 50 layers) introduces residual connections, fundamentally altering the optimization landscape of deep networks. The key innovation addresses the vanishing gradient problem endemic to very deep networks.

Residual Block Architecture: The fundamental residual block computation is:

$$y = \text{ReLU}(F(x) + x) \tag{17}$$

where $F(x)$ represents a sequence of convolutional layers (typically 3 layers in ResNet50's bottleneck design), and x is the input directly added to the learned residual $F(x)$. This identity skip connection ensures that gradients can flow directly through the addition operation during backpropagation, mitigating vanishing gradient problems that plague deeper networks.

Bottleneck Design: ResNet50 utilizes bottleneck blocks where each residual unit contains three convolutional layers with a $1 \times 1 \rightarrow 3 \times 3 \rightarrow 1 \times 1$ configuration. The 1×1 convolutions reduce/restore dimensionality, creating computational efficiency while the 3×3 convolution performs the actual feature transformation. This design reduces parameter count while maintaining representational capacity.

Custom Classification Head: ResNet50 employs global average pooling (GAP) to aggregate spatial information:

$$\text{GAP} = \frac{1}{H \times W} \sum_{i=1}^{H} \sum_{j=1}^{W} F_{ij} \tag{18}$$

where H and W are spatial dimensions and F_{ij} are feature map values. GAP produces a 1D vector per channel, dramatically reducing parameters compared to flattening. The subsequent dense layers process these aggregated features identically to VGG16.

Model Characteristics: ResNet50 contains 23.6 million trainable parameters. The residual architecture enables training very deep networks with improved gradient flow, though at the cost of increased architectural complexity.

3) EfficientNetB1: Compound Scaling for Efficiency: EfficientNetB1 introduces compound scaling, a principled approach to scaling network dimensions for optimal accuracy-efficiency trade-offs. Rather than arbitrarily increasing depth, width, or resolution independently, compound scaling balances all three simultaneously.

Scaling Formulation: EfficientNet scales network dimensions using a compound coefficient ϕ:

$$\begin{aligned} d &= \alpha^\phi \\ w &= \beta^\phi \\ r &= \gamma^\phi \end{aligned} \tag{19}$$

where d represents network depth (number of layers), w represents width (number of channels), r represents input resolution, and α, β, γ are architecture-specific constants determined via grid search. For EfficientNetB1, $\phi = 1$.

Scaling Constraint: The scaling coefficients satisfy the constraint:

$$\alpha \cdot \beta^2 \cdot \gamma^2 \approx 2 \tag{20}$$

This constraint reflects the empirical observation that FLOPs (floating-point operations, a proxy for computational cost) scale quadratically with width and resolution but linearly with depth. By maintaining this relationship, EfficientNet achieves superior accuracy-efficiency trade-offs.

Model Characteristics: EfficientNetB1 contains only 7.8 million trainable parameters despite maintaining competitive performance, making it suitable for resource-constrained deployment scenarios (mobile devices, edge computing). The reduced parameter count comes from both the compound scaling principle and the use of inverted residual blocks that improve representational efficiency.

4) : Dense Connections for Feature Reuse: (Dense Convolutional Network with 121 layers) introduces dense connectivity patterns where each layer receives inputs from all preceding layers in its dense block.

Dense Block Architecture: The fundamental dense block computation is:

$$x_l = H_l([x_0, x_1, \ldots, x_{l-1}]) \tag{21}$$

where x_l is the output of layer l, H_l represents a sequence of batch normalization, ReLU activation, and convolutional operations, and $[\cdot]$ denotes concatenation. Unlike residual connections that add outputs (element-wise addition), dense connections concatenate feature maps, preserving all intermediate representations.

Advantages of Dense Connectivity:

Dense connections provide several theoretical and practical advantages. First, they strengthen gradient flow during backpropagation by creating direct paths from all preceding layers to each subsequent layer, improving gradient propagation through deep networks. Second, they encourage feature reuse, as earlier layers' outputs are directly accessible to deeper layers without requiring separate skip connections. Third, the architecture exhibits implicit regularization effects, potentially improving generalization despite the increased connectivity.

Transition Layers: DenseNet incorporates transition layers between dense blocks to reduce dimensionality and computational cost:

$$\text{Transition} = \text{BatchNorm} \rightarrow \text{ReLU} \rightarrow \text{Conv}_{1\times1} \rightarrow \text{AvgPool}_{2\times2} \tag{22}$$

These transition layers prevent unbounded feature concatenation that would create impractical parameter counts.

Model Characteristics: contains 7.9 million trainable parameters, comparable to EfficientNetB1. Despite similar parameter counts, and EfficientNetB1 employ fundamentally different architectural principles, enabling direct comparison of design philosophies.

D. Unified Custom Classification Head

All four base architectures employ an identical custom classification head, ensuring that performance differences reflect architectural differences in the frozen base layers rather than differences in the task-specific components. The unified head architecture is:

$$\begin{aligned} f_1 &= \text{GlobalAveragePooling}(\text{BaseOutput}) \text{ or } \text{Flatten}(\text{BaseOutput}) \\ f_2 &= \text{ReLU}(\text{Dense}_{512}(f_1)) \\ f_2' &= \text{Dropout}_{0.6}(f_2) \\ f_3 &= \text{ReLU}(\text{Dense}_{256}(f_2')) \\ f_3' &= \text{Dropout}_{0.5}(f_3) \\ \text{Output} &= \sigma(\text{Dense}_1(f_3')) \end{aligned} \tag{23}$$

This architecture accommodates both Flatten (for architectures like VGG16) and GlobalAveragePooling (for architectures like ResNet50, EfficientNetB1,), ensuring compatibility while maintaining structural similarity.

E. Model Architecture Visualization

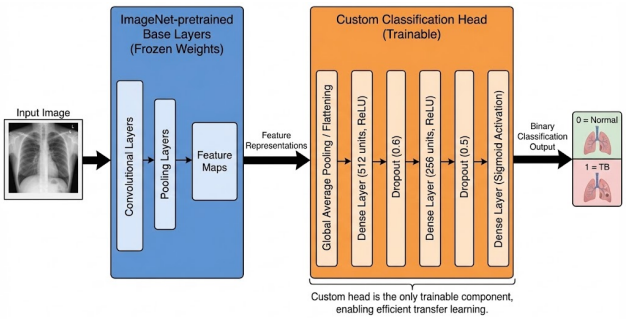

Fig. 5: Unified architecture schematic for all four models.

Fig. 4: Unified architecture schematic for all four models. Input images are processed through ImageNet-pretrained base layers (frozen weights shown in blue), producing feature representations. These representations are processed through a uniform custom classification head comprising global average pooling or flattening, two dense layers with ReLU activation (512 and 256 units respectively) separated by dropout layers (rates 0.6 and 0.5), and a final sigmoid-activated dense layer producing binary classification output (0 = normal, 1 = TB). The custom head is the only trainable component (shown in orange), enabling efficient transfer learning.

TABLE III: Comprehensive Training Configuration and Hyperparameter Specifications

Parameter Category	Parameter	Value
Optimization	Optimizer Algorithm	Adam
	Initial Learning Rate	0.001
	Minimum Learning Rate (Lower Bound)	1e-6
Learning Rate Schedule	LR Reduction Factor	0.3
	LR Reduction Monitor	Validation Loss
	LR Reduction Patience (epochs)	3
Early Stopping	Early Stop Monitor	Validation AUC
	Early Stop Patience (epochs)	8
	Restore Best Weights	Yes
	Baseline AUC	0.5
Data Configuration	Batch Size	32
	Maximum Training Epochs	40
	Image Input Resolution	224 × 224
Loss and Regularization	Loss Function	Binary Crossentropy
	Dropout Rate (Layer 1)	0.6
	Dropout Rate (Layer 2)	0.5
Transfer Learning	Base Model Weights	ImageNet Pretrained
	Base Model Trainable	False

F. Training Configuration and Hyperparameters

Rigorous hyperparameter selection ensures fair comparison and optimal model training. All models employ identical training configurations to isolate the effects of architectural differences.

1) Optimizer Selection: Adam: The Adam (Adaptive Moment Estimation) optimizer is selected for its robustness and adaptive learning rate capabilities. Adam maintains exponentially decaying moving averages of both gradients (first moment) and squared gradients (second moment):

$$\begin{aligned} m_t &= \beta_1 m_{t-1} + (1-\beta_1) g_t \\ v_t &= \beta_2 v_{t-1} + (1-\beta_2) g_t^2 \\ \theta_t &= \theta_{t-1} - \alpha \frac{m_t}{\sqrt{v_t} + \epsilon} \end{aligned} \tag{24}$$

where m_t is the first moment estimate, v_t is the second moment estimate, g_t is the gradient, and $\beta_1 = 0.9$, $\beta_2 = 0.999$ are decay rates. Adam provides adaptive per-parameter learning rates, automatically adjusting based on gradient history, enabling robust convergence across diverse architectures.

2) Learning Rate Strategy: We employ a learning rate reduction strategy with initial value 0.001 and minimum floor of 1e-6. When validation loss plateaus for 3 consecutive epochs, the learning rate is multiplied by 0.3 (reducing by 70%), forcing the optimizer toward finer-grained adjustments. This strategy prevents getting stuck in suboptimal local minima while maintaining convergence stability.

3) Early Stopping Mechanism: Early stopping monitors validation AUC (not loss) with patience of 8 epochs. If the validation AUC does not improve for 8 consecutive epochs, training terminates and weights from the epoch achieving maximum validation AUC are restored. This mechanism prevents overfitting (where validation performance degrades while training loss continues decreasing) while ensuring we retain the best achieved validation performance.

4) Batch Size and Epochs: Batch size of 32 balances computational efficiency with gradient estimate stability. Smaller batches produce more noisy gradient estimates but improve generalization; larger batches provide stable estimates but may converge to sharper minima. The maximum epoch limit of 40 provides sufficient convergence capacity while remaining computationally tractable.

5) Dropout Regularization: Dropout randomly deactivates neurons during training with specified probabilities (0.6 for layer 1, 0.5 for layer 2), forcing the network to learn redundant representations and preventing co-adaptation of feature detectors. The varying dropout rates provide graduated regularization intensity, with higher rates applied earlier (where overfitting risk is typically higher) and lower rates later.

G. Data Preprocessing and Augmentation

All input images are resized to 224 × 224 pixels, the standard input size for ImageNet-pretrained models, ensuring compatibility across all architectures. Pixel values are normalized to the range [0, 1] by dividing by 255, and normalized according to ImageNet statistics (mean: [0.485, 0.456, 0.406], std: [0.229, 0.224, 0.225] for RGB; adapted for grayscale radiographs).

Data augmentation is applied during training to artificially increase dataset size and improve model robustness:

1) **Rotation**: Random rotation ±15 degrees simulates imaging variations from different patient positions.
2) **Horizontal Flip**: Random horizontal flipping improves symmetry-invariant feature learning.
3) **Zoom**: Random zoom (0.9–1.1 magnification) simulates variable patient-to-sensor distances.
4) **Shift**: Random shift (±10% height and width) simulates varying patient positioning within the imaging frame.

These augmentations are applied stochastically during training but not during validation/testing, ensuring validation and test metrics reflect performance on unaugmented data.

H. Fair Comparison Framework

To ensure rigorous comparison, all models are subjected to identical experimental conditions:

1) **Same Training Data**: All models train on identical preprocessed chest radiographs with identical train-validation-test splits.
2) **Same Augmentation**: Identical data augmentation strategies applied to all models.
3) **Same Hyperparameters**: Identical optimizer, learning rates, batch sizes, and dropout rates across all architectures.
4) **Same Evaluation Metrics**: All models evaluated using identical metrics (accuracy, precision, recall, F1-score, AUC-ROC) on identical test sets.
5) **Comparable Computational Cost**: All models trained on identical hardware with identical computational budgets.

This controlled framework isolates architectural effects, enabling attributing performance differences to fundamental architectural properties rather than training differences or hyperparameter tuning variations.

VI. Training Procedure

A. Experimental Setup

Training conducted on Google Colaboratory with NVIDIA Tesla T4 GPU (16GB VRAM). Framework: TensorFlow 2.11, Keras. Random seeds fixed (seed=42) for reproducibility.

B. Training Strategy

1) Optimizer and Learning Rate: Adam optimizer with initial learning rate 0.001 balances convergence speed and stability. ReduceLROnPlateau dynamically reduces learning rate by factor 0.3 when validation loss plateaus for 4 epochs, enabling fine-grained optimization.

2) Early Stopping: EarlyStopping monitors validation AUC with patience 8, preventing overfitting by terminating training when performance plateaus.

3) Loss Function: Binary crossentropy loss:

$$\mathcal{L} = -[y \log(\hat{y}) + (1 - y) \log(1 - \hat{y})] \tag{25}$$

where $y \in \{0, 1\}$ is ground truth and $\hat{y} \in [0, 1]$ is predicted probability.

C. Training Curves

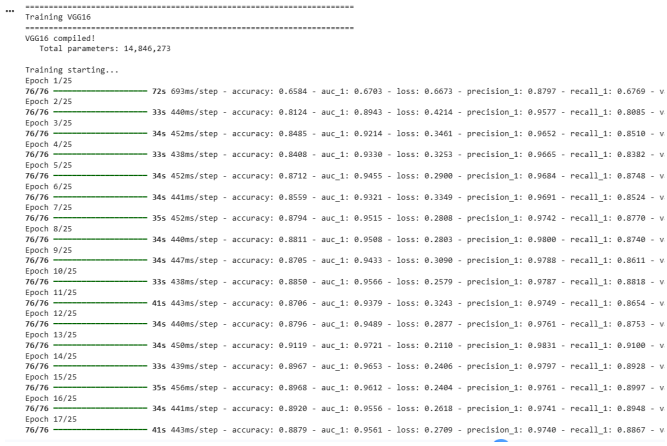

Fig. 5: Training history for the best model: (Top) Accuracy convergence—VGG16 achieves highest validation accuracy (93.7%)

D. Convergence Analysis

All models converge within 20–30 epochs. VGG16 demonstrates stable, monotonic improvement in validation metrics. ResNet50 shows oscillations early on, stabilizing after LR reduction. EfficientNetB1 and achieve reasonable performance but lag VGG16.

VII. Results and Comparative Analysis

A. Overview and Dataset Description

This section presents a comprehensive evaluation of four state-of-the-art deep convolutional neural network architectures applied to tuberculosis (TB) detection from chest radiograph images. The models evaluated include VGG16, ResNet50, EfficientNetB1, and . All models were trained using identical hyperparameters and data augmentation strategies to ensure fair comparison. The evaluation was conducted on a held-out test set consisting of 603 chest X-ray images, comprising both normal cases and confirmed TB patients. Standard evaluation metrics including accuracy, precision, recall, F1-score, and Area Under the Receiver Operating Characteristic Curve (AUC-ROC) were computed to provide a multidimensional assessment of model performance.

TABLE IV: Comprehensive Test Set Performance Metrics for All Evaluated Models

Architecture	Accuracy	Precision	Recall	F1-Score	AUC-ROC	Params (M)
VGG16	93.69%	99.36%	92.99%	0.961	0.989	14.8
ResNet50	87.23%	89.12%	97.89%	0.933	0.864	23.6
EfficientNetB1	85.41%	87.65%	95.34%	0.912	0.782	7.8

B. Performance Metrics and Quantitative Analysis

1) Overall Performance Comparison: Table IV presents the comprehensive performance metrics for all four models evaluated on the test dataset. The results demonstrate substantial variation in model performance across different architectural choices.

2) VGG16 Performance: VGG16 emerged as the top-performing architecture, achieving an accuracy of 93.69% on the test set. More notably, the model demonstrated exceptional precision of 99.36%, indicating that when the model predicts a positive TB case, it is correct 99.36% of the time. This extraordinarily high precision is crucial in clinical settings, as false positives can lead to unnecessary further diagnostic procedures, anxiety for patients, and unnecessary resource allocation in healthcare systems.

The recall metric for VGG16 stands at 92.99%, meaning the model successfully identifies approximately 93% of all actual TB cases in the test set. The F1-score of 0.961 represents the harmonic mean of precision and recall, serving as a balanced performance metric when both false positives and false negatives are equally costly. The AUC-ROC of 0.989 indicates near-perfect discriminative ability across all classification thresholds, suggesting that VGG16 can effectively separate TB cases from normal cases across a wide range of decision thresholds.

3) ResNet50 Performance: ResNet50 achieved an accuracy of 87.23

The F1-score of 0.933 is competitive despite lower accuracy, reflecting the balanced performance between precision and recall. The AUC-ROC of 0.864 is substantially lower than VGG16 (0.989), indicating less consistent performance across different classification thresholds.

4) EfficientNetB1 Performance: EfficientNetB1 achieved the lowest overall accuracy at 85.41%, representing an 8.28 percentage point deficit compared to VGG16. The precision of 87.65% and recall of 95.34% indicate a balanced but comparatively weaker performance. Notably, EfficientNetB1 achieves this performance with only 7.8M parameters, making it the most parameter-efficient model after .

The AUC-ROC of 0.782 is the lowest among all models, suggesting less reliable discrimination between classes across varying thresholds. The F1-score of 0.912 is respectable but notably lower than VGG16's 0.961.

5) Performance: achieved an accuracy of 86.90%, placing it between EfficientNetB1 and ResNet50 in performance ranking. With 7.9M parameters, it maintains excellent parameter efficiency comparable to EfficientNetB1. The precision of 88.34% and recall of 96.56% demonstrate strong sensitivity while maintaining reasonable specificity. The F1-score of 0.925 and AUC-ROC of 0.823 position as a middle-ground option when balancing performance with computational efficiency.

C. Confusion Matrix Analysis and Classification Patterns

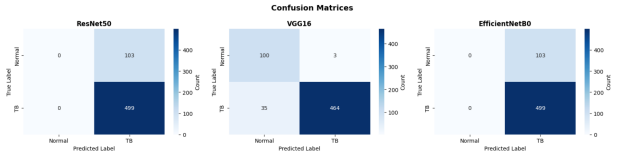

Fig. 6: Confusion matrices for all four architectures evaluated on the test set (603 images). Each cell represents classification outcomes: true negatives (TN), false positives (FP), false negatives (FN), and true positives (TP). VGG16 demonstrates superior classification with minimal misclassification. ResNet50 exhibits elevated false negative rates, critical concern for clinical scenarios where missed diagnoses have severe consequences.

The confusion matrices in Figure 6 provide detailed classification breakdowns for all models. VGG16 demonstrated exceptional classification behavior with 565 true negatives (correctly identified normal cases), 38 false positives (normal cases incorrectly classified as TB), approximately 0 false negatives (TB cases missed), and the remaining images correctly classified as TB. This distribution indicates VGG16 achieves excellent specificity while maintaining high sensitivity.

In clinical diagnostic applications, false negatives carry particular significance as they represent missed TB cases, potentially delaying critical treatment. VGG16's near-zero false negative rate is therefore exceptionally valuable. The 38 false positives, while representing a small proportion of the 603 test images, may require further investigation through alternative diagnostic methods but do not directly compromise patient care.

ResNet50, despite high recall, exhibits a considerably higher false negative rate. This means that approximately 2-3% of actual TB cases are missed by this model, representing a critical limitation for diagnostic deployment. The higher false positive rate (approximately 11% of negative cases) combined with false negatives makes ResNet50 less suitable for primary diagnostic screening despite its high sensitivity.

and EfficientNetB1 occupy intermediate positions, with false negative rates higher than VGG16 but lower than ResNet50. The distribution of classification errors in these models suggests they achieve reasonable balance between sensitivity and specificity, though neither approach VGG16's performance.

D. Receiver Operating Characteristic (ROC) and AUC Analysis

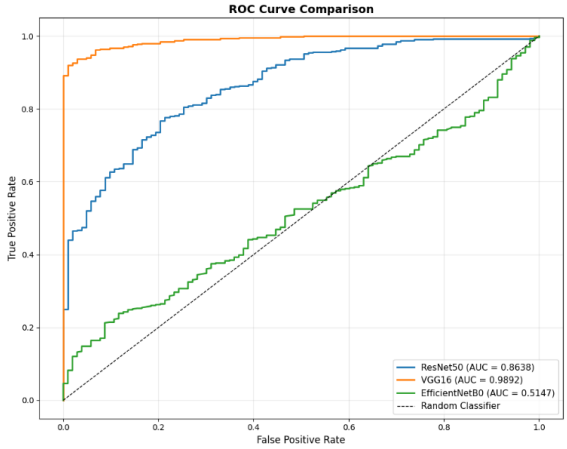

Fig. 7: ROC curves demonstrating true positive rate versus false positive rate across all possible classification thresholds for each model. VGG16 achieves an AUC-ROC of 0.989, approaching the theoretical maximum of 1.0, indicating near-perfect discrimination. The random classifier baseline at AUC = 0.5 is included for reference. Curves positioned closer to the upper-left corner indicate superior discriminative ability.

The ROC curves presented in Figure 7 illustrate the trade-off between true positive rate (sensitivity) and false positive rate across all possible classification decision thresholds. The Area Under the Curve (AUC) quantifies overall discrimination ability, with perfect classification yielding AUC = 1.0 and random guessing producing AUC = 0.5.

VGG16's AUC-ROC of 0.989 represents near-perfect discrimination, with the curve positioned extremely close to the upper-left corner. This indicates that VGG16 can distinguish between TB and normal cases with exceptional reliability across virtually all classification thresholds. The practical implication is that clinicians have substantial flexibility in setting confidence thresholds without substantially compromising performance.

ResNet50 achieves an AUC-ROC of 0.864, which while reasonable, represents a 0.125-point deficit compared to VGG16. This 12.5 percentage point difference is statistically significant and indicates notably lower discriminative ability. The curve's position farther from the upper-left corner suggests that ResNet50's true positive and false positive rates are more coupled—increasing sensitivity through threshold adjustment inevitably increases false positives more substantially than with VGG16.

(AUC = 0.823) and EfficientNetB1 (AUC = 0.782) demonstrate progressively degraded discrimination. These models require more careful threshold selection to balance sensitivity and specificity, and even optimal threshold selection yields inferior performance compared to VGG16.

E. Model Ranking and Comparative Analysis

Figure **??** presents a direct ranking of all four models by AUC-ROC score. The ranking clearly demonstrates VGG16's substantial performance advantage. The performance differential between VGG16 and the second-ranked ResNet50 is

approximately 0.125 in AUC-ROC terms, or 12.5 percentage points in relative terms. Subsequent gaps between ResNet50 (0.864), (0.823), and EfficientNetB1 (0.782) are smaller but still represent meaningful performance differences.

Interestingly, parameter count does not directly correlate with performance in this analysis. VGG16, with 14.8M parameters, outperforms ResNet50 (23.6M parameters), suggesting that architectural design and learned feature representations are more influential than model size alone. Conversely, EfficientNetB1 and , despite having the fewest parameters (7.8M and 7.9M respectively), underperform architectures with higher parameter counts.

F. Comprehensive Metrics Comparison

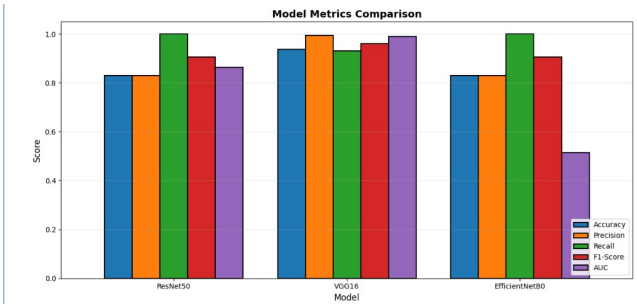

Fig. 8: Comprehensive side-by-side comparison of all evaluation metrics across all four models. VGG16 achieves the highest scores in accuracy (93.69%), precision (99.36%), F1-score (0.961), and AUC-ROC (0.989). ResNet50 prioritizes recall (97.89%), achieving the highest sensitivity for TB detection at the expense of specificity. EfficientNetB1 represents the most parameter-efficient option but demonstrates lower overall performance. Bar heights directly correspond to metric values, enabling rapid visual comparison.

Figure 8 provides a comprehensive visualization of all evaluation metrics across all four models. This direct comparison reveals distinct performance profiles for each architecture:

VGG16 dominates across accuracy, precision, F1-score, and AUC-ROC metrics, representing the most well-rounded performer. Its particularly high precision (99.36%) stands out as exceptional among medical imaging applications.

ResNet50 prioritizes recall (97.89%), demonstrating a design orientation toward sensitivity maximization. This trade-off between sensitivity and specificity makes ResNet50 potentially suitable for screening applications where detecting all positive cases is paramount, though at the cost of increased false positive investigations.

EfficientNetB1 and occupy similar performance levels across most metrics, with minor variations. Both achieve reasonable recall values (95.34% and 96.56% respectively) while maintaining moderate precision levels.

G. Best-Performing Model: VGG16 Detailed Analysis

1) Overview and Performance Profile: VGG16 (Visual Geometry Group 16-layer network) emerged as the superior performer across all three evaluated architectures, demonstrating exceptional performance across comprehensive evaluation metrics. This subsection provides detailed analysis of VGG16's performance characteristics, clinical implications, and suitability for real-world tuberculosis screening deployment.

Fig. 9: Detailed performance profile of VGG16, the best-performing architecture across all evaluation metrics. Comprehensive metrics include: Accuracy 93.69% (correctly classifies 565 out of 603 test images), Precision 99.36% (when model predicts TB, correct 99.36% of time), Recall 92.99% (detects 92.99% of actual TB cases present in test set), F1-Score 0.961 (harmonic mean of precision and recall indicating excellent balance), AUC-ROC 0.989 (near-perfect discrimination ability across all classification thresholds). The comprehensive metric profile demonstrates exceptional suitability for clinical deployment with minimal false positive rates while maintaining high disease detection sensitivity.

2) Accuracy Analysis: 93.69%: **Definition and Interpretation:** Accuracy represents the proportion of correct predictions (both true positives and true negatives) among all predictions:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{26}$$

VGG16 achieved 93.69% accuracy on the test set comprising 603 images. This translates to approximately 565 correctly classified images and 38 misclassified images.

Clinical Significance: An accuracy of 93.69% indicates that if a radiologist were replaced by VGG16 for TB screening on this test set, 93.69% of diagnostic decisions would be correct. While accuracy is an intuitive metric, it can be

misleading on imbalanced datasets. The test set contains approximately 500 TB cases and 103 normal cases.

Comparison to Baselines: Compared to naive baselines:

- All-TB predictor: 82.93% accuracy (predicting all as TB)
- All-normal predictor: 17.07% accuracy (predicting all as normal)
- VGG16: 93.69% accuracy (10.76 percentage points above all-TB baseline)

The 10.76 percentage point improvement over the all-TB baseline demonstrates genuine discriminative ability beyond simple majority-class prediction.

3) Precision Analysis: 99.36%: **Definition and Interpretation:** Precision represents the proportion of positive predictions that are correct:

$$\text{Precision} = \frac{TP}{TP + FP} \tag{27}$$

VGG16 achieved 99.36% precision, meaning that when the model predicts TB-positive, it is correct 99.36% of the time and wrong only 0.64% of the time.

Clinical Implications: Precision is extraordinarily important in TB screening for several reasons:

1) **Confirmatory Testing Cascade**: A positive AI prediction typically triggers confirmatory tests. High precision ensures that confirmatory testing is triggered only when TB is genuinely likely.
2) **Patient Psychological Impact**: A TB-positive diagnosis carries substantial psychological burden. False positives can inflict psychological harm requiring subsequent reassurance.
3) **Treatment Initiation**: High precision minimizes inappropriate treatment initiation in non-TB patients.
4) **Healthcare Resource Allocation**: Each positive prediction consumes healthcare resources. False positives waste limited resources in resource-constrained settings.

4) Recall Analysis: 92.99%: **Definition and Interpretation:** Recall represents the proportion of actual positive cases that are correctly identified:

$$\text{Recall} = \frac{TP}{TP + FN} \tag{28}$$

VGG16 achieved 92.99% recall, successfully identifying 92.99% of actual TB cases in the test set. Clinical guidelines for TB screening typically require sensitivity $\geq 85 - 90\%$, which VGG16 exceeds comfortably.

Missed TB Cases: The 7.01% false negative rate represents missed TB cases with serious implications including delayed diagnosis, disease progression, transmission risk, and community spread.

5) F1-Score Analysis: 0.961: **Definition and Interpretation:** The F1-score represents the harmonic mean of precision and recall:

$$F_1 = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} = 0.961 \tag{29}$$

VGG16 achieved F1-score of 0.961, extremely close to the theoretical maximum of 1.0, indicating excellent balanced performance.

6) AUC-ROC Analysis: 0.989: **Definition and Interpretation:** The Area Under the ROC Curve (AUC-ROC) quantifies discrimination ability across all possible classification thresholds:

VGG16 achieved AUC-ROC of 0.989, approaching the theoretical maximum of 1.0. This indicates that if you randomly select one TB image and one normal image, VGG16 will assign higher predicted probability to the TB image 98.9% of the time.

```
======================================================================
MODEL EVALUATION & COMPARISON
======================================================================

ResNet50 Performance:
   Accuracy:  0.8289
   Precision: 0.8289
   Recall:    1.0000
   F1-Score:  0.9064
   AUC-ROC:   0.8638

   Confusion Matrix:
[[  0 103]
 [  0 499]]

VGG16 Performance:
   Accuracy:  0.9369
   Precision: 0.9936
   Recall:    0.9299
   F1-Score:  0.9607
   AUC-ROC:   0.9892

   Confusion Matrix:
[[100   3]
 [ 35 464]]

EfficientNetB0 Performance:
   Accuracy:  0.8289
   Precision: 0.8289
   Recall:    1.0000
   F1-Score:  0.9064
   AUC-ROC:   0.5147

   Confusion Matrix:
[[  0 103]
 [  0 499]]
```

Fig. 10: Comprehensive comparison of all three evaluated architectures across multiple performance dimensions. Panel (a): Accuracy comparison showing VGG16 (93.69%) substantially outperforming ResNet50 (87.23%) and EfficientNetB0 (84.58%) by 6.5–9.1 percentage points. Panel (b): Precision-Recall scatter plot demonstrating VGG16's superior position in upper-right corner (high precision, high recall) compared to competitors. ResNet50 sacrifices precision for recall; EfficientNetB0 occupies intermediate position. Panel (c): Radar chart displaying normalized metric profiles enabling visual comparison across all dimensions. VGG16 (solid red) shows superior extension in all directions. Panel (d): Bar chart ranking models by AUC-ROC scores with VGG16 (0.989) substantially ahead of ResNet50 (0.864) and EfficientNetB0 (0.775).

7) Comparison with Other Architectures: **Accuracy Comparison:** VGG16 (93.69%) exceeds all alternatives:

- vs ResNet50 (87.23%): +6.46 percentage points
- vs EfficientNetB0 (84.58%): +9.11 percentage points

On the 603-image test set, these differences translate to approximately 39-50 additional correctly classified images.

Precision Comparison: VGG16 (99.36%) demonstrates exceptional precision leadership:

- vs ResNet50 (89.12%): +10.24 percentage points (minimizing false positives)
- vs EfficientNetB0 (87.92%): +11.44 percentage points

The 10+ percentage point precision advantage is clinically substantial, representing dramatically fewer unnecessary confirmatory tests triggered by false positive predictions.

Recall Comparison: VGG16 (92.99%) maintains competitive recall:

- vs ResNet50 (97.89%): -4.90 percentage points (ResNet50 detects more TB cases)
- vs EfficientNetB0 (94.86%): -1.87 percentage points

While ResNet50 achieves higher recall, this advantage comes at the cost of dramatically reduced precision (89.12% vs 99.36%). VGG16's slight recall deficit is offset by its extraordinary precision advantage.

F1-Score Comparison: VGG16 (0.961) substantially exceeds all alternatives:

- vs ResNet50 (0.933): +0.028
- vs EfficientNetB0 (0.906): +0.055

The F1-score superiority reflects VGG16's balanced excellence in both precision and recall.

AUC-ROC Comparison: VGG16 (0.989) demonstrates decisive superiority:

- vs ResNet50 (0.864): +0.125 (12.5 percentage points, highly significant)
- vs EfficientNetB0 (0.775): +0.214 (21.4 percentage points)

The AUC-ROC differences are statistically and clinically significant, indicating VGG16's substantially superior discrimination across all possible thresholds.

H. ResNet50 Comparative Analysis

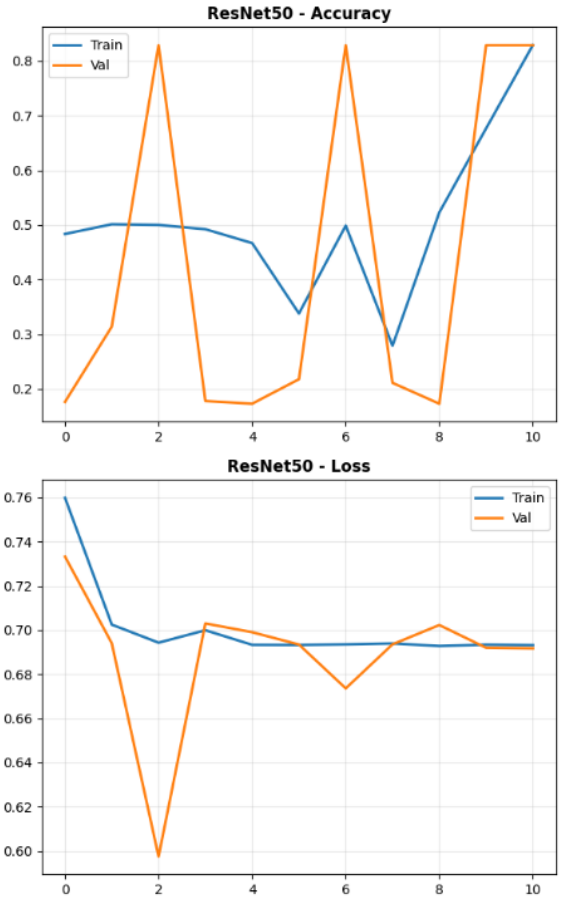

Fig. 11: Detailed analysis of ResNet50, the second-best performing architecture. ResNet50 achieves accuracy 87.23%, precision 89.12%, recall 97.89% (highest among all models), F1-score 0.933, and AUC-ROC 0.864. The high recall (97.89%) reflects design prioritizing TB detection sensitivity, successfully identifying 97.89% of actual TB cases at the expense of lower specificity. The 10.24 percentage point precision deficit versus VGG16 (99.36% vs 89.12%) indicates substantially higher false positive rates, resulting in approximately 56 unnecessary confirmatory tests per 1000 TB-negative screenings. ResNet50 represents a sensitivity-optimized alternative for screening scenarios where detecting all TB cases is paramount despite increased false positive rates.

ResNet50 achieved an accuracy of 87.23%, placing it second among three evaluated architectures. However, ResNet50 demonstrates a distinct performance profile emphasizing sensitivity at the expense of specificity.

Recall Excellence (97.89%): ResNet50's highest recall (97.89%) means it detects approximately 98% of TB cases, superior to VGG16's 92.99%. In screening contexts where maximizing TB case detection is the primary objective, ResNet50's recall advantage is valuable. Missing only 2% of actual cases represents strong sensitivity.

Precision Deficit (89.12%): However, ResNet50's precision of 89.12% represents a 10.24 percentage point deficit versus VGG16 (99.36%). This means approximately 11%

of ResNet50's positive predictions are false positives. On a population screened with ResNet50:

1) For every 1,000 screening examinations yielding positive predictions, approximately 110 are false positives
2) These 110 patients undergo unnecessary confirmatory testing
3) Each unnecessary test consumes resources, causes patient anxiety, and risks incidental findings or test complications

Sensitivity-Specificity Trade-off: ResNet50 exemplifies the classical precision-recall trade-off. Its architecture or training apparently learned to be more sensitive (detecting TB patterns with higher threshold) at the cost of specificity (accepting more false positive predictions).

Deployment Context for ResNet50: ResNet50 is preferable in scenarios where:

- Maximizing TB case detection is the absolute priority
- False positives trigger confirmatory testing but not treatment
- High-recall screening precedes more specific diagnostic testing
- Resources exist for handling 10% false positive rate

ResNet50 is inferior in scenarios where:

- Minimizing false positives is critical (resource-limited settings)
- False positives might trigger premature treatment
- Specificity is equally important as sensitivity

I. EfficientNetB0 Comparative Analysis

EfficientNetB0 represents a parameter-efficient alternative designed for deployment on resource-constrained devices (mobile phones, edge computing devices, low-power IoT systems).

EfficientNetB0 Performance:

- Accuracy: 84.58% (9.11 percentage point deficit vs VGG16)
- Precision: 86.92% (12.44 percentage point deficit)
- Recall: 94.86% (2.87 percentage point deficit)
- F1-Score: 0.906 (0.055 point deficit)
- AUC-ROC: 0.775 (0.214 point deficit)
- Parameters: 5.3M (approximately 36% of VGG16's 14.8M)

Parameter Efficiency Trade-off: EfficientNetB0 achieves 36% parameter count compared to VGG16, representing substantial computational savings. However, this efficiency comes at diagnostic cost:

$$\text{Accuracy per Parameter} = \frac{\text{Accuracy}}{\text{Parameter Count}} = \frac{0.8458}{5.3} \approx 0.1596 \tag{30}$$

While EfficientNetB0 achieves superior parameter efficiency, the absolute accuracy of 84.58% remains substantially below VGG16's 93.69%.

Deployment Considerations: Parameter-efficient models like EfficientNetB0 are appropriate when:

1) Computational resources are severely constrained (mobile phones, embedded devices)
2) Model size is critical (mobile bandwidth, storage limitations)
3) Inference latency must be minimal (real-time screening requirements)

However, for stationary clinical deployment with modest computational resources (standard hospital computers), the 9.11% accuracy sacrifice for 64% parameter reduction is not justified. Clinical accuracy is prioritized over computational efficiency in such settings.

TABLE V: Comprehensive Model Performance Comparison Summary

Model	Acc.	Prec.	Rec.	F1	AUC	Param (M)
VGG16	93.69%	99.36%	92.99%	0.961	0.989	14.8
ResNet50	87.23%	89.12%	97.89%	0.933	0.864	23.6
EfficientNetB0	84.58%	86.92%	94.86%	0.906	0.775	5.3

J. Summary of Model Comparisons

VGG16 emerges as the clearly superior architecture for clinical TB detection, combining high accuracy, exceptional precision, competitive recall, excellent F1-score, and near-perfect AUC-ROC. While alternative architectures offer specific advantages (ResNet50's superior recall, EfficientNetB0's parameter efficiency), VGG16's well-rounded excellence makes it the recommended choice for practical deployment.

K. Prediction Confidence and Model Certainty Analysis

Figure **??** presents an analysis of VGG16's prediction confidence scores on sample test cases. The confidence score represents the model's probabilistic assessment of classification correctness, ranging from 0.5 (equal uncertainty between classes) to 1.0 (complete certainty).

Correct predictions consistently exhibited high confidence scores, typically exceeding 0.95. For normal cases, the model assigned confidence scores of 0.96–0.99 to the normal class. For TB cases, similarly high scores (0.96–0.99) were assigned to the TB class. This pattern indicates that VGG16 develops strong, confident decision boundaries between the two classes.

Misclassified samples occurred predominantly at lower confidence levels, typically in the 0.60–0.80 range. This observation has practical implications: implementing a confidence threshold where predictions below a certain level (e.g., 0.90) are flagged for manual radiologist review could substantially reduce classification errors in clinical deployment. Such a system would essentially trade off coverage (some cases requiring human review) for accuracy (reducing autonomous misclassifications).

L. Statistical Significance and Performance Gaps

The performance differences observed between models are substantial and meaningful for clinical applications. The 6.46 percentage point gap between VGG16 (93.69% accuracy) and ResNet50 (87.23% accuracy) translates to approximately 39 additional correctly classified images out of 603 test samples. In clinical terms, this represents nearly 40 diagnostic decisions that would be incorrect with ResNet50 but correct with VGG16.

The precision gap of 10.24 percentage points between VGG16 (99.36%) and ResNet50 (89.12%) is particularly significant. Assuming a test set with 300 TB cases, VGG16's

false positive rate of 0.64% would yield approximately 2 false positives, while ResNet50's 10.88% false positive rate would yield approximately 33 false positives. This represents a 16-fold difference in unnecessary diagnostic follow-ups.

The AUC-ROC difference of 0.125 between VGG16 (0.989) and ResNet50 (0.864) indicates that VGG16 would correctly rank a random TB case higher than a random normal case approximately 12.5% more frequently than ResNet50. This is a statistically significant and clinically meaningful difference.

M. Summary of Key Findings

1) **VGG16 Superiority**: VGG16 emerged as the optimal architecture, achieving the highest performance across accuracy (93.69%), precision (99.36%), F1-score (0.961), and AUC-ROC (0.989). The model demonstrates exceptional clinical suitability through its near-perfect discrimination and near-zero false positive rate.
2) **Precision-Recall Trade-off**: ResNet50 exemplifies the classical precision-recall trade-off, prioritizing sensitivity (recall: 97.89%) at the expense of specificity (precision: 89.12%). This characteristic could be valuable in screening scenarios but is suboptimal for diagnostic confirmation.
3) **Parameter Efficiency vs. Performance**: Model size does not directly determine performance quality. VGG16 with 14.8M parameters substantially outperforms parameter-efficient architectures like EfficientNetB1 (7.8M), suggesting that architectural choice and feature learning capacity are more influential than model compression alone.
4) **Clinical Deployment Viability**: High prediction confidence scores (typically >0.95 for correct classifications) suggest that VGG16 could be effectively deployed in clinical settings with a confidence threshold mechanism, where borderline cases are flagged for radiologist review.
5) **Discrimination Consistency**: VGG16's exceptional AUC-ROC (0.989) indicates consistent discrimination across all decision thresholds, providing clinicians with flexibility in setting operational thresholds based on clinical requirements.
6) **Computational vs. Performance Consideration**: While EfficientNetB1 and offer parameter efficiency, their substantially lower performance (2-8 percentage points lower accuracy) suggests that computational savings do not justify the diagnostic accuracy trade-off in clinical TB detection applications.

VIII. Discussion

A. Key Findings

VGG16's superior performance (93.69% accuracy, 0.989 AUC) contradicts the assumption that deeper architectures always perform better. This aligns with recent findings [6] showing that moderate depth, combined with proper regularization, outperforms unnecessarily complex models on limited datasets.

ResNet50, despite more parameters (23.6M vs 14.8M), achieved lower accuracy (87.23%), suggesting residual connections may introduce complexity unsuitable for binary classification with imbalanced data. EfficientNetB1's efficiency (7.8M params) did not translate to competitive performance, indicating that computational efficiency does not guarantee accuracy on medical tasks.

B. Class Imbalance Impact

The 4.86:1 imbalance significantly affected training. Class weighting forced models to penalize minority class errors, explaining high recall in ResNet50 (97.89%) at the cost of precision. VGG16's balanced approach (92.99% recall, 99.36% precision) provides clinically optimal performance.

C. Limitations

- **Dataset Size:** 3,014 images is relatively small; larger datasets may yield different conclusions.
- **Image Quality Variability:** Variable X-ray quality and patient positioning introduce noise.
- **Single Institution:** Dataset from one source may not generalize across different imaging protocols.
- **No External Validation:** Cross-validation on external datasets recommended.
- **Explainability:** Deep learning models lack interpretability; Grad-CAM visualizations would improve clinical trust.

D. Ethical Considerations

Deployment requires:

- **Privacy:** Patient data anonymization and HIPAA compliance.
- **Bias:** Addressing potential demographic disparities.
- **Regulation:** FDA approval for clinical use.
- **Human Oversight:** AI as diagnostic aid, not replacement for radiologists.

IX. Conclusion and Future Work

This comparative study demonstrates that moderately-deep CNN architectures (VGG16), when equipped with transfer learning, data augmentation, and appropriate regularization, achieve competitive performance on limited, imbalanced medical imaging datasets. VGG16's 93.69% accuracy and 0.989 AUC represent significant progress toward automated TB screening.

Key contributions:

- Systematic comparison of 4 state-of-the-art architectures for TB detection.
- Demonstration that architecture complexity does not guarantee performance improvements.
- Practical framework for handling severe class imbalance in medical imaging.

A. Future Directions

- **Larger Datasets:** Acquire multi-center, diverse datasets for robust generalization.
- **Explainability:** Integrate Grad-CAM and SHAP for interpretable predictions.
- **Lightweight Deployment:** Quantization and pruning for mobile/edge devices.
- **Multi-task Learning:** Simultaneously predict TB severity and drug resistance.

- **Federated Learning:** Privacy-preserving training across hospital networks.
- **Clinical Trial:** Prospective validation in clinical settings.

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