FFT-Based Spectral Fingerprinting for Pulmonary Abnormality Detection in Chest Radiographs: A Comprehensive Methodology and Analysis

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Abstract—This paper presents a comprehensive FFT-based spectral fingerprinting methodology for pulmonary abnormality detection in chest radiographs, with tuberculosis serving as the primary validation pathology. Our approach combines frequency-domain analysis with spatial hashing to create discriminative feature representations while maintaining computational efficiency. The method achieves 95.0% accuracy on PNG datasets (400 images) and 93.13% on mixed-format datasets (583 images), demonstrating robust performance across different image formats. Key innovations include a novel cluster scoring mechanism that integrates size and spatial distribution, a conservative thresholding strategy to minimize false positives, and a database construction approach that emphasizes normal anatomical patterns. This work provides detailed algorithmic explanations and empirical validation, making it suitable for implementation in resource-constrained environments. The system performs binary classification (normal vs. abnormal) with an average processing time of 4 seconds per image (range: 2-8 seconds) and achieves consistent accuracy between 85-95% across diverse datasets.

Keywords: Medical Imaging, Pulmonary Abnormality Detection, FFT Analysis, Spectral Fingerprinting, Computer-Aided Diagnosis, Chest Radiography

1 Introduction

Pulmonary abnormalities, including tuberculosis, pneumonia, and other respiratory conditions, remain significant global health challenges, with early detection being crucial for effective treatment and containment. Automated detection systems can potentially address diagnostic gaps in resource-constrained environments, but many existing approaches require substantial computational resources and large training datasets.

This work presents a detailed FFT-based methodology for pulmonary abnormality screening that balances computational efficiency with diagnostic accuracy. While tuberculosis detection serves as our primary validation use case due to the availability of comprehensive datasets, the underlying methodology represents a general-purpose approach for detecting pulmonary abnormalities in chest radiographs. The framework can be extended to multi-class classification of various pulmonary conditions.

Our approach focuses on binary classification (normal vs. abnormal) using frequency-domain features extracted from chest radiographs, providing a solution that can operate effectively on standard hardware. The choice of tuberculosis for validation reflects data availability rather than methodological exclusivity.

The paper is organized as follows: Section II discusses related work, Section III details the comprehensive methodology, Section IV describes the experimental setup, Section V presents results and analysis, and Section VI concludes with future directions.

2 Related Work

Computer-aided diagnosis of pulmonary abnormalities has evolved from traditional image processing methods to deep learning approaches. Early works focused on texture analysis and statistical pattern recognition [2], while recent methods employ convolutional neural networks [1]. However, these often require substantial computational resources and large datasets.

Frequency domain analysis has been utilized in medical imaging for various applications. FFT-based methods offer advantages in computational efficiency and robustness to spatial variations, making them suitable for automated diagnostic systems in resource-constrained environments [3].

Our work contributes by providing a detailed, implementable methodology that combines frequency domain analysis with spatial relationship encoding in a hashing framework, enabling efficient abnormality detection with minimal computational requirements. While validated on tuberculosis detection, the approach is fundamentally designed for general pulmonary abnormality screening.

3 Comprehensive Methodology

3.1 Image Preprocessing Pipeline

The preprocessing stage ensures consistent input quality across diverse datasets. Input images undergo three main transformations:

3.1.1 Grayscale Conversion

Using the standard luminance formula:

$$I_{gray} = 0.299 \cdot I_R + 0.587 \cdot I_G + 0.114 \cdot I_B \tag{1}$$

3.1.2 Standardized Resizing

All images are resized to 1024×1024 pixels using bicubic interpolation. This specific size was chosen after extensive testing to balance frequency content preservation with computational efficiency. The resizing process employs adaptive interpolation: high-quality bicubic interpolation for upscaling and medium-quality for downscaling. This ensures that frequency characteristics are maintained while standardizing input dimensions for consistent block processing.

The 1024×1024 resolution provides optimal properties for our 8×8 block decomposition strategy, resulting in exactly 128×128 blocks (16,384 total blocks) without fractional remainders. This integer division simplifies implementation and ensures complete coverage of the image space.

3.1.3 Contrast Enhancement

Adaptive histogram equalization is applied to improve feature visibility while preserving frequency characteristics.

3.2 Block-Based Decomposition Strategy

The preprocessed image is divided into non-overlapping 8×8 pixel blocks, creating a grid of 128×128 blocks. This block size was selected based on extensive empirical analysis showing optimal balance between:

- Computational efficiency (smaller blocks require more computations)
- Feature discrimination capability (larger blocks may lose local details)
- Frequency resolution requirements

Each block undergoes intensity normalization to eliminate illumination variations:

$$B_{norm}(x, y) = \frac{B(x, y) - \mu}{\sigma + \epsilon} \tag{2}$$

where μ is the block mean, σ is the standard deviation, and $\epsilon = 10^{-10}$ prevents division by zero.

3.3 Frequency Domain Analysis

For each normalized block, we compute the 2D Fast Fourier Transform using an optimized implementation:

$$F(u, v) = \sum_{x=0}^{7} \sum_{y=0}^{7} B_{norm}(x, y) \cdot e^{-j2\pi(ux/8+vy/8)} \tag{3}$$

The frequency spectrum is shifted to center the zero-frequency component using quadrant swapping, and the magnitude spectrum is calculated:

$$M(u, v) = \sqrt{\mathrm{Re}(F(u, v))^2 + \mathrm{Im}(F(u, v))^2} \tag{4}$$

A logarithmic transform enhances feature discrimination while maintaining numerical stability:

$$L(u, v) = \log(1 + M(u, v)) \tag{5}$$

3.4 Frequency Band Separation and Energy Calculation

The frequency domain is partitioned into three concentric bands based on radial distance from the center $(3.5, 3.5)$:

- Low frequency (0-2 units): Structural information
- Mid frequency (2-3.2 units): Transitional features
- High frequency (>3.2 units): Textural details

The radial distance is computed as:

$$d = \sqrt{(u - 3.5)^2 + (v - 3.5)^2} \tag{6}$$

Energy values for each band are computed as weighted averages:

$$E_{band} = \frac{\sum_{(u,v)\in band} w(u, v) \cdot L(u, v)}{\sum w(u, v)} \tag{7}$$

where weights $w(u, v)$ emphasize regions with higher discriminative power.

3.5 Spatial Hashing with Directional Context

The hashing mechanism creates unique signatures by combining spectral features with spatial context. For each block at position (i, j), we consider its 8-connected neighbors and generate hash strings using the format:

$$\text{Hash} = E_h^i.E_l^i.E_h^k.E_l^k.\phi(k) \tag{8}$$

where:

- E_h^i, E_l^i: Current block's high and low frequency energies
- E_h^k, E_l^k: Neighbor block's spectral energies
- $\phi(k)$: Directional encoding (0: top, 1: bottom, 2: left, 4: right)

The directional encoding follows a specific numbering scheme that enables efficient storage and comparison while maintaining spatial relationship information.

3.6 Database Construction with Normal Bias

The database is constructed with intentional emphasis on normal anatomical patterns using a 3:1 ratio of normal to pathological images. This strategy is based on extensive empirical testing showing that approximately 80 normal and 60 abnormal images provide optimal performance, with diminishing returns beyond 100 images per category.

This normal-biased approach addresses a critical observation: normal anatomical structures (ribs, cardiac borders, diaphragm) exhibit consistent patterns across patients, while pathological manifestations are relatively rare and diverse in appearance. If trained with equal representation, normal anatomical features might be incorrectly classified as pathological indicators.

Hash patterns with three or more zeros in the first four energy values are excluded from the database, as these typically represent pure black patches or imaging artifacts that provide no diagnostic value. Each hash pattern stores occurrence statistics:

$$\text{HashDB}[h] = (N_h, P_h) \tag{9}$$

where N_h is normal occurrences, P_h is pathological occurrences.

3.7 Conservative Thresholding Strategy

The classification threshold was carefully designed to minimize false positives while maintaining sensitivity:

$$\text{Classify as pathological if: } \frac{N_h}{P_h} \leq 0.9 \tag{10}$$

This 0.9 threshold addresses several practical challenges:

- **Novel anatomical variations**: Accounts for unseen normal variations
- **Imaging artifacts**: Reduces sensitivity to equipment-specific artifacts
- uncertainty: Provides buffer for small sample sizes

The threshold ensures that only patterns with strong statistical evidence of pathology are classified as abnormal.

3.8 Cluster-Based Scoring Mechanism

Suspicious blocks are aggregated into connected components using 8-connectivity. Each cluster is evaluated using a comprehensive scoring function:

$$\text{Score} = \frac{\text{size} \times 0.4}{\text{distance} \times 0.6} \times 100 \tag{11}$$

where:

- **size**: Number of connected pathological blocks (weight: 0.4)
- **distance**: Euclidean distance from cluster centroid to image center (weight: 0.6)

The weighting factors reflect clinical priorities:

- Size weight (0.4): Emphasizes that pulmonary abnormalities typically present as consolidated areas
- Distance weight (0.6): Reflects that pathological findings are more likely in central lung regions

3.9 Final Decision Framework

The final classification combines cluster scores with additional validation checks:

$$\text{Final Decision} = \begin{cases} \text{Abnormal} & \text{if } \sum \text{Scores} > 1200 \\ \text{Normal} & \text{otherwise} \end{cases} \tag{12}$$

Consistency checks include spatial distribution analysis and pattern verification. The threshold of 1200 was determined through extensive cross-validation on multiple datasets.

4 Experimental Setup

4.1 Datasets and Evaluation Metrics

We evaluated our method on three distinct datasets using tuberculosis as the validation pathology due to data availability:

- **PNG Dataset**: 400 high-quality PNG images
- **Mixed Format Dataset**: 583 images with varying formats
- **JPEG Dataset**: 872 JPEG compressed images

The dataset construction followed a deliberate strategy: approximately 80 normal and 60 abnormal images formed the core training set, with additional images used for validation. This ratio proved optimal for capturing normal anatomical variability while maintaining sufficient pathological examples.

Performance was assessed using standard metrics:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{13}$$

$$\text{Sensitivity} = \frac{TP}{TP + FN} \tag{14}$$

$$\text{Specificity} = \frac{TN}{TN + FP} \tag{15}$$

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{16}$$

4.2 Parameter Optimization

Key parameters were optimized through grid search and cross-validation:

- Block size: 8×8 pixels (optimal for frequency resolution)
- Frequency bands: 3 bands (low, mid, high)
- Binning accuracy: 2 units
- Cluster threshold: 7 connected blocks
- Classification threshold: 1200

4.3 Computational Performance

The system was implemented in JavaScript with optimized FFT algorithms and achieves an average processing time of 4 seconds per image on standard hardware (Intel i7 processor, 16GB RAM). Processing times range from 2-8 seconds depending on image complexity and size. The algorithm's efficiency makes it suitable for real-time applications in resource-constrained environments.

5 Results and Analysis

TABLE 1
Comprehensive performance analysis (Tuberculosis validation)

Format	Accuracy	Sensitivity	Specificity	F1 Score
PNG (400 images)	95.0%	94.2%	95.7%	94.8%
Mixed (583 images)	93.13%	91.5%	94.3%	92.4%
JPEG (872 images)	90.2%	85.0%	95.0%	88.2%

TABLE 2
Detailed error analysis (Tuberculosis validation)

Format	False Positive	False Negative	Precision	NPV
PNG	2.0%	5.0%	96.8%	94.2%
Mixed	5.71%	8.5%	92.1%	90.3%
JPEG	2.0%	15.0%	95.2%	82.4%

The results demonstrate consistent performance across image formats, with PNG images achieving the highest accuracy (95.0%) due to their lossless compression. JPEG images show slightly reduced sensitivity (85.0%) due to compression artifacts, but maintain high specificity (95.0%). The conservative thresholding strategy effectively minimizes false positives across all formats.

While these results specifically validate the method for tuberculosis detection, the underlying methodology is designed for general pulmonary abnormality detection, with tuberculosis serving as a representative pathology due to data availability.

6 Conclusion and Future Work

This paper presented a comprehensive FFT-based methodology for pulmonary abnormality detection in chest radiographs, validated using tuberculosis detection as a representative use case. The detailed technical explanations provide a complete implementation framework while maintaining academic rigor.

Key contributions include:

- Detailed frequency domain analysis methodology with optimized implementation
- Novel spatial hashing with directional context encoding
- Conservative thresholding strategy for false positive reduction
- Comprehensive cluster scoring mechanism incorporating spatial distribution
- Extensive experimental validation across multiple datasets and formats
- Efficient implementation with average processing time of 4 seconds per image
- General-purpose framework validated on tuberculosis but extensible to other pulmonary conditions

Future work will focus on:

- Extension to multi-class classification of various pulmonary diseases
- Integration with machine learning approaches for hybrid classification
- Application to other pulmonary conditions beyond tuberculosis

The methodology provides a solid foundation for implementing efficient pulmonary abnormality screening systems in resource-constrained environments, with demonstrated effectiveness for tuberculosis detection and potential for broader application in medical image analysis.

References

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