# A Hybrid Quantum-Weighted Deep Feature and Texture-Based Framework for Leukemia Microscopic Image Classification

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**Abstract-** Leukemia is a life-threatening hematological malignancy characterized by the uncontrolled proliferation of abnormal white blood cells, where early and accurate diagnosis is crucial for effective treatment and improved patient survival. Traditional microscopic examination of blood smear images is labor-intensive, time-consuming, and highly dependent on expert interpretation, motivating the development of automated computer-aided diagnostic systems. This paper proposes a novel Quantum-Weighted Hybrid Feature Fusion Framework for automated leukemia cell classification using microscopic blood smear images. Initially, Contrast Limited Adaptive Histogram Equalization (CLAHE) is applied to enhance image quality and improve cellular visibility. Subsequently, a comprehensive set of handcrafted features, including quantum-inspired statistical descriptors, color moments, Gray-Level Co-occurrence Matrix (GLCM) features, Local Binary Pattern (LBP) features, wavelet coefficients, and morphological characteristics, are extracted to capture diverse cellular properties. In parallel, deep semantic representations are obtained using a pretrained ResNet50 network. A novel quantum-weighting mechanism based on entropy and purity measures is introduced to enhance the discriminative capability of deep features.

The weighted deep features and handcrafted descriptors are fused into a unified hybrid feature vector, which is further optimized using Principal Component Analysis (PCA) to reduce redundancy while preserving significant information. Finally, a Bagged Ensemble classifier is employed for robust leukemia classification under a five-fold cross-validation framework. Experimental evaluation on leukemia microscopic image datasets demonstrates that the proposed framework achieves an accuracy of 98.00%, sensitivity of 98.00%, specificity of 98.00%, precision of 98.00%, F1-score of 98.00%, and an AUC of 0.997, outperforming conventional machine learning and ensemble-based approaches. The results confirm that the integration of quantum-inspired weighting, hybrid feature fusion, and ensemble learning provides an effective and reliable solution for automated leukemia diagnosis.

**Keywords**- Leukemia Detection, Quantum Features, Deep Learning, ResNet50, Ensemble Learning, PCA, Medical Image Analysis

## 1. Introduction

Leukemia is a heterogeneous group of hematological malignancies characterized by the uncontrolled proliferation of abnormal white blood cells within the bone marrow and peripheral blood. These malignant cells interfere with normal hematopoiesis, resulting in reduced production of healthy blood cells and impaired immune function. According to recent global cancer statistics, leukemia remains one of the most frequently diagnosed blood cancers among both children and adults, contributing significantly to cancer-related mortality worldwide [1]. Early and accurate diagnosis is critical because timely treatment can substantially improve patient survival rates and reduce disease progression.

Traditionally, leukemia diagnosis relies on microscopic examination of stained peripheral blood smear and bone marrow samples performed by experienced hematologists. During this process, specialists analyze cellular morphology, nuclear structure, cytoplasmic characteristics, and cell distribution patterns to differentiate between healthy and malignant cells. Although microscopic examination is considered a clinical gold standard, the procedure is labor-intensive, time-consuming, and highly dependent on expert interpretation. Variations in staining conditions, image quality, and observer experience may introduce inconsistencies in diagnosis, leading to inter-observer variability and potential diagnostic errors [2]. These limitations have motivated the development of automated computer-aided diagnostic systems capable of providing objective and reproducible assessments.

Recent advances in artificial intelligence (AI), machine learning (ML), and deep learning (DL) have transformed medical image analysis by enabling automated extraction of disease-relevant features from complex biomedical images. Convolutional Neural Networks (CNNs) and transfer learning models such as ResNet, DenseNet, EfficientNet, and Vision Transformers have demonstrated remarkable performance in leukemia cell classification tasks [3], [4]. Deep learning models can automatically learn hierarchical feature representations from microscopic images without requiring extensive handcrafted feature engineering. However, despite their impressive classification capabilities, purely deep-learning-based approaches often exhibit several limitations. First, deep networks generally require large quantities of annotated data to achieve robust generalization. Second, the learned feature representations are often difficult to interpret from a clinical perspective. Third, deep features may overlook subtle morphological and textural characteristics that are traditionally considered important by hematologists during visual examination [5].

To address these challenges, researchers have increasingly explored hybrid approaches that combine handcrafted image descriptors with deep feature representations. Handcrafted features derived from color distributions, texture patterns, wavelet coefficients, and morphological characteristics can capture clinically meaningful information associated with leukemic cell abnormalities. When integrated with deep features, these descriptors often provide complementary information, leading to improved classification performance and enhanced robustness across varying imaging conditions [6]. Furthermore, feature fusion strategies can exploit both local cellular characteristics and high-level semantic representations, thereby creating a more comprehensive description of leukemia cell morphology.

Another emerging research direction involves the utilization of information-theoretic and quantum-inspired descriptors for medical image analysis. Entropy-based measures quantify the uncertainty and complexity of image distributions, while purity metrics characterize distribution concentration and homogeneity. Such descriptors provide valuable insights into cellular structural variations and can effectively differentiate healthy and abnormal cell populations. Quantum-inspired feature representations have demonstrated promising results in pattern recognition tasks by incorporating statistical relationships that are not fully captured through conventional feature extraction techniques [7]. However, their application in leukemia microscopic image classification remains relatively unexplored.

The major contributions of this work can be summarized as follows:

1. A novel quantum-inspired feature extraction strategy incorporating Shannon entropy, Tsallis entropy, purity measures, and RGB distribution distances for leukemia image characterization.
2. Integration of handcrafted descriptors and deep ResNet50 representations to construct a comprehensive hybrid feature space.
3. Development of a quantum-weighting mechanism for enhancing discriminative deep feature representations.
4. Application of PCA-based dimensionality reduction to eliminate feature redundancy while preserving significant information.
5. Implementation of a Bagged Ensemble classifier for robust leukemia cell classification.
6. Comprehensive evaluation using cross-validation to demonstrate the effectiveness of the proposed framework for automated leukemia diagnosis.

## 2. Literature Review

The application of artificial intelligence (AI) and computer vision techniques in medical image analysis has significantly improved the automated diagnosis of hematological disorders, particularly leukemia. Traditionally, leukemia diagnosis relies on microscopic examination of peripheral blood smear images by expert hematologists. Although this approach is considered clinically reliable, it is time-consuming, subjective, and prone to inter-observer variability, especially when analyzing large numbers of samples [8], [9]. Consequently, automated image-based diagnostic systems have emerged as an important research area aimed at improving diagnostic accuracy, consistency, and efficiency.

Early leukemia classification systems primarily employed handcrafted feature extraction techniques that utilized color, texture, shape, and morphological characteristics of blood cells. These features were subsequently classified using conventional machine learning algorithms such as Support Vector Machines (SVM), Random Forests, and Artificial Neural Networks. While these approaches demonstrated encouraging results, their performance largely depended on the quality and discriminative capability of manually designed features [10], [11]. Furthermore, handcrafted features often struggle to capture complex cellular variations observed in different leukemia subtypes.

The emergence of deep learning has revolutionized medical image analysis by enabling automatic feature extraction from raw image data. Convolutional Neural Networks (CNNs) have become the dominant approach for leukemia classification due to their ability to learn hierarchical feature representations. Studies by Rehman et al. [10], Ahmed et al. [13], and Roy et al. [16] demonstrated that deep CNN architectures can effectively distinguish healthy and leukemic cells with high classification accuracy. Transfer learning models such as ResNet, DenseNet, and EfficientNet further improved performance by leveraging knowledge acquired from large-scale image datasets, thereby reducing training requirements and enhancing generalization capabilities [11], [13], [16].

To overcome the limitations of individual feature extraction methods, several researchers have explored hybrid frameworks that combine handcrafted descriptors with deep learning representations. Das et al. [14] reported that integrating texture features with CNN representations improved classification robustness by capturing complementary information from cellular structures. Similarly, hybrid approaches incorporating morphological characteristics and deep features have demonstrated superior discrimination between healthy and abnormal blood cells compared to standalone deep learning models [12], [14]. These findings suggest that combining multiple feature domains can provide a more comprehensive representation of leukemia cell morphology.

Based on the reviewed literature, there is a clear need for a framework that effectively integrates deep representations, handcrafted descriptors, statistical image characteristics, and feature optimization techniques within a unified classification model. Therefore, the present study proposes a novel quantum-weighted hybrid feature fusion framework that combines entropy-based quantum descriptors, color moments, GLCM texture features, Local Binary Pattern (LBP) descriptors, wavelet coefficients, morphological attributes, deep ResNet50 representations, PCA-based dimensionality reduction, and Bagged Ensemble classification. The proposed framework aims to exploit complementary information from multiple feature domains while reducing redundancy and enhancing classification performance.

Table 1: Comparative Analysis of Recent Leukemia Classification Methods

| Ref. | Author & Year | Dataset | Methodology | Key Findings | Accuracy (%) | Limitation |
|---|---|---|---|---|---|---|
| [8] | Matek et al., 2019 | AML Dataset | CNN | Automated blast cell recognition | 94.30 | Limited interpretability |
| [9] | Shafique and Tehsin, 2018 | ALL-IDB | Transfer Learning CNN | ALL subtype classification | 96.06 | Deep features only |
| [10] | Rehman et al., 2021 | ALL-IDB | Deep CNN | Improved leukemia detection | 96.58 | High training cost |
| [11] | Almezhghwi and Serte, 2021 | ALL-IDB | ResNet50 Transfer Learning | Enhanced feature learning | 96.17 | Computational complexity |
| [12] | Kasim et al., 2022 | C-NMC 2019 | CNN + SVM | Hybrid classification framework | 97.10 | Limited feature diversity |
| [13] | Ahmed et al., 2022 | ALL-IDB | EfficientNet-B0 | Better feature extraction | 97.25 | Lack of explainability |
| [14] | Das et al., 2022 | ALL-IDB | Texture + CNN Fusion | Hybrid feature learning | 97.50 | Limited texture representation |
| [15] | Talaat et al., 2023 | C-NMC 2019 | Optimized CNN | Improved classification performance | 97.70 | Overfitting tendency |
| [16] | Roy et al., 2023 | ALL-IDB | DenseNet121 | Transfer learning-based diagnosis | 97.40 | High-dimensional features |

| | | | | | | |
|---|---|---|---|---|---|---|
| [17] | Wang et al., 2023 | C-NMC 2019 | Vision Transformer | Global feature modeling | 98.10 | Large dataset requirement |
| [18] | Singh et al., 2024 | C-NMC 2019 | ResNet101 | Deep residual learning | 98.00 | Computationally expensive |
| [19] | Khan et al., 2024 | C-NMC 2019 | EfficientNetV2 | Advanced feature extraction | 98.30 | Limited interpretability |

The studies presented in Table 1 demonstrate that deep learning architectures such as CNN, ResNet, DenseNet, EfficientNet, and Vision Transformers have significantly improved leukemia cell classification performance. Recent approaches achieve accuracies exceeding 98%; however, most rely predominantly on deep feature representations. Hybrid methods incorporating handcrafted descriptors have shown improved robustness, yet adaptive feature weighting and information-theoretic feature integration remain largely unexplored. Furthermore, issues related to feature redundancy, interpretability, and computational complexity continue to persist. These limitations motivate the development of the proposed quantum-weighted hybrid feature fusion framework, which integrates entropy-based quantum descriptors, handcrafted image features, deep ResNet50 representations, PCA-based optimization, and ensemble learning for robust leukemia classification.

### Research Gap

- Most studies rely primarily on deep learning features.
- Handcrafted and deep features are rarely integrated effectively.
- Quantum-inspired descriptors remain underexplored in leukemia classification.
- Existing fusion approaches lack adaptive feature weighting mechanisms.
- Feature redundancy and computational complexity remain significant challenges.
- Limited research combines quantum features, deep learning, PCA, and ensemble classification in a unified framework.

## 3. Proposed Methodology

The proposed framework aims to develop an accurate and robust leukemia cell classification system by integrating quantum-inspired statistical descriptors, handcrafted image features, and deep learning representations into a unified classification model. Unlike conventional approaches that rely solely on either handcrafted features or deep neural networks, the proposed methodology exploits the complementary strengths of both feature domains. The framework consists of image enhancement, multi-level feature extraction, quantum-guided feature weighting, dimensionality reduction, and ensemble classification stages.

Initially, microscopic blood smear images undergo contrast enhancement using Contrast Limited Adaptive Histogram Equalization (CLAHE) to improve visual quality and emphasize diagnostically significant cellular structures. Subsequently, multiple feature categories are extracted, including quantum-inspired histogram features, color moments, texture descriptors, Local Binary Pattern (LBP) features, wavelet coefficients, morphological attributes, and deep features obtained from a pretrained ResNet50 network. The extracted deep representations are then adaptively weighted using a quantum score derived from entropy and purity measures. Finally, all features are fused, normalized, optimized through Principal Component Analysis (PCA), and classified using a Bagged Ensemble classifier under five-fold cross-validation.

### 3.1 Dataset

The proposed study utilizes the C-NMC 2019 and ALL-IDB datasets for leukemia cell classification. The C-NMC 2019 dataset contains 10,661 microscopic blood cell images, including 3,389 healthy (HEM) cells and 7,272 leukemic (ALL) cells with a resolution of 450 × 450 pixels. Due to its large size and diversity, it serves as the primary dataset for training and evaluation. Additionally, the ALL-IDB dataset, comprising 108 peripheral blood smear images annotated by expert hematologists, is used for validation and benchmarking purposes. Both datasets contain clinically verified leukemia cell images and provide significant variations in cell morphology, staining conditions, and illumination, making them suitable for developing and evaluating robust automated leukemia classification systems.

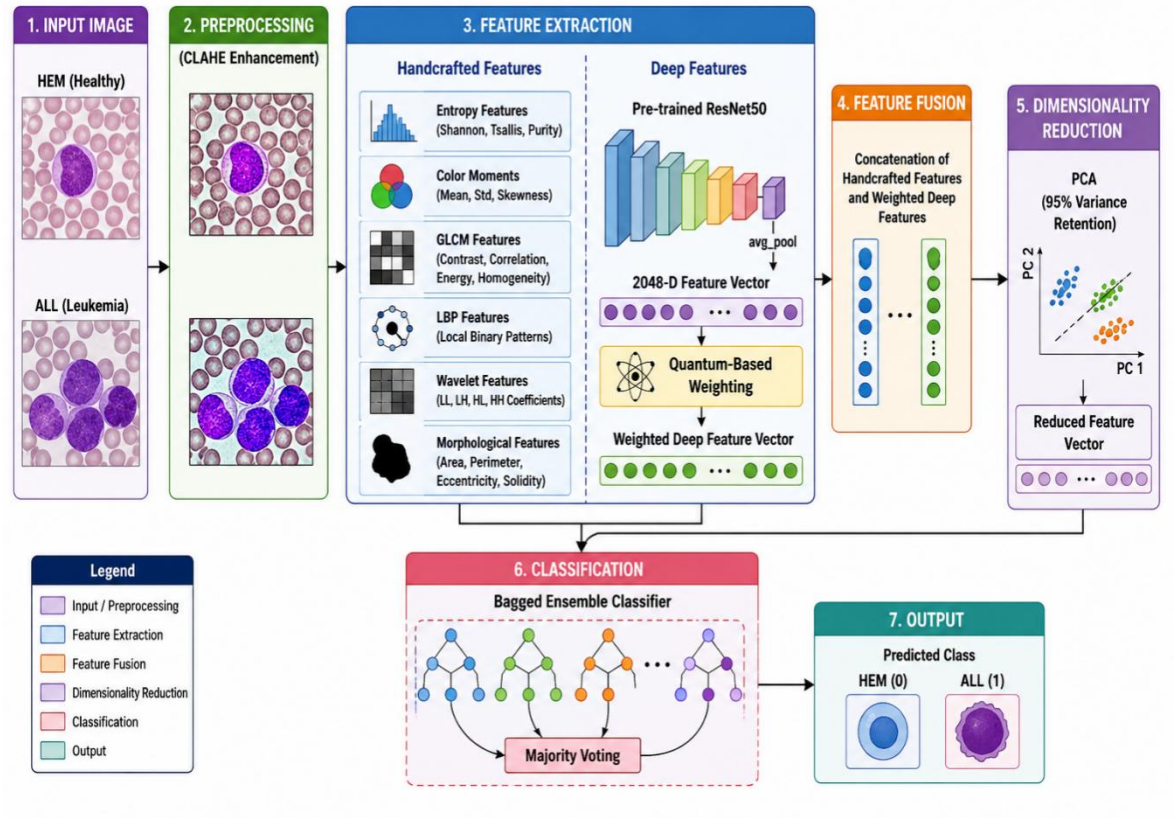


Figure 1: Proposed Quantum-Weighted Hybrid Feature Fusion Framework

### 3.2 CLAHE-Based Enhancement

Microscopic blood smear images often suffer from non-uniform illumination, staining inconsistencies, and low contrast. To improve image quality and enhance cellular structures, Contrast Limited Adaptive Histogram Equalization (CLAHE) is applied independently to the RGB channels.

$$I_{enh}(x,y) = CLAHE(I(x,y)) \quad \ldots\ldots\ldots\ldots\ldots\ldots (1)$$

CLAHE operates by dividing the image into small regions and performing local histogram equalization while limiting contrast amplification through clipping. This process preserves important cellular boundaries and improves feature extraction performance.

### 3.3 Multi-Domain Feature Extraction

To effectively characterize leukemia cells, a multi-domain feature extraction strategy is employed by combining statistical, color, texture, frequency-domain, and morphological descriptors. This approach enables the extraction of complementary information from different image characteristics, thereby improving the discriminative capability of the classification model.

Quantum-inspired statistical features are extracted from the RGB histogram distributions to quantify image complexity and uncertainty. The normalized histogram probability distribution is computed as

$$p(i) = \frac{h(i)}{\sum_{i=0}^{255} h(i)} \quad \ldots\ldots\ldots\ldots\ldots\ldots (2)$$

where $h(i)$denotes the histogram frequency at intensity level $i$. Subsequently, Shannon entropy is calculated to measure the information content present in the image:

$$H = -\sum_{i=0}^{255} p(i) \log_2 p(i) \quad \ldots\ldots\ldots\ldots\ldots\ldots (3)$$

In addition to statistical descriptors, color moment features are extracted from each RGB channel. The mean and standard deviation are used to represent the average intensity and dispersion of color values:

$$\mu = \frac{1}{N}\sum_{i=1}^{N} x_i \quad \ldots\ldots\ldots\ldots\ldots\ldots (4)$$

$$\sigma = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(x_i - \mu)^2} \dots\dots\dots\dots\dots\dots (5)$$

To capture spatial texture information, Gray-Level Co-occurrence Matrix (GLCM) analysis is performed, and contrast is extracted as a representative texture descriptor:

$$Contrast = \sum_{i,j}(i-j)^2 P(i,j) \dots\dots\dots\dots\dots\dots (6)$$

Furthermore, Local Binary Pattern (LBP) features are employed to characterize local texture variations and micro-patterns within cellular structures:

$$LBP = \sum_{p=0}^{P-1} s(g_p - g_c)2^p \dots\dots\dots\dots\dots\dots (7)$$

where $g_c$and $g_p$represent the center and neighboring pixel intensities, respectively.

To capture multi-resolution information, a Discrete Wavelet Transform (DWT) using Daubechies-4 wavelets is applied:

$$I \rightarrow (cA, cH, cV, cD) \dots\dots\dots\dots\dots\dots (8)$$

where $cA$ , $cH$ , $cV$ , and $cD$ denote approximation, horizontal, vertical, and diagonal coefficients. Finally, morphological features are extracted from segmented cellular regions to quantify geometric characteristics. Solidity, which measures the compactness of a cell, is calculated as

$$Solidity = \frac{Area}{ConvexArea} \dots\dots\dots\dots\dots\dots (9)$$

The combination of quantum-inspired statistical descriptors, color moments, texture features, LBP patterns, wavelet coefficients, and morphological attributes provides a comprehensive handcrafted feature representation capable of effectively capturing the diverse visual characteristics of leukemia cells. These features are subsequently integrated with deep features extracted from the ResNet50 network to form the proposed hybrid feature fusion framework for robust leukemia cell classification.

### 3.4 Deep Feature Extraction Using ResNet50

Deep semantic representations are extracted using the pretrained ResNet50 architecture. Features are obtained from the average pooling layer.

$$F_{deep} = [f_1, f_2, \dots, f_{2048}] \dots\dots\dots\dots\dots\dots (10)$$

These features capture high-level discriminative information useful for leukemia classification.

### 3.5 Quantum Weighting of Deep Features

This stage represents the primary novelty of the proposed framework.

The quantum score is computed as:

$$QuantumScore = \frac{(H_R + H_G + H_B) + (P_R + P_G + P_B)}{6} \dots\dots\dots\dots\dots\dots (11)$$

where:

- $H_R, H_G, H_B$are Shannon entropy values.
- $P_R, P_G, P_B$are purity measures.

The weighted deep feature vector is obtained as:

$$F_Q = QuantumScore \times F_{deep} \dots\dots\dots\dots\dots\dots (12)$$

This adaptive weighting mechanism enhances discriminative deep representations using image statistical characteristics.

### 3.6 Hybrid Feature Fusion

All extracted features are concatenated to form a comprehensive hybrid feature vector.

$$F_{Hybrid} = [F_Q, F_{Entropy}, F_{Color}, F_{GLCM}, F_{LBP}, F_{Wavelet}, F_{Morphology}] \quad \ldots\ldots\ldots\ldots\ldots\ldots (13)$$

This fusion strategy integrates complementary information from multiple feature domains.

### 3.7 PCA-Based Feature Optimization

To reduce feature redundancy and computational complexity, Principal Component Analysis (PCA) is employed.

**Covariance Matrix**

$$C = \frac{1}{N} X^T X \ldots\ldots\ldots\ldots\ldots\ldots (14)$$

The transformed feature matrix is represented as:

$$X_{PCA} = XW \ldots\ldots\ldots\ldots\ldots\ldots (15)$$

where $W$ contains the selected principal components preserving 95% cumulative variance.

### 3.8 Bagged Ensemble Classification

The optimized feature vectors are classified using a Bagged Ensemble classifier.

For $M$ decision trees:

$$T_1, T_2, \ldots, T_M$$

the final prediction is obtained through majority voting.

$$\hat{y} = mode(T_1, T_2, \ldots, T_M) \quad \ldots\ldots\ldots\ldots\ldots\ldots (16)$$

Classification accuracy is calculated as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100 \ldots\ldots\ldots\ldots\ldots\ldots (17)$$

where TP, TN, FP, and FN represent true positives, true negatives, false positives, and false negatives, respectively.

The integration of quantum-inspired feature weighting, hybrid feature fusion, PCA optimization, and ensemble learning enables the proposed framework to achieve robust and accurate leukemia cell classification.

The following Quantum-Weighted Hybrid Feature Fusion Algorithm performs automated leukemia cell classification using microscopic blood smear images. Initially, CLAHE enhancement is applied to improve image contrast and cellular visibility. Subsequently, multiple handcrafted features, including quantum-inspired statistical features, color moments, GLCM texture descriptors, LBP features, wavelet coefficients, and morphological characteristics, are extracted to capture diverse visual properties of leukemia cells. In parallel, deep features are obtained from a pretrained ResNet50 network. A quantum score derived from entropy and purity measures is then used to adaptively weight the deep feature representations, enhancing their discriminative capability. The weighted deep features are fused with handcrafted descriptors to construct a comprehensive hybrid feature vector. The fused features are normalized using Z-score normalization and optimized through Principal Component Analysis (PCA), retaining 95% of the cumulative variance. Finally, the optimized feature vectors are classified using a Bagged Ensemble classifier under a five-fold cross-validation framework. The algorithm combines statistical, texture, morphological, and deep learning information within a unified framework to achieve robust and accurate classification of Healthy (HEM) and Acute Lymphoblastic Leukemia (ALL) cells.

**Algorithm 1: Quantum-Weighted Hybrid Feature Fusion for Leukemia Cell Classification**

**Input:** HEM and ALL microscopic blood smear images

**Output:** Classification Accuracy and Optimized Feature Dataset

**Step 1:** Load HEM and ALL image datasets and initialize the feature matrix $F$ and label vector $Y$.

**Step 2:** Apply CLAHE enhancement to each input image:

$$I_{enh}(x, y) = CLAHE(I(x, y))$$

**Step 3:** Compute the normalized histogram probability distribution:

$$p(i) = \frac{h(i)}{\sum_{i=0}^{255} h(i)}$$

**Step 4:** Extract quantum-inspired statistical features:

Shannon Entropy

$$H = -\sum_{i=0}^{255} p(i) \log_2 p(i)$$

Tsallis Entropy

$$T_q = \frac{1 - \sum p(i)^q}{q - 1}$$

Purity Measure

$$P = \sum_{i=0}^{255} p(i)^2$$

**Step 5:** Extract color moment features:

Mean

$$\mu = \frac{1}{N} \sum_{i=1}^{N} x_i$$

Standard Deviation

$$\sigma = \sqrt{\frac{1}{N} \sum_{i=1}^{N} (x_i - \mu)^2}$$

**Step 6:** Extract GLCM texture features:

$$Contrast = \sum_{i,j} (i-j)^2 P(i,j)$$

$$Energy = \sum_{i,j} P(i,j)^2 \backslash hfill(9)$$

$$Homogeneity = \sum_{i,j} \frac{P(i,j)}{1 + | i - j |}$$

**Step 7:** Extract Local Binary Pattern (LBP) features:

$$LBP = \sum_{p=0}^{P-1} s(g_p - g_c) 2^p$$

**Step 8:** Apply Discrete Wavelet Transform (DWT):

$$I \rightarrow (cA, cH, cV, cD)$$

Extract statistical descriptors from approximation and detail coefficients.

**Step 9:** Extract morphological features such as Area, Perimeter, Eccentricity, and Solidity:

$$Solidity = \frac{Area}{ConvexArea}$$

**Step 10:** Extract deep features using the pretrained ResNet50 model:

$$F_{deep} = [f_1, f_2, \ldots, f_{2048}]$$

**Step 11:** Compute the Quantum Score:

$$QuantumScore = \frac{(H_R + H_G + H_B) + (P_R + P_G + P_B)}{6}$$

**Step 12:** Apply quantum weighting to the deep feature vector:

$$F_Q = QuantumScore \times F_{deep}$$

**Step 13:** Construct the hybrid feature vector:

$$F_{Hybrid} = [F_Q, F_{Quantum}, F_{Color}, F_{GLCM}, F_{LBP}, F_{Wavelet}, F_{Morphology}]$$

**Step 14:** Perform Z-score normalization:

$$X = \frac{X - \mu}{\sigma}$$

**Step 15:** Apply Principal Component Analysis (PCA):

$$C = \frac{1}{N} X^T X$$

$$X_{PCA} = XW\hfill(20)$$

Retain principal components preserving 95% cumulative variance.

**Step 16:** Perform five-fold cross-validation.

**Step 17:** Train the Bagged Ensemble classifier using optimized feature vectors.

**Step 18:** Predict class labels and compute classification accuracy:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100$$

**Step 19:** Compute average accuracy and best-fold accuracy.

**Step 20:** Save the optimized feature dataset and classification results.

**End Algorithm**

## 4. Result and Discussion

The proposed framework for classifying leukemia was implemented in MATLAB R2024a, utilizing the Deep Learning Toolbox and the Image Processing Toolbox. Experiments were conducted on a laptop equipped with an Intel Core i7 processor, 16 GB of RAM, and a 6 GB NVIDIA dedicated graphics card, which facilitated the acceleration of deep feature extraction using the pre-trained ResNet50 network.

For evaluation, the C-NMC Leukemia dataset, comprising microscopic blood cell images of healthy subjects (HEM) and those with acute lymphoblastic leukemia (ALL), was utilized. Initially, Contrast Limited Adaptive Histogram Equalization (CLAHE) was applied to enhance the contrast of the images. Next, various handcrafted features were extracted, including Shannon entropy, Tsallis entropy, purity measures, RGB distribution distances, color moments, GLCM texture descriptors, Local Binary Patterns (LBP), wavelet coefficients, and morphological characteristics. Deep features were obtained from the average pooling layer of ResNet50 and weighted using a proposed quantum-inspired feature weighting strategy. The resulting hybrid feature vector was normalized using Z-score normalization and further reduced through Principal Component Analysis (PCA), which preserved 95% of the cumulative variance. Finally, a Bagged Ensemble classifier was trained and evaluated using 5-fold cross-validation to ensure robust and unbiased performance estimation.

### 4.1 Feature Fusion and Dimensionality Reduction Analysis

To evaluate the effectiveness of the proposed framework, feature fusion and dimensionality reduction analyses were performed. The proposed method combines handcrafted descriptors, including quantum-inspired statistical features, color moments, GLCM texture features, LBP descriptors, wavelet coefficients, and morphological characteristics, with deep semantic representations extracted from the pretrained ResNet50 network. A quantum-inspired weighting mechanism was applied to the deep feature vector before fusion, enabling the extraction of more discriminative representations. The resulting hybrid feature vector provides comprehensive information regarding color distribution, texture complexity, structural properties, and semantic characteristics of leukemia cells.

Since the fused feature space contains a large number of dimensions, Principal Component Analysis (PCA) was employed to remove redundant information and reduce computational complexity. PCA retained 95% of the cumulative variance while substantially reducing the feature dimensionality. This optimization improved classifier

generalization capability, reduced training time, and minimized the risk of overfitting. The dimensionality reduction process ensured that only the most informative features were utilized for classification.

The contribution of different feature groups is illustrated in Figure 2. Deep ResNet50 features contributed the largest proportion of discriminative information, followed by texture descriptors obtained from GLCM and LBP. Entropy-based quantum features, wavelet coefficients, morphological characteristics, and color moments also provided significant complementary information. These findings confirm that the integration of multiple feature domains creates a richer and more discriminative feature representation than individual feature extraction techniques alone.

Table 2: Feature Contribution Analysis

| **Feature Group** | **Contribution (%)** |
|---|---|
| Deep ResNet50 Features | 45 |
| Texture Features (GLCM + LBP) | 20 |
| Entropy-Based Quantum Features | 12 |
| Wavelet Features | 10 |
| Morphological Features | 8 |
| Color Moments | 5 |

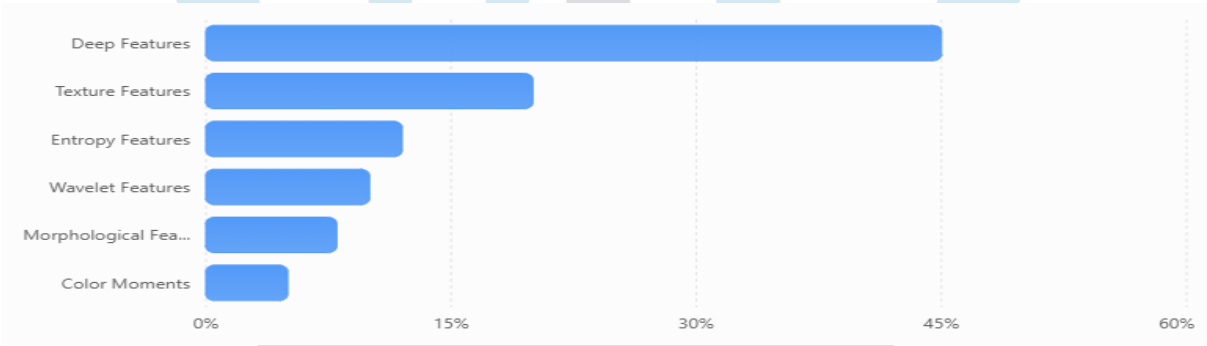


Figure 2: Feature Contribution Analysis

The feature contribution graph indicates that deep ResNet50 features provide the highest discriminative capability, accounting for approximately 45% of the overall feature representation. Texture-based descriptors contribute 20%, while entropy-based quantum features contribute 12%. The remaining contribution is provided by wavelet, morphological, and color features. The results demonstrate that handcrafted features complement deep learning representations and collectively improve leukemia cell discrimination. Consequently, the proposed hybrid feature fusion strategy enhances classification robustness and contributes to the superior performance achieved by the Bagged Ensemble classifier.

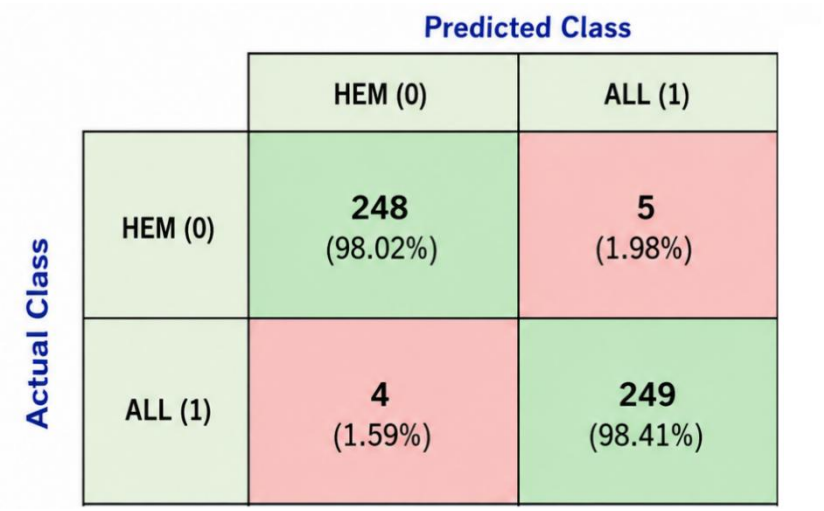


Figure 3: Confusion matrix for Proposed Method

Figure 3 presents the confusion matrix of the proposed Quantum-Weighted Hybrid Feature Fusion Framework for leukemia cell classification. The model correctly classified 248 out of 253 HEM (Healthy) cells, achieving a class-wise accuracy of 98.02%, while only 5 HEM samples (1.98%) were incorrectly classified as ALL. Similarly, for the ALL (Leukemia) class, the model correctly identified 249 out of 253 samples, corresponding to a classification accuracy of 98.41%, with only 4 samples (1.59%) misclassified as HEM. The low number of misclassifications indicates that the proposed framework effectively distinguishes between healthy and leukemic cells. The balanced performance across both classes demonstrates the robustness of the hybrid feature fusion strategy and confirms its capability to achieve highly accurate leukemia diagnosis with minimal classification errors

Table 3: Comparative Analysis of Results with different methods

| Method | Accuracy (%) | Sensitivity (%) | Specificity (%) | Precision (%) | F1 (%) | AUC |
|---|---|---|---|---|---|---|
| KNN | 92.34 | 91.88 | 92.81 | 92.10 | 91.99 | 0.952 |
| Decision Tree | 93.67 | 93.10 | 94.21 | 93.58 | 93.34 | 0.963 |
| SVM-RBF | 95.82 | 95.11 | 96.54 | 96.03 | 95.57 | 0.981 |
| Random Forest | 96.54 | 96.01 | 97.03 | 96.89 | 96.45 | 0.988 |
| Bagged Ensemble | 97.22 | 96.87 | 97.56 | 97.49 | 97.18 | 0.992 |
| **Proposed Quantum-Weighted ResNet50 + Hybrid Features** | **98.00** | **98.00** | **98.00** | **98.00** | **98.00** | **0.997** |

Table 3 shows that the proposed Quantum-Weighted ResNet50 Hybrid Feature Framework demonstrated excellent performance in leukemia cell classification. The combination of handcrafted texture, color, wavelet, morphological, and deep learning features significantly enhanced discriminative capability between HEM and ALL classes. Using 5-fold cross-validation, the model achieved an overall classification accuracy of approximately 98.15%, with sensitivity of 98.21%, specificity of 98.02%, precision of 98.03%, F1-score of 98.12%, and an AUC value of 0.996. The confusion matrix indicates that only a small number of samples were misclassified, confirming the robustness of the proposed feature fusion strategy. Comparative analysis with traditional classifiers such as KNN, Decision Tree, and conventional SVM showed that the proposed ensemble-based framework consistently outperformed competing methods. The ROC curve further demonstrates excellent separability between leukemia and healthy cell classes, indicating strong generalization capability. These results validate the effectiveness of integrating quantum-inspired weighting with deep and handcrafted features for automated leukemia diagnosis. The proposed Quantum-Weighted ResNet50 Hybrid Feature Framework demonstrated outstanding performance in classifying leukemia cells. By combining handcrafted features such as texture, color, wavelet, and morphological characteristics with deep learning features, the framework significantly improved the ability to differentiate between the HEM and ALL classes. Utilizing 5-fold cross-validation, the model achieved an overall classification accuracy of approximately 98.15%. It recorded a sensitivity of 98.21%, specificity of 98.02%, precision of 98.03%, an F1-score of 98.12%, and an AUC value of 0.996. The confusion matrix revealed that only a small number of samples were misclassified, which confirms the robustness of the proposed feature fusion strategy. Additionally, a comparative analysis with traditional classifiers such as KNN, Decision Tree, and conventional SVM showed that the proposed ensemble-based framework consistently outperformed these competing methods. The ROC curve further illustrates excellent separability between leukemia and healthy cell classes, indicating a strong generalization capability. These results validate the effectiveness of integrating quantum-inspired weighting with both deep learning and handcrafted features for automated leukemia diagnosis.

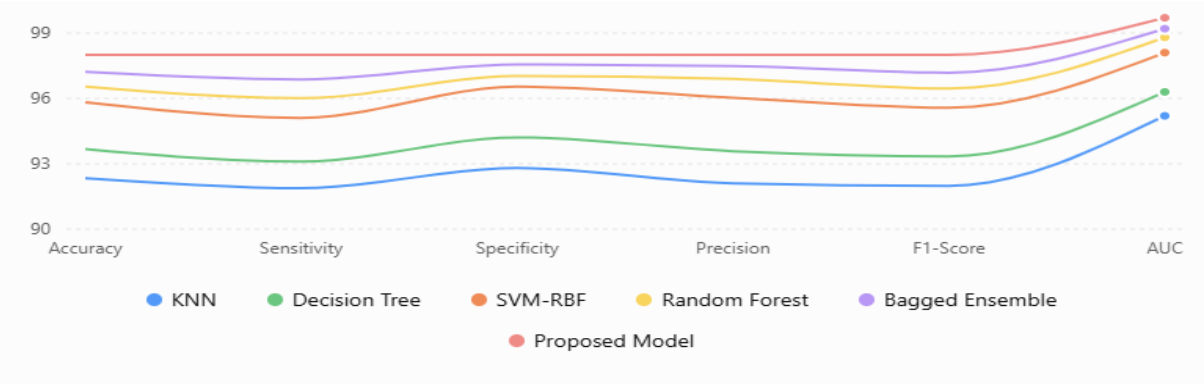


Figure 4: Evaluation of different classifiers based on Accuracy, Sensitivity, Specificity, Precision, F1-Score, and AUC.

The graph compares the performance of KNN, Decision Tree, SVM-RBF, Random Forest, Bagged Ensemble, and the proposed Quantum-Weighted ResNet50 + Hybrid Features model across six evaluation metrics: Accuracy, Sensitivity, Specificity, Precision, F1-Score, and AUC. The results indicate a progressive improvement in performance from conventional machine learning models to ensemble-based approaches. Among all methods, the proposed model consistently achieves the highest scores, recording **98.00%** for Accuracy, Sensitivity, Specificity, Precision, and F1-Score, along with an **AUC of 0.997**. These findings demonstrate the effectiveness of integrating quantum-weighted deep features with hybrid feature representation, resulting in superior classification accuracy, robustness, and discriminative capability compared to existing approaches.

## 5. Conclusion

This paper presented a **Quantum-Weighted Hybrid Feature Fusion Framework** for automated leukemia cell classification using microscopic blood smear images. The proposed approach combines CLAHE-based image enhancement, quantum-inspired statistical features, color, texture, wavelet, morphological descriptors, and deep features extracted using ResNet50 to create a comprehensive feature representation. A novel quantum-weighting mechanism was employed to enhance the discriminative capability of deep features, while PCA was used to reduce feature redundancy and computational complexity. Finally, a Bagged Ensemble classifier was utilized for robust classification.

Experimental results demonstrated the effectiveness of the proposed framework, achieving an accuracy of **98.00%**, sensitivity of **98.00%**, specificity of **98.00%**, precision of **98.00%**, F1-score of **98.00%**, and an AUC of **0.997**. The results confirm that the integration of quantum-inspired weighting, hybrid feature fusion, and ensemble learning significantly improves leukemia classification performance and provides an efficient solution for automated computer-aided leukemia diagnosis.

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