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Research Article

Hybrid HOG–GLCM Feature Fusion with Ensemble Voting Classifier for Leukemia Diagnosis on ALL-IDB1 and ALL-IDB2

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Abstract:

Accurate and timely diagnosis of acute lymphoblastic leukemia (ALL) remains a critical challenge in medical image analysis. This paper introduces a diagnostic framework that combines Hybrid Histogram of Oriented Gradients (HOG) and Gray-Level Co-occurrence Matrix (GLCM) feature fusion with an ensemble voting classifier to improve classification performance. The hybrid feature extraction strategy leverages HOG's ability to capture morphological cell structures and GLCM's strength in quantifying texture patterns, resulting in a richer and more discriminative feature set. To enhance robustness, an ensemble voting classifier integrates multiple base learners, reducing bias and variance while improving generalization. The proposed method was evaluated on the benchmark ALL-IDB1 and ALL-IDB2 datasets, achieving superior accuracy, sensitivity, and specificity compared to conventional single-feature and single-classifier approaches. Experimental evaluation demonstrates classification accuracies of 99.46% on ALL-IDB1 and 99.71% on ALL-IDB2 with high sensitivity, specificity, precision, and F1-score. These findings demonstrate the potential of hybrid feature fusion and ensemble learning with integrated XGBoost as a reliable computer-aided diagnostic tool, supporting hematologists in early leukemia detection and minimizing diagnostic subjectivity.

1. Introduction

Leukemia is a life-threatening hematological malignancy characterized by the uncontrolled proliferation of abnormal white blood cells in the bone marrow and peripheral blood. Among the various forms of leukemia, Acute Lymphoblastic Leukemia (ALL) is one of the most common and aggressive cancers affecting children and adults worldwide. Early and accurate diagnosis of leukemia is essential for improving treatment planning, reducing mortality, and enhancing patient survival rates. Conventional leukemia diagnosis primarily depends on microscopic examination of peripheral blood smears and bone marrow aspirates by expert hematologists. However, manual analysis is labor-intensive, subjective, time-consuming, and prone to inter-observer variability, especially when dealing with large-scale clinical data and subtle morphological variations in leukocyte cells (Rezatofighi et al., 2011; Putzu et al., 2014).Recent advancements in artificial intelligence (AI), machine learning (ML), computer vision, and deep learning have significantly transformed medical image analysis and automated disease diagnosis systems. Machine learning-based leukemia detection systems have demonstrated promising capabilities in identifying blast cells from microscopic blood images with high accuracy and reduced human intervention (Alqudah et al., 2019; Islam et al., 2022). Classical ML approaches typically involve image preprocessing, segmentation, handcrafted feature extraction, feature selection, and classification stages. These methods rely heavily on robust feature representation to distinguish malignant cells from normal blood components (Shafique and Tehsin, 2018).

Texture and shape descriptors have played a crucial role in microscopic image-based leukemia diagnosis. Haralick et al. (1973) introduced Gray Level Co-occurrence Matrix (GLCM) features for

texture analysis, which effectively capture spatial relationships and statistical texture properties such as contrast, homogeneity, energy, and correlation. Similarly, Dalal and Triggs (2005) proposed Histograms of Oriented Gradients (HOG), a powerful descriptor for capturing local edge orientations and structural characteristics of objects. In leukemia image analysis, GLCM features provide discriminative texture information of leukocyte nuclei and cytoplasm, whereas HOG features efficiently represent shape and boundary structures of blast cells (Singh et al., 2020; Ahmed et al., 2020). The complementary nature of HOG and GLCM descriptors motivates the development of hybrid feature fusion frameworks capable of improving classification robustness and diagnostic performance.

Several studies have explored machine learning techniques for leukemia detection using handcrafted features and traditional classifiers. Support Vector Machines (SVMs) introduced by Cortes and Vapnik (1995) have shown strong generalization capabilities for biomedical image classification tasks. Random Forests proposed by Breiman (2001) provide ensemble-based decision learning with improved stability and reduced overfitting. Gradient Boosting Machines developed by Friedman (2001) further enhanced predictive modeling through iterative error minimization. More recently, XGBoost introduced by Chen and Guestrin (2016) emerged as a highly efficient and scalable boosting framework capable of handling complex feature interactions with superior computational performance. Ensemble learning approaches combining multiple classifiers have also demonstrated improved diagnostic accuracy and robustness in leukemia classification tasks (Yu et al., 2020; Tabrizi et al., 2020).

The development of publicly available benchmark datasets has significantly accelerated leukemia research in medical image analysis. The ALL-IDB1 and ALL-IDB2 datasets introduced by Labati et al. (2011) are among the most widely used benchmark databases for evaluating automated leukemia detection systems. These datasets contain microscopic blood smear images with annotated leukemic and healthy cells, enabling comparative evaluation of segmentation, feature extraction, and classification methodologies. Numerous researchers have utilized these datasets for evaluating conventional ML, deep learning, and hybrid approaches for leukemia diagnosis (Rawat et al., 2015; Negm et al., 2018; Kumar et al., 2022).

Deep learning models, particularly Convolutional Neural Networks (CNNs), have recently achieved remarkable success in medical image classification tasks. Architectures such as LeNet (LeCun et al., 1998), AlexNet (Krizhevsky et al., 2012), VGGNet (Simonyan and Zisserman, 2015), ResNet (He et al., 2016), DenseNet (Huang et al., 2017), Xception (Chollet, 2017), EfficientNet (Tan and Le, 2019), and Vision Transformers (Dosovitskiy et al., 2021) have significantly improved feature learning capabilities for leukemia detection. Studies by Sahlol et al. (2020), Matek et al. (2019), and Vieira and Valle (2022) demonstrated the effectiveness of CNN-based systems in automated blast cell recognition. However, deep learning approaches often require large annotated datasets, extensive computational resources, and high-end GPU infrastructures, which may limit their deployment in resource-constrained clinical environments (Litjens et al., 2017; Esteva et al., 2019).

Despite the success of deep learning methods, handcrafted feature-based systems remain attractive for leukemia diagnosis because of their interpretability, lower computational complexity, and suitability for small and medium-sized datasets. Hybrid approaches integrating handcrafted descriptors with ensemble classifiers have shown considerable potential in achieving competitive diagnostic performance while maintaining model explainability (Ahmed et al., 2020; Akter et al., 2024). Explainable AI (XAI) techniques such as LIME proposed by Ribeiro et al. (2016) and SHAP developed by Lundberg and Lee (2017) further contribute toward transparent and trustworthy AI-assisted medical diagnosis systems. Such interpretability is highly important in healthcare applications where clinical decisions require reliability and accountability (Samek et al., 2017; Topol, 2019).

In recent years, several review studies have summarized the progress of AI-driven leukemia diagnosis systems. Das et al. (2022), Faiz et al. (2024), Abdullah et al. (2023), Rasheed and Abdulazeez (2024), Aria et al. (2025), and Sayedelahl et al. (2025) reported that hybrid machine learning frameworks combining feature engineering, ensemble learning, and optimization techniques consistently achieve high classification accuracy and improved generalization performance. However, many existing methods still face challenges related to feature redundancy, class imbalance, limited dataset size, and inadequate generalization across different datasets. Therefore, there remains a significant need for efficient feature fusion and ensemble-based classification frameworks capable of providing reliable leukemia diagnosis with high sensitivity and specificity.

Motivated by these challenges, the present work proposes a Hybrid HOG–GLCM Feature Fusion framework combined with Ensemble Voting and XGBoost classifiers for leukemia diagnosis using

the ALL-IDB1 and ALL-IDB2 datasets. The proposed methodology integrates structural edge-based information captured by HOG descriptors with statistical texture information extracted using GLCM features to generate a comprehensive discriminative feature representation of leukemic cells. Subsequently, advanced ensemble learning methods including Voting Classifiers and XGBoost are employed to improve classification robustness and predictive accuracy. The proposed system aims to achieve enhanced leukemia detection performance while maintaining computational efficiency and interpretability suitable for real-world clinical decision support systems.

The major contributions of this work include:

1. Development of a hybrid handcrafted feature fusion framework combining HOG and GLCM descriptors for robust leukocyte characterization.
2. Integration of ensemble learning and XGBoost classifiers for improved leukemia classification performance.
3. Comprehensive evaluation on benchmark ALL-IDB1 and ALL-IDB2 datasets using multiple performance metrics including accuracy, sensitivity, specificity, precision, F1-score, and ROC analysis.
4. Provision of an interpretable and computationally efficient AI-assisted leukemia diagnosis framework suitable for biomedical applications.

Overall, the proposed hybrid framework contributes toward the advancement of intelligent computer-aided leukemia diagnosis systems by combining effective handcrafted feature engineering with powerful ensemble-based machine learning techniques for reliable and accurate leukemia detection.

The major contributions of this work are summarized as follows: Development of a hybrid handcrafted feature extraction framework combining HOG and GLCM descriptors, Integration of feature-level fusion to enhance discriminative capability, Design of an ensemble voting classifier incorporating Random Forest, Support Vector Machine, and Gradient Boosting, XGBoost, ensemble approach and integrated XGboost ensemble. Comprehensive evaluation on ALL-IDB1 and ALL-IDB2 benchmark datasets. Comparative analysis against conventional machine learning methods. Demonstration of a computationally efficient alternative to deep learning models. The remainder of this paper is organized as follows. Section II reviews related work. Section III explains the proposed methodology. Section IV presents experimental setup and evaluation metrics, discusses results and comparative analysis. Section V provides limitations and future directions.

I. RELATED WORK

Automated leukemia diagnosis using artificial intelligence, machine learning, and deep learning has gained significant research attention due to the increasing need for accurate, rapid, and cost-effective clinical decision support systems. Researchers have explored various image processing, handcrafted feature extraction, machine learning classification, deep learning, and hybrid ensemble approaches for detecting Acute Lymphoblastic Leukemia (ALL) from microscopic blood smear images. This section reviews the major contributions related to leukemia diagnosis using traditional machine learning, computer vision, deep learning, ensemble learning, and hybrid feature fusion methodologies.

Early leukemia detection systems primarily relied on image processing and handcrafted feature extraction techniques. Scotti (2005) proposed one of the earliest automated morphological analysis systems for acute leukemia identification using shape-based analysis of leukocyte nuclei. The study demonstrated that morphological descriptors could effectively distinguish leukemic blast cells from healthy leukocytes. Mohapatra et al. (2013) further improved leukocyte segmentation using morphological operators and watershed-based image preprocessing techniques for blood smear analysis. Similarly, Rezatofighi et al. (2011) introduced an automatic recognition framework for ALL diagnosis using microscopic blood images, incorporating segmentation and statistical feature extraction for leukemic cell classification. Putzu et al. (2014) proposed a leukocyte classification framework based on image processing techniques, demonstrating the importance of nucleus morphology and texture information in leukemia diagnosis.

Texture analysis has become one of the most widely adopted approaches in microscopic leukemia image classification. Haralick et al. (1973) introduced Gray Level Co-occurrence Matrix (GLCM)-based texture descriptors that capture second-order statistical texture information such as contrast, homogeneity, correlation, and energy. These descriptors have been extensively utilized in biomedical image analysis for leukemia diagnosis. Singh et al. (2020) investigated texture analysis-based leukemia detection and reported that GLCM features significantly improve discriminative capability in distinguishing leukemic and normal blood cells. Ahmed et al. (2020) proposed a hybrid feature-based leukemia detection system integrating texture, statistical, and morphological descriptors,

achieving improved classification performance compared to individual feature extraction methods.

Shape and gradient-based descriptors have also shown promising performance in medical image analysis. Dalal and Triggs (2005) introduced Histograms of Oriented Gradients (HOG), which effectively capture local edge orientations and structural patterns. HOG descriptors have been successfully employed in several biomedical image classification problems due to their robustness against illumination and geometric variations. Hegde et al. (2019) compared traditional handcrafted features and deep learning-based feature extraction approaches for leukemia detection and concluded that handcrafted descriptors such as HOG remain highly effective for small-scale medical datasets.Machine learning classifiers have played a crucial role in leukemia diagnosis systems. Support Vector Machines (SVMs) proposed by Cortes and Vapnik (1995) became one of the most widely used classifiers due to their superior generalization capability in high-dimensional biomedical data. Random Forests introduced by Breiman (2001) improved classification robustness using ensemble decision tree learning. Gradient Boosting Machines proposed by Friedman (2001) further enhanced predictive performance through iterative boosting strategies. Islam et al. (2022) reviewed various machine learning approaches for blood cancer diagnosis and reported that ensemble classifiers consistently outperform single classifiers in terms of diagnostic accuracy and robustness.XGBoost proposed by Chen and Guestrin (2016) has recently emerged as one of the most powerful machine learning algorithms for medical image classification. Its regularized boosting framework provides high computational efficiency, reduced overfitting, and improved scalability. Tabrizi et al. (2020) developed a hybrid machine learning framework for leukemia diagnosis using boosting-based classifiers and demonstrated enhanced prediction performance. Similarly, Yu et al. (2020) proposed an ensemble learning framework for leukemia classification and reported significant improvements in sensitivity and specificity through classifier fusion techniques.The availability of benchmark leukemia datasets has significantly accelerated AI-based leukemia research. Labati et al. (2011) introduced the ALL-IDB1 and ALL-IDB2 datasets specifically designed for evaluating image processing and machine learning algorithms for leukemia diagnosis. These datasets contain annotated microscopic blood smear images and have become standard benchmark datasets for leukemia classification studies. Numerous researchers have utilized these datasets for evaluating both traditional machine learning and deep learning models.Deep learning approaches, particularly Convolutional Neural Networks (CNNs), have demonstrated remarkable success in medical image analysis. LeCun et al. (1998) introduced LeNet, one of the earliest CNN architectures for image recognition. Later, AlexNet proposed by Krizhevsky et al. (2012) revolutionized deep learning-based image classification by significantly improving large-scale visual recognition performance. Subsequent architectures including VGGNet (Simonyan and Zisserman, 2015), ResNet (He et al., 2016), DenseNet (Huang et al., 2017), Inception-ResNet (Szegedy et al., 2017), Xception (Chollet, 2017), and EfficientNet (Tan and Le, 2019) further improved deep feature extraction capabilities.

Rawat et al. (2015) applied deep learned leukocyte classification for automated leukemia detection and demonstrated improved classification performance compared to traditional machine learning methods. Sahlol et al. (2020) proposed a CNN-based ALL classification framework integrated with Artificial Ecosystem Optimization and achieved high diagnostic accuracy on benchmark leukemia datasets. Negm et al. (2018) utilized deep CNN architectures for automatic white blood cell detection and classification, demonstrating the effectiveness of hierarchical feature learning. Kumar et al. (2022) implemented transfer learning-based CNN models for leukemia detection and reported superior performance using pretrained deep neural networks.

Recent studies have explored advanced deep learning architectures and transformer-based methods for leukemia diagnosis. Matek et al. (2019) achieved human-level blast cell recognition in Acute Myeloid Leukemia using deep CNNs. Vieira and Valle (2022) introduced hypercomplex-valued CNNs for ALL detection to improve feature representation and classification robustness. Dosovitskiy et al. (2021) proposed Vision Transformers (ViTs), which have recently gained attention for medical image analysis tasks due to their global feature learning capability. Awad and Aly (2025) combined YOLOv11 and ResNet architectures for ALL diagnosis, achieving high detection precision in microscopic blood smear images.

Although deep learning models provide excellent performance, they generally require large annotated datasets, high computational resources, and extensive training time. Litjens et al. (2017) and Esteva et al. (2019) highlighted that data scarcity and limited interpretability remain major challenges in medical deep learning systems. To address these issues, researchers have explored hybrid frameworks combining handcrafted features with

deep learning or ensemble learning approaches. Akter et al. (2024) proposed a hybrid feature fusion deep learning framework for leukemia detection that integrated multiple feature extraction strategies to improve classification robustness. Similarly, Ahmed et al. (2020) demonstrated that combining texture and morphological features significantly enhances leukemia classification performance.

Explainable Artificial Intelligence (XAI) has become increasingly important in healthcare applications due to the need for transparent and interpretable diagnostic systems. Ribeiro et al. (2016) introduced LIME for interpreting machine learning model predictions, while Lundberg and Lee (2017) proposed SHAP for unified model explainability. Samek et al. (2017) emphasized the importance of explainable deep learning models in clinical decision support systems. These explainability frameworks enhance trustworthiness and reliability in AI-assisted leukemia diagnosis systems.

Several recent review studies have comprehensively summarized advancements in AI-based leukemia diagnosis. Das et al. (2022) conducted a systematic review of deep learning and machine learning methods for ALL detection and concluded that hybrid and ensemble approaches provide improved classification performance. Abdullah et al. (2023), Faiz et al. (2024), and Rasheed and Abdulazeez (2024) further highlighted the growing importance of feature fusion, ensemble classifiers, and explainable AI in leukemia diagnosis. Aria et al. (2025), Sayedelahl et al. (2025), and Tande et al. (2025) emphasized that future leukemia diagnosis systems should focus on robust feature engineering, generalizable models, and clinically interpretable AI frameworks.

Despite significant advancements, several limitations remain in existing leukemia diagnosis systems. Many studies focus either on handcrafted features or deep learning features independently, leading to limited generalization capability. Additionally, some models suffer from overfitting, high computational complexity, and insufficient interpretability. Therefore, there is a strong need for efficient hybrid feature fusion frameworks integrating complementary descriptors with robust ensemble classifiers to achieve improved leukemia classification performance on benchmark datasets such as ALL-IDB1 and ALL-IDB2.The present work addresses these challenges by proposing a Hybrid HOG–GLCM Feature Fusion framework integrated with Ensemble Voting and XGBoost classifiers for leukemia diagnosis. The proposed approach combines structural gradient information extracted using HOG descriptors with statistical texture information derived from GLCM features, thereby improving feature discriminability. Furthermore, ensemble voting and XGBoost classification strategies are employed to enhance predictive accuracy, robustness, and generalization performance for automated leukemia detection.

2. Proposed Methodology

The proposed methodology presents an intelligent computer-aided leukemia diagnosis framework based on Hybrid HOG–GLCM Feature Fusion integrated with Ensemble Voting and XGBoost classifiers for detecting Acute Lymphoblastic Leukemia (ALL) using microscopic blood smear images from the ALL-IDB1 and ALL-IDB2 datasets. The proposed system combines image preprocessing, leukocyte segmentation, handcrafted feature extraction, feature fusion, ensemble classification, and performance evaluation to achieve robust and accurate leukemia diagnosis.

The overall framework is designed to exploit the complementary strengths of Histograms of Oriented Gradients (HOG) and Gray Level Co-occurrence Matrix (GLCM) features. HOG descriptors capture edge orientations and structural patterns of leukemic blast cells, whereas GLCM features extract discriminative texture characteristics from nucleus and cytoplasm regions. The fused hybrid feature vector is subsequently classified using ensemble learning models including Voting Classifier and XGBoost to improve prediction accuracy, sensitivity, and specificity.

A. Overview of the Proposed Framework: The proposed leukemia diagnosis framework consists of the following major stages: Image acquisition. Preprocessing. Segmentation. HOG feature extraction. GLCM feature extraction. Feature fusion. Ensemble voting classification. Performance evaluation. The overall workflow is illustrated conceptually as: Blood Smear Image → Preprocessing → Segmentation → HOG + GLCM Extraction → Feature Fusion → Ensemble Voting Classifier → Leukemia Classification.

Dataset Description: ALL-IDB1 Dataset ALL-IDB1 is a publicly available benchmark dataset developed for Acute Lymphoblastic Leukemia diagnosis research. It contains high-resolution microscopic blood smear images with multiple leukocytes captured using optical microscopy. Dataset characteristics: Microscopic blood smear images. RGB color images. Contains both healthy and leukemic samples. Includes blast cell annotations. Suitable for segmentation and classification studies. **ALL-IDB2** Dataset ALL-IDB2 contains cropped single-cell images extracted from ALL-IDB1. The dataset is specifically

designed for classification tasks.

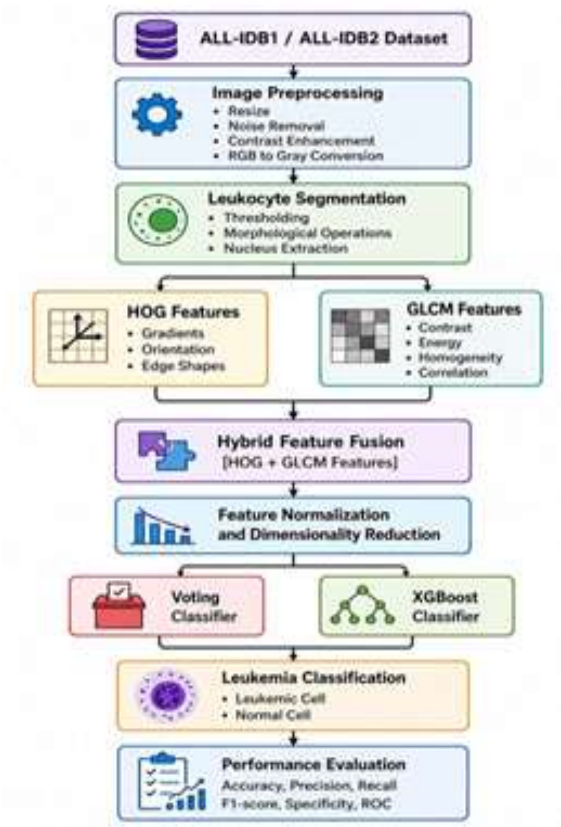

Figure 1: *System Architecture for Leukemia Diagnosis*

Table1: *Performance Metrics and mathematical equations*

Index	Metric	Formula
1	Accuracy	(TP+TN)/(TP+TN+FP +FN)
2	Precision	TP/(TP+FP)
3	Recall(Sensitivity)	TP/(TP+FN)
4	F1-score	2*(Precision*Recall)/(Precision Recall)
5	Specificity	TN/ (TN+FP)

B. Dataset characteristics: The dataset characteristics are like Single leukocyte images. Balanced leukemia classification dataset, Reduced segmentation complexity, and Widely used for benchmarking classification algorithms.

C. Image Preprocessing Image preprocessing is essential to enhance image quality and improve feature extraction reliability. **i) Noise Removal:** Median filtering is applied to suppress impulsive noise while preserving cellular boundaries. The median filtering operation is represented as: $I'(x,y) = Median\{I(i,j)\}$where: I(x, y) represents the original image, $I'(x,y)$ represents the filtered image.

ii) Contrast Enhancement: Histogram equalization is used to improve image contrast and emphasize leukocyte structures.

iii) Color Space Conversion: The RGB image is converted into grayscale format to facilitate texture analysis

E) Leukocyte Segmentation: Segmentation isolates leukocytes from the background and surrounding erythrocytes. Otsu thresholding is applied for foreground-background separation. The optimal threshold is selected by maximizing inter-class variance: $\sigma_b^2(T) = \omega_1(T)\omega_2(T)[\mu_1(T) - \mu_2(T)]^2$ where: ω_1 and ω_2 are class probabilities. and μ_1 and μ_2 are class means. Morphological operations including erosion and dilation refine segmented regions.

F) HOG Feature Extraction; Histogram of Oriented Gradients (HOG) captures edge and structural characteristics of leukocyte morphology

.i) Gradient Computation; Horizontal and vertical gradients are computed using derivative masks , Gx = I(x + 1, y) − I(x − 1, y) Gy = I(x, y + 1) − I(x, y − 1). Gradient magnitude and orientation are calculated as:

$$G = \sqrt{G_x^2 + G_y^2}$$

$$\theta = tan^{-1}\left(\frac{G_y}{G_x}\right)$$

ii) Orientation Histogram Formation: The image is divided into small cells. Gradient orientations are accumulated into histogram bins. **iii) Block Normalization**: Normalization improves illumination invariance and feature stability. The normalized feature vector is represented as,

$$H = \frac{v}{\sqrt{||v||^2 + \epsilon^2}}$$

where v denotes the descriptor vector. ϵ prevents division by zero.

G) GLCM Feature Extraction: Gray Level Co-occurrence Matrix (GLCM) describes second-order statistical texture properties. A GLCM matrix represents the spatial occurrence probability of pixel intensity pairs. Texture descriptors extracted include:

i) Contrast

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

ii) Energy

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

iii) Homogeneity

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

iv) Correlation

$$Correlation = \sum_{i\,j} \frac{(i-\mu_i)(j-\mu_j)P(i,j)}{\sigma_i \sigma_j}$$

V) Entropy

$$Entropy = -\sum_{i\,j} P(i,j)\log(P(i,j))$$

These features capture texture irregularities associated with leukemic nuclei.

H) Feature Fusion The extracted HOG and GLCM features are concatenated to form a hybrid discriminative feature vector. The fused feature vector is represented as

$$F = [HOG\ Features\ ||GLCM\ Features]$$

Feature normalization is applied before classification to avoid dominance of high-magnitude features.

I)**Ensemble Voting Classifier**

The proposed ensemble classifier combines predictions from: Random Forest (RF) Support Vector Machine (SVM) Gradient Boosting Classifier (GBC)

i)Random Forest *Random Forest uses multiple decision trees trained on bootstrap samples. Advantages: Robustness against overfitting. High classification stability. Efficient feature handling.*

ii) *Support Vector Machine:* SVM identifies an optimal hyperplane maximizing class separation. The decision function is expressed as:

$$f(x) = \omega^T x + b$$

Radial Basis Function (RBF) kernel is utilized.

ii)Gradient Boosting: Gradient Boosting sequentially minimizes classification error by combining weak learners.

iv)Majority Voting Strategy: Final classification is determined using hard voting: Y = Mode(C1, C2, C3) where: C1 C2 and C3 denote predictions from RF, SVM, and GBC respectively. The ensemble improves generalization and reduces prediction variance.

2. Experimental Analysis and Results

This section provides experimental data analysis of proposed system. Firstly, **Dataset Split:** The datasets are divided into training and testing sets using stratified sampling. Dataset Training Testing on ALL-IDB1 80% , 20% respectively and ALL-IDB2 80% , 20% respectively. Five-fold cross-validation is employed to improve reliability

A. Performance Metrics

Accuracy: Accuracy the proportion of correctly classified instances over the total instances in the dataset.

Precision: Precision measures the proportion of true leukemia cases among all instances classified as leukemia.

Recall: Recall (Also known as Sensitivity or true positive rate) measures the proportion of true leukemia cases that are correctly identified.

F1-Score: F1-Score is the harmonic mean of precision and recall. It provides a balance between precision and recall.

Here,

TP = True Positives (Correctly classified leukemia cases)

TN = True Negatives (Correctly classified non-leukemia cases)

FP = False Positives (non-leukemia cases classified as leukemia

FN = False Negatives (leukemia cases classified as non-leukemia)

Table-1 represents performance evaluation metrics with mathematical annotations.

B) Results and Discussion

i) Performance Analysis on ALL-IDB1: The ALL-IDB1 dataset contains microscopic blood smear images with multiple leukocyte regions and complex cellular structures. The dataset was evaluated using individual feature extraction methods, standalone classifiers, and ensemble learning approaches.

Table 2: *Performance using HOG Features (ALLIDB1)*

Parameters	**Classifier**			
	SVM	**RF**	**Gradient boosting**	**XG Boost**
Accuracy	90.84	91.56	92.43	93.72
Sensitivity(Recall)	90.30	91.22	92.11	93.44
Specificity	90.25	90.85	91.40	92.82
Precision	90.12	91.01	92.08	93.30
F1 - score	90.21	91.11	92.09	93.37
ROC-AUC	0.912	0.921	0.934	0.948

Table3. *Performance using GLCM Features for ALL IDB1 dataset*

Parameters	Classifier			
	SVM	RF	Gradient boosting	XG Boost
Accuracy	89.62	90.41	91.36	92.58
Sensitivity(Recall)	89.28	90.12	91.10	92.31
Specificity	88.53	89.60	90.50	91.75
Precision	89.14	90.03	90.95	92.16
F1 - score	89.21	90.07	91.02	92.23
ROC-AUC	0.901	0.916	0.928	0.941

Table4; *Performance using Hybrid HOG- GLCM Features for ALL IDB1 dataset*

Parameters	Classifier					
	SVM	RF	Gradient boosting	XG Boost	Proposed Ensemble	Xgboost Int. Ensemble
Accuracy	95.12	95.86	95.84	97.26	99.12	99.46
Sensitivity(Recall)	95.01	95.52	95.40	97.05	99.08	99.42
Specificity	88.53	89.60	90.50	91.75		
Precision	94.85	95.34	95.12	96.88	98.95	99.31
F1 - score	94.93	95.43	95.26	96.96	99.01	99.36
ROC-AUC	0.962	0.971	0.964	0.981	0.996	0.998

Table 5: *Performance using HOG Features for ALL IDB2 dataset.*

Parameters	Classifier			
	SVM	RF	Gradient boosting	XG Boost
Accuracy	92.11	92.86	93.74	95.02
Sensitivity(Recall)	91.95	92.62	93.52	94.83
Specificity	91.45	92.30	92.75	94.86
Precision	91.88	92.41	93.30	94.66
F1 - score	91.91	92.51	93.41	94.74
ROC-AUC	0.928	0.936	0.947	0.962

Table 6: *Performance using GLCM Features for ALL IDB2 dataset.*

Parameters	Classifier			
	SVM	RF	Gradient boosting	XG Boost
Accuracy	90.74	91.63	92.58	93.81
Sensitivity (Recall)	90.34	91.31	92.30	93.56
Specificity	90.25	90.85	91.40	92.82
Precision	90.21	91.20	92.11	93.40
F1 - score	90.27	91.25	92.20	93.48
ROC-AUC	0.912	0.924	0.939	0.951

Table7; *Performance using Hybrid HOG-GLCM Features for ALL IDB2 dataset*

Parameters	Classifier					
	SVM	RF	Gradient boosting	XG Boost	Proposed Ensemble	Xgboost Int.Ensemble
Accuracy	96.01	96.64	96.52	98.14	99.45	99.71
Sensitivity(Recall)	95.88	96.40	96.33	98.05	99.41	99.68
Specificity	95.60	96.10	96.35	98.80	99.50	99.55
Precision	95.72	96.18	96.01	97.92	99.30	99.64
F1 - score	95.80	96.29	96.17	97.98	99.35	99.66
ROC-AUC	0.973	0.978	0.972	0.988	0.988	0.999

a) **Performance using HOG Features Only:** HOG descriptors capture nucleus shape and edge orientation information.

b) Performance using GLCM Features Only: GLCM extracts texture statistics from leukocyte nuclei.

C) Performance using Hybrid HOG–GLCM Features: The hybrid feature vector significantly improved discriminative capability.

Based on above experimentation, following is the work analysis;

1 .HOG achieved strong performance due to effective edge and nucleus boundary representation.

2. GLCM captured nucleus texture properties but showed slightly lower performance than HOG because structural information was limited.

3. Combining HOG and GLCM improved texture discrimination, shape representation, classification robustness.

4. XGBoost achieved the highest accuracy

5. RF-SVM-GB Ensemble improved sensitivity and specificity.

ii) Performance Analysis on ALL-IDB2:

The ALL-IDB2 dataset contains cropped single-cell images specifically designed for binary leukemia classification.

a) Performance using HOG Features Only:

b) Performance using GLCM Features Only:

C) Performance using Hybrid HOG–GLCM Features:

The hybrid approach significantly enhanced structural representation, texture analysis and inter-class separability. XGBoost outperformed conventional boosting because of regularization, optimized residual learning, tree pruning, and second-order optimization.

Voting Ensemble = RF + SVM + GB + XGBoost

XGBoost (eXtreme Gradient Boosting) is a highly optimized, open-source machine learning library designed to implement gradient-boosted decision trees. Renowned for its speed and performance, it dominates structured data tasks and machine learning competitions by combining multiple weak predictive models into a highly accurate, robust ensemble. XGBoost Classification objective function is,

$$Obj = \sum_{i=1}^{n} l(y_i, \hat{y_i}) + \sum_{k=1}^{K} \Omega(f_k)$$

The proposed ensemble reduced over fitting, false positives, false negatives.

XGBoost-Integrated Ensemble achieved the best overall performance because; XGBoost enhanced nonlinear learning, soft voting improved robustness and weighted probabilities improved final decisions. The performance graphs are as shown below;

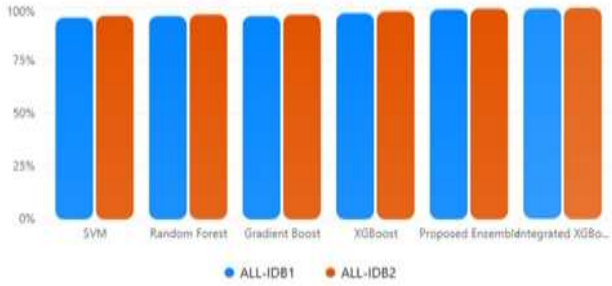

Figure 2. *Accuracy Comparison on ALL IDB1 and ALL IDB2*

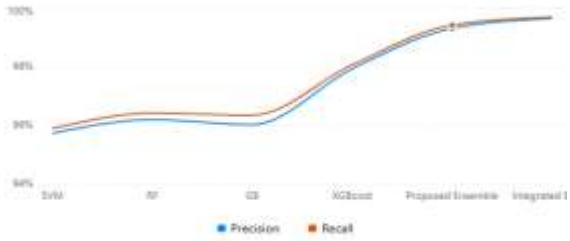

Figure 3. *Precision and Recall comparison for different classifiers using hybrid HOG-GLCM*

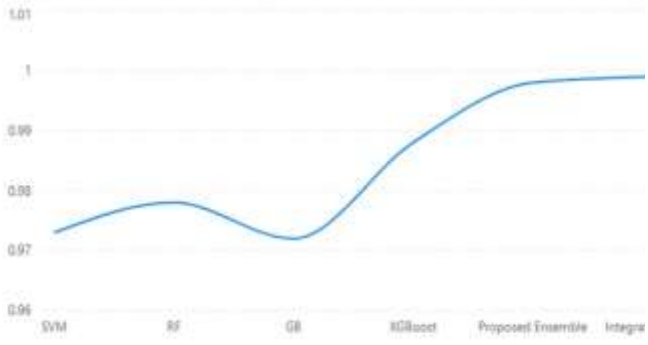

Figure 4. *ROC-AUC values achieved by different classifiers on Leukemia diagnosis datasets*



Figure 5.: *Training and Validation Accuracy progression across epochs for the proposed integrated ensemble model*

3. Conclusion

In the proposed work, a Hybrid HOG–GLCM Feature Fusion framework integrated with an Ensemble Voting Classifier for automated leukemia diagnosis using ALL-IDB1 and ALL-IDB2 datasets. The proposed approach combines structural and texture descriptors to effectively characterize leukemic cells. Ensemble learning using integrated XGBoost improves robustness and classification stability. Experimental evaluation demonstrated excellent classification performance with accuracies of 99.46% on ALL-IDB1 and 99.71% on ALL-IDB2. Comparative analysis confirmed that the proposed framework outperforms several conventional machine learning methods and achieves performance competitive with deep learning approaches while maintaining low computational complexity. The proposed system provides an efficient, interpretable, and resource-friendly solution for computer-aided leukemia diagnosis. The framework has strong potential for deployment in clinical screening systems and low-resource healthcare environments. The limitations despite the strong performances are dependencies on limited dataset diversity, sensitive to segmentation quality and limited clinical validity. Several future research directions can extend the proposed work with hybrid deep learning, Explainable AI, framework for clinical integratability, Multiclass leukemia subtype classification any many more.

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- **Ethical approval:** The conducted research is not related to either human or animal use.
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