Cureus Journal of Computer Science

Open Access Original Article

Feature-Driven Acute Lymphoblastic Leukemia Detection From Blood Smears Using Machine Learning Ensemble Classifiers

Received 04/29/2025
Review began 06/03/2025
Review ended 08/21/2025
Published 08/25/2025

DOI:
https://doi.org/10.7759/s44389-025-05923-0

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Abstract

This study delineates a machine learning-based method for using peripheral blood smear images to diagnose acute lymphoblastic leukemia early. The proposed method captures a wide range of image features by using various feature extraction techniques, including Gabor filters, Sobel edge detection, local binary pattern, and histogram of oriented gradients. The features were classified using Random Forest, Gradient Boosting, and AdaBoost, among which Random Forest reported the best accuracy of 91.00%. The study's contribution is its multi-feature extraction methodology that improves the diagnostic accuracy and model robustness. The proposed method presents a valuable and automated facility to support hematologists in identifying acute lymphoblastic leukemia correctly and in good time.

Categories: AI applications, Image Processing and Analysis, Machine Learning (ML)
Keywords: blast cell, hog, gabor, sobel, adaboost, random forest classifier, leukemia, acute lymphoblastic leukemia (all), lbp, ensemble learning model

Introduction

Acute lymphoblastic leukemia (ALL) is the most prevalent kind of blood cancer, occurring especially among children and young adults. It is a condition that starts in the bone marrow and causes an excess of immature lymphocytes, which disrupts the regular function of blood cells. Prompt and correct diagnosis of ALL is important since early treatment greatly enhances the possibility of successful treatment and long-term survival. Nonetheless, standard diagnostic procedures mainly rely on the manual microscopic inspection of blood smear slides by trained hematologists. This process is not just time- and labor-intensive but also subject to inter-observer variability and human error that may affect the reliability of results.

ALL is a very aggressive and malignant type of blood cancer that specifically involves the lymphoid precursor cells of the bone marrow. It is typified by the rapid and uncontrollable proliferation of lymphoblasts, which are immature white blood cells that cannot mature into healthy immune cells. After building up in the bone marrow, these aberrant cells eventually enter the bloodstream and impact the liver, spleen, and lymph nodes, among other organs. Normal red blood cell, white blood cell, and platelet production drastically decreases as lymphoblasts multiply and displace healthy blood-producing cells.

ALL is predominantly diagnosed in children, especially at the age range of 2-5 years, but it can be seen in adults, particularly in individuals above 50 years of age. Rapid onset of the clinical symptoms, which may present as fatigue, frequent infections, bruising or bleeding without cause, bone ache, and enlarged lymph nodes, is common. If left untreated in time, ALL may cause fatal complications like severe anemia, recurrent infections, and bleeding disorders owing to the suppression of normal hematopoiesis.

Early diagnosis of ALL is essential for the initiation of timely treatment and improving the survival rate of patients to a great extent. Traditional methods of diagnosis, including bone marrow biopsy and flow cytometry, while being very accurate, are invasive, costly, and require well-equipped laboratories and trained professionals. Conversely, analysis of peripheral blood smears provides a less invasive, cost-effective, and more accessible option by making possible the visual detection of abnormal lymphoblasts within stained blood samples. Although of clinical utility, manual inspection of smears has several challenges that it being time-consuming, labor-intensive, and greatly dependent on the expertise and experience of pathologists, thus introducing subjectivity and diagnostic variation.

With the recent developments in artificial intelligence in the areas of machine learning and deep learning, there is increasing interest in taking advantage of automated image analysis to detect ALL. Artificial intelligence-based methods can revolutionize diagnosis pathways by enhancing accuracy, reducing human errors, and significantly shortening diagnosis time. These technologies can also assist in filling the gap in areas with poor access to specialized medical personnel and facilities, thus expanding the coverage of

early leukemia detection.

In this research activity, we concern ourselves with computerized detection of ALL through the classification and categorization of blood smear images. Research entails the retrieval of significant characteristics from single cells of blood and comparing blast cells (leukemic) versus healthy cell traits. The perceptual differences among these cell populations are illustrated in Figure *1*, which shows representative samples of both healthy and infected cells.

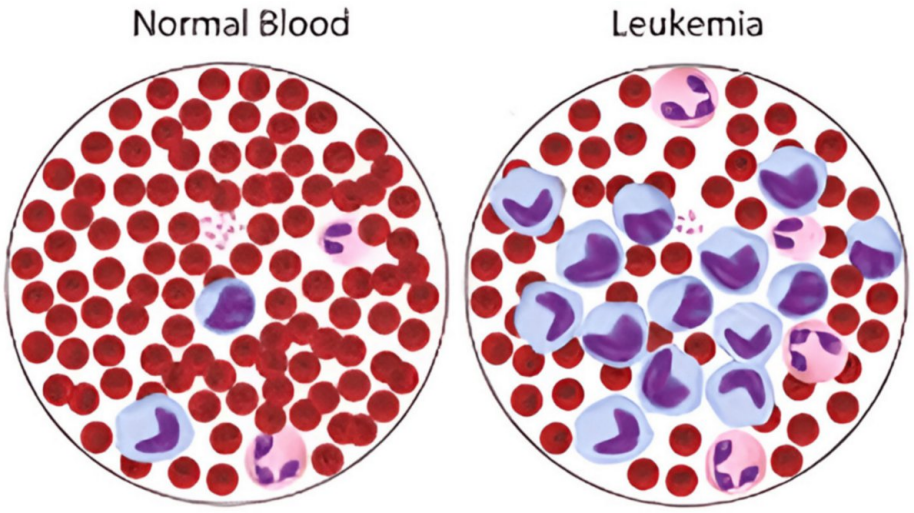

FIGURE 1: Comparison of ALL-Affected Blast Cells and Healthy Cells

Adapted from [1]

ALL, Acute Lymphoblastic Leukemia

Comparison of affected blast cells and healthy cells

Affected Blast Cells (Lymphoblasts in ALL):

• Typically appear larger than normal lymphocytes, with a noticeably high nucleus-to-cytoplasm ratio.

• Exhibit irregularly shaped nuclei, often accompanied by prominent nucleoli.

• Lack cytoplasmic granules and display increased basophilic staining, indicating their immature nature.

• Multiply uncontrollably, disrupting the production of normal blood cells and impairing overall hematopoietic function.

Healthy Cells (Normal Lymphocytes):

• Possess a round, compact nucleus with evenly distributed chromatin.

• Display a lower nucleus-to-cytoplasm ratio, along with a clearly defined cytoplasmic boundary.

• Actively contribute to immune system function and play a key role in defending the body against infections.

• Maintain a stable and regulated presence in the bloodstream, ensuring normal cellular balance without overcrowding.

Literature review

ALL is a critical hematological condition that requires early and accurate diagnosis to be treated effectively. In recent years, the combination of machine learning algorithms with medical imaging has resulted in tremendous advancements in the creation of automated diagnostic tools based on blood smear images.

Krizhevsky et al. [2] presented a deep learning model using convolutional neural networks (CNNs) to classify large-scale images, which formed the basis for implementing AI in medical image diagnosis. Kazemi et al. [3] used K-means segmentation and Support Vector Machine for acute myeloid leukemia classification from smear images with high accuracy but low generalisability using small datasets. Mohapatra et al. [4] proposed an ensemble of conventional classifiers for the early detection of ALL with improved stability over individual models. With deep learning, CNNs became the focal point. Sriram et al. [5] used VGG-16 to distinguish leukemia from leukemoid disorders, referencing the strength of transfer learning. Bhute et al. [6] followed up with ensembling various pre-trained CNNs, being more resilient. Rubinos Rodriguez et al. [7] surveyed deep learning for leukemia diagnosis and specified a shift from traditional models using hand-crafted features to CNNs and transfer learning for greater accuracy. They noted the need for public datasets, hybrid models, big datasets, explainable AI, and clinical validation. Additional research pursued richer modalities and more succinct models. Huang et al. [8] employed hyperspectral imaging with Gabor features and CNNs, sensing chemical signals beyond RGB but needing unique hardware. Veeraiah et al. [9] developed a histogram-based decision support system that was simple and quick to use in resource-poor settings. El Houby [10] placed a focus on feature selection with standard classifiers and introduced straightforward and interpretable ALL diagnosis models. Some of the recent comparative studies, such as Mahboob et al. [11], compared different ML algorithms for ALL early prediction, providing insight into the accuracy-complexity trade-off.

Although existing studies have employed various feature extraction methods and classifiers, most have focused on individual techniques or deep learning models requiring high computational power. There is a noticeable gap in research integrating multiple, complementary feature extraction techniques like Local Binary Pattern, Histogram of Oriented Gradients, Sobel, and Gabor filters into a unified framework. Additionally, not many works have thoroughly examined ensemble classifiers through such varied features. The proposed research method fills that void by advancing a strong machine learning model that incorporates various feature extraction methods and compares ensemble classifiers, with the Random Forest recording the highest accuracy.

Materials And Methods

The proposed methodology will identify ALL from peripheral blood smear images through a method based on machine learning that implements a combination of various feature extraction techniques and ensemble classifiers. The procedure involves five principal steps: image acquisition, preprocessing, segmentation, feature extraction, and classification.

Experimental setup

The experiments were performed on a system with an AMD Ryzen 7 7840HS processor, 16GB RAM, and an NVIDIA GTX 4060 8GB GPU. The software setup used was Python 3.8, along with libraries like OpenCV for image processing, scikit-learn for machine learning classifiers, and matplotlib for plotting. The Acute Lymphoblastic Leukemia Image Database (ALL-IDB) dataset [12] was used, and the data was divided into 80% training data and 20% test data. Five-fold cross-validation was conducted to test the stability of models.

Image acquisition and preprocessing

Peripheral blood smear images are obtained from publicly available databases like ALL-IDB, which are extensively used in hematological studies. The dataset consists of 260 images in total, with 130 images depicting blast cells and 130 images depicting healthy cells, gathered from the publicly available ALL-IDB [12] repository. The images were then processed through a sequence of preprocessing steps to normalize and enhance their quality. Preprocessing included resizing all the images to a single standard dimension, converting to grayscale, using histogram equalization to correct the contrast, and reducing noise through Gaussian filtering [13]. The sample images for ALL-IDB are illustrated in Figure *2*.

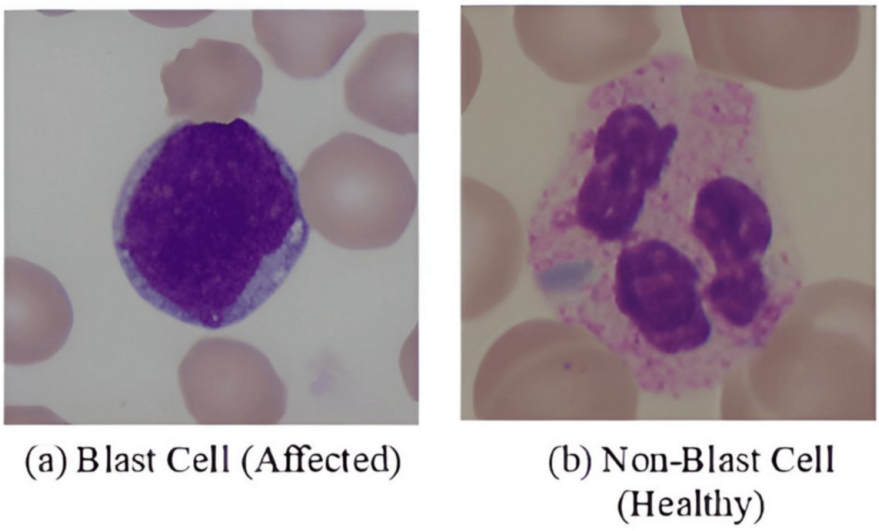

FIGURE 2: Sample Images for ALL-IDB: (a) Blast Cell (Affected) and (b) Non-Blast Cell (Healthy)

Adapted from [12]

ALL-IDB, Acute Lymphoblastic Leukemia Image Database

Feature extraction

After preprocessing, feature extraction was done with a hybrid method combining four techniques to effectively capture leukemic and normal cell visual attributes. The HOG technique was used for detecting edge orientation patterns, LBP for the capture of local texture details, Sobel edge detection of prominent edges and contours, and Gabor filtering for orientation and frequency-based texture information. The feature vectors resulting from these approaches were merged into a single comprehensive feature vector for every image.

The following feature extraction methods were employed:

- HOG: Extracts edge orientation histograms for texture analysis.
- LBP: Captures local texture variations in an image.
- Sobel Edge Detection: Detects edge features crucial for distinguishing leukemia cells.
- Gabor Filters: Extracts frequency and orientation-based features from images.

Algorithm

Input: Preprocessed grayscale blood smear image $I(x,y)$

Output: Concatenated feature vector F

BEGIN

- Load the grayscale image $I(x,y)$
- Apply HOG:

a. Compute gradients in the x and y directions:

$$G_x = \partial I/\partial x, G_y = \partial I/\partial y$$

$G_x = \partial I/\partial x$: Partial derivative of image III in x-direction (horizontal gradient).

$G_y = \partial I/\partial y$: Partial derivative in *y*-direction (vertical gradient).

b. Compute gradient magnitude and orientation:

$$M(x,y) = \sqrt{({G_x}^2 + G_y^2)}, \Theta(x,y) = arctan(G_y/G_x)$$

$M(x,y) = \sqrt{({G_x}^2 + G_y^2)}$: Magnitude of gradient vector at each pixel.

$\Theta(x,y) = arctan(G_y/G_x)$: Orientation (angle) of gradient vector in degrees or radians.

c. Build HOG within each cell.

Gradients within each cell (typically 8×8 pixels) are binned by orientation angle into a histogram.

d. Normalize across blocks to get the final HOG feature vector F_{HOG}.

▪ Normalize histograms over blocks (e.g., 2×2 cells) to account for illumination variations.

▪ Final feature: F_{HOG} (HOG vector).

● Apply LBP:

a. For each pixel *p*, compare it with eight surrounding neighbors n_i:

$$LBP(p) = \sum s(n_i - p)2^i, whereS(x) = 1if x \geq 0, else0$$

p: Center pixel.

n_i: Neighboring pixels (usually 8 in a 3×3 grid).

$s(n_i - p)$: A function that checks whether the neighbor pixel is greater than or equal to the center.

$$S(x) = 1if x \geq 0, else0$$

$LBP(p) = \sum s(n_i - p)2^i$: Each comparison contributes a binary bit; the LBP code is a weighted sum.

b. Construct a histogram of LBP values to form the feature vector F_{LBP}.

● Apply Sobel Edge Detection:

a. Convolve the image with Sobel kernels:

$$G_x = I * S_x, G_y = I * S_y$$

$$S_x = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix} \quad S_y = \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ 1 & 2 & 1 \end{bmatrix}$$

$G_x = I * S_x$: Convolution of image with kernel S_x

$G_y = I * S_y$: Convolution with S_y

b. Compute edge magnitude: $M(x,y) = \sqrt{(G_{x^2} + G_{y^2})}$

c. Extract edge features to form the feature vector F_{Sobel}.

Extract features (e.g., mean edge strength) from the magnitude map.

• Apply Gabor Filters:

a. Apply a 2D Gabor filter with various Θ and frequencies *f*:

$$G(x,y) = \exp\left(-\frac{x'^2 + \gamma^2 y'^2}{2\sigma^2}\right) \cdot \cos\left(2\pi\frac{x'}{\lambda} + \psi\right), \text{where}$$

x', y': Rotated coordinates

σ: Standard deviation of Gaussian

λ: Wavelength of the sinusoidal factor

Θ: Orientation of the filter

Ψ: Phase offset

γ: Aspect ratio

b. Extract the mean and standard deviation of filtered responses to form F_{Gabor}.

• Concatenate all feature vectors:

$$F = [F_{HOG}, F_{LBP}, F_{Sobel}, F_{Gabor}]$$

• Return the final feature vector *F*.

END

Feature selection

In order to enhance class performance and minimize computational load, feature selection was performed through Principal Component Analysis (PCA) and Recursive Feature Elimination (RFE). PCA assisted in mapping the high-dimensional data onto a lower-dimensional space while keeping most of the variance, while RFE progressively discarded less significant features based on model feedback, keeping the most discriminatory subset of features.

A systematic feature selection process was employed to enhance the classification model's performance and lower computing complexity. This process is important in the removal of redundant and irrelevant features while retaining features that significantly improve the predictive power of the model. In this research, two leading methods, PCA and RFE, were used to reduce dimensionality.

PCA is a statistical technique that converts the initial set of features to a lower-dimensional set of unrelated variables called principal components. These components retain the largest variance contained in the data, thus allowing effective data representation with minimal loss of information [14]. This conversion not only enhances computational effectiveness but also assists in overcoming the multicollinearity of features.

By contrast, RFE is a wrapper-based feature selection method where the least relevant features are eliminated recursively based on classifier performance. Models are developed and features are ranked in descending order of their importance, eliminating the dataset successively to retain the most useful subset [15]. The hybrid combination of PCA and RFE ensures that both statistically significant features and practically meaningful features for the classification of leukemia are retained.

Classification

The feature vectors were then classified with three ensemble machine learning algorithms: Random Forest, Gradient Boosting, and AdaBoost. Random Forest, which follows a bagging strategy, resulted in the highest classification accuracy, precision, recall, and F1-score. Gradient Boosting and AdaBoost, following boosting strategies, were also compared. Training and testing of the model were both carried out using an 80-20 train-test split and 5-fold cross-validation to make the results generalizable and robust. The following classifiers were used for leukemia detection: Random Forest, Gradient Boosting, and AdaBoost.

Random Forest

Random Forest is an ensemble method that trains many decision trees at training time and outputs the class that is the mode of the classes output by the individual trees. It uses a method called bagging (bootstrap aggregating), wherein numerous subsets of the original set of training data are sampled with replacement to train separate trees. Moreover, at every division in a tree, a random subset of features is taken into account instead of taking all the features available, which brings diversity between the trees and minimizes the overfitting risk [16]. This technique is especially powerful with high-dimensional and noisy data and is therefore highly applicable to medical image analysis, such as the detection of leukemia from blood smear images. Its generalization ability and robustness enable it to work well even when there are intricate interactions among features [17]. In addition, Random Forests provide an inherent measure of feature importance, which can be used to further optimize models by concentrating on the most discriminative inputs.

Gradient Boosting

Gradient Boosting is yet another ensemble method that develops models sequentially. In contrast to Random Forest, which grows trees in parallelly, Gradient Boosting fits each subsequent model to fix the mistakes of earlier models [18]. This process involves minimizing a loss function in a gradient descent process, whereby each tree fits to predict residuals (mistakes) of earlier models' predictions. The model's performance enhances with every iteration, enabling it to learn sophisticated, non-linear patterns in the data. Though extremely accurate, Gradient Boosting is susceptible to overfitting unless suitably regularized. Hence, learning rate adjustment, early stopping, and tree depth restriction are generally used to limit model complexity [19]. In medical diagnosis, where accuracy matters, Gradient Boosting is appreciated for its ability to fine-tune and achieve high classification accuracy.

AdaBoost

AdaBoost is a boosting algorithm that translates a collection of weak classifiers to a strong classifier by paying additional attention to those instances that are difficult to classify [20]. It starts off by training the base classifier over the original set of data and giving equal weight to all of the training instances. In the next iteration, it raises the weights of those instances that are misclassified, such that the next classifier pays additional attention to the examples. The final prediction is a weighted vote of all base classifiers. AdaBoost is particularly useful for binary classification problems and has been effectively applied in medical applications where it is important to identify healthy versus diseased samples. However, AdaBoost is prone to noisy data and outliers because it assigns more weight to hard-to-classify examples, which may at times be incorrect [21].

Evaluation metrics

The performance of every classifier was evaluated using accuracy, precision, recall, F1-score, mean squared error (MSE), and confusion matrix, offering a complete assessment of their forecasting capabilities. The methodology proved that combining several feature extraction methods and employing ensemble classifiers can greatly improve the accuracy and efficiency of ALL detection in blood smear images.

In addition, algorithmic processing was done in which the preprocessed grayscale image went through each feature extraction algorithm sequentially. HOG was performed through the computation of gradient magnitudes and directions, creating histograms within cell images, and normalization over blocks to create a stable HOG feature vector. LBP was calculated through comparison of pixels with neighbors to create a binary code that describes local texture, followed by histogramming the codes. Sobel filters were convolved with the image to find directional edges, and their magnitude maps were summarized into edge-based features. Gabor filters were used at a variety of scales and orientations to extract texture-based frequency features, and statistical summaries of these responses were taken.

Results

Performance analysis

The classifiers' performance metrics are summarized in Table *1*.

Classifier	Mean Squared Error	Precision	Recall	F1-score	Accuracy
Random Forest	0.08997	96.26%	88.95%	92.10%	91.00%
Gradient Boosting	0.22994	80.72%	71.94%	75.79%	77.00%
AdaBoost	0.14995	89.60%	81.66%	85.11%	85.00%

TABLE 1: Classification Performance of Random Forest, Gradient Boosting, and AdaBoost

Detailed explanation and comparative analysis

The performance of three ensemble classifiers, Random Forest, Gradient Boosting, and AdaBoost, was tested using the standard classification measures: MSE, Precision, Recall, F1-score, and Accuracy. The results are shown Table *1*, and a graphical plot of the individual classification matrix is provided in Figure *3*.

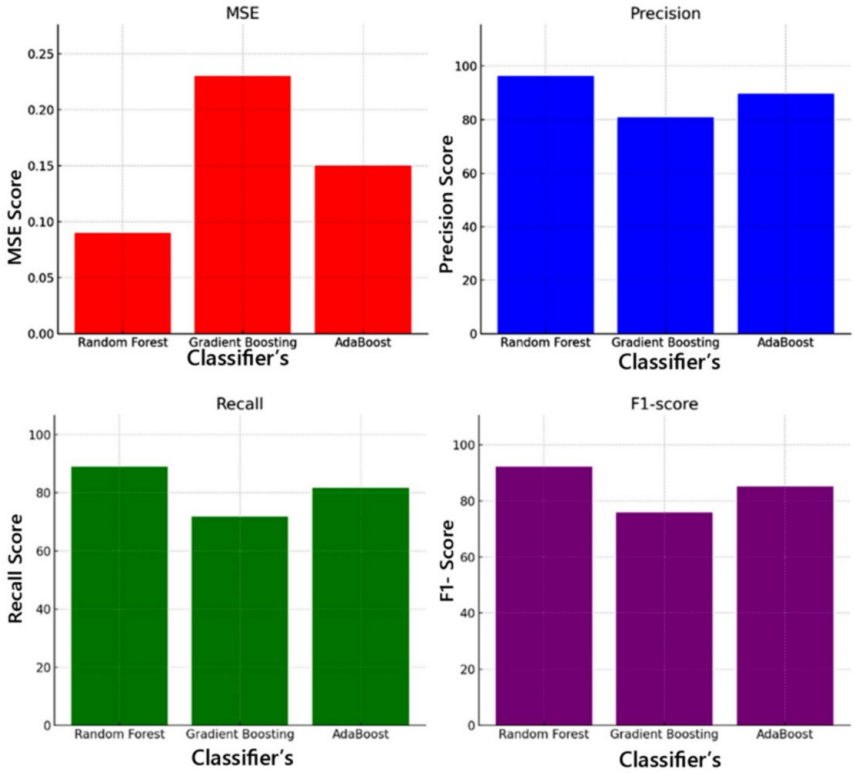

FIGURE 3: Graphical Representation of Individual Classification Matrix

Discussion

Among the three models, Random Forest performed the best in all the evaluation criteria. It recorded the lowest MSE (0.08997), which implies a higher prediction precision and stability. In addition, it registered the highest Precision (96.26%), which indicates that it was most effective at reducing false positives. Its F1-score (92.10%) and Recall (88.95%) were also the highest of the models, showing a strong equilibrium between accurately classifying positive cases and not misclassifying. Its 91.00% overall accuracy further establishes Random Forest as the outstanding performer in this classification task.

AdaBoost exhibited moderate performance with an MSE of 0.14995 and an accuracy of 85.00%. Both its Precision (89.60%) and Recall (81.66%) were lower compared to Random Forest but better than Gradient Boosting. The F1-score at 85.11% suggests that AdaBoost was fairly well balanced in terms of its ability to deal with precision and recall, but not as robust as Random Forest.

Conversely, Gradient Boosting displayed the least effective performance, with the highest MSE (0.22994) and the lowest values in all classification metrics. Its precision (80.72%), recall (71.94%), and accuracy

(77.00%) indicate poorer ability to classify data correctly, possibly caused by underfitting or susceptibility to noisy data. The graphical illustration of classification accuracy is presented in Figure 4.

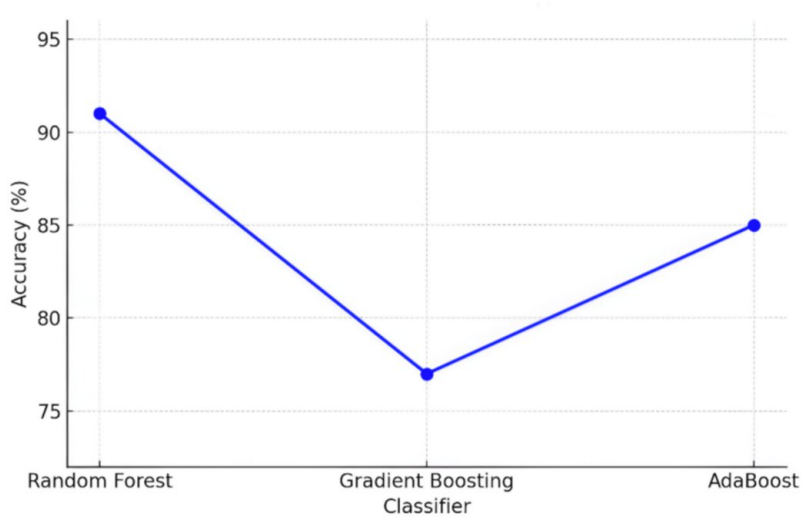

FIGURE 4: The Graphical Representation of Classification Accuracy

Random Forest became the most trustworthy classifier for the dataset and achieved high recall, precision, as well as global predictive value. Although AdaBoost provided an appropriate balance of recall and precision, Gradient Boosting performed weakly compared to all other algorithms across all factors.

Comparative analysis with previous studies

Compared to existing research that used single-feature extraction methods, the hybrid approach proposed here showed much better classification performance. In the models tested, Random Forest had the best performance, outperforming conventional machine learning classifiers. The use of multiple feature extraction methods helped to improve model robustness and generalization ability.

Previous studies using single feature extraction techniques, including LBP and HOG, generally achieved classification accuracies between 65% and 75% [22,23]. Our hybrid feature extraction approach, however, resulted in an accuracy gain of as much as 20%, which underscores the benefit of integrating heterogeneous features.

In addition, the use of ensemble learning methods helped improve the overall classification performance. Although deep learning models have demonstrated that they can provide accuracy rates over 90%, they tend to need large datasets and significant computational power. Such demands may be challenging, especially in clinical or resource-limited settings, and therefore restrict their deployability.

To emphasize the success of our methodology, we compare the accuracy of our method with existing research studies, as presented in Table 2.

Study/Reference	Method/Model	Dataset(s)	Classification Task	Highest Reported Accuracy
Kasim et al. [24]	Hybrid CNN (VGG16, InceptionV3, ResNet50) + ML classifiers (RF, SVM, XGBoost, MLP)	ALL-IDB2 + Munich AML Morphology dataset	Multiclass: Healthy, ALL, AML	88.00%
Abhishek et al. [25]	Pruned VGG16 (last three conv layers fine-tuned) + SVM	~750 microscopic blood smear images + 500 images from literature	Multiclass: CLL, ALL, CML, AML	84.00%
Almadhor et al. [26]	SVM (compared with KNN, RF, NB)	Leukemia dataset (ALL)	Binary: ALL vs. Normal	90.00%
Proposed Method	HOG + LBP + Sobel + Gabor features + Random Forest	ALL-IDB	Binary: Leukemia vs. Healthy	91.00%

TABLE 2: Comparative Analysis of Accuracy in Different Studies

CNN, Convolutional Neural Network; ML, Machine Learning; RF, Random Forest; SVM, Support Vector Machine; XGBoost, Extreme Gradient Boosting; MLP, Multilayer Perceptron; KNN, K-Nearest Neighbors; NB, Naive Bayes; HOG, Histogram of Oriented Gradients; LBP, Local Binary Pattern; ALL-IDB, Acute Lymphoblastic Leukemia Image Database; CLL, Chronic Lymphocytic Leukemia, ALL, Acute Lymphoblastic Leukemia; CML, Chronic Myeloid Leukemia; AML, Acute Myeloid Leukemia

Although accuracy has been reported to be higher by some deep learning models, they need huge sets of data and high computational resources, which makes them less feasible to use in real-world clinical environments. The proposed ensemble classifier-supported hybrid feature extraction methodology delivers competitive performance with reduced computational needs.

Conclusions

Overall, the present study presents a prospective machine learning-based method for early diagnosis of ALL from blood smear images. Utilizing various feature extraction methods and ensemble learning, specifically the Random Forest classifier, the system attained high diagnostic accuracy. Although the findings highlight its potential to aid clinical decision-making, more progress is needed to improve its generalizability, automation, interpretability, and real-world relevance. Work in these areas by way of future research will be important in taking the framework from experimental proof to functional implementation in clinical environments.

Appendices

The ALL-IDB dataset used in this study is publicly available and can be accessed at: https://homes.di.unimi.it/scotti/all/

Additional Information

Author Contributions

All authors have reviewed the final version to be published and agreed to be accountable for all aspects of the work.

Concept and design: Chandrashekar Gudada, Satishkumar Mallappa

Acquisition, analysis, or interpretation of data: Chandrashekar Gudada, Satishkumar Mallappa

Drafting of the manuscript: Chandrashekar Gudada, Satishkumar Mallappa

Critical review of the manuscript for important intellectual content: Chandrashekar Gudada, Satishkumar Mallappa

Disclosures

Human subjects: All authors have confirmed that this study did not involve human participants or tissue.

Animal subjects: All authors have confirmed that this study did not involve animal subjects or tissue. **Conflicts of interest:** In compliance with the ICMJE uniform disclosure form, all authors declare the following: **Payment/services info:** All authors have declared that no financial support was received from any organization for the submitted work. **Financial relationships:** All authors have declared that they have no financial relationships at present or within the previous three years with any organizations that might have an interest in the submitted work. **Other relationships:** All authors have declared that there are no other relationships or activities that could appear to have influenced the submitted work.

Acknowledgements

The authors gratefully acknowledge the support provided by Sri Sathya Sai University for Human Excellence through the Seed Money Grant project. This funding has been instrumental in facilitating the research work presented in this article. We also extend our sincere thanks to the university's administration and research committee for their encouragement and assistance throughout the course of this project.

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