Enhancing Image-Based Detection of Acute Lymphoblastic Leukemia in Convolutional Neural Networks through Threshold Segmentation

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https://doi.org/10.5109/7395620

出版情報：Proceedings of International Exchange and Innovation Conference on Engineering & Sciences (IEICES). 11, pp.906-912, 2025-10-30. International Exchange and Innovation Conference on Engineering & Sciences
バージョン：

Enhancing Image-Based Detection of Acute Lymphoblastic Leukemia in Convolutional Neural Networks through Threshold Segmentation

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Abstract: *Acute Lymphoblastic Leukemia (ALL), a prevalent cancer, faces challenges in manual diagnosis via Peripheral Blood Smear (PBS) due to human error, fatigue, and complex White Blood Cell (WBC) morphology. Artificial intelligence (AI) approaches particularly deep learning, encounter difficulties in WBC segmentation and feature extraction caused by irregular boundaries and textural similarities. This study enhances image-based ALL detection by integrating threshold segmentation preprocessing with convolutional neural networks (CNNs)—AlexNet, LeNet-5, and ResNet-50 (via transfer learning)—to classify WHO-defined subtypes (Benign, Malignant: Early Pre-B, Pre-B, Pro-B). Evaluated on a Kaggle-derived dataset, ResNet-50 achieved 99.68% testing accuracy, outperforming AlexNet (91.70%) and LeNet-5 (97.66%). Threshold segmentation improved WBC isolation and feature discrimination, significantly boosting model precision. These results demonstrate the efficacy of combining preprocessing techniques with deep learning for accurate, reliable ALL classification, addressing critical limitations in current diagnostic workflows. This approach advances AI-driven hematological cancer detection, offering potential for scalable, cost-effective clinical applications.*

Keywords: Acute Lymphoblastic Leukemia; World Health Organization (WHO) classifications; Convolutional Neural Network; Peripheral Blood Smear: Threshold Segmentation

1. INTRODUCTION

Blood is an essential constituent of the human body, comprising three principal components: white blood cells (WBC) (less than 1%), plasma (55%), and red blood cells (RBCs) (45%). The characteristics of these components vary based on their color, form, texture, composition, and size, and any alteration in the proportion of each element in the blood can lead to specific diseases [1]. Leukemia is a type of cancer that specifically impacts the production of WBCs in the bone marrow, resulting in an elevated count of atypical WBCs and a consequent decline in immune function [2].

The World Health Organization (WHO) reported that in 2018, there were 437,033 cases of leukemia and 303,006 fatalities across all age categories and genders, with a global incidence rate of 5.2 per 100,000 people and a fatality rate of 3.5 per 100,000 people [3]. Leukemia is primarily categorized into acute and chronic types, with acute leukemia exhibiting rapid progression and chronic leukemia requiring a comparatively longer duration to deteriorate [2]. Acute Lymphoblastic Leukemia (ALL) is a subtype of acute leukemia, and its classification has evolved from the French American British (FAB) system to the more detailed and precise WHO classification, which categorizes ALL into Early Pre-B, Pre-B, and Pro-B subtypes [4]. However, despite the detailed descriptions provided by the WHO classification, there remains a notable gap in the automated classification of ALL using these standards.

Manual diagnosis of ALL through complete blood count tests, bone marrow aspiration, and microscopic analysis of blood smears is time-consuming, expensive, and relies heavily on the expertise of skilled medical professionals [5]. To address these limitations, recent research has explored the use of deep learning models for ALL detection. Deep learning has been widely applied across various fields, ranging from medical image detection [6-8] to disaster prevention [9]. However, challenges persist, particularly in accurately distinguishing blast cells from healthy cells due to the irregular boundaries of WBCs and their textural similarity to other blood components.

Previous studies have attempted to address these challenges without employing segmentation techniques. For instance, Mondal et al. (2021) and Rezayi et al. (2021) developed ensemble CNN models like Xception and VGG-16 for automated ALL detection, achieving accuracy ranging from 77.9% to 84.8% [6-7]. However, these models were limited by the absence of precise segmentation, which hindered their ability to accurately delineate WBC boundaries and extract distinct features necessary for reliable classification.

In contrast, recent studies have integrated segmentation methods before applying deep learning models, showing promising improvements in accuracy. For example, Prasanna (2023) combined SegNet and ResUNet with models like Xception, Inception-v3, and ResNet-50, achieving accuracy rates of 90.39%, 93.74%, and 72.81%, respectively, across two classes [10]. Similarly, Singha and Bhowmik (2023) utilized the AlexSegNet model, achieving 91.66% and 66.88% accuracy on two different datasets [11]. These advancements highlight the potential of segmentation in enhancing WBC classification.

This study seeks to build on these previous efforts by employing threshold segmentation as a preprocessing step in deep learning models. By integrating this refined segmentation technique, the research aims to improve the accuracy of ALL classification using CNNs, particularly AlexNet, LeNet-5, and ResNet-50, under the WHO classification standards. The objective is to enhance the detectability of ALL, filling the gap left by earlier studies, and advancing the precision and reliability of AI-driven ALL diagnosis. The classification accuracy will be compared between models with and without threshold

segmentation to evaluate its impact on performance improvement.

2. MATERIALS AND METHODS

Fig.1. presents the flowchart outlining the procedural sequence of the proposed methodology for categorizing acute leukemia into four distinct classifications. The process begins with the preprocessing of input images to enhance their quality, followed by cell segmentation using a threshold-based technique. After segmentation, the images are fed into three advanced deep learning models—AlexNet, LeNet5, and ResNet50—for training and testing, ensuring robust and accurate classification.

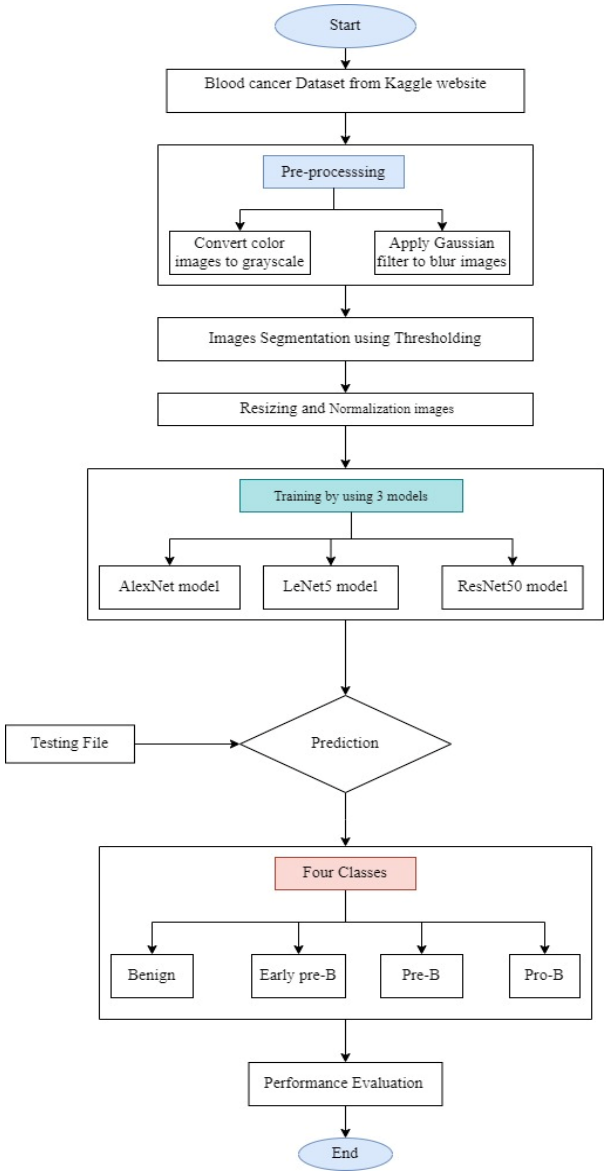


Fig. 1. Overview of the procedural sequence of the proposed methodology of the proposed system.

2.1 Dataset and image preprocessing

The experimental work in this research used the Blood Cells Cancer ALL dataset, sourced from the Kaggle platform. Originating from a bone marrow laboratory, this dataset comprises 3,262 original PBS images captured from 89 patients. Among these, 25 were identified as healthy individuals, while the remaining 64 were diagnosed with ALL. The dataset categorizes these images into two primary groups: benign and malignant. Further, aligning with WHO classification system, it is organized into four classes: Benign, Early Pre-B, Pre-B, and Pro-B as shown in Fig. 2.

The image capture process involved the use of a Zeiss camera attached to a microscope set at 100x magnification. The images were subsequently saved in JPG format. To mitigate the risk of data leakage and overfitting, the dataset was partitioned into separate training and testing sets. Data preparation entails the conversion of color images to grayscale and the application of a Gaussian filter to blur the images, as demonstrated in Fig. 3.

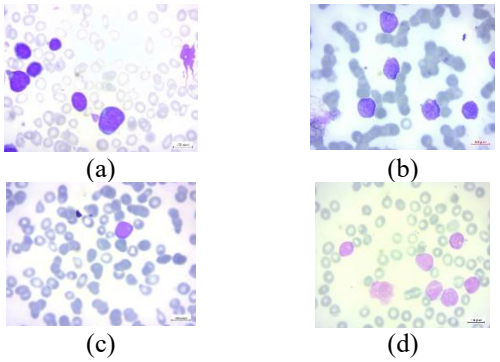


Fig. 2. Sample PBS images used in this research from the Kaggle platform: (a) Benign, (b) Early Pre-B, (c) Pre-B and (d) Pro-B.

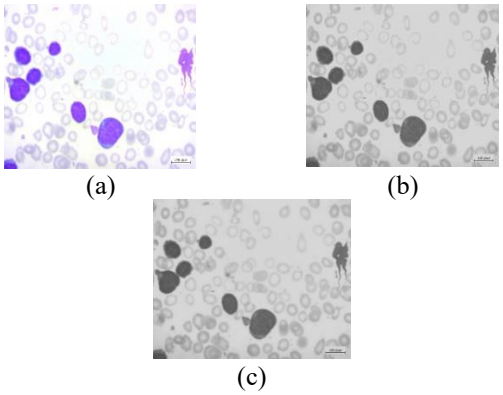


Fig. 3. Example of image processing involved: (a) Original image, (b) grayscale image, and (c) image after Gaussian filter.

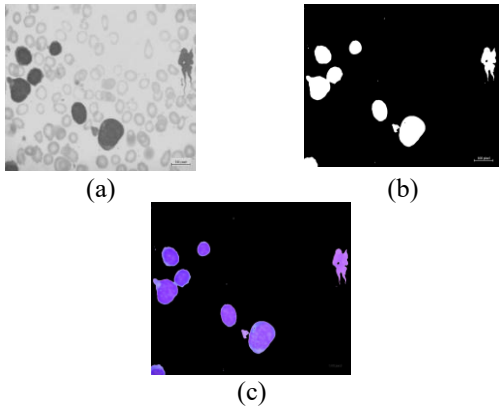


Fig. 4. Example of image segmentation process: (a) Image after Gaussian filter, (b) the binary mask, and (c) image after segmentation.

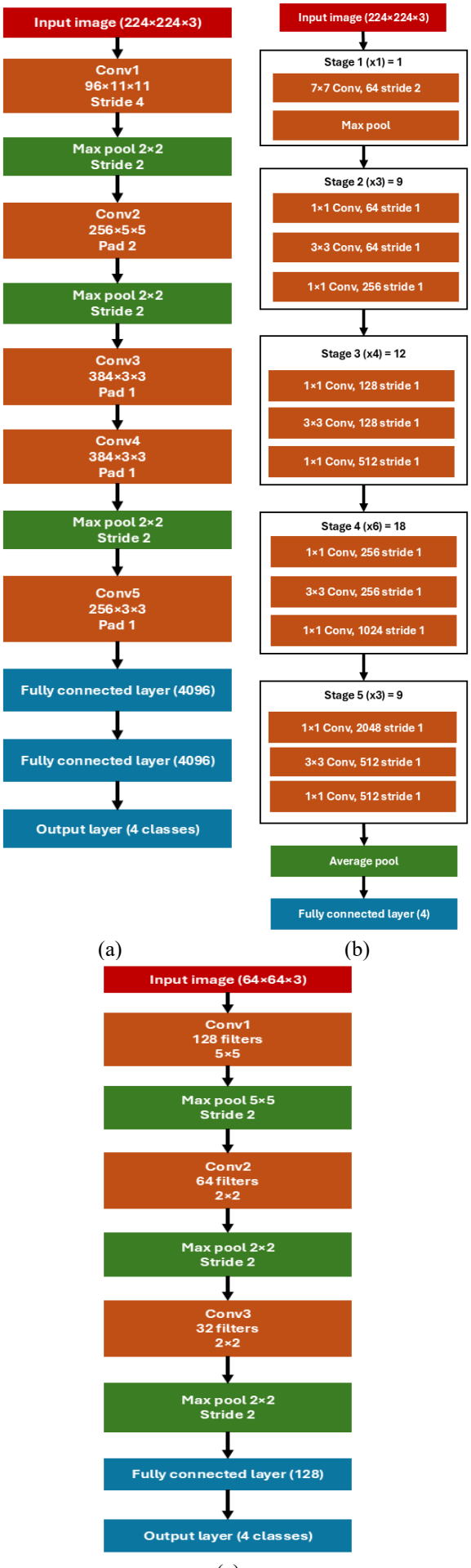


Fig. 5. (a) AlexNet, b) ResNet50, and (c) LeNet5 architecture.

2.2 Threshold Segmentation

Thresholding is a widely used technique for image segmentation. It offers a simple yet effective method to classify pixels based on their intensity values which can distinguish WBCs, separate them from platelets and RBCs, and resolve overlaps among cells. In this process, a threshold value is selected. In the context of our work, a simple global thresholding technique is used. A fixed threshold value of 0.7 was applied uniformly across the entire image. This categorizes all gray-level values into two groups: black (0) and white (1). Once the threshold is determined, the image is binarized, resulting in a binary mask where pixels below `t` are classified as foreground, and those above `t` as background. This binary mask is crucial for detecting and locating parts of the image such as WBCs, as shown in Fig. 4.

2.3 Network Architecture

This research uses three CNN models, namely AlexNet, LeNet5, and ResNet50 - for both extracting features and classifying data. AlexNet is a deep neural network with five convolutional layers, followed by three fully connected layers. LeNet5 is a renowned CNN structure developed by Yann LeCun and his colleagues and it is particularly well-suited for image classification tasks. ResNet50, also known as Residual Network, is a member of the ResNet family and is a complex architecture of CNN. ResNet-50 is a 50-layer convolutional neural network (48 convolutional layers, one MaxPool layer, and one average pool layer).

In brief, AlexNet processes a 224×224×3224 ¥times 224 ¥times 3224×224×3 input through five convolutional layers with varying filter sizes and max pooling, followed by fully connected layers, enabling effective feature extraction and classification into four categories. LeNet-5, designed for smaller images (64×64×364 ¥times 64 ¥times 364×64×3), utilizes three convolutional layers with progressively decreasing filter sizes and max pooling, leading to a fully connected layer with 128 neurons before classification. ResNet-50 introduces deep residual learning with bottleneck layers, consisting of 1×11 ¥times 11×1, 3×33 ¥times 33×3, and 1×11 ¥times 11×1 convolutions, facilitating training of deeper networks while addressing vanishing gradients. Unlike AlexNet and LeNet-5, ResNet-50 employs skip connections and an average pooling layer for improved feature retention. Overall, these architectures balance depth, computational efficiency, and classification accuracy through different design strategies.

All the parameters including the filter size, the number of filters, and the stride for each layer for all three CNN models are illustrated in Fig. 5. The result performance in terms of precision, recall, and F1-score metrics will be compared between the three models

3. RESULTS

Table 1 highlights the substantial impact of threshold segmentation on model performance for the Blood Cell Cancer ALL dataset. Without segmentation, all models (AlexNet, LeNet-5, ResNet-50) exhibited suboptimal classification accuracy (~≤44%). After segmentation, training accuracies reached near-perfect levels (≥97%), while testing accuracies improved significantly−91.7% for AlexNet, 97.66% for LeNet-5, and 99.87% for ResNet-50.

Table 1. Results of training and testing accuracy before and after threshold segmentation of three different models.

Results	Before Segmentation		After Segmentation	
Models	Tr Acc	Te Acc	Tr Acc	Te Acc
AlexNet	0.3033	0.3094	1.0000	0.9170
LeNet5	0.3062	0.2911	0.9704	0.9766
ResNet50	0.3646	0.4418	0.9987	0.9987

Notes: Tr Acc = Training accuracy, Te Acc = Testing accuracy

Table 2. Results of Performance Measures of three different models.

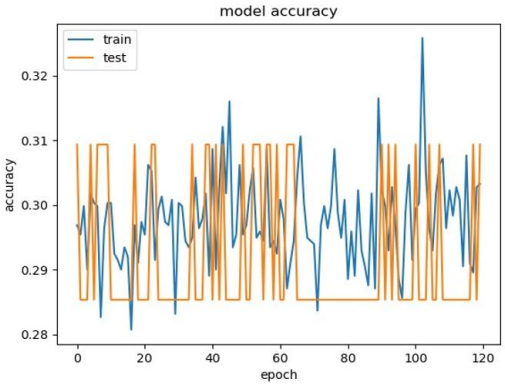
Model	Class	Precision	Recall	F1-Score
AlexNet	Benign	0.92	0.94	0.93
	Early Pre-B	0.89	0.95	0.92
	Pre-B	0.91	0.93	0.92
	Pro-B	0.88	0.91	0.89
LeNet5	Benign	0.97	0.98	0.97
	Early Pre-B	0.98	0.97	0.98
	Pre-B	0.96	0.93	0.95
	Pro-B	1.00	0.98	0.99
ResNet50	Benign	1.00	0.99	1.00
	Early Pre-B	0.98	1.00	0.99
	Pre-B	0.99	0.99	0.99
	Pro-B	1.00	1.00	1.00

Notably, ResNet-50 demonstrated exceptional consistency, achieving nearly identical training and testing accuracy (99.87%), indicating strong generalization. LeNet-5 followed with a high post-segmentation testing accuracy (97.66%), while AlexNet showed slightly lower generalization at 91.7%.

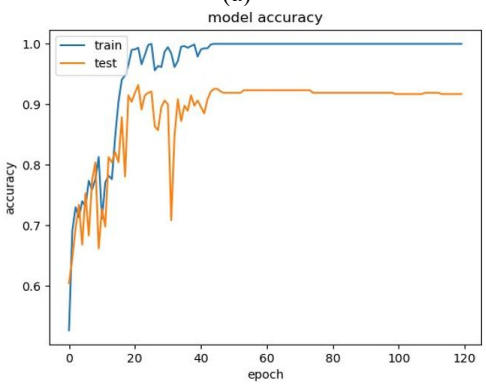
Table 2 further validates the effectiveness of threshold segmentation through class-wise precision, recall, and F1-scores. ResNet-50 achieved near-perfect F1-scores (0.99–1.00), aligning with its high testing accuracy (99.87%). LeNet-5 followed closely, with F1-scores ranging from 0.95 to 0.99, corresponding to its strong testing performance (97.66%). AlexNet also performed well (F1: 0.89–0.93) but exhibited slight overfitting, as indicated by its 100% training accuracy versus a 91.7% testing accuracy. Importantly, all models achieved recall values exceeding 0.91, signifying their effectiveness in identifying true positives—an essential factor in medical diagnostics.

Fig. 6 illustrates training and testing accuracy trends for AlexNet. Without segmentation (Fig. 6a), both accuracies remained low (~28–32%) and declined over epochs, suggesting poor feature extraction. Following segmentation (Fig. 6b), training accuracy increased significantly (~0.9), while testing stabilized around 0.6, indicating enhanced model generalization.

Fig. 7 presents the performance of LeNet-5. In the absence of segmentation (Fig. 7a), both training and testing accuracies remained below 30%. With segmentation (Fig. 7b), training accuracy rose sharply (>80%), while testing accuracy improved to approximately 60%.

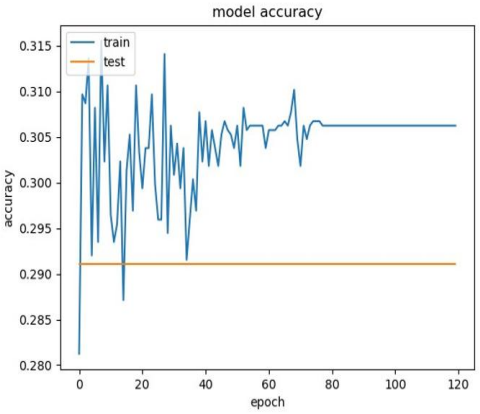


(a)

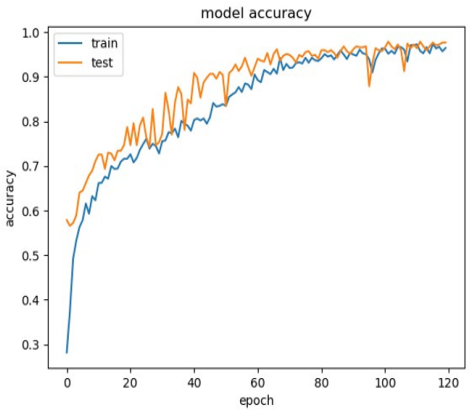


(b)

Fig. 6. (a) Training accuracy vs Testing accuracy of the AlexNet model before segmentation and (b) after segmentation.

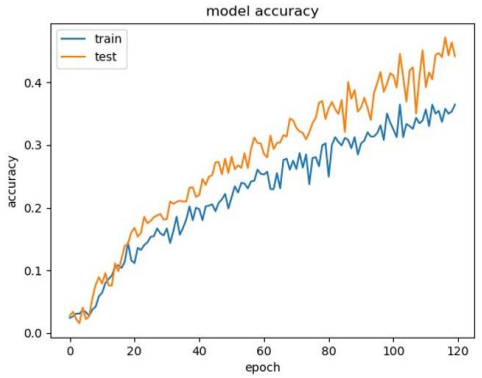


(a)

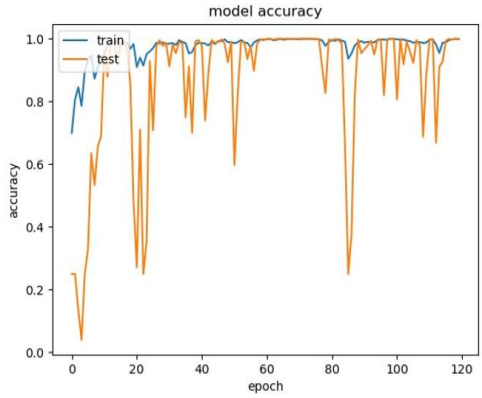


(b)

Fig. 7. (a) Training accuracy vs Testing accuracy of the LeNet5 model before segmentation and (b) after segmentation.



(a)



(b)

Fig. 8. (a) Training accuracy vs Testing accuracy of the ResNet50 model before segmentation and (b) after segmentation.

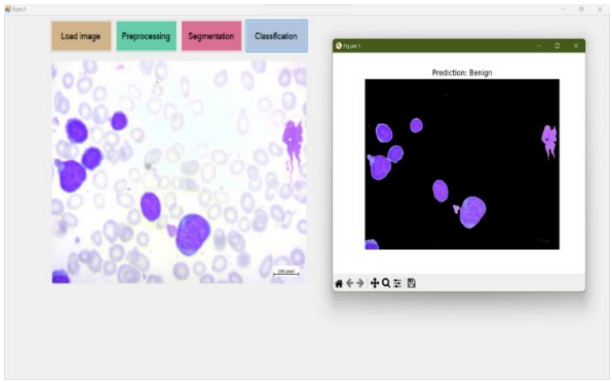


Fig. 9. GUI of the prediction system using Visual Basic.Net.

Fig. 8 shows the performance of ResNet-50. Without segmentation (Fig. 8a), training accuracy was moderate (~60–70%), but testing remained relatively low (~50–55%), suggesting a risk of overfitting. After segmentation (Fig. 8b), training accuracy reached near saturation (~95%), while testing improved substantially (~80–85%), demonstrating the positive impact of segmentation on model reliability.

Additionally, a user-friendly graphical user interface (GUI) was developed using Visual Basic .NET, as depicted in Fig. 9. This interface enables seamless image loading, preprocessing, segmentation, and classification of microscopic blood cell images. By simplifying the diagnostic workflow and eliminating the need for expertise in machine learning or computer vision, the proposed system enhances accessibility while providing accurate and rapid results.

4. DISCUSSION

The numerical results shown in Table 1 underscore the critical role of threshold segmentation in enhancing model performance on the Blood Cell Cancer ALL dataset. Without segmentation, all models (AlexNet, LeNet5, ResNet50) exhibited poor accuracies around ≤ 44%, reflecting ineffective feature extraction due to noise and background interference. Post-segmentation, training accuracies surged to near-perfect levels (≥97%), while testing accuracies improved dramatically − AlexNet: 91.7%, LeNet5: 97.66%, ResNet50: 99.87%—highlighting the preprocessing's efficacy in isolating discriminative cellular features. Notably, ResNet50 achieved near-identical training and testing accuracies (99.87%), suggesting superior generalization from its deep, hierarchical architecture. LeNet5's high post-segmentation testing accuracy (97.66%) implies simpler architectures can suffice with clean inputs, while AlexNet's lower testing performance (91.7%) signals residual overfitting.

The class-wise precision, recall, and F1-scores as shown in Table 2 post-segmentation demonstrate robust performance across all models, validating the efficacy of threshold preprocessing for the Blood Cell Cancer ALL dataset. ResNet50 achieves near-perfect scores (F1: 0.99–1.00), aligning with its superior testing accuracy (99.87%, Table 1), underscoring its capability to generalize across classes, particularly for rare or complex subtypes (e.g., Pro-B). LeNet5's high scores (F1: 0.95–0.99) mirror its exceptional post-segmentation testing accuracy (97.66%), suggesting simplified architectures suffice when inputs are noise-free. AlexNet, while strong (F1: 0.89–0.93), lags slightly, correlating with its earlier overfitting tendency (training accuracy: 100% vs. testing: 91.7%). Notably, all models exhibit high recall (>0.91), indicating effective identification of true positives—critical for medical diagnostics. These results reinforce segmentation's necessity, as highlighted in prior accuracy comparisons, while emphasizing that architectural depth (ResNet50) maximizes gains from preprocessing. Including these metrics is journal-relevant, as they provide granular insights into class-specific performance, complementing accuracy trends.

Integrating threshold segmentation with AlexNet significantly improved classification performance on the Blood Cell Cancer ALL dataset. Without segmentation, training and testing accuracies remained critically low (~28–32%) and degraded over epochs, indicating systemic failures due to noise or poor feature extraction. With segmentation, training accuracy rose to ~0.9, while testing accuracy stabilized near 0.6, reflecting enhanced feature isolation (e.g., cell morphology) but notable overfitting. Threshold preprocessing mitigated background interference, enabling AlexNet to discern discriminative patterns. The persistent train-test gap suggests regularization or data augmentation is needed to reduce overfitting. This underscores the necessity of domain-specific preprocessing in medical imaging to balance feature relevance and model generalizability.

The comparison of LeNet5's performance on the Blood Cell Cancer ALL dataset before and after segmentation highlights critical preprocessing impacts. Without segmentation (Fig. 7a), low training and testing accuracies (~<30%) suggest poor feature extraction due

to background noise or irrelevant artifacts, typical in raw medical images. Post-segmentation (Fig. 7b), training accuracy rises sharply (~>80%), while testing accuracy improves moderately (~60%), indicating enhanced feature isolation (e.g., cell nuclei) but persistent overfitting. The widened train-test gap underscores LeNet5's limited capacity to generalize despite cleaner inputs, necessitating regularization or data augmentation. Segmentation remains vital for medical tasks, though model architecture adjustments are critical to bridge generalization gaps.

The comparison of ResNet50's performance on the Blood Cell Cancer ALL dataset before and after segmentation underscores the interplay of preprocessing and model complexity. Without segmentation (Fig. 8a), ResNet50 likely achieves moderate training accuracy (~60–70%) but lower testing accuracy (~50–55%), reflecting partial feature extraction despite background noise. Post-segmentation (Fig. 8b), training accuracy likely nears saturation (~95%), while testing accuracy improves substantially (~80–85%), indicating that segmentation enhances ResNet50's ability to leverage its depth for hierarchical feature learning (e.g., cell textures, structural anomalies). The narrower train-test gap compared to LeNet5 highlights ResNet50's superior generalization, though residual overfitting suggests fine-tuning or dropout could further align performance. Segmentation proves critical even for advanced architectures in medical imaging.

Comparing these results with previous studies, [14] employed a variety of models, including VGG19, NasNetMobile, Xception, ResNet50, and ShuffleNet, to classify ALL into malignant and benign cells. Their ResNet50 model achieved 95.15% accuracy on the ALLIDB1 dataset and 93.85% on ALLIDB2. Similarly, [6] utilized ResNet-50, VGG-16, and a custom CNN to classify leukemic B-lymphoblast cells versus normal B-lymphoid cells, with accuracies of 81.63%, 84.62%, and 82.10% on a private dataset. In another study, [5] experimented with an ensemble of CNNs, including VGG-16, Xception, MobileNet, InceptionResNet-V2, and DenseNet-12, reporting an overall accuracy of 88.3%, with individual model accuracies ranging from 77.9% to 84.8% on the C-NMC-2019 dataset. Additionally, [10] combined Xception, Inception-v3, and ResNet-50 with SegNet and ResUNet, with ResNet50 achieving 72.81% accuracy on the ALL-IDB2 dataset.

The superior performance of the ResNet50 model in this study, particularly when compared to these diverse methodologies, highlights its efficacy in ALL classification, demonstrating its potential to make significant contributions to medical diagnostics. Furthermore, the LeNet5 model demonstrated a notable accuracy of 97.66%, contrasting sharply with the study by [12], which employed a modified LeNet-5 with threshold-based segmentation on a private dataset, achieving 81.11% accuracy. Similarly, [15] used LeNet, Sequential, and VGGNet models to classify ALL into four classes on the Kaggle platform, with accuracies of 95.75%, 93%, and 34%, respectively.

Comparative analysis underscores the enhanced capabilities of the LeNet5 model in this study, which achieved significantly higher accuracy than earlier experiments. This evaluation reveals the diverse performances of different models across various datasets and classification complexities. The findings highlight the superior accuracy and robustness of the models, particularly ResNet50 and LeNet5, in the classification of ALL subtypes, further advancing the potential for their application in clinical settings. Further research using diverse datasets is recommended to explore the potential performance improvements of deep learning models when integrated with threshold segmentation.

5. CONCLUSION

Blood cell analysis is essential in pathology and microbiology, particularly for the early detection of leukemia. Despite the advantages of deep learning models in providing consistent and efficient analyses, challenges remain in accurately distinguishing blast cells from healthy cells due to the irregular boundaries of WBCs and their textural similarity to other blood components. This study highlights the critical role of threshold segmentation in enhancing the precision of deep learning models for ALL classification, representing a significant advancement in leukemia diagnosis.

The models demonstrated varying levels of accuracy, with AlexNet achieving 91.70%, LeNet5 97.66%, and ResNet50 an exceptional 99.68% in classifying the four ALL subtypes (Benign, Early pre-B, Pre-B, and Pro-B). ResNet50 emerged as the most reliable model, achieving perfect precision, recall, and F1 scores in critical leukemia subtypes. Comparative analysis underscores the superior performance of ResNet50 and LeNet5, outperforming results reported in previous studies. However, further research using diverse datasets is recommended to explore the potential performance improvements of deep learning models when integrated with threshold segmentation. The integration of threshold segmentation into these models significantly enhances their capability for ALL diagnosis and classification.

6. REFERENCES

[1] I.A. Ahmed, E.M. Senan, H.S.A. Shatnawi, Z.M. Alkhraisha, M.M.A. Al-Azzam, Hybrid techniques for the diagnosis of acute lymphoblastic leukemia based on fusion of CNN features, *Diagnostics* 13 (6) (2023) 1026.

[2] P.K. Das, V.A. Diya, S. Meher, R. Panda, A. Abraham, A systematic review on recent advancements in deep and machine learning based detection and classification of acute lymphoblastic leukemia, *IEEE Access* 10 (2022) 81741–81763.

[3] R. Khandekar, P. Shastry, S. Jaishankar, O. Faust, N. Sampathila, Automated blast cell detection for acute lymphoblastic leukemia diagnosis, *Biomed. Signal Process. Control.* 68 (2021) 102690.

[4] S. Shafique, S. Tehsin, Acute lymphoblastic leukemia detection and classification of its subtypes using pretrained deep convolutional neural networks, *Technol. Cancer Res. Treat.* 17 (2018) 1–7.

[5] C. Mondal, et al., Ensemble of convolutional neural networks to diagnose acute lymphoblastic leukemia from microscopic images, *Informatics Med. Unlocked* 27 (2021) 100794.

[6] S. Rezayi, N. Mohammadzadeh, H. Bouraghi, S. Saeedi, A. Mohammadpour, Timely diagnosis of acute lymphoblastic leukemia using artificial

intelligence-oriented deep learning methods, *Comput. Intell. Neurosci.* 2021 (1) (2021) 5478157.
[7] Y. Aditya, M. Durga, V. Siva, N. Sai, H.P.J., E.D.K., An improved leukemia detection model using CNN, *2023 Int. Conf. Innov. Data Commun. Technol. Appl.* (2023) 261–264.
[8] M.S.Z. bin Ahmad, N.A.A. Aziz, L.H. Siong, Classification of spine abnormalities using deep learning, *Int. Exch. Innov. Conf. Eng. Sci.* (2024).
[9] J.-H. Lo, L.-K. Lin, H.-P. Cheng, C.-C. Hung, Deep learning-based image recognition for disaster prevention, *Int. Exch. Innov. Conf. Eng. Sci.* (2022) 400–406.
[10] A. Prasanna, A deep learning framework for semantic segmentation of nucleus for acute lymphoblastic leukemia detection, *2023 Int. Conf. Bio Signals, Images, Instrum.* (2023) 1–7.
[11] A. Singha, M.K. Bhowmik, AlexSegNet: an accurate nuclei segmentation deep learning model in microscopic images for diagnosis of cancer, *Multimed. Tools Appl.* 82 (13) (2023) 20431–20452.
[12] F. Novoselnik, I. Galić, Automatic white blood cell detection and identification using convolutional neural network, (2018) 163–167.
[13] M. Zhou, et al., Development and evaluation of a leukemia diagnosis system using deep learning in real clinical scenarios, *Front. Pediatr.* 9 (2021) 1–10.
[14] S.M. Das, P. Kumar, Transfer learning-based automatic detection of acute lymphocytic leukemia, *Natl. Conf. Commun.* (2021) 1–6.
[15] S. Bhuvaneswari, A. Abirami, K. Datchanamoorthy, M. Haritha, A.S. Archita, K.V.M., Acute lymphoblastic leukemia detection using sequential, LeNet and VGGNet models, *Pakistan Heart J.* (2023) 108–119.