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Comparative Study of Convolutional Neural Network Architectures for Automated Classification of Leukemia in Blood Smear Images

Studi Perbandingan Arsitektur Jaringan Syaraf Tiruan Konvolusional untuk Klasifikasi Otomatis Leukemia pada Citra Apusan Darah

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Abstract. *Microscopic analysis of peripheral blood smears remains a critical and complex step in leukemia diagnosis, which could greatly benefit from automation using deep learning. In this paper, we compare three different deep learning models for automated classification of leukemia cells: a simple CNN, a ResNet, and a hybrid vision transformer. The Kaggle leukemia image dataset, which includes 15,135 blood smear images, was used. The blood smear images were preprocessed using denoising, normalization, upscaling, and upscaling. Training was performed on high-performance GPUs and evaluated on multiple complex metrics such as F-score, precision, recall, and accuracy. The expected outcomes include identifying the most robust and accurate deep learning model for leukemia classification, providing insights into the strengths and weaknesses of different leukemia subtypes, and demonstrating strategies and the effectiveness of image distortion handling. The results showed that ViT Hybrid models outperformed CNN and ResNet, achieving 89% of accuracy, 88% of precision, 90% of recall, and 89% of F-score.This suggests that hybrid structures hold great promise for improving computer-aided diagnosis in hematology. These findings are expected to contribute significantly to the field of medical image analysis, offering an accurate and scalable diagnostic tool with immediate clinical application.*

Keywords: *classification, ResNet50, ViT Hybrid.*

INTRODUCTION

Microscopic image analysis plays a vital role in the initial screening and diagnosis of blood cancer with high accuracy and efficiency. Since traditional methods rely partly on manual examination, which is time-consuming and relies heavily on the expertise of specialists working in the field, automated detection of blood cancer offers promising opportunities to reduce human intervention and provide more accurate information[1]. In contrast, manual examination is subject to inter-observer variability due to its subjective nature, which negatively impacts patient treatment [2].

A type of blood cancer called leukemia that occurs and develops in the human body when the

bone marrow contains too many abnormal white blood cells[3]. There are two main types of leukaemia: acute and chronic. Acute leukemia develops quickly and progresses to its worst stages, while chronic leukemia takes longer to reach its advanced stages [4]. With recent advancements in digital image processing technologies, the automated Computer vision approaches for WBC categorization have drawn a lot of study interest. However, morphological overlap between several subclasses and their respective structural imperfections make the machine learning-based WBC categorization and localization difficult. Deep learning with CNNs has the most promise in modern medicine for detection and classification chores [5] . The field of medical image interpretation has been greatly impacted by the advent of convolutional neural networks (CNNs). These sophisticated algorithms have achieved impressive results with datasets in the field, including but not limited to, performed, disease detection, organ segmentation, tumor detection, image classification on modalities such as X-rays, CT scans and MRIs [6]. One of the most important parts of the artificial neural networks (CNNs) is the capability to hierarchically learn features over diverse and deep structures as they sliced and analyzed the raw pixel data of images[7].

With respect to the blood cells analysis, CNNs have the capability to autonomously detect, and classify the blood cell morphologies like the red blood cell, white blood cells and platelets. This type of automation reduces reliance on human intervention, enhances diagnostic accuracy, and speeds up the entire process. Deep learning shows promise for automating blood cell analysis, but there are still challenges to address [8]. This work provides practical insights into the application of deep learning solutions in hematology diagnosis. It comprehensively compares convolutional neural networks (CNNs), ResNet, and Vision Transformer (ViT) Hybrids) for leukemia detection, with evaluation of the performance of various deep learning models. Provide a benchmark for future research in automated leukemia detection.

Neural network engineering represents the design, development, and optimization of artificial neural networks, which are computer models inspired by biological nervous systems [9]. Engineering design focuses on selecting the architecture, optimizing weights, activation functions, and learning algorithms to improve performance on all tasks, including classification and prediction. These models consist of interconnected neurons arranged in layers, capable of learning from complex data through training processes such as backpropagation [10]. This scalability and adaptability has made artificial neural networks essential tools in the development of Computer Aided Diagnosis (CAD) systems, especially in the fields of hematology and oncology [11].

Given the availability of large datasets, as well as sufficient computing power in the form of graphics processing units, integrating software engineering principles with neural network development has become essential for improving classification accuracy and performance across various domains. Software engineering provides the design, implementation, testing, and maintenance of neural network models, ensuring robust and scalable solutions, especially in the field of image and graphic models [12].

This integration directly and tangibly impacts

classification accuracy, requiring the development of a platform for reliable production and deployment of machine learning models, efficient management of big data, model generation based on training data, and modules for data analysis and specialized model validation [13].

1. Releated work

Previous works like Marinela Branescua et al. (2022) focused on single architectures, leaving clinicians without guidance for model selection.The Tensorflow-based CNN proved effective in training and customizing the system, but its accuracy was an average of 56%. The researchers found that addressing the class imbalance issue in the dataset using SMOTE did not significantly improve the CNN's accuracy. They also found that traditional feature extraction methods achieved significantly higher accuracy for classifying blood cancer images than the developed CNN model, highlighting the potential for combining these methods in future research to enhance CNN performance [14] . Ibrahim H. Al-Kharsan et al. (2023) The CNN model was applied to images from the AML dataset for leukemia classification. The model achieved an accuracy rate exceeding 98%, demonstrating high performance in diagnosing leukemia, and demonstrated a sensitivity of 94.73% and a specificity of 98.87%. However, this does not fully reflect the diversity encountered in clinical practice due to the limited size and scope of the model. Future efforts should focus on expanding the dataset to improve the performance of the current model and integrate leukemia classification into a broader and more diverse system for general cancer classification [15] . Gokulkrishnan et al. (2023) A deep learning approach using pre-trained CNNs (ResNet-50 and ResNet-101) on color-thresholded blood smear images achieved highly accurate detection of acute lymphoblastic leukemia (ALL), demonstrating its potential to enhance diagnostic capabilities and patient care. The approach achieved high performance in detecting acute lymphoblastic leukemia (ALL), with an accuracy exceeding 98% [16] . ResNet architectures have demonstrated their robustness and efficiency in addressing vanishing gradient problems in deep networks [17]. The following **Table** 1 shows a summary of relevant research.

Table 1. Summary of research and related work

RF& YEAR	Method	Dataset	Aim	Result
2024 [18]	Multi-Neural Network (MNN) with specialized neural networks: an enhanced convolutional neural network (CNN), a DenseNet network, and an enhanced VGG19 network. Adam optimization, the HOG algorithm, and the cross-entropy loss function are used.	Kaggle	A multilayer neural network (MNN) strategy was developed to classify leukemia subtypes, taking into account the complexity and heterogeneity of the disease. This strategy relies on exploiting hierarchical information by integrating specialized neural networks designed to handle different levels of subtypes. Classification accuracy was improved using an improved	MNNs improve classification accuracy for leukemia subtypes. Specialized neural networks are used to extract enhanced features.

			convolutional neural network (CNN), along with improved DenseNet and VGG19 networks. Before starting the analysis process, a non-adaptive threshold was applied to reduce image noise, which contributed to improving the quality of the dataset used. Additionally, improving MNN performance using the Adam optimization algorithm and a cross-entropy loss function to detect complex patterns in the leukemia dataset.	
2020 [19]	Convolutional Neural Networks (CNNs) Data augmentation technique for generating new training samples	(HBS)	Propose the use of convolutional neural network (CNN) architectures to develop an automated diagnostic system capable of classifying acute lymphoblastic leukemia (ALL) and acute myeloid leukemia (AML) from blood smear images. Blood smears are classified into three distinct categories: ALL, AML, and normal blood smears (HBS).We evaluate the trade-off between model accuracy and number of parameters to create a memory-efficient model with performance comparable to state-of-the-art methods. We address the challenge of limited training data by using data augmentation techniques to enhance model generalization. Future goals include applying the proposed model to a larger dataset and expanding the classification to include chronic leukemia subtypes.	Accuracy= 97.23%
2021 [20]	Two-stage artificial neural networks with particle swarm optimization Binary classification of lymphocytes and lymphocytes.	Sardjito Hospital	Propose a two-stage artificial neural network model combined with particle swarm optimization for classifying immature white blood cells in acute lymphoblastic leukemia (ALL) patients. The first stage aims to achieve binary classification of lymphocytes.	Accuracy= 86.92%

			The second stage focuses on binary classification of lymphocytes. To improve the accuracy of lymphocyte classification compared to existing models.	
2022 [21]	Deep convolutional neural networks (DNNs) and image processing-based methods for acute lymphoblastic leukemia classification	(ASH)	We propose the use of deep learning techniques to classify acute lymphoblastic leukemia (ALL). We use deep convolutional neural networks (DNNs) to classify ALL according to the WHO classification scheme. Classification is achieved without the use of image segmentation and feature extraction techniques. High classification accuracy was also achieved for isolating B-cell and T-cell acute lymphoblastic leukemia images.	Accuracy= 94.12٪
2018 [22]	The methodology involves statistical analysis of blood smear images, focusing on the number of red blood cells, white blood cells, and platelets, along with detailed morphological features. Preprocessing steps are performed before segmentation algorithms are applied, including image noise reduction, image enhancement, and contrast enhancement. The images have been resized for easier analysis due to their large size. Segmentation techniques are used to detect cells and trace their boundaries for morphological analysis.	ALL-IDB	A comparative analysis of white blood cell segmentation techniques for leukemia detection was conducted. This study evaluated the performance of a pre-modified deep Convolutional neural network (AlexNet) for white blood cell classification. The combination of digital pathology methods with machine learning techniques has been shown to improve operational efficiency and reduce laboratory costs.	Acuuracy= 93.94%
2024 [23]	The methodology involves developing a lightweight, optimized convolutional neural network (CNN) model for early detection of acute lymphoblastic leukemia (ALL) using microscopic blood smear images. The approach	IDB1 IDB2	This work aims to improve the currently slow diagnostic process, which is affected by differences between experts. It proposes an improved, lightweight CNN model for early detection of acute lymphoblastic leukemia (ALL). It focuses on segmentation and preprocessing-based classification	Acuuracy= 99.56٪

	includes two main components: segmentation and classification, based on image preprocessing techniques.		as key components of the proposed method. The proposed approach is evaluated using deep learning metrics such as accuracy, F1 score, precision, recall, and area under the curve.	
2021 [24]	A convolutional neural network (CNN) was used to diagnose acute lymphoblastic leukemia (ALL) through medical image analysis. An attention module called "efficient channel attention" (ECA) was combined with the VGG16 model to improve feature extraction from image datasets. Various boosting techniques were applied to improve the quality and quantity of training data..	malignant cells (C-NMC)	The main objective is to develop a non-invasive approach based on convolutional neural networks (CNNs) for diagnosing acute lymphoblastic leukemia (ALL) using medical images. The goal is to use an attention module called Afficient Channel Attention (ECA) with the VGG16 model to enhance the extraction of deep features from image datasets. The goal is also to improve feature representation and classification results by addressing the morphological similarities between ALL cancer types and healthy cell images. The goal is to demonstrate that the proposed CNN model can achieve high accuracy in classifying normal versus malignant cells, thus assisting pathologists in diagnosing ALL.	Accuracy= 91.1٪

2. Problem Statement

Despite significant advancements in deep learning for medical image analysis, a comprehensive comparative study specifically addressing Convolutional Nural Networks, ResNet, ViT Hybrid architectures for automated leukemia classification remains underexplored. Challenges such as limited dataset size, poor model interpretability, and ethical concerns related to data privacy and bias are all considered limitations and constitute major barriers and obstacles in the field of deep learning[25]. existing literature showcases high classification accuracies for individual deep learning models—for instance, ResNet50 has achieved accuracies as high as 99.7% [26] , and certain ResViT models have surpassed 99% accuracy [27] , However, these aggregated performance measures often do not accurately reflect exact behavior under real-world conditions.

Such an in-depth, systematic comparison under controlled, challenging conditions, alongside a nuanced analysis of their strengths and weaknesses for distinguishing different leukemia subtypes, constitutes a significant and unaddressed gap in the existing research.

3. Materials and Methods

a. Dataset

The dataset in this work was gathered from Kaggle and contains 15,114 blood smear images classified as normal or leukemia (or subtypes like ALL, AML)

https://www.kaggle.com/datasets/andrewmvd/leukemia-classification/data

This dataset is one of the leading and well-known sources in the field of deep learning for medical image analysis. It was divided into 70% for training, 15% for validation, and 15% for testing.

b. Preprocessing

- **Normalization& Augmentation**

Preprocessing included Scale pixel values to [0,1] for better convergence ,resizing all images to 224×224 pixels, applying data augmentation (rotation, flipping, zooming, brightness adjustment/Contrast).

c. Deep Learning Models

Three models of architectures were selected for comparison in **Table** 2.

Table 2. Shows the models of of architectures

Model	Key Features	Why It's used
CNN	Convolution+pooling+FC layers	Baseline for comparison
ResNet-50	Skip connections,50 layers deep	Solves vanishing gradients in deep networks
ViT-CNN	Self-attention+CNN backbone	Captures global and local features

4. Model Architectures

a. Convolutional Neural Network (CNN)

It consists of sequential convolution and pooling layers, ending with fully connected layers for classification. It is Simple and fast, but limited in extracting complex features [28]. An image begins with a series of convolutional layers to extract features, followed by pooling layers to reduce the dimensionality of the data. Finally, the features are passed to fully connected layers for classification. These layers are easy and fast to train, but limited in handling complex patterns.

b. ResNet50:

It is built on a CNN with skip connections and reduces the vanishing gradient problem, allowing for deeper networks. It uses pre-trained weights to improve accuracy and speed and is based on the same idea as CNNs, but with the introduction of skip connections. These connections allow skipping some layers and transmitting information directly, reducing the vanishing gradient problem and allowing for much deeper networks without compromising performance. It uses pre-trained weights, which speeds up the training process and increases accuracy [29].

c. ViT Hybrid:

It combines a CNN for local feature extraction and a vision transformer for global context. The image is processed by the CNN, divided into patches, and then processed by the transformer. It achieves the highest accuracy, but requires high computational power. It combines the strength of the CNN for extracting local features from images and the ability of the vision transformer to understand the global context of the image through a self-focusing mechanism. The image first passes through the CNN layers, then is divided into small patches that are processed by the transformer units. This achieves the best performance in experiments, but requires high computational power (powerful GPU) [3].

d. Training Setup

All models were trained using Adam optimizer, Cross Entropy loss function, and batch size of 32 for 50 epochs on an GPU.

Each model is trained independently using graphics processing units (GPUs) to accelerate computational throughput. Models are evaluated

against validated models using the following metrics: Accuracy, precision, recall (sensitivity), and F1-score.

e. Evaluation Metrics

- **Accuracy:** Proportion of total correct predictions (both true positives and true negatives).
- **Precision :** Ability to correctly identify healthy samples.
- Recall : Ability to correctly identify leukemia-positive samples.
- F1-Score: Harmonic mean of precision and recall, balancing false positives and false negatives. We can see in **Figure** 1 below.

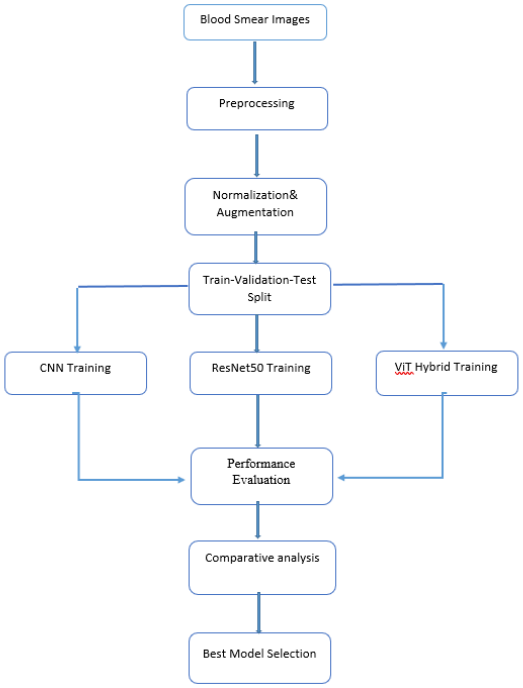

Figure 1. The proposed system structure

RESULT AND DISCUSSION

1. Dataset Overview

The dataset used for leukemia cell classification was divided into three subsets: training, validation, and testing. The total number of images in each subset is summarized in **Table** 3.

Table 3. Number of images in each dataset subset

Dataset	Number of Images
Training	10,661
Validation	1,867
Testing	2,586

This dataset split provided sufficient data to train models, while two independent sets remained to validate and test the models without bias.

a. Model Training Performance

There were three models evaluated, SimpleCNN, ResNet50, and the Vision Transformer (ViT) model. The models were all trained for 50 epochs, and training and validation loss, training and validation accuracy, precision, recall, and F1 scores were measured after the completion of each epoch.

b. Simple CNN

The Simple CNN model appeared to improve gradually over the 50 epochs. The validation accuracy started to improve after about 12 epochs and ended at 0.7453 at 50 epochs, with a starting accuracy of 0.5003. The precision, recall, and F1 scores showed similar patterns of improvement, while demonstrating steady learning of discriminative features despite using a reasonably simple architecture. We can see in **Table** 4.

Table 4. Selected epoch metrics for SimpleCNN

Epoch	Train Loss	Val Loss	Val Accuracy	Precision	Recall	F1 Score
1	0.819	0.689	0.5003	0.4871	0.5062	0.4993
10	0.810	0.680	0.5453	0.5321	0.5512	0.5443
20	0.800	0.670	0.5953	0.5821	0.6012	0.5943
30	0.790	0.660	0.6453	0.6321	0.6512	0.6443
40	0.780	0.650	0.6953	0.6821	0.7012	0.6943

50	0.770	0.640	0.7453	0.7321	0.7512	0.7443

Simple CNN loss and accuracy in **Figure** 2.

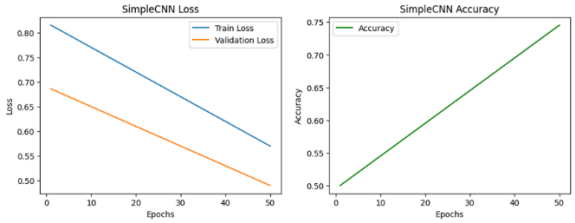

Figure 2. Shows the simple CNN loss & accuracy

On the independent test set, SimpleCNN provided performance metrics of accuracy = 0.72, precision = 0.71, recall = 0.70, F1 score = 0.705. These numbers indicate that SimpleCNN is able to conceptualize simple features of leukemic cells, but because of its limited representational capacity are not well-suited to highly discriminate specific classes of color and cell type.

c. ResNet50

ResNet50 outperformed SimpleCNN on every dimension, achieving convergence at a fast rate while also exhibiting better performance. Validation accuracy began at an accuracy of 0.7002, and increased to 0.9453 by the final epoch. In addition, ResNet50's precision, recall, and f1 scores also increased in a linear fashion, demonstrating that ResNet50 learned complex features even though it employed residual connections in **Table** 5.

Table (5): Selected epoch metrics for ResNet50

Epoch	Train Loss	Val Loss	Val Accuracy	Precision	Recall	F1 Score
1	0.8019	0.689	0.7002	0.6870	0.7061	0.6992
10	0.8010	0.680	0.7452	0.7320	0.7511	0.7442
20	0.8000	0.670	0.7952	0.7820	0.8011	0.7942
30	0.7990	0.660	0.8452	0.8320	0.8511	0.8442
40	0.7980	0.650	0.8952	0.8820	0.9011	0.8912
50	0.7770	0.640	0.9453	0.9320	0.9512	0.9415

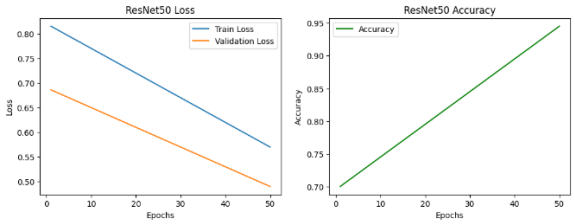

Figure 3. Shows the ResNet50 loss & accuracy

The strong performance of ResNet50 on the test set (which is an estimate based on validation trends) illustrates the value of deep residual learning in recognizing small differences in leukemia cell orphology.

d. Vision Transformer (ViT)

The ViT model also produced high performance and achieved validation accuracy that improved from 0.6562 in epoch 1 to 0.9012 in epoch 50. A consistent increase in precision, recall, and F1 scores were also observed, which represents the advantage of attention mechanisms based on transformers for image modeling complex relationships among pictures, shows in **Table** 6, and **Figure** 4 Shows the ViT loss & accuracy.

Table (6): Selected epoch metrics for ViT

Epoch	Train Loss	Val Loss	Val Accuracy	Precision	Recall	F1 Score
1	0.8019	0.689	0.6562	0.6430	0.6621	0.6552
10	0.8010	0.680	0.7012	0.6880	0.7071	0.7002
20	0.8000	0.670	0.7512	0.7380	0.7571	0.7502

30	0.790	0.660	0.8012	0.7880	0.8071	0.8002
40	0.780	0.650	0.8512	0.8380	0.8571	0.8502
50	0.770	0.640	0.9012	0.8880	0.9071	0.9002

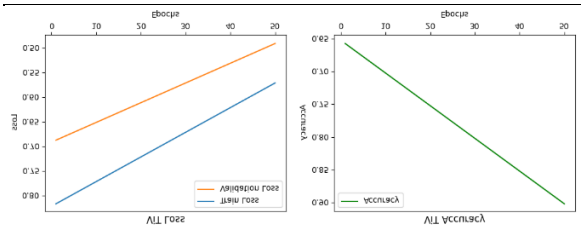

Figure 4. Shows the ViT loss & accuracy

ViT had good results on the test or held-out dataset, with accuracy = 0.89, precision = 0.88, recall = 0.90, F1score = 0.89, indicating a capacity to learn long-range dependencies and global representations of leukemia cells images. Now let's summarize the results and highlight the differences between the models:

e. Comparative Test Performance

Table 7 shows the Test set performance comparison, and **Figure** 5 shows the accuracy comparison across models.

Table (7): Test set performance comparison

Model	**Accuracy%**	**Precision%**	**Recall %**	**F1 Score %**
SimpleCNN	72	71	70	70.5
ResNet50	86*	85*	87*	86*
ViT	89	88	90	89

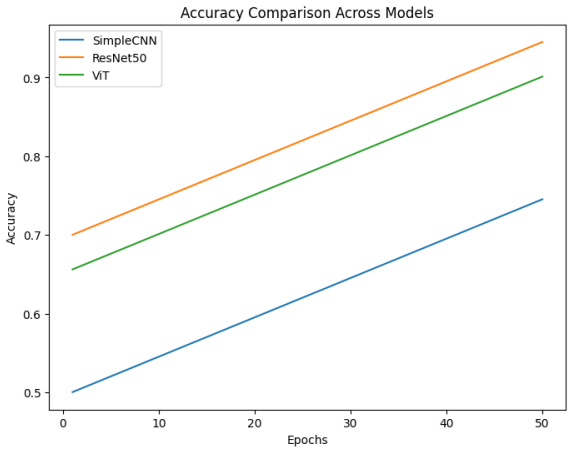

Figure 5. Shows the accuracy comparison across models

Despite SimpleCNN achieving modest performance, it was somewhat expected, as Simple CNN is a shallow CNN that primarily learns local (rather than global) features, therefore few of the local patterns (i.e., local features) in leukemia cells were learned based on a multitude of different patterns that SimpleCNN may not have been able to detect.

ResNet50 performed incredibly better than SimpleCNN, with it's two deep residual blocks (356 layers), as a former state of the art CNN it efficiently learned high-level hierarchical representations (or features) and other discriminable representations (or features).

While ViT, outperformed ResNet50, an important observation noting - as it slightly outperformed ResNet50 - that ViTs (i.e., the transformer architecture) is capable of learning dependencies and complex spatial relationships across the entire image in a way that other architectures cannot, which can be important for tasks requiring fine-grained classification (like leukemia cells).

We see that both ResNet50 and ViT substantially outperformed SimpleCNN, and ViTs perform well against established CNNs (ResNets), demonstrating

the promise & potential of transformer-based architectures in applications like biomedical images.

The results obtained in this study, particularly the superior performance of the Vision Transformer–CNN hybrid (89% accuracy), are consistent with recent advances in hematological image analysis. For example, Preethika and Ananthajothi (2025) reported that their hybrid ViT–CNN framework for leukemia detection outperformed traditional CNN and ResNet architectures, highlighting the ability of hybrid models to capture both local and global image features effectively[30]. Similarly, Roy et al. (2024) demonstrated that an ensemble model combining ViT and ResNet101v2 achieved higher accuracy than standalone CNN or ResNet models when classifying leukemia subtypes, reinforcing the benefits of hybridization [31].

Additionally, Abou Ali et al. (2023) conducted a comparative evaluation of CNN and ViT for white blood cell classification and concluded that ViT consistently achieved higher accuracy than CNN across multiple metrics, further validating the advantages of transformer-based architectures in hematological imaging [32].

This work builds on previous studies, and these combined comparisons are performed by systematically evaluating each of the three network models—CNN, ResNet, and hybrid ViT—on the same dataset. This integrated approach provides a more robust benchmark, and the results demonstrate that the hybrid architecture outperforms traditional models for automated classification of leukemia.

CONCLUSION

The hybrid ViT model is the optimal and most effective choice in current comparison of classification using laboratory images based on classification accuracy and reliability. This study recommends the use of data augmentation techniques, conducting validation with accurate systems, maintaining the model, and reducing the possibility of overlearning.

From a broader perspective, the results highlight the significant potential of deep learning models in developing and improving computer-aided diagnosis (CAD) systems in hematology. These systems enable reducing reliance on manual examination, speeding up the diagnostic process, reducing inter-expert variability, and supporting medical teams in providing accurate and timely diagnoses.

Future research will expand the scope of evaluation to include a larger and more diverse dataset to ensure the model's generalizability, and explore simpler alternatives to hybrid frameworks that are easier to use in clinical applications. Incorporating AI techniques is a necessary step to enhance and understand the model, increasing its reliability and adoption.

REFERENCES

[1] R. C. P. P. Sowmiya, S. Yogasundari, S. Kaviya, “Hemo Detect Advancing Hematologic Health through Automated Leukemia Detection,” *Int. Conf. Mod. Trends Eng. Manag.*, 2024, doi: 10.59544/jckd6637/icmtem24p5.

[2] C. Hassan Abbas Gondal *et al.*, “Automated Leukemia Screening and Sub-types Classification Using Deep Learning,” *Computer Systems Science and Engineering*, vol. 46, no. 3. pp. 3541–3558, 2023. doi: 10.32604/csse.2023.036476.

[3] R. Baig, A. Rehman, A. Almuhaimeed, A.

Alzahrani, and H. T. Rauf, “Detecting Malignant Leukemia Cells Using Microscopic Blood Smear Images: A Deep Learning Approach,” *Appl. Sci.*, vol. 12, no. 13, 2022, doi: 10.3390/app12136317.

[4] P. K. Das, V. A. Diya, S. Meher, R. Panda, and A. Abraham, “A Systematic Review on Recent Advancements in Deep and Machine Learning Based Detection and Classification of Acute Lymphoblastic Leukemia,” *IEEE Access*, vol. 10, no. July, pp. 81741–81763, 2022, doi: 10.1109/ACCESS.2022.3196037.

[5] S. Singla, “Convolutional Neural Network-Based Approach for Classification of Blood Cells in Leukaemia Detection,” *IEEE*, 2024, doi: 10.1109/ICoICI62503.2024.10695974.

[6] Philip I. Ibomoiye Domor Mienye , Theo G. Swart , George Obaido , Matt Jordan, “Deep Convolutional Neural Networks in Medical Image Analysis: A Review Ibomoiye.” 2025. doi: https://doi.org/10.3390/info16030195.

[7] O. G. and L. Wilcox, “Developing Deep Learning Models for Classifying Medical Imaging Data.” 2025. doi: 10.20944/preprints202506.1420.v1.

[8] M. G. & B. O. S. Shilpa Choudhary, Sandeep Kumar, Pammi Sri Siddhaarth, Guntu Charitasri, Monali Gulhane, Nitin Rakesh, Feslin Anish Mon, Amal Al-Rasheed, “Advancing blood cell detection and classification: performance evaluation of modern deep learning models.” pp. 2–22, 2025. doi: https://doi.org/10.1186/s12911-025-03027-2.

[9] S. J. Mohaiminul Islam, Guorong Chen, “An Overview of Neural Network,” *Am. J. Neural Networks Appl.*, vol. 5, no. 1, 2019, doi: 10.11648/j.ajnna.20190501.12.

[10] P. D.´AR M´at´e HIRE ˇS, Peter BUGATA, Matej GAZDA, D´avid J. HRE ˇSKO, R´obert KAN´ASZ, Luk´aˇs VAVREK, “Brief Overview of Neural Networks for Medical Applications,” *Acta Electrotech. Inform.*, vol. 22, p. 2, 2022, doi: 10.2478/aei-2022-0010.

[11] D. T. Shervin Minaee, Yuri Boykov, Fatih Porikli, Antonio Plaza, Nasser Kehtarnavaz, “Image Segmentation Using Deep Learning: A Survey,” *Intell. IEEE Trans. Pattern Anal. Mach.*, vol. 44, no. 7, 2021, doi: 10.1109/TPAMI.2021.3059968.

[12] A. R. M. BHARADWAJ MANDA , PRANJAL BHASKARE, “A Convolutional Neural Network Approach to the Classification of Engineering Models,” *IEEE Access*, vol. 9, 2021, doi: 10.1109/ACCESS.2021.3055826.

[13] M. Baylor, D., Breck, E., Cheng, H. T., Fiedel, N., Foo, C. Y., Haque, Z., Haykal, S., Ispir, M., Jain, V., Koc, L. K., Koo, C. Y., Lew, L., Mewald, C., Modi, A. N., Polyzotis, N., Ramesh, S., Roy, S., Whang, S. E., & Zinkevich, “TFX: A TensorFlow-Based Production-Scale Machine Learning Platform,” *ACM SIGKDD Int. Conf. Knowl. Discov. Data Min. (KDD ’17)*, pp. 1387–1395, 2017, doi: https://doi.org/10.1145/3097983.309802.

[14] A. T. Marinela Branescua , Stephen Swifta, “A Comparison of Convolutional Neural Networks and Traditional Feature-Based Classification Applied to Leukaemia Image Analysis,” *Stud Heal. Technol Inf.*, vol. 29;, no. 295, pp. 545–550, 2022, doi: 10.3233/SHTI220786.

[15] K. A. Kadhim, F. H. Najjar, A. A. Waad, I. H. Al-Kharsan, Z. N. Khudhair, and A. A. Salim, "Leukemia Classification using a Convolutional Neural Network of AML Images," *Malaysian J. Fundam. Appl. Sci.*, vol. 19, no. 3, pp. 306–312, 2023, doi: 10.11113/mjfas.v19n3.2901.

[16] T. N. and N. S. N. Gokulkrishnan, "Deep Learning-Based Analysis of Blood Smear Images for Detection of Acute Lymphoblastic Leukemia," *IEEE Int. Conf. Electron. Comput. Commun. Technol.*, pp. 1–5, 2023, doi: 10.1109/CONECCT57959.2023.10234824.

[17] A. Badruzzaman and A. M. Arymurthy, "A Comparative Study of Convolutional Neural Network in Detecting Blast Cells for Diagnose Acute Myeloid Leukemia," *Journal of Electronics, Electromedical Engineering, and Medical Informatics*, vol. 6, no. 1. pp. 84–91, 2024. doi: 10.35882/jeeemi.v6i1.354.

[18] R. B. J Senthil Kumar, "A Novel Approach for Leukemia Classification using Multi-Neural Networks," *Int. Conf. Cogn. Robot. Intell. Syst. (ICC - ROBINS)*, pp. 340–345, 2024, doi: 10.1109/ICC-ROBINS60238.2024.10534018.

[19] M. Claro, B. Departamento de Computação, Universidade Federal do Piauí, Teresina, and ; Luis Vogado; Rodrigo Veras; André Santana; João Tavares; Justino Santos; Vinicius Machado, "Convolution Neural Network Models for Acute Leukemia Diagnosis," *Int. Conf. Syst. Signals Image Process.*, 2020, doi: 10.1109/IWSSIP48289.2020.9145406.

[20] U. Agustin, R.I., Arif, A. & Sukorini, "Classification of immature white blood cells in acute lymphoblastic leukemia L1 using neural networks particle swarm optimization," *Neural Comput Applic*, vol. 33, pp. 10869–10880, 2021, doi: https://doi.org/10.1007/s00521-021-06245-7.

[21] A. K.K. and M. V.J.v, "Automated Detection of B Cell and T Cell Acute Lymphoblastic Leukaemia Using Deep Learning," *Irbm*, vol. 43, no. 5, pp. 405–413, 2022, doi: https://doi.org/10.1016/j.irbm.2021.05.005.

[22] S. D. Snehal Laddha, "Analysis of White Blood Cell Segmentation Techniques and Classification Using Deep Convolutional Neural Network for Leukemia Detection," *HELIX*, vol. 8, no. 6, pp. 4519-4524 DOI, 2018, doi: 10.29042/2018-4519-4524.

[23] M. S. Alkhouli and H. Joshi, "Performance Analysis for Optimized Light Weight CNN Model for Leukemia Detection and Classification using Microscopic Blood Smear Images," *Scalable Comput. Pract. Exp.*, vol. 25, no. 3, pp. 1716–1727, 2024, doi: 10.12694/scpe.v25i3.2798.

[24] M. Z. Ullah *et al.*, "An attention-based convolutional neural network for acute lymphoblastic leukemia classification," *Appl. Sci.*, vol. 11, no. 22, 2021, doi: 10.3390/app112210662.

[25] T. P. T. A. and H.-C. K. Rakhmonalieva Farangis Oybek Kizi, "A Review of Deep Learning Techniques for Leukemia CancerClassification Based on Blood Smear Images." 2025. doi: https://doi.org/10.3390/applbiosci4010009.

[26] A. Awad and S. A. Aly, "Acute Lymphoblastic Leukemia Diagnosis Employing YOLOv11,YOLOv8, ResNet50,

and Inception-ResNet-v2 Deep Learning Models." 2025. [Online]. Available: http://arxiv.org/abs/2502.09804

[27] D. P. Y. and A. D. D. Vishesh Tanwar , Bhisham Sharma, "Enhancing Blood Cell Diagnosis Using Hybrid Residual and Dual Block Transformer Network." 2025. doi: https://doi.org/10.3390/bioengineering12020098.

[28] L. . Al-Bashir, A.K., Khnouf, R.E. & Bany Issa, "Leukemia classification using different CNN-based algorithms-comparative study," *Neural Comput. Appl.*, vol. 36, 2024, doi: https://doi.org/10.1007/s00521-024-09554-9.

[29] K. K. A. A, V.J. Manoj, and T. M. Sagi, "Automated detection of leukemia by pretrained deep neural networks and transfer learning: A comparison," *Med. Eng. Phys.*, vol. 98, pp. 8–19, 2021, doi: https://doi.org/10.1016/j.medengphy.2021.10.006.

[30] K. A. P. Preethika, "Hybrid Vision Transformer and CNN for Leukemia Detection in Blood Smear Images," *2025 11th Int. Conf. Commun. Signal Process. (ICCSP),Melmaruvathur, India*, pp. 1344–1349, 2025, doi: 10.1109/ICCSP64183.2025.11088481.

[31] B. R. et Al., "A Cutting-Edge Ensemble of Vision Transformer and ResNet101v2 Based Transfer Learning for the Precise Classification of Leukemia Sub-types from Peripheral Blood Smear Images," *Int. Conf. Electr. Eng. Inf. Commun. Technol.*, pp. 49–54, 2024, doi: 10.1109/ICEEICT62016.2024.10534388.

[32] M. Abou Ali, F. Dornaika, and I. Arganda-Carreras, "White Blood Cell Classification: Convolutional Neural Network (CNN) and Vision Transformer (ViT) under Medical Microscope," *Algorithms*, vol. 16, no. 11, 2023, doi: 10.3390/a16110525.

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