2024 International Conference on Advancement in Computation & Computer Technologies (InCACCT)

Enhancing Leukemia Diagnosis through Machine Learning: A Customized ResNet50 Approach

Modigari Narendra
Assistant Professor Senior Grade 1
School of Computer Science and Engineering
Vellore Institute of Technology, Chennai, India
modigari.narendra@vit.ac.in

Sumit Negi
Post Graduate Student
School of Computer Science and Engineering
Vellore Institute of Technology, Chennai, India
sumit.negi2022@vitstudent.ac.in

***Abstract*—Leukemia, a form of cancer affecting the blood and bone marrow, presents a significant challenge in healthcare due to its varied subtypes and complex classification process. This study addresses the need for accurate and efficient leukemia classification, with a specific focus on acute lymphoblastic leukemia (ALL), by proposing a comprehensive methodology integrating machine learning techniques. Through meticulous data preprocessing, including Otsu's Thresholding for segmentation and feature extraction using the ResNet50 convolutional neural network (CNN), the study establishes a robust foundation for leukemia image analysis. With the Lazy Predict library, the research streamlines model selection, ultimately leading to the development of a customized ResNet50 CNN model. This model with additional layers for feature extraction and classification, demonstrates superior performance compared to traditional approaches, achieving an accuracy of 0.87 and a balanced accuracy of 0.83. Notably, the custom model exhibits faster inference times, indicating its potential for real-time leukemia diagnosis. By advancing computer-assisted leukemia diagnosis, this research contributes to improving healthcare outcomes and lays the groundwork for future applications of machine learning in leukemia management.**

Keywords—Leukemia Classification, ResNet50, Lazy Predict, LGBMClassifier, XGBClassifier, Medical Diagnostics

I. INTRODUCTION

The entire organism relies on the circulatory system to supply vital nutrients through the bloodstream. Blood comprises three main components: erythrocytes (red blood cells), leukocytes (white blood cells), and thrombocytes (platelets). Red blood cells (RBCs) play a crucial role in oxygenating all cells, while platelets contribute to blood clotting in case of injuries. White blood cells (WBCs) serve as defenders against viruses and diseases, constituting only 1\% of blood volume but holding paramount importance for the immune system. Changes in the quantity of White Blood Cells in blood plasma are indicative of diseases. There are five types of WBCs: lymphocytes, monocytes, neutrophils, eosinophils, and basophils. Any deviation in the white blood cell count raises concerns. Leukemia, often associated with low WBC counts, can be detrimental when the WBC quantity is unusually high [1,2].

Leukemia, a potentially fatal cancer, disrupts the normal functioning of blood and bone marrow due to the rapid proliferation of abnormal white blood cells. These aberrant cells compromise the immune system and hinder the production of RBCs and platelets. Acute leukemia, growing rapidly with severe symptoms, differs from chronic leukemia. Leukemia is further classified into lymphocytic and myelogenous types, the former involving abnormal growth of cells developing into lymphocytes and the latter affecting hematopoietic cells leading to abnormal RBCs, WBCs, and platelet development. The f main types of leukemia include Acute Lymphocytic Leukemia, Acute Myelogenous Leukemia (AML), Chronic Lymphocytic Leukemia (CLL), and Chronic Myelogenous Leukemia (CML). Acute Lymphoblastic Leukemia stands out as the most common childhood cancer, with a majority of cases occurring in otherwise healthy individuals. Genetic factors, including familial susceptibility and environmental elements, play a role in some cases, characterized by chromosome abnormalities and genetic alterations related to the lymphoid system . Although ALL represents 80% of pediatric leukemia cases, it constitutes only 20% of adult leukemia cases. Diagnosing ALL involves intricate procedures, and survival rates exceeding 90% in developed nations are attributed to modern risk-adapted therapies and supportive care.

II. BACKGROUND STUDY

Numerous researchers have endeavored to develop computer assisted methods for analyzing microscopic images of cells, specifically targeting the automatic diagnosis and classification of acute lymphocytic leukemia. This objective is paramount for ensuring timely and precise detection, which significantly influences patient therapy and recovery. The existing methodologies in this domain vary in their approaches, each presenting unique contributions and challenges. Das et al. [3] utilizes a k-means clustering method based on color to extract lymphocytes from microscopic images. Following image segmentation, attributes such as shape, texture, and color are extracted, employing techniques like Gray-level co-occurrence matrix (GLCM) and gray-level run-length matrix (GRLM). Prin-

Principal Component Analysis (PCA) is then applied for dimensional reduction. The segmentation of white blood cell (WBC) nuclei benefits from the utilization of HSI, Lab color space, and the k-means algorithm, as demonstrated by Rajpurohit et al. [4]. The integration of features from the first and last convolutional layers with the propagation of input images enhances the accuracy of Convolutional Neural Network (CNN) models. This research focuses on improving the generalization potential of the system and the localization of WBC nuclei. A discrete orthonormal S-transform is employed by Mishra et al. [5] for the detection of ALL, utilizing PCA and linear discriminant analysis to minimize dimensionality. The selected features are then fed into a hybrid classifier based on AdaBoost and a random forest, demonstrating potential applicability to acute myeloid leukemia.

Jothi et al. [6] developed a graphical user interface employing BSA-based clustering for segmenting ALL images. The STRSFFQR algorithm efficiently identifies high-quality features, while the integration of the Jaya algorithm facilitates the separation of malignant leukemia cells. By combining Jaya with diverse classification algorithms, the accuracy of the segmentation process is enhanced. Mishra et al. [7] used the Support Vector Machine (SVM) for classification with the gray-level run length matrix for feature extraction. The SVM classifier achieves a high accuracy of 96.97% using the GLRL feature on the ALL-IDB1 dataset.

Reena et al. [8] utilized DeepLabv3 for leukocyte segmentation, and AlexNet was combined for the classification of lymphocytes and achieved an average precision of 98.42% and a classification accuracy of 98.87%. Abdeldaim et al. [9] propose an alternative approach involving a multi-step procedure, encompassing image format conversion, contrast enhancement, thresholding, background elimination, noise reduction, and data normalization, with different normalization algorithms employed in the final stage to enhance classification performance.

In their study, Aftab et al. [10] conducted a comparative analysis between the Spark BigDL framework and the Keras model. Their findings revealed that the Spark BigDL framework outperformed the Keras model in terms of efficiency and precision. Additionally, the implementation of histogram leveling and morphological techniques further enhanced the efficiency of their approach compared to previous methods.

Table I provides a comparative analysis of recent advancements in the detection and classification of Acute Lymphoblastic Leukemia. The table outlines the segmentation techniques, features extracted, classifiers utilized, and datasets employed in each study. Techniques such as K-means clustering, the Triangle method of thresholding, and manual segmentation are employed for segmentation, while features including color, texture, shape, and statistical measures are extracted. Classifiers range from Support Vector

Machines (SVM) and Convolutional Neural Networks (CNN) to ensemble methods like Random Forest and K-nearest Neighbors (KNN). Datasets utilized include ALL-IDB1, ALL-IDB2, LISC, and private datasets. This comprehensive overview highlights the diversity of approaches in the field and their respective contributions to the detection and classification of ALL.

In the culmination of various segmentation, feature extraction, and classification methods, it becomes evident that traditional machine learning algorithms are favored for unsupervised segmentation tasks, while supervised algorithms excel in classification tasks. However, the emergence of deep learning, particularly transfer learning, stands out for its remarkable performance, even with limited datasets [11]. The proposed approach offers a more efficient solution compared to previous methodologies.

TABLE I

A COMPARATIVE ANALYSIS OF RECENT ADVANCEMENTS IN DETECTION & CLASSIFICATION OF ALL

Reference	Segmentation	Features	Classifier	Dataset
[3]	K-means	Color, shape, texture, P.C.A	S.V.M	ALL-IDB1
[4]	K-means	N/A	C.N.N	BCC, ALL-IDB1
[5]	Triangle method of thresholding	DOST,PCALDA	Random forest	ALL-IDB1
[6]	B.S.A	Statistical Wavelet, shape	Roughset	ALL-IDB
[7]	Watershed algorithm	GLRLM	SVM	ALL-IDB1
[8]	Deeplab v3+	N/A	AlexNet	LISC
[9]	Colour model to CMYK	Color, texture, shape, Wavelet	KNN, Naïve Bayes	ALL-IDB
[10]	RGB images into Gray	BigDLlib Transfer learning	CNN with Softmax	A.S.H
[11]	Zack algorithm	GLDM,GLCM	SVM	ALL-IDB
[12]	Gaussian Distribution	Otsu Adaptive	CNN	MISCR
[13]	Manual segmentation	Color geometry, texture	CNN	ALL-IDB
[14]	FCM	Statistical LDP	Deep CNN	ALL-IDB2
[15]	K-mediod	Shape, color, text	uAreNN	ALL-IDB,Atlas
[16]	Manual Segmentation	Chi Square	CNN	ALL-IDB
[17]	Darknet53 and ShufeNet	PCA	Ensemble KNN	LISC
[18]	N/A	Transfer learning ChiSqaure	S.V.M, WBC's Net	Private datasets

The primary contributions of this proposed approach are outlined below:

- Develop a customized ResNet50 CNN model for leukemia classification, achieving high accuracy in leukemia classification.
- Automate model evaluation using Lazy Predict, facilitating efficient selection of machine learning classifiers.
- Superior performance of the custom ResNet50 model, with an accuracy of 0.87 and balanced accuracy of 0.83, contributing to improved leukemia detection.
- Faster inference times of the custom model, making it suitable for real-time leukemia diagnosis in resource-constrained healthcare environments.
- Contribution to healthcare research by advancing computer assisted leukemia diagnosis, paving the way for future applications of machine learning in improving leukemia management and healthcare outcomes.

III. PROPOSED METHODOLOFY

A. Dataset

The dataset used in the proposed work is C-NMC leukemia dataset [19] which is publicly available. The leukemia dataset comprises a total of 10,661 images, out of which 7272 Acute lymphoblastic leukemia images and the remaining are normal images. This structured organization

facilitates a clear delineation between the two classes within the leukemia dataset.

B. Proposed Methodology

Leukemia images typically consist of microscopic images of blood smears or bone marrow aspirates stained with special dyes. Classification of leukemia images involves the use of machine learning and computer vision techniques to automatically identify and differentiate between normal and abnormal cells. Convolutional neural networks are commonly used for leukemia image classification due to their ability to learn hierarchical features directly from the images. These networks are trained on labeled datasets containing images of both normal and malignant cells, learning to discriminate between the two classes based on the extracted features. Transfer learning, where pre-trained CNN models are fine-tuned on leukemia datasets, can also be employed to leverage knowledge from larger, related datasets and improve classification performance. Sample images of both Leukemia and normal are shown in Figure 1. This section provides a comprehensive explanation of the proposed methodology utilizing a pretrained ResNet50 CNN model. A two-fold methodology is proposed for leukemia classification. Initially, the images in the dataset are fed into ResNet50 Convolutional Neural Network and then the features are extracted. The extracted features are given to multiple classifiers at a time with LazyPredict library for classification. Subsequently, a novel approach is introduced leveraging a customized model based on ResNet50. Again, the features are extracted from the custom CNN model designed and tested against multiple classifiers with the LazyPredict Library.

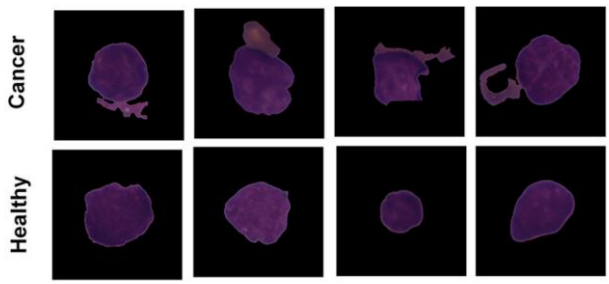

Fig. 1. Leukemia images samples for two classes cancer and healthy cell

C. Preprocessing

Otsu's Thresholding is initially applied to perform image segmentation, separating foreground and background, which is crucial for isolating relevant features. Subsequently, binary thresholding is employed to refine the segmentation process further and enhance the contrast between foreground and background regions. Black areas in the images were removed to reduce irrelevant features and improve model training efficiency. This preprocessing step involved identifying and cropping out black regions from the images, resulting in a reduction of unnecessary pixel counts and optimization of memory usage during model training. The resulting images after these steps are shown in Figure 2. To address the imbalance in the dataset and improve model generalization, data augmentation techniques including rotation, flipping, and scaling, were applied.

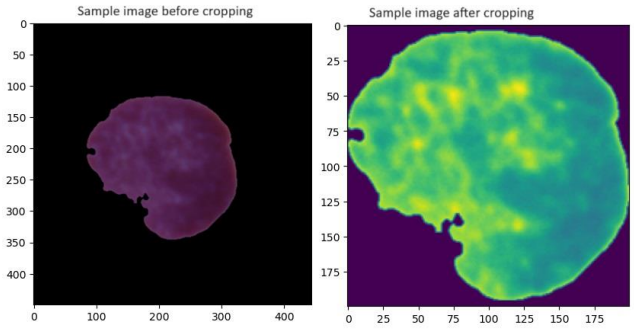

Fig. 2. Preprocessed images with segmentation and cropping

D. Feature Extraction

In this study, pre-trained Convolutional Neural Network-based architectures ResNet50 architecture was chosen to extract features, with images reshaped to dimensions (-1, 224, 224, 3). Prior to implementing feature selection techniques, the features extracted from ResNet50 comprise a total of 2,048 features.

Algorithm 1: Customized ResNet Model Approach with Lazy Predict

Input: Leukemia image data

Output: Trained model for leukemia classification

1. Data Preprocessing: Load and preprocess leukemia image data as described earlier
2. Data Augmentation: Perform data augmentation with operations such as rotation, flipping, and scaling
3. Model Compilation: Initialize the ResNet50 base model with pre-trained weights from ImageNet Exclude the top layers of the ResNet50 model.
   Add custom layers on top of the base model for feature extraction and classification.
   Compile the model using the Adam optimizer with a specific learning rate and binary cross-entropy loss function.
   Set evaluation metrics such as accuracy for model performance assessment.
4. Feature Extraction: Freeze the weights of pre-trained layers to retain learned features during training.
5. Model Training and Evaluation: Use Lazy Predict to evaluate a variety of classification models on the preprocessed data and select the best-performing model based on results.
6. Fine-Tuning: Fine-tune the selected model by adjusting hyperparameters or unfreezing specific layers for further optimization

E. Custom ResNet50 convolution Neural Network

The ResNet50 model and is pretrained on the ImageNet dataset and consists of 50 layers, including 48 convolutional layers, 1 MaxPooling layer, and 1 AveragePooling layer. The top classification layer is excluded by setting include top parameter to False, and the input shape parameter is set to (224, 224, 3). A new fully connected output layer is then added to the ResNet50 model. The output of the previous layer is flattened into a 1D array using the Flatten() layer. For multi-class classification with 4 classes, a Dense() layer

with a softmax activation function is used. For compilation, the model employs the sparse categorical loss function, the Adam optimizer, and the accuracy metric to measure performance. The model is trained for 50 epochs with a batch size of 32 while shuffling the data. ResNet50 utilizes skip connections to add the output of one layer to the next, reducing the complexity of time. It behaves as a 34-layer network with the same number of filters when the output feature map size remains the same and doubles the number of filters when the feature map size is halved. The architecture of customized ResNet50 is shown in Figure 3 and a summary is given in Table II.

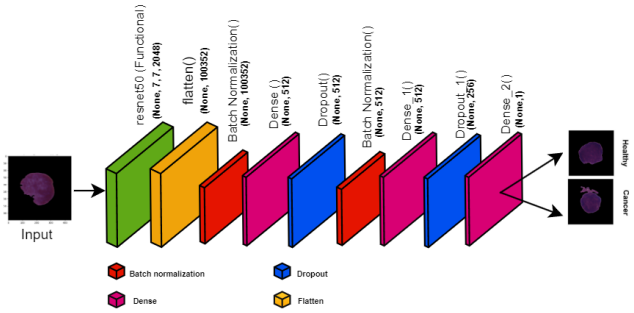

Fig.3. Proposed Custom ResNet50 Architecture

TABLE II
SUMMARY OF CUSTOM MODEL

Layer (type)	Output Shape / Param #
resnet50 (Functional)	(None, 7, 7, 2048) 23587712
flatten (Flatten)	(None, 100352) 0
batch normalization (Batch Normalization)	(None, 100352) 401408
dense (Dense)	(None, 512) 51380736
dropout (Dropout)	(None, 512) 0
batch normalization 1 (Batch Normalization)	(None, 512) 2048
dense 1 (Dense)	(None, 256) 131328
dropout 1 (Dropout)	(None, 256) 0
dense 2 (Dense)	(None, 1) 257
Total params	75503489 (288.02 MB)
Trainable params	75248641 (287.05 MB)
Non-trainable params	254848 (995.50 KB)

F. Lazy Predict Classifier

Lazy Predict automates the evaluation of a wide range of machine learning models on a given dataset, eliminating the need for manual tuning and extensive experimentation. The LazyClassifier class from the lazypredict.Supervised module is utilized for this purpose. Using Lazy Predict significantly reduces the time and effort required for model selection and evaluation, making it a valuable tool for rapid prototyping and initial exploration of machine learning pipelines.

IV. Experimental Results Analysis

This section elaborates on the outcomes proposed methodology and the evaluation metrics employed in this study. The first approach with the CNN model has given an accuracy of 0.76 and results in overfitting and the same can be observed from accuracy and loss plots shown in Figures 4 and 5.

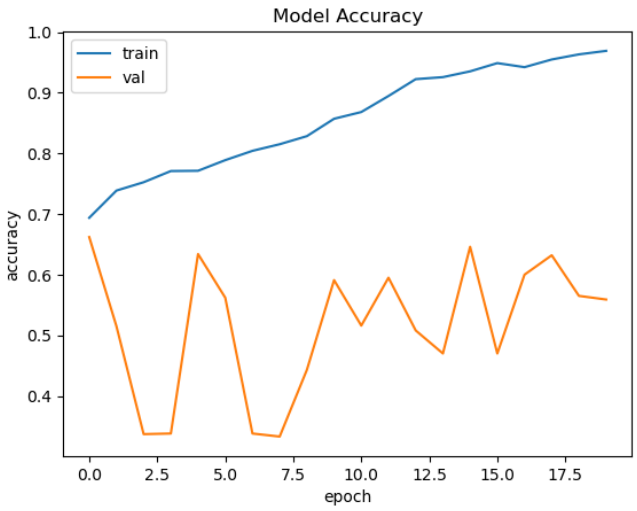

Fig. 4. Traditional ResNet50 model accuracy with the dataset

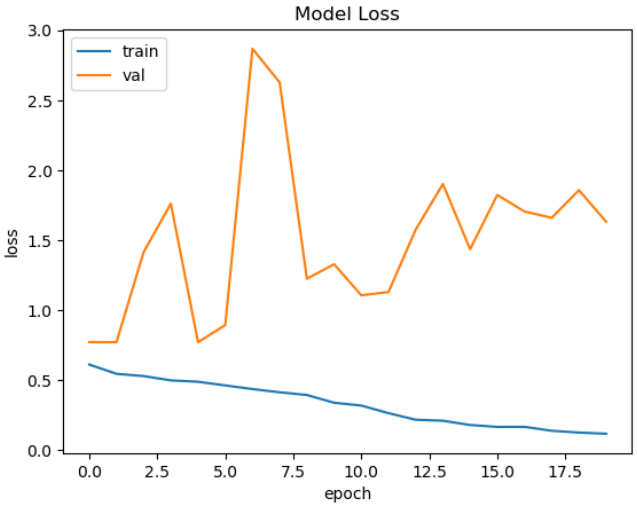

Fig.5. Traditional ResNet50 model accuracy with the dataset

The performance of different classifiers using the traditional ResNet50 model is given in Table III. Among the top-performing classifiers, the Support Vector Classifier (SVC) achieved the highest accuracy of 0.86 with a balanced accuracy (the arithmetic mean of sensitivity and specificity) of 0.80, followed by the XGBoost Classifier (XGBClassifier) and the LightGBM Classifier (LGBMClassifier). The computational time varied significantly across different classifiers, with the AdaBoost Classifier being the most time-consuming, taking approximately 133.90 seconds.

TABLE III

PERFORMANCE METRICS ON RESTNET 50 USING LAZY PREDICT

Model	Accuracy	Balanced Accuracy	ROC AUC	F1 Score	Time Take(s)
SVC	0.86	0.80	0.80	0.86	91.80
XGBClassifier	0.85	0.79	0.79	0.84	77.70
LGBMClassifier	0.84	0.78	0.78	0.84	47.41
LinearDiscriminantAnalysis	0.83	0.78	0.78	0.82	20.74
RidgeClassifierCV	0.83	0.78	0.78	0.82	16.90
RidgeClassifier	0.83	0.78	0.78	0.82	2.69

LogisticRegression	0.80	0.76	0.76	0.80	3.43
AdaBoostClassifier	0.81	0.76	0.76	0.81	133.90
ExtraTreesClassifier	0.83	0.76	0.76	0.82	9.38
RandomForestClassifier	0.83	0.76	0.76	0.82	44.31
Perceptron	0.78	0.75	0.75	0.79	1.51
KNeighborsClassifier	0.81	0.75	0.75	0.80	2.11
BaggingClassifier	0.79	0.75	0.75	0.79	342.86
SGDClassifier	0.78	0.74	0.74	0.78	6.47
PassiveAggressiveClassifier	0.78	0.74	0.74	0.78	2.76
LinearSVC	0.77	0.74	0.74	0.77	36.30
NuSVC	0.82	0.73	0.73	0.81	117.89
CalibratedClassifierCV	0.81	0.72	0.72	0.79	96.80
NearestCentroid	0.71	0.71	0.71	0.72	1.08
BernoulliNB	0.70	0.70	0.70	0.71	1.26
GaussianNB	0.69	0.70	0.70	0.70	1.26
DecisionTreeClassifier	0.74	0.70	0.70	0.74	44.96
ExtraTreeClassifier	0.68	0.63	0.63	0.69	0.95
QuadraticDiscriminantAnalysis	0.72	0.54	0.54	0.62	26.74
LabelSpreading	0.33	0.52	0.52	0.19	11.81
LabelPropagation	0.33	0.52	0.52	0.19	10.95
DummyClassifier	0.70	0.50	0.50	0.57	0.81

The custom ResNet50 model introduced several enhancements compared to the traditional ResNet50 architecture. These modifications aimed to enhance feature extraction capabilities and optimize the model for leukemia classification tasks. Utilizing transfer learning and fine-tuning strategies, the bespoke model efficiently employed pre-trained ResNet50 weights, thereby adapting to the unique features present in the leukemia image dataset. From Table IV it can be observed that the custom ResNet50 model proposed outperformed the traditional model, with an overall accuracy of 0.87 and a balanced accuracy of 0.83, showcasing the effectiveness of the additional convolutional layers and feature extraction techniques incorporated into the custom architecture. The AdaBoost Classifier and the XGBoost Classifier emerged as the top performing classifiers in the custom model, achieving an accuracy of 0.87 each. The custom model also demonstrated relatively faster inference times compared to the traditional model, with most classifiers completing the classification task in less than 10 seconds.

TABLE IV

CUSTOMIZED RESNET50 MODEL PERFORMANCE METRICS

Model	**Accuracy**	**Balanced Accuracy**	**ROC AUC**	**F1 Score**	**Time Taken(s)**
AdaBoostClassifier	0.87	0.83	0.83	0.87	1.04
LabelSpreading	0.82	0.83	0.83	0.83	9.09
SVC	0.84	0.83	0.83	0.84	2.37
LabelPropagation	0.82	0.83	0.83	0.83	6.39
CalibratedClassifierCV	0.82	0.83	0.83	0.82	0.48
LogisticRegression	0.82	0.83	0.83	0.82	0.09
SGDClassifier	0.81	0.83	0.83	0.81	0.03
RidgeClassifierCV	0.81	0.83	0.83	0.82	0.02
RidgeClassifier	0.81	0.83	0.83	0.82	0.03
PassiveAggressiveClassifier	0.81	0.83	0.83	0.81	0.06
LGBMClassifier	0.87	0.83	0.83	0.87	0.14
LinearDiscriminantAnalysis	0.81	0.83	0.83	0.81	0.08
NuSVC	0.81	0.83	0.83	0.82	9.00
LinearSVC	0.81	0.83	0.83	0.82	0.07
XGBClassifier	0.87	0.82	0.82	0.87	0.09
GaussianNB	0.79	0.82	0.82	0.80	0.04
QuadraticDiscriminantAnalysis	0.79	0.82	0.82	0.80	0.06
KNeighborsClassifier	0.85	0.82	0.82	0.85	0.19
DecisionTreeClassifier	0.83	0.82	0.82	0.83	0.11
RandomForestClassifier	0.83	0.81	0.81	0.83	2.48
NearestCentroid	0.77	0.81	0.81	0.78	0.10
BaggingClassifier	0.83	0.81	0.81	0.83	0.35
ExtraTreesClassifier	0.83	0.81	0.81	0.83	1.87
ExtraTreeClassifier	0.82	0.81	0.81	0.83	0.05
Perceptron	0.74	0.79	0.79	0.75	0.09
BernoulliNB	0.74	0.79	0.79	0.75	0.05
DummyClassifier	0.70	0.50	0.50	0.57	0.03

Figure 6 compares the accuracy of original and custom ResNet50 models with various machine learning models including SVC, XGBClassifier, LGBMClassifier, and LinearDiscriminantAnalysis. It appears that the custom ResNet50 model has a higher accuracy than the original ResNet50 model with most of the classification algorithms.

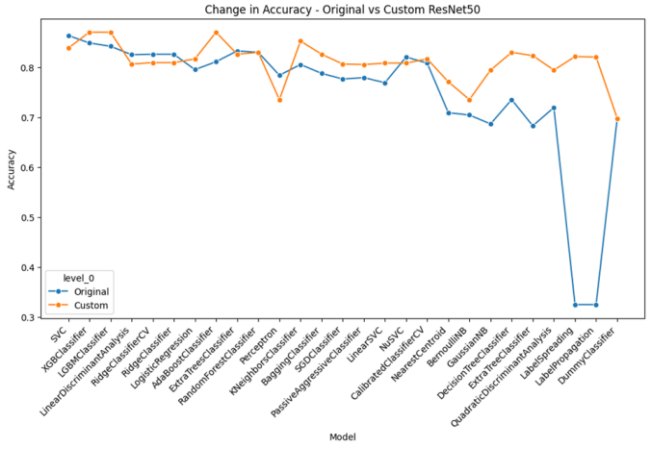

Fig.6. Accuracy comparison of different classifiers between two models

V. CONCLUSION AND FUTURE SCOPE

In conclusion, the study aimed to develop an effective approach for the classification of leukemia using machine learning techniques, focusing on the detection of acute lymphoblastic leukemia (ALL) in microscopic images. Leveraging a custom ResNet50 convolutional neural network (CNN) model and Lazy Predict for classification, a methodology involving preprocessing the leukemia image dataset, extracting features using the ResNet50 architecture, and evaluating various classifiers to identify the best-performing model. The study demonstrated the superior performance of the custom model over traditional methods, achieving an overall accuracy of 0.87 and a balanced accuracy of 0.83. Notably, the custom model exhibited faster inference times compared to its counterparts, indicating its suitability for real-time leukemia diagnosis applications. These results underscore the potential of machine learning in improving leukemia detection accuracy and highlight the efficacy of the proposed methodology in achieving competitive performance metrics. The study contributes to the growing body of research in computer-assisted leukemia diagnosis and sets a foundation for future investigations aimed at leveraging machine learning for improved healthcare outcomes in leukemia management.

REFERENCES

[1] P. Ghanem, A. Zouein, M. Mohamad, M. H. Hodroj, T. Haykal, S. Abou Najem, H. Y. Naim, and S. Rizk, "The vitamin e derivative gamma tocotrienol promotes anti-tumor effects in acute myeloid leukemia cell lines," Nutrients, vol. 11, no. 11, p. 2808, 2019.

[2] W. H. Abir, M. F. Uddin, F. R. Khanam, T. Tazin, M. M. Khan, M. Masud, S. Aljahdali et al., "Explainable ai in diagnosing and anticipating leukemia using transfer learning method," Computational Intelligence and Neuroscience, vol. 2022, 2022.

[3] P. K. Das, P. Jadoun, and S. Meher, "Detection and classification of acute lymphocytic leukemia," in 2020 IEEE-HYDCON. IEEE, 2020, pp. 1–5.

[4] S. Rajpurohit, S. Patil, N. Choudhary, S. Gavasane, and P. Kosamkar, "Iden tification of acute lymphoblastic leukemia in microscopic blood image using image processing and machine learning algorithms," in 2018 International con ference on advances in computing, communications and informatics (ICACCI). IEEE, 2018, pp. 2359–2363.

[5] S. Mishra, B. Majhi, and P. K. Sa, "Texture feature based classification on microscopic blood smear for acute lymphoblastic leukemia detection," Biomedical Signal Processing and Control, vol. 47, pp. 303–311, 2019.

[6] G. Jothi, H. H. Inbarani, A. T. Azar, and K. R. Devi, "Rough set theory with jaya optimization for acute lymphoblastic leukemia classification," Neural Computing and Applications, vol. 31, pp. 5175–5194, 2019.

[7] S. Mishra, B. Majhi, and P. K. Sa, "Glrlm-based feature extraction for acute lymphoblastic leukemia (all) detection," in Recent Findings in Intelligent Computing Techniques: Proceedings of the 5th ICACNI 2017, Volume 2. Springer, 2018, pp. 399–407.

[8] M. R. Reena and P. Ameer, "Localization and recognition of leukocytes in peripheral blood: A deep learning approach," Computers in Biology and Medicine, vol. 126, p. 104034, 2020.

[9] A. M. Abdeldaim, A. T. Sahlol, M. Elhoseny, and A. E. Hassanien, "Computer aided acute lymphoblastic leukemia diagnosis system based on image analysis," Advances in Soft Computing and Machine Learning in Image Processing, pp. 131–147, 2018.

[10] M. O. Aftab, M. J. Awan, S. Khalid, R. Javed, and H. Shabir, "Executing spark bigdl for leukemia detection from microscopic images using transfer learning," in 2021 1st International Conference on Artificial Intelligence and Data Analytics (CAIDA). IEEE, 2021, pp. 216–220.

[11] C. Ananth, K. Mystica, M. Sridharan, S. A. James, and T. A. Kumar, "An advanced low-cost blood cancer detection system." International Journal of Early Childhood Special Education, vol. 14, no. 5, 2022.

[12] R. Agrawal, S. Satapathy, G. Bagla, and K. Rajakumar, "Detection of white blood cell cancer using image processing," in 2019 International Conference on Vision Towards Emerging Trends in Communication and Networking (ViTECoN). IEEE, 2019, pp. 1–6.

[13] T. Pansombut, S. Wikaisuksakul, K. Khongkraphan, A. Phon-On et al., "Convolutional neural networks for recognition of lymphoblast cell images," Computational Intelligence and Neuroscience, vol. 2019, 2019.

[14] K. K. Jha and H. S. Dutta, "Mutual information based hybrid model and deep learning for acute lymphocytic leukemia detection in single cell blood smear images," Computer methods and programs in biomedicine, vol. 179, p. 104987, 2019.

[15] A. I. Shahin, Y. Guo, K. M. Amin, and A. A. Sharawi, "White blood cells identification system based on convolutional deep neural learning networks," Computer methods and programs in biomedicine, vol. 168, pp. 69–80, 2019.

[16] D. Kumar, N. Jain, A. Khurana, S. Mittal, S. C. Satapathy, R. Senkerik, and J. D. Hemanth, "Automatic detection of white blood cancer from bone marrow microscopic images using convolutional neural networks," IEEE Access, vol. 8, pp. 142 521–142 531, 2020.

[17] S. Saleem, J. Amin, M. Sharif, M. A. Anjum, M. Iqbal, and S.-H. Wang, "A deep network designed for segmentation and classification of leukemia using fusion of the transfer learning models," Complex & Intelligent Systems, pp. 1–16, 2021.

[18] A. I. Shahin, Y. Guo, K. M. Amin, and A. A. Sharawi, "White blood cells identification system based on convolutional deep neural learning networks," Computer methods and programs in biomedicine, vol. 168, pp. 69–80, 2019.

[19] R. Gupta, S. Gehlot, and A. Gupta, "C-nmc: B-lineage acute lymphoblastic leukaemia: A blood cancer dataset," Medical Engineering & Physics, vol. 103, p. 103793, 2022