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RESEARCH ARTICLE

LEUKNET: A DEEP LEARNING MODEL FOR EARLY DETECTION AND CLASSIFICATION OF LEUKEMIA

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Abstract – Leukemia is a critical condition affecting the blood and lymphatic systems, requiring timely and accurate detection for effective treatment. Traditional microscopic analysis, though effective, relies heavily on the skill of the pathologist, leading to potential delays in diagnosis. In this research, a novel introduced LeukNet proposed for identifying the different types of leukaemia in its early stages. Initially, the images of the blood smear are preprocessed using Adaptive Gaussian filters to removing noise artifacts. Sobel detector is used to detecting the edges in horizontal and Vertical from the images. Based on the edges, the deep learning-based GoogleNet is used for extracting the blood cell features. Further, the classification is performed by Multi-Layer Perceptron. It classifies the smear of blood images into five different classes: Normal, Acute leukemia (ALL), Acute lymphoblastic leukemia (ALL), Chronic lymphoblastic leukemia (CLL), and Chronic myeloid leukemia (CML). The effectiveness of the proposed LeukNet method using metrics like F1 score, sensitivity, accuracy, and specificity. The proposed LeukNet model achieved a classification accuracy 98.76%. The proposed LeukNet model enhanced the total accuracy by 2.90%, 6.57%, and 8.48% better than LD-C-NMC, ALL-delt and DeepLeukNet respectively.

Keywords *– Adaptive Gaussian filters, deep learning, edge detection, blood smear images, Multi- Layer Perceptron.*

1. INTRODUCTION

A microscopic analysis of blood cells is the best method for detecting and diagnosing leukemia. Leukemia is a dangerous condition affecting the lymphatic system and blood-forming tissues of the body [1]. Leukaemia is defined as the abnormal production of white blood cells by the bone marrow. Acute leukaemia and chronic leukaemia are two important subtypes. ALL, AML, CLL, and CML are other kinds of leukaemia [2]. The image shows the morphological differences distinguish leukemia cells from healthy cells. The blood sample are drawn by a pathologist with training, and then the blood slide is to detect for these cells. Staining enables for the inspection of the cells under a high-quality microscope to identify the morphological features of the different blood cell components, including blasts, RBC, parasites, WBC, any other abnormal condition, and platelets [3]. Immature lymphocytes cause ALL, a type of cancer. Leukemic cells invade several organs, including the spleen, liver, lymph nodes, brain, and nervous system, and spread quickly in the blood [4].

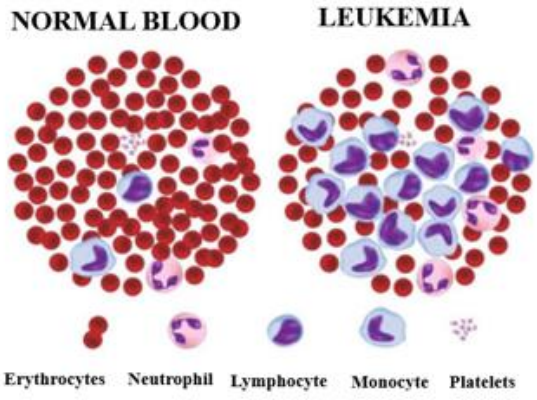

Figure 1. Normal and Leukemia cell

The diagnosis is typically made manually by a skilled pathologist examines the white cell abnormalities under a microscope to identify the presence of malignancy. Pathologists specifically look for lymphoblasts in peripheral blood, which are white cells with a changed morphology [5]. Pathologists specifically look for lymphoblasts in peripheral blood, which are white cells with a changed morphology [6]. Low-grade B-cell lymphoproliferative illness CLL has a wide racial disparity and is thought to be 6.9 instances per 100,000 people on a yearly basis in western countries [7]. CLL is more common in men than in women, and the incidence increases progressively with age. Currently, the start of CLL treatment is postponed until the start of Disease progression (transformation of high-grade lymphoma, the

organomegaly, general symptoms, or bone marrow failure), as well as in cases of chronic autoimmune symptoms [8, 9]. Despite this, it is tempting to believe that early intervention benefits some patients when the tumor mass is smaller and they are in better health when they are diagnosed. Therefore, it is necessary to improve risk stratification for CLL patients. Adult patients with AML achieve complete remission at a rate of 50% to 80% with aggressive treatment [10]. Despite these positive outcomes, most responding patients will short relapse, with about 30–40% of young patients and less than 20% of patients over the age of sixty being long-term survivors [11]. CML is a malignant condition of hematopoietic stem cells (HSCs) that makes for 15%–20% of all adult leukemia [12,13]. Leukemia reduces immunity, leaving patients more vulnerable to illnesses, while treatments like chemotherapy often lead to severe side effects such as fatigue, hair loss, and organ damage. [14] The financial burden of managing the disease is significant, placing considerable stress on patients and their families. [15] In addition to physical challenges, leukemia also causes emotional strain, with anxiety and depression being common among both patients and caregivers. Moreover, there is always a risk of relapse, result in ongoing cycles of treatment and uncertainty. The main study is as follows,

- In this work, a novel deep learning LeukNet model has been proposed for identifying the different types of leukaemia in its early stages.
- Initially, Blood smears images are collected from publicly available sources and images are pre-processed using adaptive Gaussian filters to reducing noise.
- Sobel edge detector is used to detecting horizontal edges and vertical edges of the millet crop images.
- Based on these edges, the deep learning-based GoogleNe**t** is used for extracting the blood cell features.
- Finally, multi-layer perceptron is used to classify types of Leukemia namely normal, ALL, CLL, AML and CML.

The remaining sections of this work were separated into the five categories listed below. The review of relevant literature is presented in Section 2, followed by the proposed approach in Section 3, Section 4 discusses the results and discussion and Section 5 explains the conclusion and future scope.

2. LITERATURE SURVEY

In the literature has described many techniques for automated leukaemia identification using microscopic images over the years. In this section, a few frameworks are briefly studied.

In 2021 Genovese, A., et al., [18] examined the machine learning methodology for the categorization of ALL blood samples as lymphoblast and normal focus quality estimate and adaptive unsharpening. The approach on a public ALL database demonstrates that, regardless of the CNN used, deep CNNs trained using the proposed method's unsharpened images increase the accuracy of lymphoblast detection.

In 2022 Pandey, M.K. and Pal, S., [19] devised the machine learning based identifying for chronic phase (CML). It involves analyzing patient data and identifying critical features that are help in the diagnosis or prognosis of CML. In the results, the four models with the highest accuracy, 96.66% are RF sfs, KNN sves, SVC sfs, and SVC rbf.

In 2021 Karami, K., et al., [20] introduce using machine learning to detect acute myeloid leukemia (AML). Several feature selection methods were employed to extract a set of necessary features for the purpose of modeling data. According to the results, GBT outperforms all other feature selection methods using a 0.930 AUC, 85.17% accuracy, and feature selection utilizing the Relief technique in forecasting the proportion of AML patients that survive.

In 2022 Venkatesh, K., et al., [21] devised to identify AML, to calculate the amount of white and red blood cells, as well as use a microscope to look for any abnormal health issues. The dataset includes lymphocytes, abnormal monocytes, and normal monocytes. The experimental accuracy rate of 97%, beat several deep learning techniques currently in use.

In 2020 Claro, M., et al., [22] introduce to detect deep learning Models of Convolution Neural Nets for the Identification of Acute Leukemia. In capable of differentiating between healthy blood slides and blood slides with ALL and AML is presented (HBS). A precision of 97.23% and an accuracy of 97.18% were attained in the studies, which included 16 datasets totally 2,415 images.

In 2022 Jawahar, M., et al., [23] proposed a ALNett, a deep convolutional neural network used for Acute Lymphoblastic Leukemia classification. The use of cluster layer to raise the accuracy of the classification by identifying and grouping similar features within the data. The proposed ALNet model, based on the experimental data, not only had the lowest computational complexity but also achieved the highest classification accuracy with an F1 score of 0.96% and 91.13%, respectively.

In 2024 Ogunbiyi, T., et al., [24] devised the application of gene expression data for acute leukemia classification. Utilizing Recursive Feature Elimination (RFE) and a Multilayer Perceptron (MLP) for classification, the features are the most crucial factors. The combined technique is successful, as evidenced by recall, F1-Score, accuracy, and precision rates for leukemia subtype categorization that are close to 99%.

In this literature review, limit their practical applicability and effectiveness in actual situations, particularly in settings with limited resources. Additionally, there may be concerns about the lack of comprehensive evaluation or real-world testing under varying conditions. To address these issues, a novel LeukNet introduce for accurate classification of Leukemia.

3. PROPOSED METHODOLOGY

In this section, a novel LeukNet model has been proposed for classifying the Leukemia from the dataset. Figure.1 shows the general process of the proposed LeukNet methodology.

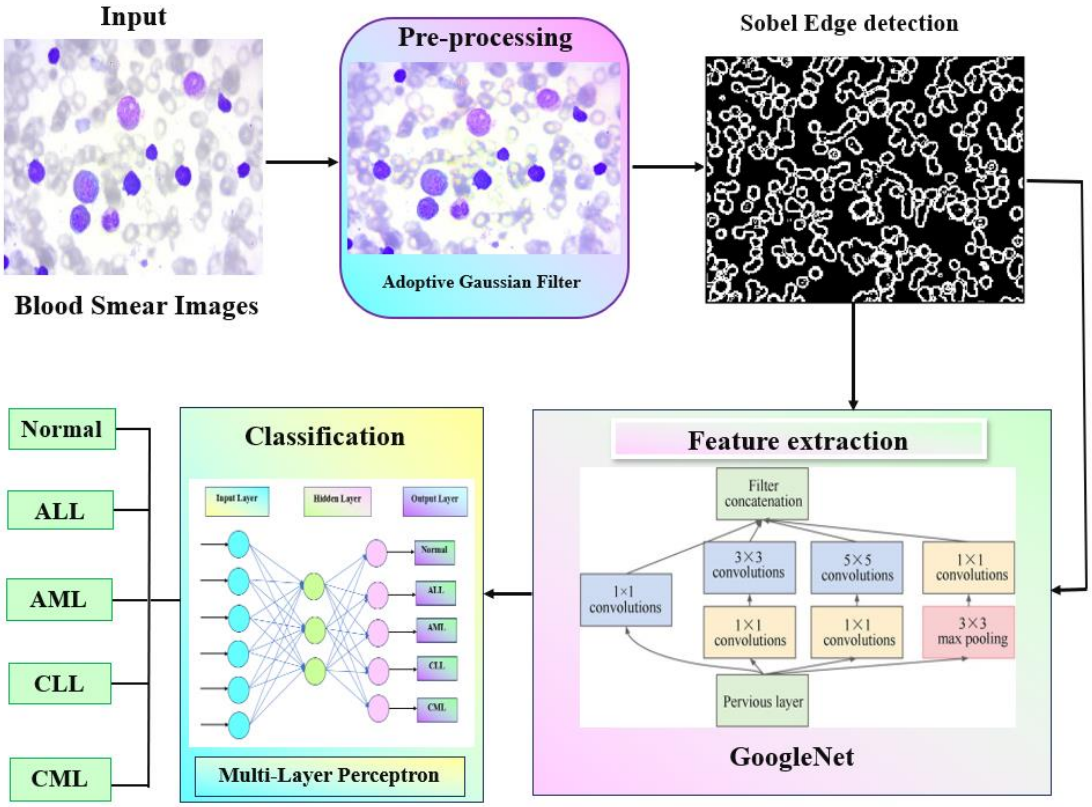

Figure 2. Proposed LeukNet methodology

3.1 Dataset acquisition

In this study the blood sample images are collected from two widely known dataset libraries like Kaggle and ALL-IDB. The collection includes five types of leukemia images, each one with a size of 2560x1920 in BMP formats. The collective formats are designed to tune the suggested method to decide the types of leukemia chronic are CML, CLL and acute are ALL, AML.

3.2 Pre-processing using AGF

Adaptive Gaussian filters (AGF) are used to pre-process photos and eliminate noise artifacts. An innovative method of sharpening and smoothing is the adaptive Gaussian filter (AGF). The digital Gaussian filter in two dimensions will be represented as follows:

$$G(x,y) = \frac{1}{\sqrt{2\pi\sigma}} e\left(-(x^2+y^2)/2\sigma^2\right), \quad (1)$$

Where σ^2 is the filter kernel's size and the Gaussian filter's variance $l(-l \le x, y \le l)$ is often determined by subtracting values from the kernel that are less than five percent of its maximum value. The one-dimensional Gaussian filter is expressed as:

$$G(x) = \frac{1}{\sqrt{2\pi\sigma}} exp\left(-x^2/2\sigma^2\right). \quad (2)$$

Large filter variances are effective in mitigating noise when using the Gaussian filter for noise suppression; however, they also cause the image to warp in areas where there are sharp variations in pixel brightness. In addition, the Gaussian filter causes phantom edges, edge disappearing, and displacement of edge positions. AGF effectively reduces noise while preserving edges, making it an essential step for enhancing image quality before further processing.

3.3 Sobel Edge detection

Sobel edge detector is used to detecting edges for the horizontal edges and vertical edges. The majority of edge detection techniques operate under the assumption that an edge only exists where there is an image-wide intensity gradient or discontinuity. Using this assumption, an edge will be detected if one found the points where the image's derivative of the intensity value throughout was higher. The adaptive Gaussian filter operation is the foundation of the Sobel edge detection operator. The periodicity of pixel value changes is described by Adaptive Gaussian filter operation. The first difference-based operator's algorithms are the simplest to implement on hardware when compared to other edge detection techniques. A certain weight is added to the center point in the Sobel algorithm in order to decrease noise.

$$U_q = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 3 \end{bmatrix} \qquad U_p = \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ 1 & 2 & 3 \end{bmatrix}$$

Vertical operator Horizontal operator

In the Sobel algorithm, gradients are calculated at each location of the image using both vertical and horizontal masks. Therefore, moving the horizontal and vertical masks over the entire image starting from the upper left corner. Until it reaches the end of the row on the image, the mask moves to the right before starting again from the leftmost second row of the image. The Sobel operator highlights edges by marking areas with significant intensity changes across the image.

3.4 GoogleNet

Convolutional neural networks of the GoogleNet type were constructed with the Inception architecture. The network selects from a range of sizes for convolutional filters using Inception modules. These modules are arranged by an Inception network in a stack on top of one another, occasionally using stride 2 max-pooling layers, the grid resolution are halved. In contrast to earlier cutting-edge architectures like AlexNet and ZF-Net, the GoogleNet architecture is significantly different. This is achieved by utilizing a number of techniques such as global average pooling and 1×1 convolution.

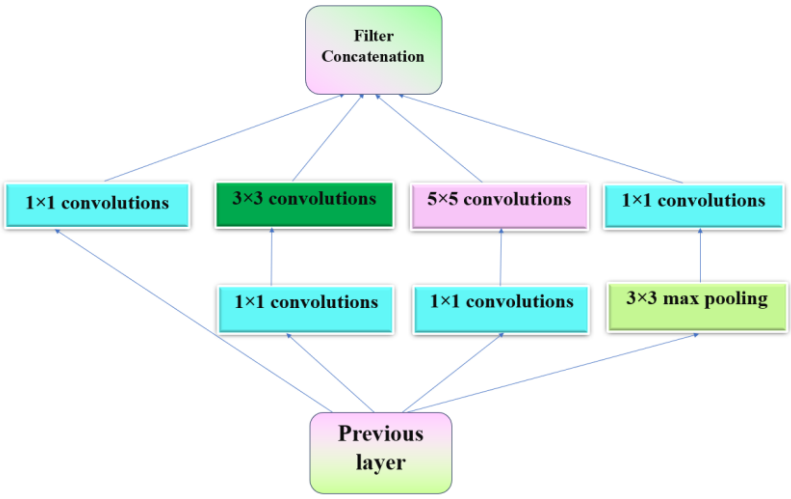

Figure 3. Architecture of GoogleNet Inception Module

A simple mathematical model of an inception module with three types of operations (1×1, 3×3, and 5×5) with concatenated outputs:

$$Inception = Concat\left(Conv_{1x1}(X), Conv_{3x3}(X), Conv_{5\times5}(X), Pool(X)\right) \quad (3)$$

where X is the input to the inception module, and Concat is the concatenation of feature maps along the channel dimension. Its efficient structure with less parameters and unique use of 1x1 convolutions to image classification applications. This architecture allows GoogleNet to achieve high precision using fewer parameters, which makes it effective for large-scale image classification tasks. This architecture allows GoogleNet to achieve high performance with fewer parameters and reduced computational cost, making it efficient for large-scale image classification tasks.

3.5 Multi-Layer Perceptron

Multilayer perceptron (MLP) is used to classify kinds of Leukemia namely normal, ALL, CLL, AML and CML. Its components are typically a layer of input, a layer of output, one or more hidden layers. Weighted connections are used to link each node in the network to nodes in neighboring layers. The MLP employs nonlinear activation functions to give the model nonlinearity, allowing it to identify intricate connections and patterns in the data. During training, the network adjusts the weights of these connections techniques, like gradient descent, to reduce the discrepancy between expected and realized results. MLPs are frequently utilized for a variety of tasks, including as categorization, regression, and pattern recognition, due to their ability to learn from data and model intricate relationships. This process iterates until a desirable level of predictive accuracy is attained. The visual representation of MLP shown in Figure 4.

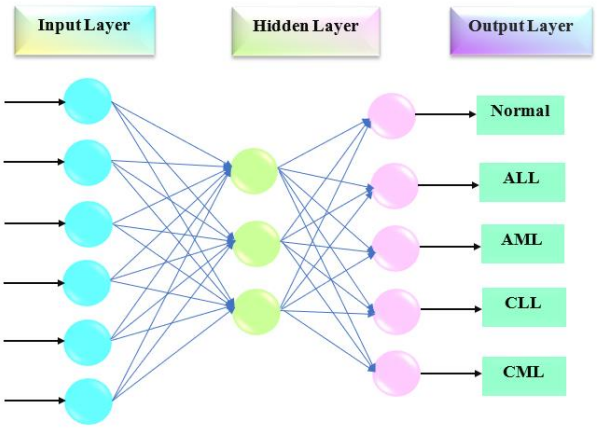

Figure 4. The schematic representation of Multi-Layer Perceptron

The perceptron algorithm adapts the connection weights immediately after processing each individual data point, relying on the discrepancy between the perceptron's generated output and the intended outcome. The linear perceptron, an abridged variant of the least mean squares algorithm, characterizes this process. This is achieved by reducing the corrections applied to the weights, guaranteeing that the perceptron converges towards the sought-after output. The calculation of these corrections is as follows:

$$\sum(n) = \frac{i}{2}\sum_{j=0} e^2\,(n) \quad (4)$$

Difference in each weight is calculated using gradient descent like in the following:

$$\Delta wji(n) = -\eta\left(\frac{\partial \sum(n)}{\partial vj(n)}\right) yi(n) \quad (5)$$

Where yi indicate the output of the previous neuron, while the learning rare is indicated by η, and ensures that the weights coverage to a stable response without oscillations. The computed derivative is significantly dependent on the generated local field vj. The final corrections are computed by iterating through the algorithm until the error is minimized, ensuring the MLP produces the desired output with high accuracy. The MLP ability to adjust weights dynamically and use data to learn from, making it an effective tool for classifying complex patterns such as leukemia types.

4. RESULT AND DISCUSSION

The result analysis of the LeukNet model is implemented using MATLAB-R2022b. The experiment dataset is used to blood sample images commonly available two dataset library namely Kaggle and ALL-IDB.

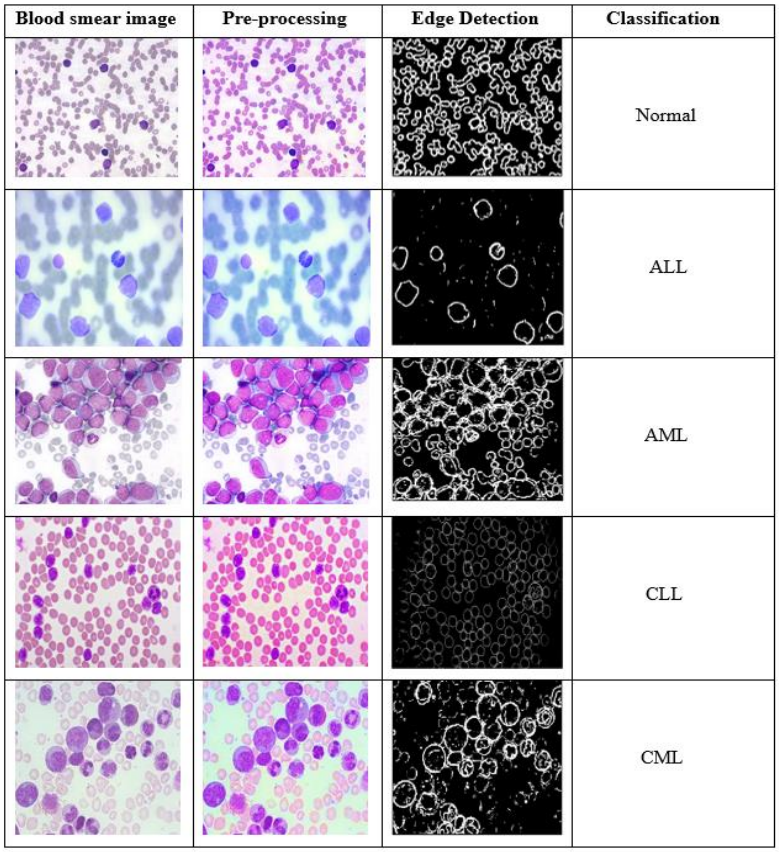

Figure 5. The experimental result of proposed LeukNet model

4.1 Performance analysis

The following statistical measures, including accuracy, precision, recall, specificity, and F1 score, are used to evaluate the efficacy of the classification technique.

$$Specificity = \frac{T_{neg}}{T_{neg}+F_{pos}} \quad (6)$$

$$Precision = \frac{T_{pos}}{T_{pos}+F_{pos}} \quad (7)$$

$$Recall = \frac{T_{pos}}{T_{pos}+F_{neg}} \quad (8)$$

$$Accuracy = \frac{T_{pos}+T_{neg}}{Total\ no.of\ samples} \quad (9)$$

$$F1\ score = 2\ (\frac{Precision*Recall}{Precision+Recall}) \quad (10)$$

where T_{pos} and T_{neg} indicates the actual benefits and drawbacks of the sample images, F_{pos} and F_{neg} shows the sample images false positives and negatives. The effectiveness of the proposed network for categorizing various Leukemia are demonstrated in table.1 and it is visually displayed in Figure 6.

Table 1. performance analysis LeukNet model

Classes	Accuracy%	Specificity%	Precision%	Recall%	F1 score%
Normal	99.12	98.87	95.22	91.80	94.24
ALL	98.2	97.52	90.37	93.39	96.71
AML	99.67%	89.30	93.25	95.31	90.43
CLL	98.18	91.73	97.69	97.37	88.35

CML	98.55	95.39	98.16	79.41	91.46

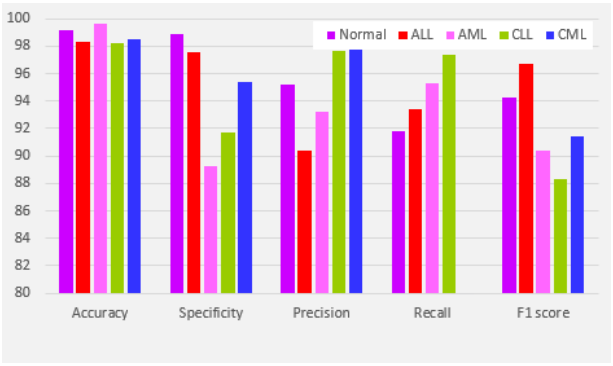

Figure 6. Performance analysis proposed LeukNet

Figure 6 shows the performance of proposed model for five classes that includes Normal, ALL, CLL, AML, CML. The proposed approach produced accurate results of 99.12%, 98.29%, 99.67%, 98.18% and 98.55% for normal, ALL, CLL, AML, CML.

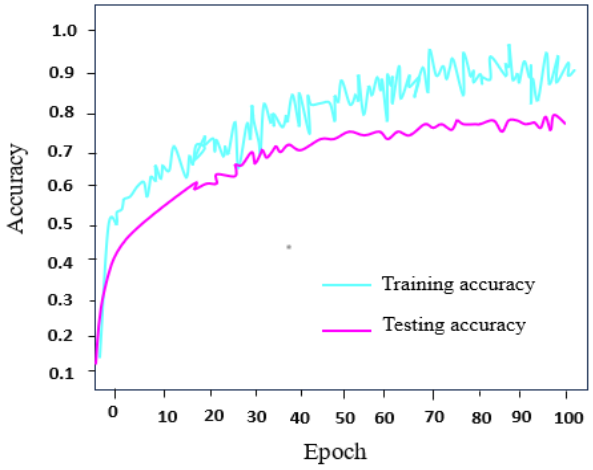

Figure 7. Training and Testing accuracy of the proposed method

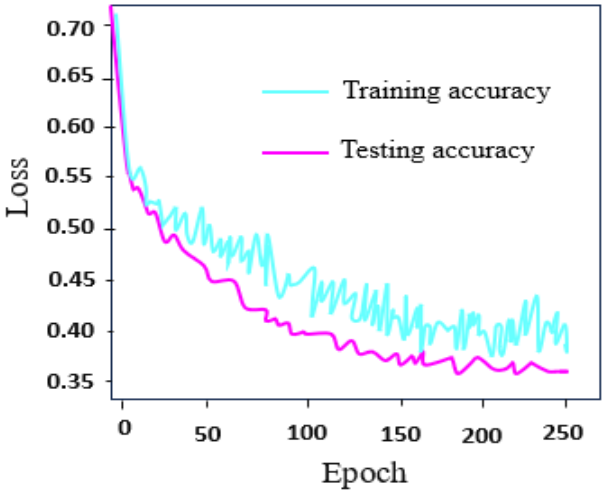

Figure 8. Training and Testing loss of proposed method

The proposed LeukNet model seen in Figure 7 and 8 has achieved high precision in testing as well as teaching. The Performance metrics is measured by F1 score, specificity, recall, accuracy, and precision. The proposed approach achieves high accuracy 98.76%.

4.2 Comparative analysis

In this research presents a comparison study of LeukNet model in comparison of other deep learning models. To show results of the LeukNet model are more effective, compared the effectiveness of existing techniques using specificity, F1 score, accuracy, and recall.

Table 2. Comparative analysis of the proposed method with existing techniques

Networks	Accuracy	Specificity	Precision	Recall	F1 score
CNN	95.89 %	91.95%	95.49 %	90.13 %	85.38 %
DenseNet	92.27 %	94.49%	91.23 %	93.20 %	90.37 %
GoogleNet	90.38 %	95.48%	93.17 %	94.32 %	92.14 %
MLP	98.76 %	98.36%	96.36 %	97.42 %	98.90 %

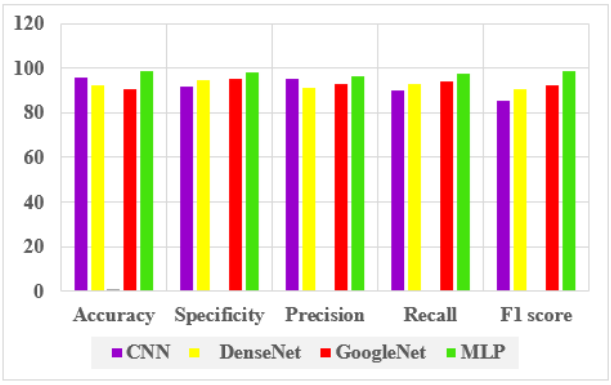

Figure 9. Comparison of existing deep learning network and proposed network

Figure 9 shows that the comparative analysis of LeukNet method obtained 98.76% of accuracy, 98.36% of specificity, 96.36% of precision, 97.42% of Recall and 98.90% of F1score respectively. The proposed technique improves the accuracy range of 2.90%, 6.57%, and 8.48% better than LD-C-NMC, ALL-delt and DeepLeukNet respectively. However, in comparison to the proposed method, the previously described strategies do not perform as well. The proposed LeukNet system has demonstrated higher performance compared to existing methodologies, with a higher accuracy rate of 98.76%. The maximum F1 score of the method is 98.90% which is higher compared to the maximum F1 scores of all other proposed techniques. The proposed approach outperforms the existing methodologies with a specificity rate of 98.36%.

Table 3. Comparison of accuracy with existing and proposed work

Author	Methods	Accuracy (%)
Talaat, and Gamel., [1]	LD-C-NMC	96.97%
Perveen, S., et al., [5]	ALL-delt	97.18%
Saeed, U., et al., [7]	DeepLeukNet	97.01%
Proposed	LeukNet	98.76%

Table 3 shows that proposed LeukNet model improves the overall accuracy of 2.90%, 6.57%, and 8.48% better than LD-C-NMC, ALL-delt and DeepLeukNet respectively. The comparison above indicates that in terms of precision, the proposed LeukNet model outperforms the current models.

5. CONCLUSION

In this research, a novel deep learning based LeukNet model has been proposed for identifying the types of leukaemia in its early stages. Initially, the images of the blood smear are preprocessed using Adaptive Gaussian filters to removing noise artifacts. Sobel detector is used to detecting the edges in horizontal and Vertical from the blood smear images. Based on the edges, the deep learning-based GoogleNet is used for extracting the blood cell features. Further, the classification is performed by Multi-Layer Perceptron. It classifies the smear of blood images into five different classes: Normal, ALL, CLL, AML, and CML. The classification of the proposed LeukNet model was 98.76%. The proposed LeukNet model enhanced the total accuracy by 2.90%, 6.57%, and 8.48% better than LD-C NMC, ALL-delt and DeepLeukNet respectively. Future, work will improve the accuracy of the proposed LeukNet by integrating the advanced optimization algorithms for efficient detection of Leukemia.

CONFLICTS OF INTEREST

The authors declare that there is no conflict of interest.

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