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# Leukemia detection using SegNet and faster region-based convolutional neural network

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**ABSTRACT**

Prevention of cancer is mostly attained by surveillance of the transformation zones. White blood cells (WBCs) are established in the bone marrow and intemperate growth of WBC leads to leukemia. Hematologists examine the microscopic images in manual method for predicting leukemia, but it is very complex process and without any guaranteed for accurate. In this proposed study, deep learning techniques involved to segment and classify the three types of leukemia like acute lymphocytic leukemia (ALL), acute myeloid leukemia (AML) and chronic lymphocytic leukemia (CLL) using the BioGps dataset. The purpose of deep learning in medical science enhances the accuracy and precision of determining leukemia in early stages. In this study, introducing a sigmoid stretching (SS) in pixel enhancement for preprocessing; SegNet (St) is comfort to extract the structural features of the leukocytes and to segment the normal and blast cells for a clear classification; faster region-based convolutional neural network (faster R-CNN) carried under the process of classification and optimization done by dragon fly algorithm. The result of this work achieves best accuracy related to the existing techniques of convolutional neural network (CNN) such as support vector machine (SVM), k-nearest neighbors (kNN) and Bayesian model. This study achieves the accuracy rate of 97%, precision rate of 94% and sensitivity rate of 90% respectively with low complexity.



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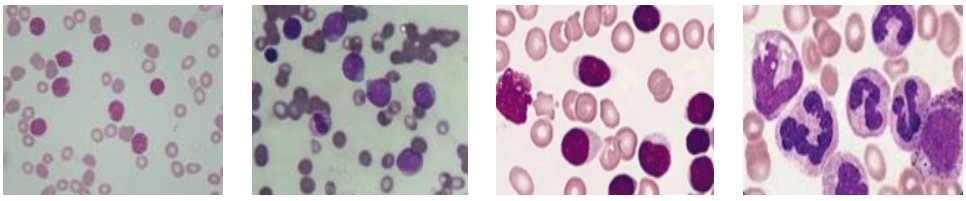
## 1. INTRODUCTION

Leukemia is a classification of blood cancer in which abnormal white blood cells (WBC) form in the bone marrow [1]. According to Global Cancer Observatory (GLOBOCAN), an estimated 9,000 peoples are affected by leukemia in 2021. Figure 1 presents microscopic images of different types of leukemia. Acute lymphoblastic leukemia (ALL) is characterized by the presence of immature lymphoblasts in Figure 1(a). Acute myeloid leukemia (AML), which presents irregularly shaped nucleoli and myeloblasts is shown in Figure 1(b). Chronic lymphocytic leukemia (CLL) is characterized by mature, small lymphocytes with a distinctive, "smudged" appearance in Figure 1(c). An increased number of myeloid precursor cells in various stages of differentiation is shown in Figure 1(d). ALL arises in children age group between 2 to 8 years old, AML arises at any age, but most common in age group between 2 to 20 years old, CLL takes place the age group of above 70 years old and rarely affects the teenagers, chronic myeloid leukemia (CML) emanates at the age group of 60 to 65 years. Here, AML is rapidly spreading into the other blood cells. One of most

common tests for detecting leukemia is the smear test [2], [3]. Blood samples are obtained and subjected to various tests in order to predict leukemia. The tests are: i) complete blood count with differential: used to determine the counts of different types of leukocytes and for categorizing the type of cancer; ii) flow cytometry: this test determines the type of cancer cell due to the presence or absence of protein markers on the cell surface; and iii) peripheral smear examination: this examination looks for variations in the number and shape of leukocytes [4], [5].

Early detection of leukemia is a very challenging task for hematologists in nowadays. Therefore, hematologists examine blood tissues under an optical microscope on a consistent level to accurately classify and detect blast cells. It is difficult to separate and identify the cytoplasm and nucleus is engaged with the segmentation approach [6]–[8]. Recently deep learning (DL) and machine learning (ML) techniques play a vital role such as analyze the medical image, medical image classification and cancer detection [9]–[11]. In going to deeper layer, there must be little difficult to trained the networks [12]. By engaging advanced DL models such as convolutional neural network (CNN) [13], RegNet [14], LSTM [15], YOLO [16] and so on utilized to detecting leukemia. In this paper, pixel brightness (sigmoid stretching) technique is used for preprocessing, Seg-net in DL used for segmentation and feature extraction. For classification, faster region-based convolutional neural network (faster R-CNN) is applied and to reduce the responding time and reaches higher accuracy.

This paper was incorporated as follows five sections: part 2 depicts brief about the existing techniques. Proposed feature extraction, segmentation, classification and optimization techniques explained in the part 3. Performance analysis and comparison part done in part 4 and part 5 concludes with a conclusion.



(a) (b) (c) (d)

Figure 1. Microscopic images of different types of leukemia (a) ALL, (b) AML, (c) CLL, (d) CML

## 2. RELATED WORKS

In recent days, several DL techniques were put forward by researchers mainly to improve the accuracy of blood cell images. These advancements primarily focus on improving the classification, segmentation, and detection of different types of blood cells particularly for diagnosing hematological disorders such as leukemia. Furthermore, advanced preprocessing techniques are enhancing the robustness and generalizability of deep learning models in the analysis of blood cell images.

Thanh *et al.* [17] had put forward to DL techniques utilized to distinguish normal and anomalous cases. In preprocessing, histogram equalization involves to upgrade the contrast of a poor brightness image and predicting the distribution of pixel densities, translational operations are used to shift an image along both X and Y axis with corresponding displacement values and middle of each axis. Image reflection process also included. But activation function is not improved, so it reaches low accuracy. Rajesh and Sathiamoorthy [18] had developed genetic based k-nearest neighbor (G-kNN) algorithm involved to classify the leukemia. Herein integrates the genetic algorithm (GA) and k-nearest neighbor (kNN) algorithm. Preprocessing framework composed of two processes, image noise canceling by median filter approach and enhances the image by G-kNN algorithm. It chooses the best k value with minimum misclassification rate. But, Small number of datasets only feed.

Shafique and Tehsin [19] had proposed a AlexNet is activated to identify ALL in an automatic manner and classify its subtypes. The images were taken by public available datasets. Four sets of datasets had been noted as different colors (red-green-blue (RGB), hue, saturation, value (HSV), luminance, chrominance blue, chrominance red (YcbCr) and high bit rate (HBR)). For the total datasets, ALL detection was good but, the classification was lower than the RGB image datasets. Ahmed *et al.* [20] had proposed CNN is used to identify the varieties of leukemia. The datasets are picking up by the two commonly available leukemia data sources are ALL image database and Ash Image Bank. Feature extractions carry off convolutional and pooling layer. Stochastic gradient descent (SGD) and ADAM optimizers are applied.

Kumar *et al.* [21] had proposed a Dense CNN framework to classify the two types of leukemia such as ALL and multiple myeloma (MM). The datasets had been collected from SMS Spam research. Here, data augmentation introduced two processes, first one is rotating the images corresponding to certain degrees and

second one is upgrading only the edges or boundaries of the original image. Univariate feature selection had been introduced and selects the features based on univariate statistical tests. But its computational time is more. Loey *et al.* [22] had developed two proposed models using transfer learning for detecting leukemia. The datasets are taken from kaggle and ASH image bank. The first technique entails extracting features from input photos and attaining the corresponding parameters of the final FC layer before accessing the classification part, whereas the next step tends to network-fine tuning procedure. The first classification method has three several steps namely: Image preprocessing by using RGB, Feature extraction by using AlexNet, SVM and linear discriminants (LDs) models are utilized for classification. The second classification model has only dual steps: first step is same as that of first model and AlexNet is induced for edge detection as well as identification. Herein, second model reaches the low performance metrics.

Dasariraju *et al.* [23] had devised the random forest (RF) algorithm used to detect and classify the undeveloped leukocytes. Publicly accessible datasets are employed, and the segmentation method includes picture format conversion and structural processes to fragment the characteristics of the blood cell's nucleus and cytoplasm. In every image, 14 features and 2 which are of new nucleus-colored features were extracted. Here in only limited morphological features were added. Most of the data were imbalanced and did not detect the variance of leukemia. Das *et al.* [24] had developed a GLCM (gray level co-occurrence matrix) and glrlm (gray level run length matrix) algorithms are employed to extract the nucleus characteristics and detect ALL. The datasets were taken by ALL Image Database. The SVM is to classify the WBCs. Here, CLAHE applied to upgrade the sample quality. But SVM takes more time to train the large datasets. Shaheen *et al.* [25] had devised the identification of AML using AlexNet and Lenet-5 models and compared the performance of these both models. The datasets were derived from Acevedo *et al.* When comparing the both two models on the performance analysis, the second model reaches low accuracy. But, AlexNet reaches high accuracy and detect only one type of leukemia like AML. From this study various deep learning methods are comfortable to get high accuracy. In this proposed system, SegNet is a type of CNN architecture used to get high accuracy and low memory space for bounding boxes.

## 3. PROPOSED SYSTEM

In this research, deep learning techniques involved to segment and classify the three types of leukemia like ALL, AML and CLL using the BioGps dataset. The purpose of deep learning in medical science enhances the accuracy and precision of determining leukemia in early stages. In this study, introducing a SS in pixel enhancement for preprocessing; St is comfort to extract the structural features of the leukocytes and to segment the normal and blast cells for a clear classification; faster R-CNN carried under the process of classification and optimization done by dragon fly algorithm. Figure 2 shows the overall process of the proposed method.

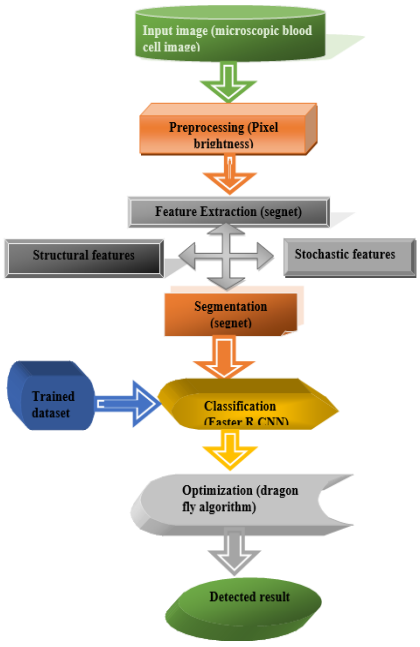



Figure 2. Schematic diagram of proposed method

### 3.1. Data acquisition

Blood sample images involved in this study are taken from the commonly available BioGPS dataset library [26]. Four types of leukemia images with size of 2560×1920 in BMP format constitute the dataset [27]. The merged forms of images are intended to train the proposed model to decide the types of leukemia.

### 3.2. Data preprocessing

The goal of preprocessing is to improve the image by inhibiting unwanted distortions or enhancing some specific features that are essential for further processing and analysis tasks. Herein, two techniques such as sigmoid stretching in pixel brightness transformation and image cleaning are involved. (i) Sigmaroid stretching in the transformation of pixel brightness: The characteristics of the pixel itself dictate the transformation and pixel brightness. The congruent value of the input pixel is the single factor that determines the output pixel's value in pixel brightness transformation. The sigmoid function is a non-linear activation function that is continuous.

$$g(u,v) = \frac{1}{1+e^{(c*(t-fs(u,v)))}} \quad (1)$$

The above (1) implies $fs(u,v)$ - original image; $g(u,v)$ - improved pixel value; c - contrast factor; t - threshold value. By altering the contrast factor 'n' and threshold value 't' it is possible to tailor regulate the overall image quality. (ii) Image cleaning: it is also required to be performed. The term solidity (S) required to be measured for image cleaning. Each component with a solidity value lesser than the threshold value is eliminated. The formula for solidity (S) is (2)

$$S = \frac{Area}{Convex\ area} \quad (2)$$

### 3.3. Extracting features

The aim of this phase was to create a set of descriptions that could be used to classify the leukocytes. It helps to minimize the quantity of redundant data from the datasets. Herein, SegNet is involved extracting the structural features of the cytoplasm and nuclei. The structural features of nucleus like convexity, circularity and convexity are identified in which helps to detect the leukemia. The following (3)-(5) are related to structural features:

$$Sol\ (solidity) = \frac{area\ of\ nucleus}{area\ of\ convex\ hull} \quad (3)$$

$$Convex\ (convexity) = \frac{perimeter\ of\ convex\ hull}{perimeter\ of\ nucleus} \quad (4)$$

$$Cir\ (circularity) = \frac{(perimeter\ of\ nucleus)^2}{4\pi(area\ of\ nucleus)} \quad (5)$$

### 3.4. Segmentation

Detecting and classifying the objects is the most vital role in a computer vision. The goal of this process is to segregate the object in the image. In this process, SegNet is introduced to fragment the blast and normal cell of the WBC. The main contribution in SegNet was to avoid transposed convolution, because it leads to uneven overlap. Figure 3 shows the architecture diagram of SegNet. The encoder network resembles to the thirteen convolutional layers in the very deep convolutional (VGG 16) network without fully connected layers intended for image classification. Figure 4 demonstrates the up-sampling of SegNet. The decoder uses pooling indices of corresponding maximum pooling steps to perform up-sampling. Figure 3 shows the architecture of SegNet.

For setting the window 2×2, stride 2 which is done, then the outcome of the pooling layer is sampled by the factor 2. Before sub-sampling, the boundary characteristics must be retained in the encoder feature maps. Using maximal pooling, each decoder in the network up samples the map of features. The maps of sparse features are produced at this step. Then, the normal cells and blast cells are divided into two different images and with congruent colors.

### 3.5. Classification

In this section, the images are recognized utilizing faster R-CNN. Faster R-CNN is choosing to achieve high accuracy and reliability for determining leukemia. Firstly, the extracted features are trained to the faster R-CNN. The input image is fed into pre trained or initialized CNN to generate a feature. Here, VGG16 is involved to CNN block. The region proposal network gives rise to proposal for this region, in

which the object lies; a mini network is slid over through a convolutional feature that is the outcome of the final layer and it takes less computational time. Finally, the FC layers were accustomed to classifies the target and adjust the bounding box of the target that means to classify the types of leukemia.

$$Intersection\ of\ union\ = \frac{u}{v} \tag{6}$$

The (6) depicts the intersection of union. Here by, $u$- area of intersection between anchor and ground truth box; $v$- area of union of the anchor. It delivers the classification on the blast cell severity and chronic level for classifying the leukemia cases. The faster R-CNN architecture is shown in Figure 5.

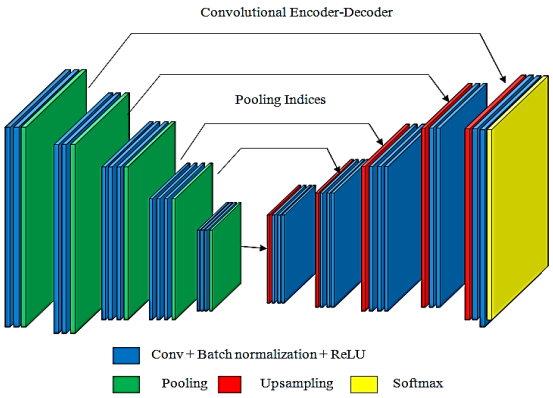



Figure 3. Architecture of SegNet

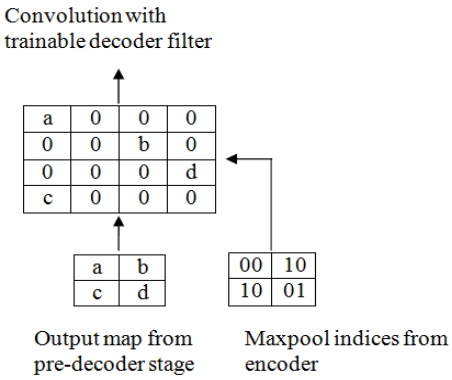



Figure 4. Up-sampling of SegNet

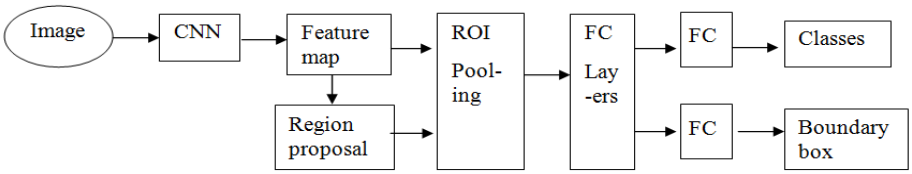



Figure 5. Faster R CNN architecture

### 3.6. Optimization

Essentially, optimization is a unique method of problem solving where certain objectives are fulfilled by adjusting the neural network's internal parameter weights. where the optimization is done using the dragon fly technique. The weight changing in the optimization process is the path to parity of exploration and exploitation.

$$s_j = -\sum_{i=1}^{M} \quad Y - Y_i \tag{7}$$

The (7) implies the calculation for separation. Hither, $Y$- depicts the current location of the individual; $Y_i$ - depicts the location for the $i^{th}$ neighboring element; M- depicts the total count of individual in the element throng and $s$- depicts the separation motion for the $j^{th}$ individual.

$$a_j = \frac{\sum_{i=1}^{M} \quad v_i}{M} \tag{8}$$

The above (8) denotes the alignment calculation. Hither, $a_j$ is the alignment motion for the $j^{th}$ individual and $v$ is the velocity for the $i^{th}$ neighboring element.

$$c_i = \frac{\sum_{i=1}^{M} \quad Y_i}{M} - \quad Y \tag{9}$$

The (9) implies the adhesion calculation and $c_i$ is the adhesion for $i^{th}$ individual, $M$ is the neighborhood size, $Y_i$ is the location of $i^{th}$ neighboring element and $Y$ is the current element individual. The two more features are added to improve the performance of dragon fly algorithm is memory-based hybrid dragon fly algorithm. Finally, it helps to achieve the correct image format, high optimal value and convergence speed.

### 3.7. Detection

The classified images are identified for the three types of leukemia. The difference was predicted as a shape, sponginess of the tissues and multiple of the blast cells. It is used to display the final result of the test data.

## 4. RESULT AND DISCUSSIONS

The experimental setup of this paper was implemented by MATLAB 2019a. In this result analysis, the blood smear images are taken from BioGps dataset to detect at the leukemia at the early stages. The proposed deep learning-based method was evaluated using various performance metrics to ensure its effectiveness in identifying abnormal blood cells. Based on collected data, the proposed method was assessed based on specificity, precision, F1 score, recall, and accuracy.

### 4.1. Preprocessing

It is applied to enhance the image quality. In this study, sigmoid stretching is used to enhance the contrast. Here, $A_{en}$ is the average intensity value and $A_{in}$ is the average intensity of image.

$$Measure\ of\ contrast\ = \frac{A_{en} - A_{in}}{A_{in}} \tag{10}$$

Some blood smear samples usually acquired with the intent of enhancing contrast and classification are achieved using the methods are mentioned above. The contrast measures of five images are depicted as a Table 1. The above table and graphs are clearly shows that the measure of contrast is high for sigmoid stretching than histogram equalization method and fuzzy logic-based method.

Table 1. Measure of contrast Performance measure analysis for segnet:

| Enhancing technique | Img 1 | Img 2 | Img 3 | Img 4 | Img 5 |
|---|---|---|---|---|---|
| Histogram equalization | 0.587 | 0.636 | 0.454 | 0.381 | 0.765 |
| Fuzzy logic | 0.745 | 0.837 | 0.768 | 0.598 | 0.821 |
| Sigmoid stretching, c=2 | 1.038 | 0.945 | 1.134 | 0.856 | 1.264 |
| Sigmoid stretching, c=5 | 1.143 | 1.896 | 1.654 | 0.978 | 1.529 |

This technique is a crucial component of the total face recognition accuracy rate for improving face detection accuracy while reducing the number of false negatives and positives. The parameters used for detection are ACC, PRE, Re $F_1$ score, cw, and $fre$ which are defined as: $tp$ (true positive); $tn$ (true negative); $fp$ (false positive) and $fn$ (false negative). The (12) implies the formula for $p_e$ (precision). Class weights are used to balance the classes. The class weight (cw) for each class is formulated as (15). Whereas, $fre$ - frequency of each class; N- the count of pixel in the class; TN is the count of pixel in the image.

$$Accuracy = \frac{tp+tn}{tp+fp+fn+tn} \quad (11)$$

$$p_e = \frac{tp}{tp+fp} \quad (12)$$

$$r_e = \frac{tp}{tp+fn} \quad (13)$$

$$F1\ score = \frac{2(p_e.r_e)}{(p_e+r_{e)}} \quad (14)$$

$$cw = \frac{1}{fre} \quad (15)$$

$$fre = \frac{N}{TN} \quad (16)$$

As shown in Table 2, the blast cell has the highest weight (8.2034) because of its critical role in detecting leukemia, followed by the normal cell (1) and the background (0.5643). SegNet incorporates class weights into the final layer of the architecture to balance the learning process, ensuring the model does not favor more frequent classes and improving sensitivity towards less represented blast cells. According to Table 3, SegNet has an overall accuracy of 0.96, an Intersection over Union (IoU) of 0.79, a weighted IoU of 0.89, and a Mean F1-score of 0.78. All of these metrics demonstrate SegNet's efficiency in segmenting blood smear images.

Table 4 provides a breakdown of class-wise performance metrics, demonstrating high accuracy for blast cells (097), normal cells (095), and background (092). Additionally, the Mean F1-scores for all three classes support the model's ability to successfully distinguish between different cell types. Here blast cell reaches the high accuracy than the other classes and maximum F1 score achieves the background.

Table 2. Class weight of three classes

| Name | Class weight |
|---|---|
| Blast Cell | 8.2034 |
| Normal Cell | 1 |
| Background | 0.5643 |

Table 3. Valuation metrics of SegNet

| Accuracy | Mean IoU | Weighted IoU | Mean $F_1$ score |
|---|---|---|---|
| 0.96 | 0.79 | 0.89 | 0.78 |

Table 4. Class metrics of three classes

| Name | Accuracy | IoU | Mean $F_1$ score |
|---|---|---|---|
| Blast Cell | 0.97 | 0.88 | 0.79 |
| Normal Cell | 0.95 | 0.87 | 0.82 |
| Background | 0.92 | 0.90 | 0.84 |

### 4.2. Comparative analysis

In this proposed study, the testing methodology is used to detect the leukemia in early stages. The SegNet is used to avoid transposed convolution. It is noted, that the SegNet reaches high reaches high accuracy than the other previous techniques such as dual threshold method, enhanced SVM and Bayesian model. Table 5 represents the accuracy and precision results of these different methods by highlighting the advantages of SegNet in achieving more precise and accurate blood cell classification. The accuracy of dual threshold method, enhanced SVM, and Bayesian model are 56%, 67% and 88%.

Table 5. Accuracy and precision result for different methods

| Methods | Accuracy | Precision |
|---|---|---|
| Dual threshold method | 56 | 45 |
| Enhanced SVM | 67 | 78 |
| Bayesian model | 88 | 89 |
| SegNet | 97 | 94 |

From the above comparison SegNet reaches the maximum accuracy 97% and precision 94% compared to other methods like dual threshold method, enhanced support vector machine and Bayesian model. The segmented images are subjected to faster region-based convolutional neural network (R-CNN) to classify the leukemia based on severity level and the Table 6 represents comparison of faster R-CNN classifier with support vector machine, k nearest neighbor. The faster R-CNN classifier firstly well trained the trained data and then move to estimate the test data.

Table 6. comparison of faster R-CNN with other classifiers

| Classifiers | Accuracy | Specificity | Sensitivity |
|---|---|---|---|
| SVM | 86 | 89 | 85 |
| kNN | 92 | 90 | 91 |
| Faster R-CNN | 95 | 92 | 90 |

According to Table 7, the proposed model enhances the accuracy of 2%, 0.23% and 0.5% better than SVM, RF, and AlexNet**.** As a result, the predicted results of the proposed model for leukemia recognizing in images are quite reliable. Compared to traditional machine learning techniques like RF and SVM, the proposed deep learning approach provides more precise and accurate classifications, reducing the likelihood of misdiagnosis. Additionally, when compared to AlexNet, which is a widely used CNN architecture, faster R-CNN offers enhanced object localization and segmentation, making it more suitable for medical imaging tasks.

Table 7. Comparison of proposed model with the existing models

| Authors | Techniques | Accuracy |
|---|---|---|
| Dasariraju S. *et al.* [23] | RF | 96.77% |
| Das, *et al.* [24] | SVM | 95% |
| Shaheen M. *et al.* [25] | AlexNet | 96.5% |
| Proposed method | Faster R-CNN | 97% |

According to Table 8, to attain high levels of precision, classic networks like convolutional neural network (CNN), deep neural network (DNN), and deep belief network (DBN) use a huge number of parameters, which increases the difficulty. With fewer parameters used in Table.8, the suggested model keeps its good performance while reducing complexity. To demonstrate the system's speed, the suggested model employs a restricted number of GFLOPs. Additionally, the suggested model's leukemia diagnosis procedure involving a dermoscopic with 7.1 GFLOPS takes 111 milliseconds (ms). Compared to other earlier DL architectures such as CNN, DNN, and DBN, the complexity is radically reduced. The proposed approach outperforms the current DL methods based on this comparison. The computational complexity of the proposed optimization algorithm using the Dragonfly Algorithm and faster R-CNN is discussed. The model maintains high performance while reducing computational complexity compared to conventional deep learning architectures like CNN, DNN, and DBN. Specifically: The proposed model operates with 7.1 GFLOPS, indicating fewer floating-point operations compared to CNN (15.1), DNN (9.3), and DBN (9.5). The proposed model achieves a processing time of 546 ms on the CPU. The model processes images in 111 ms on the GPU. This reduced computational load demonstrates the efficiency of the proposed optimization strategy in achieving accurate leukemia detection while minimizing resource consumption.

Table 8. Computational complexity comparison of existing methods with proposed model

| Model | GFLOPS | CPU (ms) | GPU (ms) |
|---|---|---|---|
| CNN | 15.1 | 888 | 215 |
| DNN | 9.3 | 652 | 139 |
| DBN | 9.5 | 744 | 143 |
| R-CNN (ours) | 7.1 | 546 | 111 |

### 4.3. Clinical setting

In this section, a clinical implication of the proposed faster R-CNN was illustrated for efficiently detecting the leukemia disease using blood smear images likely in a real-world clinical setting. It begins with the patient visiting a hospital, where blood smear images are collected as input for diagnosis. These blood smear images are then processed by the faster R-CNN model, which analyses them to predict the location of leukemia. The prediction results are then sent back to the doctor in the hospital for assisting in refining the patient's diagnosis and advises on an appropriate treatment plan for the patient. This streamlined process

supports timely and accurate diagnosis to assist in effective patient care in real-time. This approach enhances accuracy by targeting specific leukemia types (blast cell, normal cell) and reducing diagnostic complexity.

## 5. CONCLUSION

The primary intent of this study is to segment the normal and blast cells or undeveloped cells in the peripheral blood smear images into separate images. After, extracting the features and feed into SegNet. Segnet (St) requires less memory space comparing to the other bounding box segmentation. The provided sigmoid stretching (SS) boosts the image contrast level while also upgrading the image quality. Faster R-CNN can be trained in all possible ways to detect and classify the leukemia with low error rate. According to the final results, it has been concluding this proposed framework improves the image quality compare to other methods. The accurate detection of the leukemia is done using the comparative analysis of accuracy, specificity and sensitivity. This proposed work achieves the accuracy of 95%, specificity of 92% and sensitivity of 90% respectively. Detecting leukemia using deep learning has practical real-world applications in improving diagnostic accuracy, and accessibility. Deep learning algorithms are analyzing the blood smears images to identify leukemic cells with high precision, often surpassing traditional methods. Additionally, it can be deployed in resource-limited settings through automated diagnostic tools, expanding access to quality healthcare and potentially improving patient outcomes. In future, our model improves the Multi-Modal Data Fusion, and will be extended with the advanced recognizing network to improve the accuracy.

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## AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

| Name of Author | C | M | So | Va | Fo | I | R | D | O | E | Vi | Su | P | Fu |
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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

## CONFLICT OF INTEREST STATEMENT

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## INFORMED CONSENT

The authors certify that they have explained the nature and purpose of this study to the above-named individual, and they have discussed the potential benefits of this study participation. The questions the individual had about this study have been answered, and we will always be available to address future questions.

## ETHICAL APPROVAL

Our research guide reviewed and ethically approved this manuscript for publishing in this journal.

## DATA AVAILABILITY

Data sharing not applicable to this article as no datasets were generated or analyzed during the current study.

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