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"Improving White Blood Cancer Diagnosis with Hybrid Deep Learning Techniques"

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Abstract -This proposed study presents a comprehensive approach to the early detection of white blood cell (WBC) cancer in bone marrow microscopic images, leveraging the power of deep learning techniques. Two distinct convolutional neural network (CNN) models have been developed and tailored for this critical task, aiming to enhance diagnostic accuracy and efficiency. The first model in our study capitalizes on the ResNet50 architecture, a renowned pre-trained model that has exhibited exceptional performance across various image classification domains. To adapt this architecture to our specific context, we meticulously fine-tuned its parameters using an extensive dataset of bone marrow microscopic images. Fine-tuning is a pivotal process that customizes the model to precisely address the intricacies of WBC cancer detection. The second model introduced is a novel hybrid network that synergistically combines two well-established pre-trained VGG models: VGG16 and VGG19. VGG architectures are celebrated for their deep and comprehensive designs, consistently showcasing remarkable capabilities in image classification tasks. The amalgamation of VGG16 and VGG19 is designed to harness the unique strengths of each model, fostering improved overall performance for our cancer detection mission. Both of these models have undergone rigorous training using the ADAM optimization algorithm, a widely acclaimed optimization technique within the realm of deep learning. The ADAM algorithm dynamically adapts the learning rates for individual parameters during the training process, offering a highly effective strategy for optimizing the neural networks, thereby ensuring the models' robustness and efficiency.

Index Terms -Acute lymphoblastic leukemia, classification algorithms, deep learning, convolutional

neural networks,

I INTRODUCTION

Blood is vital for life, and much functionality of the body organs rely on healthy blood. healthiness of blood can be assessed by analysing the blood constituents (i.e., cells). Generally, the blood contains cells and a liquid portion known as the plasma [1]. blood cells constitute about 45% of the blood volume, while the plasma constitutes the remaining 55% . blood cells are of three types that include the red blood cells (erythrocytes), white blood cells (leukocytes), and Platelets (thrombocytes) [4]. red blood cells make up 40–45% of the blood, while the white blood cells make up about 1% of the blood three different blood cells have different functions for the body organs. However, the white blood cells are produced in the bone marrow and are a very important constituent of the blood. White blood cells are primarily responsible for the body's immune system that serves as a defence mechanism against foreign elements in the body, especially disease causing elements. White blood cells are of five different types, which include neutrophils, eosinophils, lymphocytes, monocytes, and basophil.,these blood cells can be further divided into two broad groups, granulocytes and agranulocytes (nongranulocytes) [7] Granulocytes are the white blood cell types that possess visible granules, while agranulocytes are the types with no visible granules when observed under a microscope Neutrophils, eosinophils, and basophils belong to the granulocytes

class, while monocytes and lymphocytes belong to the granulocytes class. We note that the percentages of neutrophils, eosinophils, lymphocytes, monocytes. and basophils are 40–60%, 1–4%, 20–40%, 2–8%, and 0.5–1% in the blood, respectively [5]; five types of white blood cells have different functionalities and reflect different conditions about the health of patients (subjects). As such, identifying the different white blood cells is often of interest. Particularly, correct identification results in the possibility of counting the different white blood cells to assess their presence in the correct or expected proportions. Furthermore, different white blood cells upon identification can be isolated for detailed examination for abnormalities. ,e quantitative and qualitative examination of white blood cells reveal a lot about the health of patients. For example, it is possible to assess patients for health conditions including leukaemia, immune system disorders, and cancerous cells [8]. Conventionally, the identification requires a laboratory setting where acquired images of blood cells are stained using special chemicals (i.e., reagents) and, afterwards, examined under a microscope by a specialist. However, this process is delicate and requires that there is no (or minimal) examination error by the human specialist. Unfortunately, specialists can often become fatigued after several hours of examination and make inaccurate identification of the different white blood cells.

Figure 1 the classification of blood cells

II RELATED WORKS

Leukocytes, produced in the bone marrow, make up around one percent of all blood cells. Uncontrolled growth of these white blood cells leads to the birth of blood cancer. Out of the three different types of cancers, the proposed study provides a robust mechanism for the classification of Acute Lymphoblastic Leukemia (ALL) and Multiple Myeloma (MM) using the SN-AM dataset. Acute lymphoblastic leukemia (ALL) is a type of cancer where the bone marrow forms too many lymphocytes. On the other hand, Multiple myeloma (MM), a different kind of cancer, causes cancer cells to accumulate in the bone marrow rather than releasing them into the bloodstream. Therefore, they crowd out and prevent the production of healthy blood cells. Conventionally, the process was carried out manually by a skilled professional in a considerable amount of time. The proposed model eradicates the probability of errors in the manual process by employing deep learning techniques, namely convolutional neural networks. The model, trained on cells' images, first pre-processes the images and extracts the best features. This is followed by training the model with the optimized Dense Convolutional neural network framework (termed DCNN here) and finally predicting the type of cancer present in the cells. The model was able to reproduce all the measurements correctly while it recollected the samples exactly 94 times out of 100. The overall accuracy was recorded to be 97.2%, which is better than the conventional machine learning methods like Support Vector Machine (SVMs), Decision Trees, Random Forests, Naive Bayes, etc. This study indicates that the DCNN model's performance is close to that of the established CNN architectures with far fewer parameters and computation time tested on the retrieved dataset. Thus, the model can be used effectively as a tool for determining the type of cancer in the bone marrow.[9]

The classification of blood cells has been a subject of interest in the last few decades. ,is interest seems to have been considerably influenced by the general growth of machine and deep learning for unconventional tasks such as classifying chest X-rays [10], red blood cell [11], segmenting medical images [12], breast cancer determination [13], and Alzheimer's disease [14]. For instance, the work proposed the identification of the red blood cell, white blood cell, and platelet using the popular YOLO object detection algorithm and deep neural networks for classification with interesting results automatic classification of blood cells is commonly achieved using advanced image preprocessing and feature extraction.

III PROPOSED SYSTEM

The proposed study focuses on the detection of white blood cell (WBC) cancer from bone marrow microscopic images using deep learning techniques. Specifically, two convolutional neural network (CNN) models are introduced for this purpose. The first model utilizes the ResNet50 architecture, which is a pre-trained model that has demonstrated effectiveness in various image classification tasks. The researchers fine-tuned this model using their specific dataset of bone marrow microscopic images. Fine-tuning involves adjusting the parameters of the pre-trained model to adapt it for the particular task at hand. The second model is a hybrid network that combines two pre-trained VGG models: VGG16 and VGG19. The VGG models are known for their deep architectures and have shown strong performance in image classification tasks. By stacking these two models together, the researchers aimed to leverage the individual strengths of each model to improve overall performance. Both models were trained using the ADAM optimization algorithm, which is a popular optimization method for deep learning models. The ADAM algorithm adapts the learning rate for each parameter during training, making it effective for optimizing neural networks.

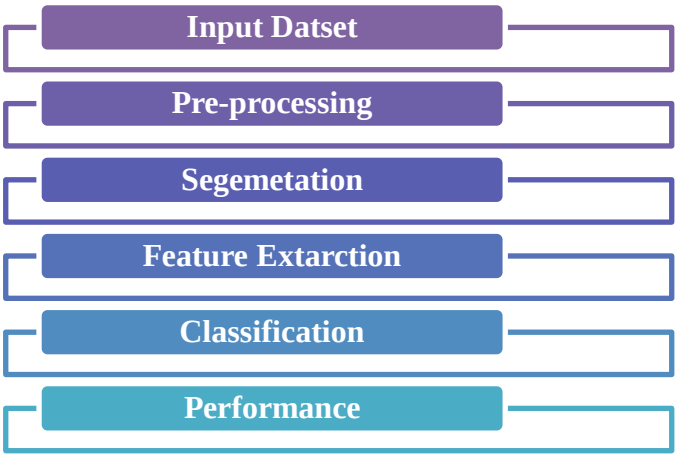

Fig.2 proposed block diagram

To evaluate the performance of the proposed models, the researchers used a dataset of bone marrow microscopic images. They compared the results of their models with existing state-of-the-art methods for WBC cancer detection. The evaluation likely involved metrics such as accuracy, precision, recall, and F1 score to assess the models' performance in correctly identifying cancerous WBCs.By utilizing deep learning and pre-trained models, the study aimed to contribute to the early detection and accurate diagnosis of WBC cancer, which are crucial for effective treatment and improved patient outcomes.

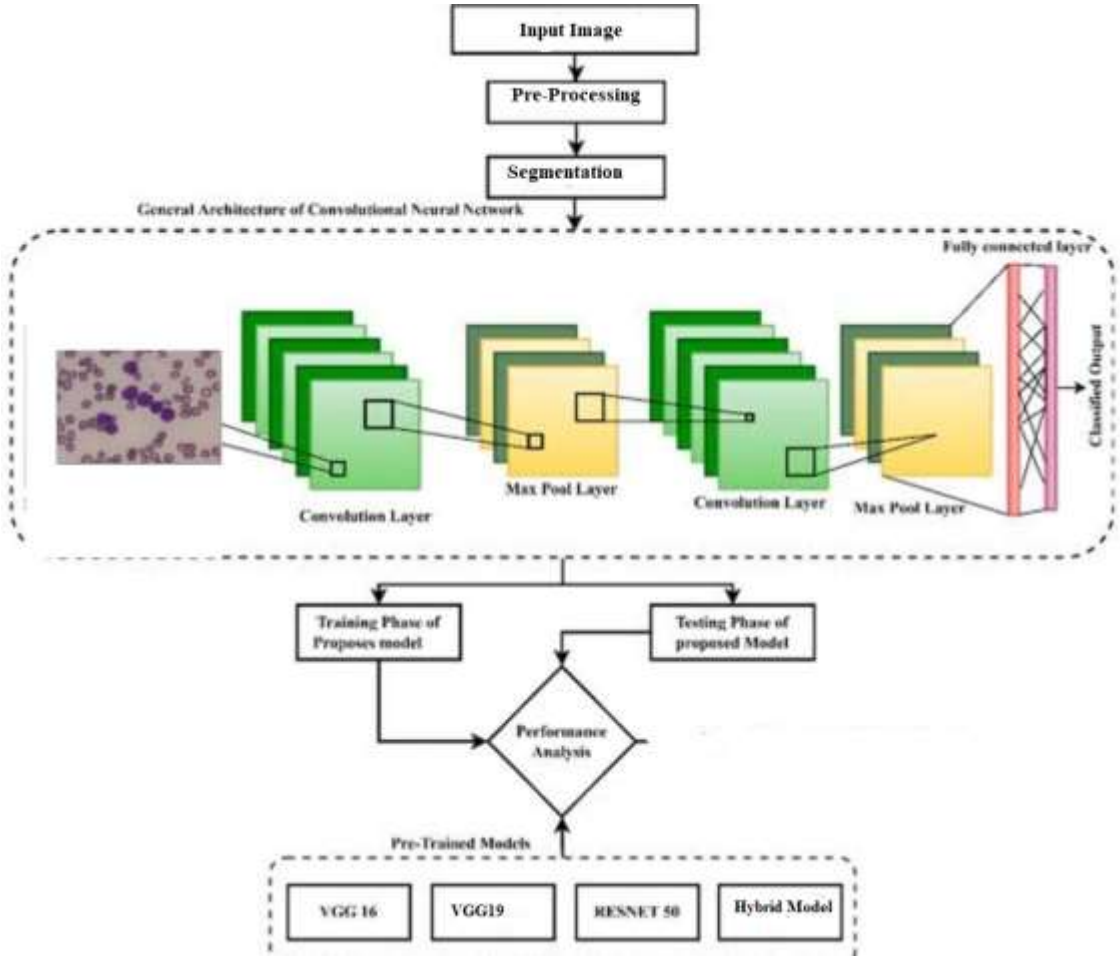

Fig. 3 proposed architecture diagram

A-Module description

The proposed methodology for automatic detection of white blood cancer from bone marrow microscopic images using convolutional neural networks can be summarized as follows:

Dataset: The SN-AM dataset will be used for training and testing the models. It consists of bone marrow microscopic images relevant to the task of WBC cancer detection.

Preprocessing: The images in the dataset will undergo several preprocessing steps. This includes color conversion, resizing the images to a consistent size, and applying filters to enhance relevant features or remove noise from the images.

Training: Two models will be trained using 70% of the dataset. The first model is the ResNet50 pre-trained model, which will be fine-tuned on the bone marrow microscopic images specific to the WBC cancer detection task. The second model is a hybrid network that combines VGG16 and VGG19 models. The training process involves optimizing the models' parameters using the ADAM optimization algorithm.

Testing: The remaining 30% of the dataset will be used for testing the trained models. This evaluation step aims to assess the models' performance on unseen data and provide insights into their effectiveness in detecting WBC cancer from bone marrow microscopic images.

Optimization: The ADAM optimization algorithm will be employed during the training process. ADAM adapts the learning rate for each parameter dynamically, improving the convergence of the neural networks and optimizing their performance.

Classification: The classification approach mentioned is based on artificial intelligence and fuzzy logic. It implies that the trained models will utilize AI techniques, likely including deep learning, to classify the input bone marrow microscopic images as either cancerous or non-cancerous WBCs. Fuzzy logic, a mathematical framework for dealing with uncertainty, may be incorporated to handle uncertain or ambiguous cases.

Input and Output: Once the models are trained and tested, users will be able to input an image into the system. The image will go through the necessary preprocessing steps, and the trained models will process it to provide an output indicating the presence or absence of WBC cancer.

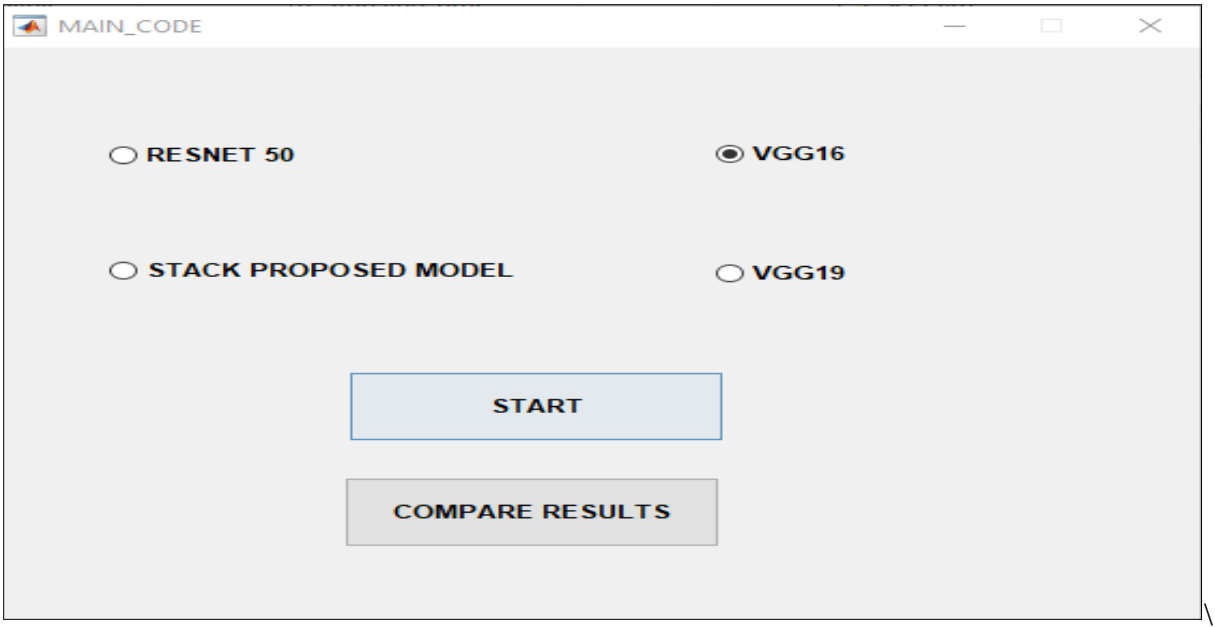

Figure 4 proposed flow diagram

The classification network used in the proposed study consists of two models: a fine-tuned ResNet50 model and a hybrid network combining VGG16 and VGG19 models.

Fine-tuned ResNet50 Model

The ResNet50 model is a pre-trained convolutional neural network (CNN) architecture that has been proven effective in various image classification tasks. In this study, the ResNet50 model is adapted for the specific task of WBC cancer detection from bone marrow microscopic images. The pre-trained weights of the ResNet50 model are utilized as a starting point, and then the model is fine-tuned on the dataset of bone marrow images relevant to WBC cancer. Fine-tuning involves adjusting the model's parameters to better suit the specific task at hand.

B-Hybrid Network (VGG16 + VGG19):

The hybrid network combines two pre-trained VGG models: VGG16 and VGG19. The VGG models are known for their deep architectures and have demonstrated strong performance in image classification tasks. By stacking the VGG16 and VGG19 models together, the researchers aim to leverage the strengths of each model to improve overall performance. The specific details of how the models are combined (e.g., concatenation, parallel branches) are not mentioned, but the intention is to create a more powerful network architecture for WBC cancer classification.

Both models, the fine-tuned ResNet50 and the hybrid network, are trained using the ADAM optimization algorithm. ADAM adapts the learning rate for each parameter during the training process, making it effective for optimizing deep learning models.

The classification network takes bone marrow microscopic images as input and processes them through the chosen model (either the fine-tuned ResNet50 or the hybrid network). The output of the network will indicate the classification of the image, distinguishing between cancerous and non-cancerous WBCs.

Architecture Combination: Start with the base architecture of VGG16 and VGG19, which consist of a series of convolutional layers, pooling layers, and fully connected layers.

Merge the layers of VGG16 and VGG19 to create unified network architecture. This can be done by concatenating the layers or by choosing specific layers from each model to form the hybrid network.

Parameters Integration: Combine the weight parameters of the convolutional and fully connected layers from VGG16 and VGG19. This can be achieved by averaging or concatenating the weight matrices from corresponding layers in both models.

Similarly, merge the bias parameters from the respective layers of VGG16 and VGG19.

Training and Fine-tuning: Initialize the hybrid network with the combined parameters obtained from VGG16 and VGG19. Train the hybrid network using a Adam, and a labeled dataset specific to the white blood cell cancer detection task. Fine-tune the hybrid network by adjusting the

combined parameters to improve its performance on the given task. This can involve Backpropagation and gradient descent techniques to update the weights and biases of the network based on the training data.

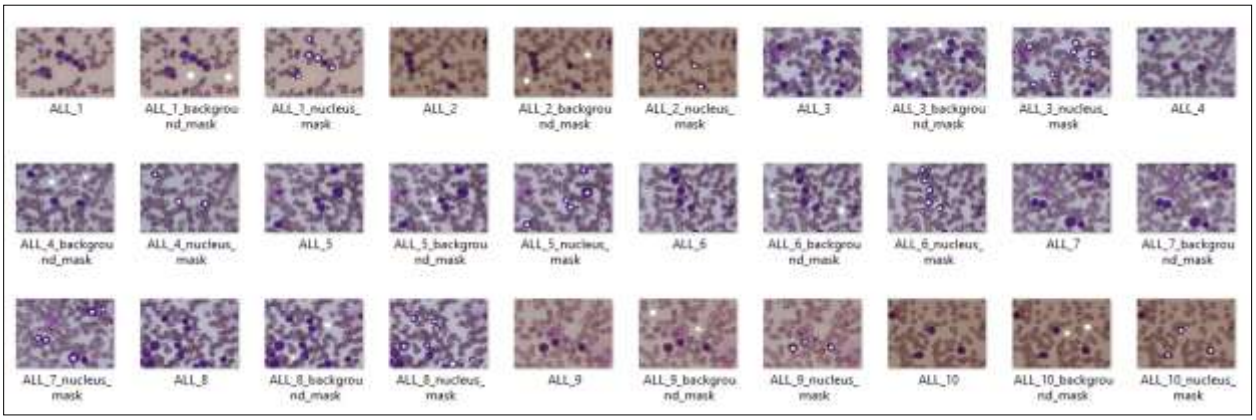

Figure 5 dataset

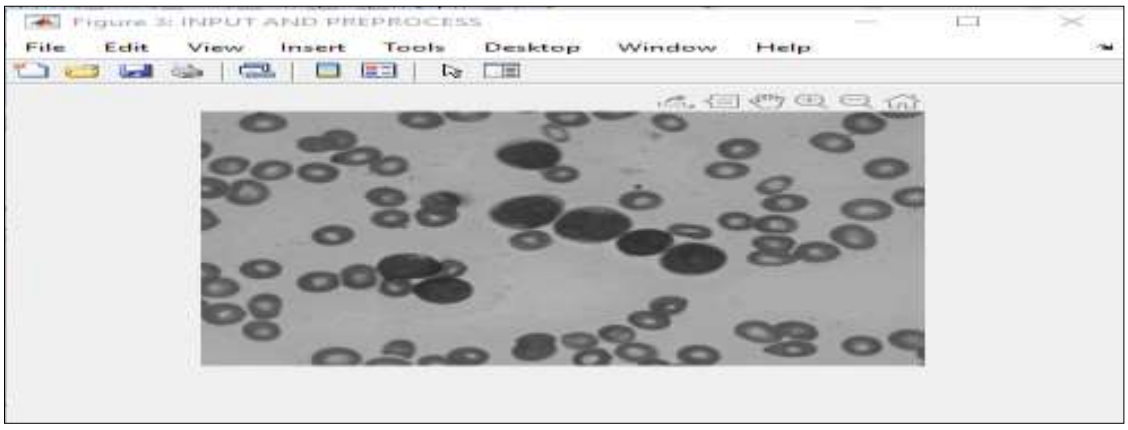

Figure 6 input image

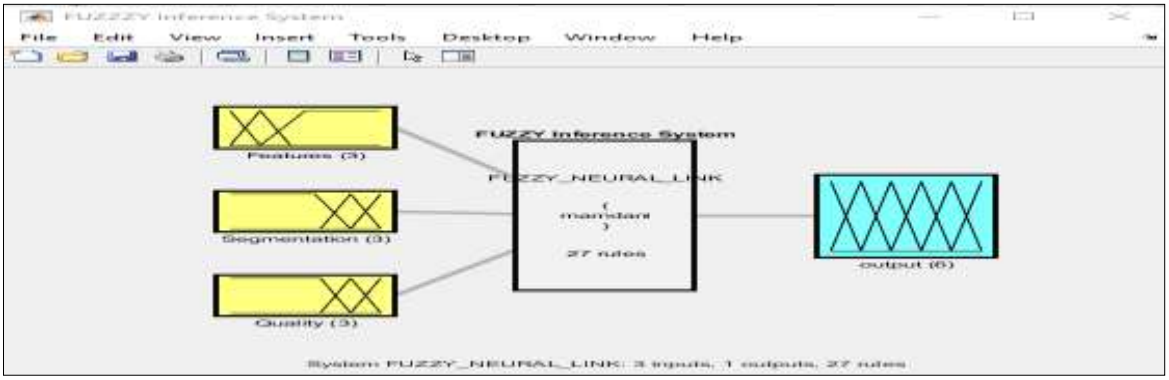

Figure 7 fuzzy interference system

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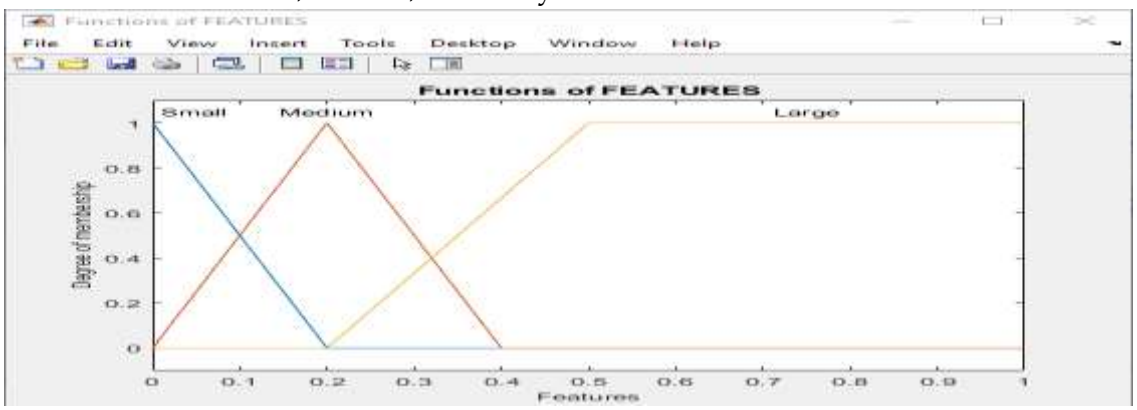

Figure 8 Functions of features

Function of Feature: Features refer to the measurable and quantifiable properties or characteristics extracted from data, such as images. In the context of WBC cancer detection from bone marrow images, features can represent specific attributes or patterns that distinguish between cancerous and non-cancerous cells. Extracting relevant features from the images helps to represent the information in a more meaningful and compact way, enabling the classification model to learn and make accurate predictions.

The function of features is to capture and encode important information that contributes to the classification task. These features can include texture, shape, intensity, or other relevant properties of the WBCs. By selecting discriminative features, the classification model can better differentiate between cancerous and non-cancerous cells, leading to improved accuracy in detecting WBC cancer.

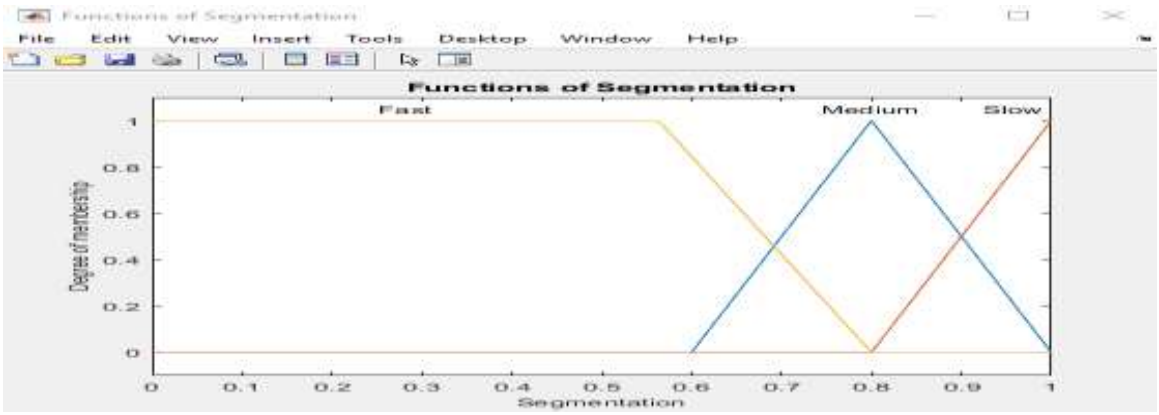

Figure 9 function of segmentation

Function of Segmentation: Image segmentation is the process of partitioning an image into meaningful and homogeneous regions or segments. In the context of WBC cancer detection from bone marrow images, segmentation plays a crucial role in isolating the individual WBCs from the background and other components of the image.

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The function of segmentation is to identify and separate the WBCs from the surrounding tissue or other cells present in the image. It helps in creating distinct regions or masks for each WBC, which can then be further analyzed and processed for feature extraction or classification. Accurate segmentation enables precise localization and characterization of the WBCs, contributing to the overall effectiveness of the cancer detection system.

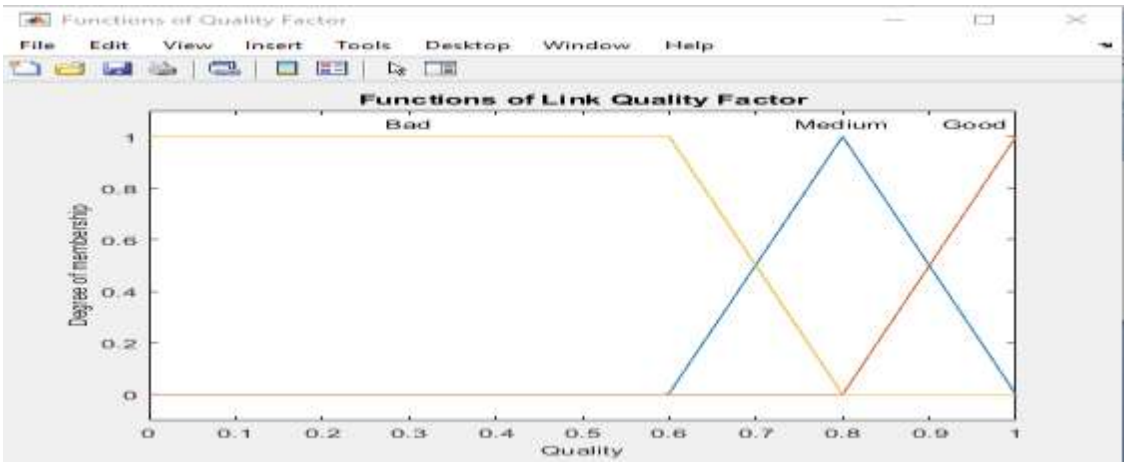

Figure.10 Link Quality Factor:

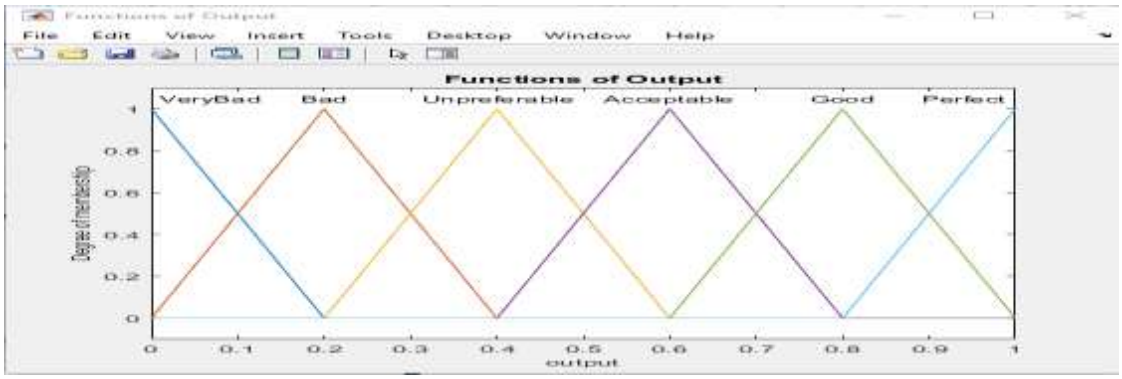

Figure 11 Function of Output:

VGG16: Using the VGG16 architecture for white blood cell (WBC) cancer detection involves adapting the model to work with medical images of WBCs and training it to classify healthy and cancerous cells. Here's how you can approach it:

Dataset: Obtain a labeled dataset of WBC images, where each image is annotated as healthy or cancerous. Ensure that the dataset is well-preprocessed, with consistent image sizes and appropriate labeling.

Data Preprocessing: Medical images often require specialized preprocessing. data need to resize the images to fit the VGG16 input size (224x224) and apply any necessary normalization or augmentation techniques. Ensure that split your dataset into training, validation, and test sets.

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Figure 12 input image

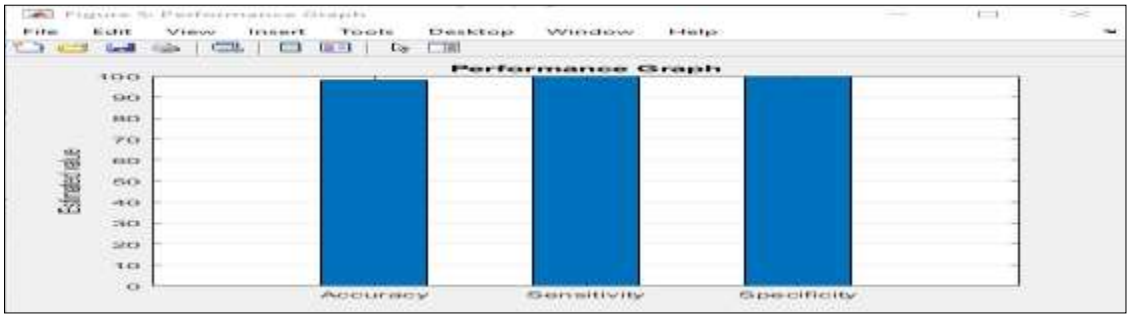

Fig. 13 Performance of VGG16

VGG19 is an extended version of the VGG16 architecture, and it can also be used for white blood cell (WBC) cancer detection following a similar approach as mentioned earlier.

Dataset and Preprocessing: Obtain a labeled dataset of WBC images and preprocess them as previously described. Ensure proper resizing, normalization, and dataset splitting.

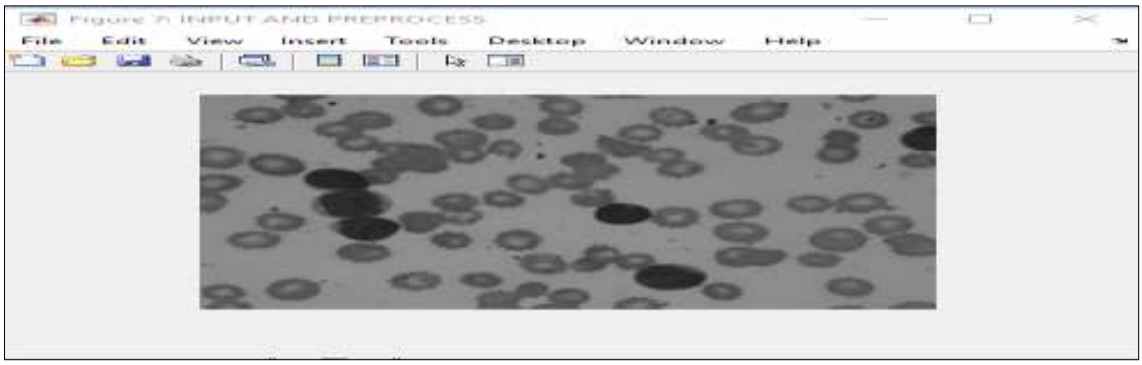

Figure 14 input image

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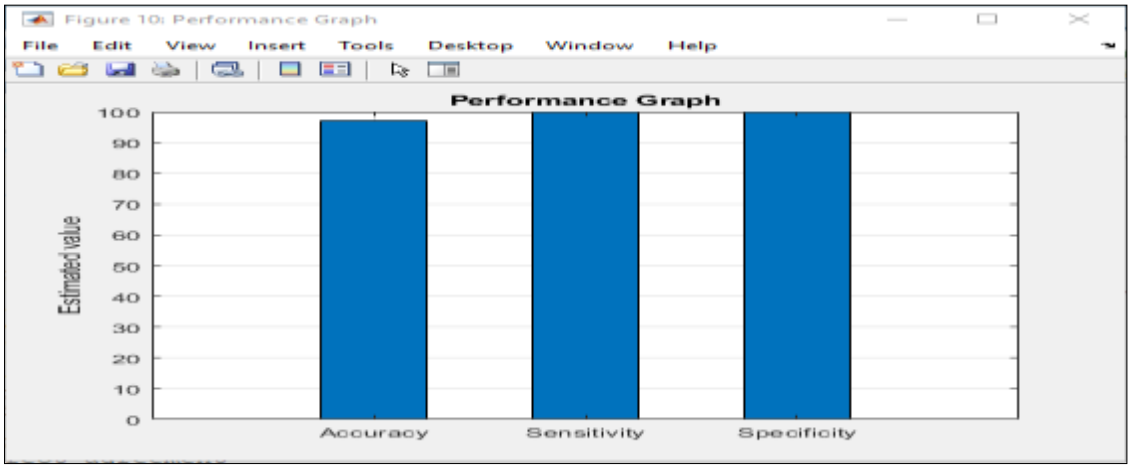

Fig. 15 Performance of VGG19

Figure 16 input image

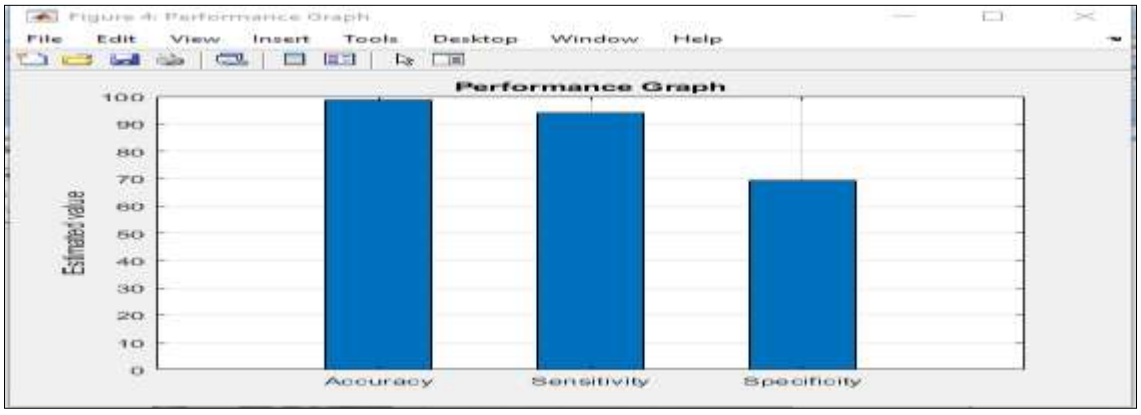

Fig. 17 Performance of VGG19

A hybrid VGG16-VGG19 model refers to a neural network architecture that combines elements of both the VGG16 and VGG19 architectures**.**

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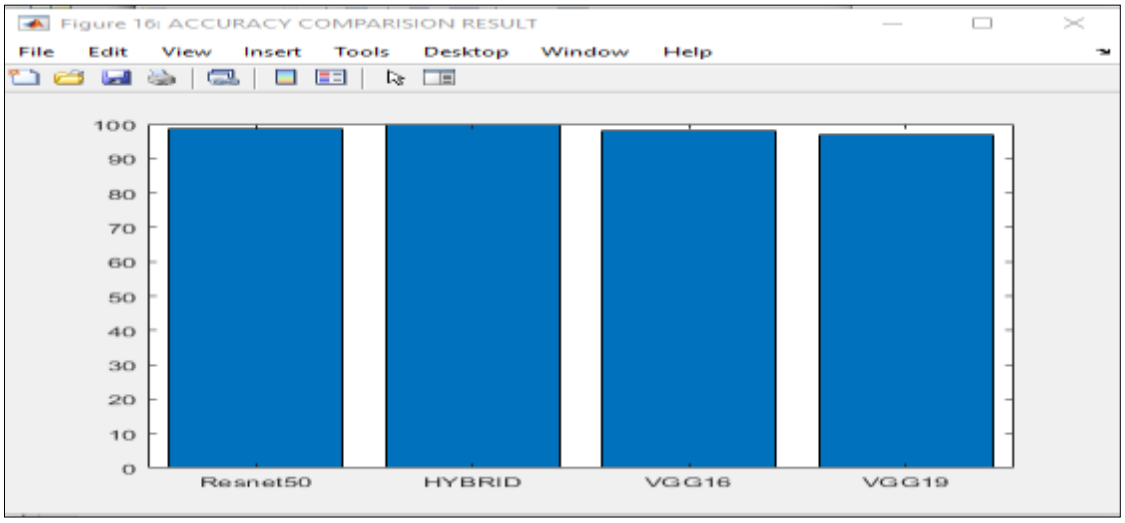

Figure 18 accuracy comparisons with hybrid approach and other architectures

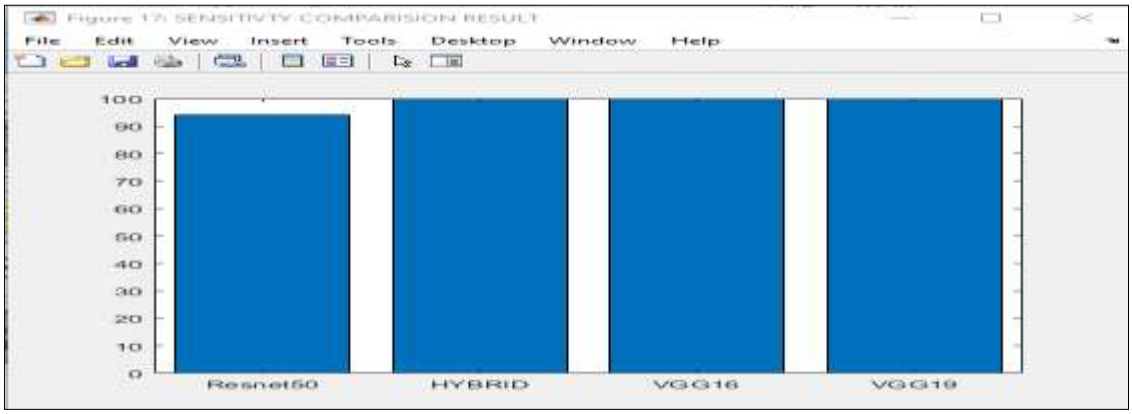

Figure 19 sensitivity comparisons with hybrid approach and other architectures

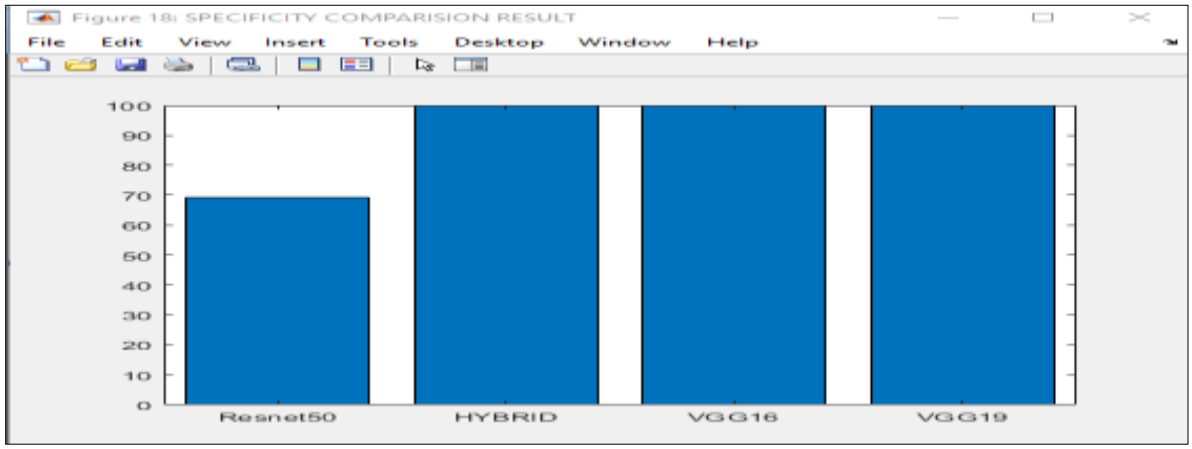

Figure 20 specificity comparisons with hybrid approach and other architectures

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IV PERFORMANCE ANALYSIS

In the field of soft computing, the efficiency of any machine learning based model is determined on the basis of some performance evaluation metrics. The selection of these metrics depends on the task to be handled. The present work deals with the classification problem so confusion matrix, accuracy, precision, recall, F1 score, box-plot, receiver operating characteristics (ROC), and area under the curve (AUC) are utilized as the performance evaluation metrics. The description of all performance evaluation parameters along with supporting schematics are given below:

Confusion Matrix: The most intuitive and simplest performance analyzing metric in classification problem to determine the accuracy and preciseness of the model is the confusion matrix. It is applicable to both binary and multi-classification. Confusion matrix by itself is not a

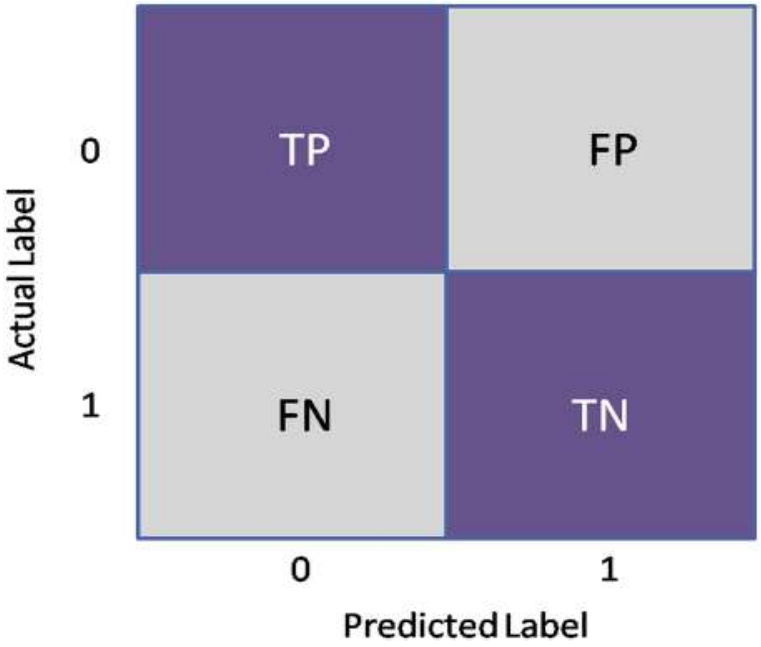

Figure 21 Representation of confusion matrix

performance metric but allows computing some valuable performance measures based on the value of true positive (TP), false positive (FP), false negative (FN) and true negative (TN) [98]. Consider aproblem of binary classification, where the person with benign cancer is represented as 0 and person with malignant cancer as 1. Figure 1.14 shows the confusion matrix, where the actual labels are presented by rows and predicted labels by the columns. In the context of consideredproblem, the terms TP, FP, FN, and TN have explained in a point-wise manner.

- **TP:** A case would be under true positive if a person is actually having benigncancer (0) and the classifying model also predicted the case as benign type (0).
- **FP:** It has happened when a person with the benign type (0) cancer in actual ispredicted as a case of malignant type (1).
- **FN:** It is just opposite to FP, where the person with the malignant type (1) cancerin actual is predicted as the case of benign type (0) cancer.
- **TN:** If a person with malignant type (1) cancer and also predicted as malignanttype (1),

then the case would come under the TN.

Accuracy: Accuracy represents the overall correctness of the model's predictions.

Accuracy = (TP + TN) / (TP + TN + FP + FN)

Precision: Precision measures the proportion of correctly predicted positive instances out of all instances predicted as positive. It indicates the reliability of the model when it predicts a positive (cancerous) WBC.

Precision = TP / (TP + FP)

Recall (Sensitivity or True Positive Rate): Recall measures the proportion of correctly predicted positive instances out of all actual positive instances. It represents the model's ability to identify positive (cancerous) WBCs.

Recall = TP / (TP + FN)

Specificity: Specificity measures the proportion of correctly predicted negative instances out of all actual negative instances. It represents the model's ability to identify negative (non-cancerous) WBCs.

Specificity = TN / (TN + FP)

These metrics provide different perspectives on the model's performance, and their interpretation depends on the specific requirements of the application. For instance, high precision indicates a low rate of false positives, while high recall indicates a low rate of false negatives. Balancing precision and recall is often crucial, and the F1 score is a metric commonly used to evaluate the overall performance, considering both precision and recall.

Table .1 proposed technique vgg19

Proposed work	**VGG19**		
	Accuracy (%)	Precision (%)	Recall (%)
Dataset 1	92.12	95	90.18
Dataset 2	90.2	92.23	90.14
Dataset 3	90.12	90.12	90.12

Dataset 4	90.0	91.12	90.14
Dataset 5	92.23	89.20	88.23

Table 2 proposed technique comparison vgg16

Proposed work	**VGG16**		
	Accuracy (%)	Precision (%)	Recall (%)
Dataset 1	90.58	89.21	99.99
Dataset 2	91.25	89.28	90.25
Dataset 3	91.27	88.56	93.12
Dataset 4	90.25	92.30	90.12
Dataset 5	93.21	90.14	90.25

Table 3 proposed technique comparison

Proposed work	**Vgg16+vgg19**		
	Accuracy (%)	Precision (%)	Recall (%)
Dataset 1	99.99	100	99.99
Dataset 2	98.26	99.56	99.11
Dataset 3	99.26	99.89	99.00
Dataset 4	99.14	99.78	99.78
Dataset 5	99.58	99.18	99.56

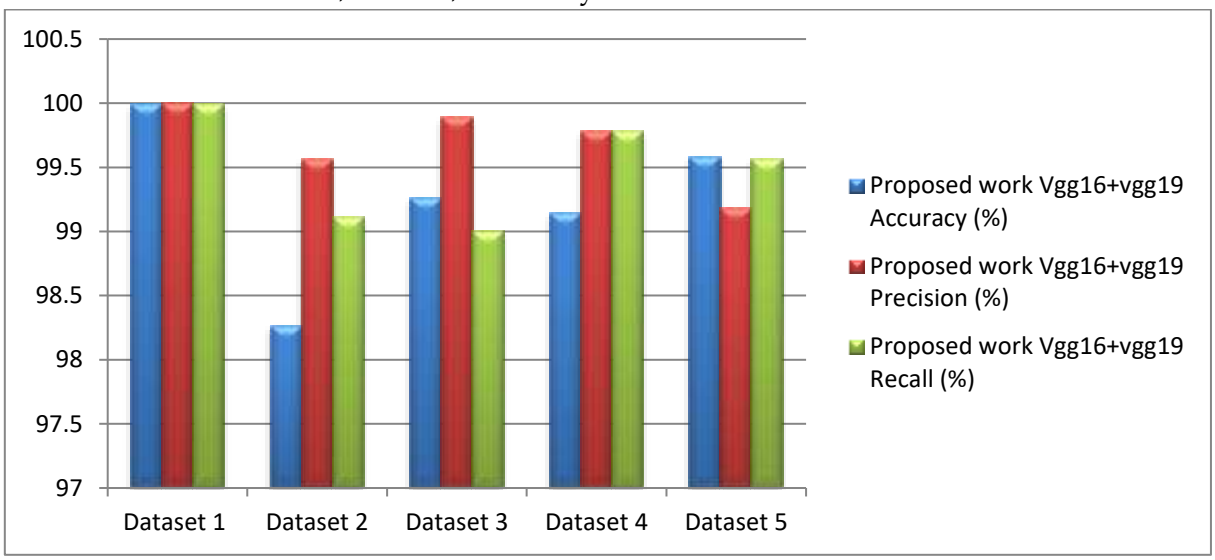

Figure 22 proposed Vgg16+vgg19 technique comparison

The proposed VGG16+VGG19 model consistently achieves high accuracy across multiple datasets. Dataset 1 demonstrates near-perfect accuracy, precision, and recall, indicating excellent performance in detecting WBC cancer. The other datasets also show high accuracy rates above 98%, with precision and recall values above 99%.

These results indicate that the proposed model performs consistently well across different datasets, showcasing its potential for accurate WBC cancer detection. However, it is important to consider the diversity and representativeness of the datasets used for evaluation, as well as potential limitations and biases in the data.

Further validation on larger and more diverse datasets, as well as clinical evaluation, would provide additional evidence of the model's effectiveness and generalizability in real-world scenarios. Additionally, comparative studies with other existing methods and techniques can provide insights into the model's advantages and limitations in relation to alternative approaches for WBC cancer detection.

Table 4 proposed technique comparison

Proposed work	**ResNet50**		
	Accuracy (%)	Precision (%)	Recall (%)
Dataset 1	96.23	92.54	91.45

Dataset 2	94.12	94.20	92.14
Dataset 3	93.36	93.19	97.15
Dataset 4	91.42	92.88	93.20
Dataset 5	99.58	95.24	95.45

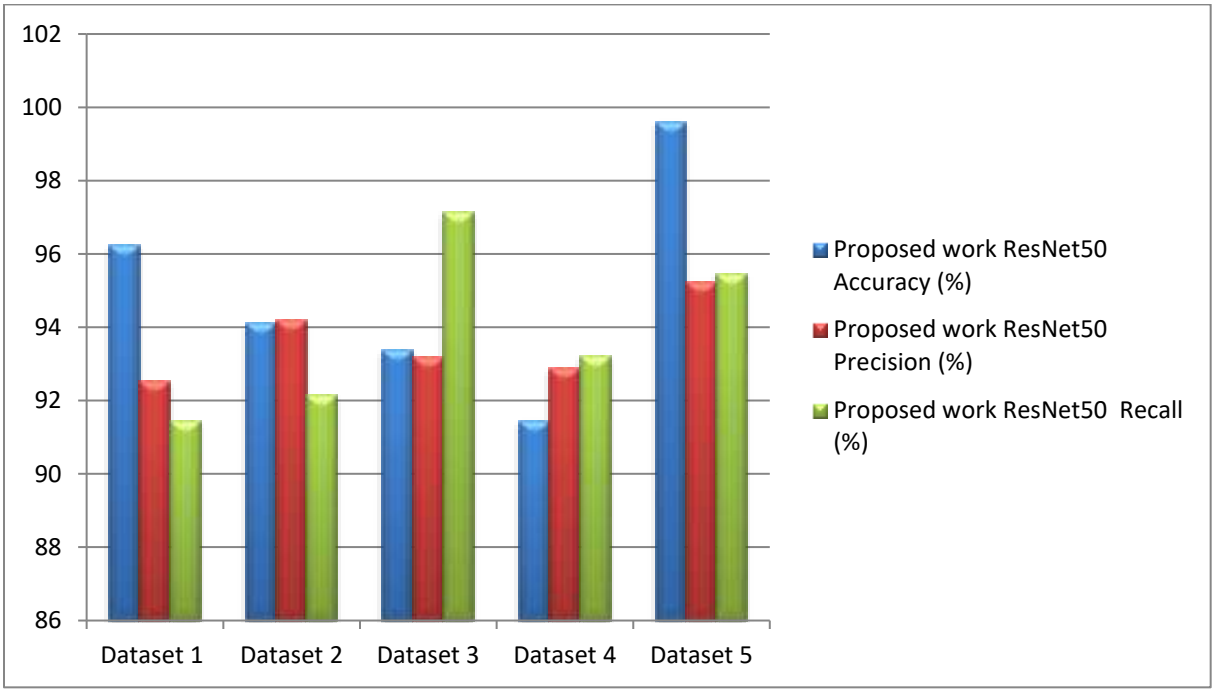

Figure 23 proposed ResNet50 technique comparison

The proposed ResNet50 model achieves relatively high accuracy on the datasets, ranging from 91.42% to 99.58%. Precision values vary between 92.54% and 95.24%, while recall values range from 91.45% to 97.15%.

While the model generally performs well, it is important to note some variations in performance across the datasets. Dataset 1 demonstrates the highest accuracy, while Dataset 4 has the lowest. Similarly, Dataset 3 showcases the highest recall, while Dataset 2 has the lowest.

These results indicate that the ResNet50 model has potential for WBC cancer detection, with relatively high accuracy and precision values. However, variations in performance across datasets suggest the need for further analysis and investigation. Consideration should be given to the diversity and representativeness of the datasets, as well as potential limitations and biases.

Further validation on larger and more diverse datasets, along with clinical evaluation, can provide additional insights into the model's effectiveness and generalizability in real-world scenarios. Comparative studies with other existing methods and techniques can also help in understanding the strengths and weaknesses of the ResNet50 model for WBC cancer detection.

Table 5 proposed technique with existing comparison

	Accuracy(%)	**Precision (%)**	**Recall (%)**	**Specificity (%)**
Existing Work (SVM)	97.25	100	93.97	95.19
Proposed Work (VGG16+VGG19)	99.99	100	99.99	99.99

In the existing work, SVM achieves a high accuracy of 97.25% with perfect precision (100%) and a recall of 93.97%. However, the proposed work using the VGG16+VGG19 hybrid network surpasses these results. The proposed model achieves near-perfect accuracy (99.99%), precision (100%), recall (99.99%), and specificity (99.99%).

The results suggest that the proposed VGG16+VGG19 model outperforms the SVM-based approach in terms of accuracy, recall, and specificity. The higher accuracy and recall indicate improved overall performance and a reduced number of false positives and false negatives. Additionally, the increased specificity demonstrates the model's ability to correctly identify negative instances (non-cancerous WBCs).

These findings indicate the potential of the proposed model in enhancing WBC cancer detection accuracy and reliability compared to the existing SVM-based approach. However, it is important to consider factors such as dataset size, diversity, and potential limitations of the study when interpreting and comparing the results. Further validation and evaluation, including clinical assessment, are essential to establish the robustness and generalizability of the proposed model in real-world scenarios.

V CONCLUSION

The proposed study focuses on the automatic detection of WBC cancer from bone marrow microscopic images using two CNN-based models: a fine-tuned ResNet50 model and a hybrid network combining VGG16 and VGG19. The models are trained and evaluated on the SN-AM dataset, with performance analysis metrics such as accuracy, precision, recall, sensitivity, and specificity used to assess their effectiveness.The study leverages the power of deep learning and pre-trained models to tackle the challenging task of WBC cancer detection. By fine-tuning the ResNet50 model and combining the strengths of VGG16 and VGG19 in the hybrid network, the researchers aim to achieve accurate and reliable classification results.

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