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Classifying Anemia Diseases based on VGG-16 and CBAM Attention Mechanism Models

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Abstract Anemia is a major public health concern and has a significant impact on women and children worldwide. This condition is caused by a lack of sufficient Red Blood Cells (RBCs). Traditionally, anemia diagnosis has relied on invasive techniques that require blood samples, leading to pain and discomfort. This study explores deep learning techniques for automating and enhancing anemia detection accuracy using the Blood Cell Count and Detection (BCCD) dataset. We employ the VGG16 convolutional neural network architecture augmented with the Convolutional Block Attention Module (CBAM) to boost feature representation and performance. The BCCD dataset, consisting of 364 images with 4888 labeled blood cells, was used for training and evaluation. Our enhanced VGG16 model achieved accuracy for RBCs, WBCs, and platelets with values of 0.84, 0.93, and 0.92, respectively, effectively identifying various blood cell types and detecting anemia. Precision-recall analysis and confusion matrix metrics confirmed the robustness of the model, with high precision and recall rates and minimal false positives and negatives. These results suggest that advanced deep learning models with attention mechanisms, such as CBAM, can significantly improve medical diagnostics by providing reliable, efficient, and accurate early disease detection tools. Future development will be directed towards fine-tuning and validating the proposed model on other medical imaging datasets for clinical applications.

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Keywords: *Anemia detection, VGG16, CBAM, deep learning, convolutional neural network.*

1. INTRODUCTION

Anemia is a major public health concern and has a significant impact on women and children worldwide [1]. The World Health Organization (WHO) reports that about (42%) of children under six and (40%) of pregnant women globally are anemic, affecting roughly (33%) of the world's population due to iron deficiency [2]. This condition occurs when the body lacks sufficient red blood cells or when its structure is compromised. Anemia can also result from haemoglobin (Hb) levels falling below normal owing to increased red blood cell destruction, blood loss, defective cell production, or reduced red blood cell count [3]. The symptoms of anemia depend on its cause and severity. Anemia may be so mild that it does not cause any symptoms. However, symptoms usually appear and worsen as anemia worsens. Early anemia detection is vital to prevent irreversible organ damage. The forms of anemia include sickle cell, thalassemia, aplastic, and iron or vitamin deficiency anemia, each with specific causes varying from mild to severe [4].

Human blood contains red blood cells (RBCs), white blood cells (WBC), and platelets. All blood cells are counted in a Complete Blood Count (CBC), and for this, cell segmentation and identification are important. Considering the details of this test, it is imperative to diagnose issues such as Anemia. This study focuses on RBC counting and the identification of abnormalities and Anemia on a peripheral blood film through digital image processing [5]. In particular, for models that use given datasets, such as blood smears and microscopy images, Convolution Neural Networks (CNN) have been used to carry out model training and model validation. The model has proven to be highly effective in the detection of peculiarities of blood composition associated with anemia, which can subsequently help diagnose the disease at an early stage [618-].

One of the advantages of anemia diagnosis based on fingernail, hand, and conjunctival images is that it does not pose any risks to the patient, but also has limitations. These include challenges in accuracy owing to skin colour variations, variable impacts, the presence of medical conditions, and patient diversity. Additionally, concerns regarding data quality, privacy, costs, approval processes, and clinical validation have arisen. This diagnostic method should be used in conjunction with other diagnostic tests and physician assessments. Addressing these constraints requires thorough research, extensive validation, and careful implementation. Deep learning is a reliable method for feature learning and automatic pattern classification [19-27]. Specifically, Vgg16 utilizes weight sharing and local connections to optimize the two-dimensional data structure, reduce parameters, and simplify the learning process, thereby accelerating the network. This study [28-35] used Vgg16, which also focuses on model complexity, some pre-classification mechanisms, and typical Vgg16 problems that include overfitting and vanishing gradient problems [1].

In this study, the Vgg16 model was improved with a Convolutional Block Attention module (CBAM) to increase the model's ability to extract features for anemia detection. The Vgg16 model was trained using a set of images of different blood cells from the BCCD dataset. The performance evaluation of the Vgg16 model used a test set of smeared images of different blood cells from the BCCD dataset. The experimental environment was a computer with an Intel COR i9 CPU, RTX4080Ti-13G GPU, RAM 64 GB and python 9.13.

2. RELATED WORK

This section presents previous approaches employed for identifying anemia using deep learning (DL) models. Magdalena et al.[2] proposed the application of DL techniques to diagnose anemia using conjunctival images by means of convolutional neural networks (CNN). Using CNN, researchers were able to differentiate normal palpebral conjunctiva images from images indicative of anemia. These included 1,440 conjunctival images for training purposes, 160 for validation purposes, and 400 for evaluation. This approach achieved 94% accuracy, and the average precision, recall, and F-score values were 0. 94, 0. 94, and 0. 93, respectively. In [36], a structured cell detection algorithm for isolating red blood cells (RBCs) from an image was proposed. The image was first converted to grayscale and then a binary image was created using a threshold value of 140 to distinguish WBCs from RBCs. The binary image was subtracted from the original image to obtain the RBCs, which were used for further analysis.

Lorenzo Putzu and Cecilia Di Ruberto applied image processing and segmentation to identify white blood cells from pictures taken with the microscope. First, the Zack algorithm finds the background of the image and then histogram equalises the CMYK colour model component to detect the WBCs of the sample. L. Putzu et al. have applied the watershed segmentation technique for the separation of WBC groups with an accuracy of 92% for 33 images [37]. K. Jha et al. [38] employed image processing and morphological methods to segment and count WBCs, achieving 85% accuracy on 20 images. The study in [39] also used the Zack algorithm and histogram equalization for WBC detection. Z. Alreza and A. Karimian used watershed segmentation to separate clumped leucocytes and extracted features such as texture, color, average, variance, standard deviation, and entropy. These features were classified using a support vector machine (SVM) [40-46], which achieved 93% accuracy for leucocyte counts. Alam and Islam [47] use the YOLO (You Only Look Once) [48] which is a deep learning algorithm to detect and count three types of blood cells. From the above analysis, they extracted and modified images of blood smear samples from the BCCD dataset and fine-tuned the YOLO model to accurately detect and count WBCs, RBCs, and platelet counts. lac, additional unlabeled cells were counted by the proposed YOLO model, which was tested on several smear image datasets and achieved high accuracy. The classification was performed in a study by Acevedo et al. [49], who used a trained convolutional neural network to differentiate between eight types of blood cells. Two architectures were employed: Inceptionv3 and VGG-16 were first employed to extract features for training support vector machine classifiers, and the networks were further optimized to produce two models for classifying the eight blood cell types. Wang et al. [50] used two modern approaches of object detection for leukocyte identification, namely the YOLO algorithm and SSD. These are based on feature extraction using convolutional neural networks to solve the problem of segmentation while introducing the problem of multi-true target identification [51-71].

3. METHODOLOGY

3.1 Dataset

The publicly available BCCD dataset was used, comprising 364 annotated smear images for blood cell detection, categorized into three classes: RBC, WBC, and platelets. The JPEG images measured 640 × 480 pixels and included 4,888 labels distributed as 4,155 RBCs, 372 WBCs, and 361 platelets. Platelets account for approximately 20% of the RBC diameter, while WBCs account for approximately twice that of RBCs, with a diameter ratio of 0.2:1:2, as illustrated in Figure 1. Table 1 shows the division of the dataset into training and testing for the three classes.

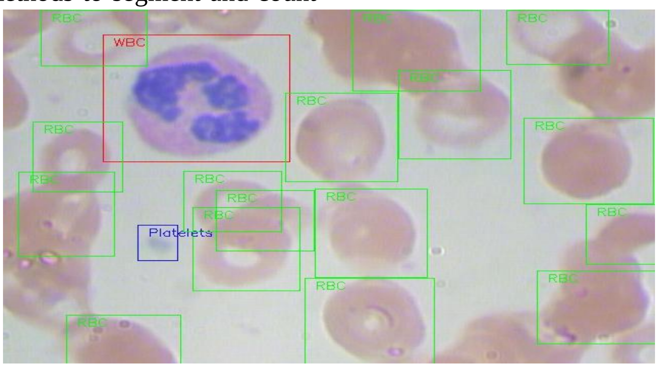

Figure. 1: *Images of blood cells from the BCCD dataset.*

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Table 1*: BCCD dataset*

Class	Training (80 %)	Testing (20%)
Red Blood Cell (RBC)	3310	843
White Blood Cell (WBC)	297	75
Platelets	301	60

3.2 Processing Methodology

Digital blood images are first acquired, followed by the selection of optimal image enhancement and filtering techniques to segment RBCs and WBCs using suitable algorithms. Subsequently, the RBC boundaries were identified. Figure 2 illustrates the overall workflow used to detect anemia.

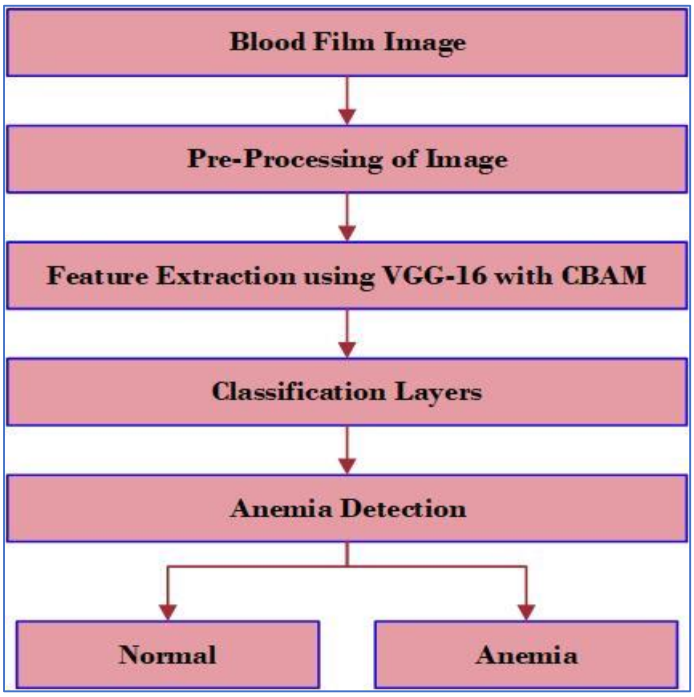

Figure. 2: *Workflow for anemia detection using VGG16.*

3.3 Pre-Processing Steps

In the VGG16 model, preprocessing is essential for optimal data preparation. This involves eliminating unwanted features from the images. The preprocessing pipeline, as illustrated in Figure 5, includes several stages that are performed on all images prior to training. These stages are 1) rescaling image pixels to enhance edges and isolate the region of interest (ROI) from the background, 2) removing noise and detecting RBC edges, 3) improving image quality, and 4) image augmentation, as illustrated in Figure 3.

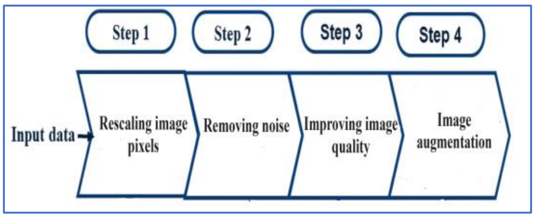

Figure.3: Pre-processing steps.

All the images were resized to 224 × 224 pixels to match the VGG16 input size. Contrast normalization was used to sharpen the red blood cell edges, aiding the identification of overlapping areas. Because the range of the RGB image pixel values differed, the loss function was changed. To overcome this, the image pixels were normalized to the range [0,1] whereby the total loss for all pixels remained constant. As part of this rescaling, the learning rate was normalized to the same

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value as that in the previous work. The second-order derivative Laplacian filter was used to employ the local noise estimator function that enhanced the removal of blur and noise, although it was successful in a 3 × 3 window size with λ=0. 5. From the above results, we observe that the Laplacian filter is mainly sensitive to the horizontal and vertical directions and edges. An improvement in image quality was noted, which was due to morphological operations, such as erosion and dilation. In the case of abnormal images, erosion reduces the area size of the region of interest, followed by dilation which expands the region of interest for segmentation, enabling the visualization of red blood cell elements distant from background features.

4. Proposed VGG16 Model with CBAM

VGG16 plays a crucial role in the automated detection of anemia in blood images by leveraging deep-learning techniques. This study aims to develop a VGG16 network in which the microscopic blood image is segmented to the pixel level and then the images are classified into anemic and healthy red blood cell elements through a two-tier process. Traditionally, CNN-based models are deep multilayer architectures that can examine microscopic images to extract useful information [59]. The VGG16 model, pre-trained on ImageNet, was used and fine-tuned for the given task. Transfer learning can be used to leverage pre-trained weights and adapt the model to detect anemia.

In this study, the proposed model is developed with an attention mechanism that focuses on important information in the image to analyze morphological abnormalities in blood images. The attention mechanism was integrated into the VGG16 model to enhance the model's ability to extract important features more accurately and efficiently. The mechanism of attention focuses on the most important areas in the image by assigning higher weights to these areas than to the less important parts. Thus, replacing the softmax layer with the attention mechanism in the VGG16 architecture makes the model more effective in extracting features. Although the softmax layer is less computationally complex than the attention mechanism, the attention mechanism achieves accuracy and improves the effectiveness of the model by enhancing its ability to focus on the most important information. Figure 4 shows the architecture of the proposed attention mechanism.

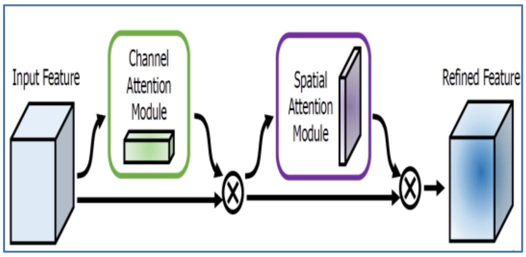

Figure 4: *Architecture of CBAM.*

It consists of two components: the channel attention module (CAM) and spatial attention module (SAM). The CAM captures the correlation between channels across spatial locations, whereas the SAM captures the correlation between spatial locations across different channels. By combining CAM and SAM, as shown in Equation 1, CBAM enables VGG16 to dynamically adjust its focus on both channel and spatial features, leading to improved performance in various computer vision tasks. And Average Pooling ($F_{avg}^{c,s}$) and Max Pooling $F_{max}^{c,s}$ are applied along the spatial dimensions (height and width) to obtain the pooling features for each channel، note that c represents channel and s represents spatial.

$$F'' = M_s(F) \times F' \quad (1)$$

Where F' represents the output of the channel attention mechanism ،while $M_s(F')$ represents the output of the spatial attention mechanism.

For the channel attention mechanism, a Multi-Layer Perceptron (MLP) and sigmoid function (σ) is used, and then the resulting attention map ($M_c(F)$ is then multiplied by the original features(F).

$$M_c(F) = \sigma\left(MLP(F_{avg}^{c}) + MLP(F_{max}^{c})\right) \quad (2)$$

Thus:

$$F' = M_c(F) \times F \quad (3)$$

The spatial attention mechanism depends on the convolutional layer (CONV) with a 7×7 filter and sigmoid function، as shown in Equation 4.

$$M_s(F'') = \sigma\left(CONV\left([F_{avg}^{s};\ F_{max}^{s}]\right)\right) \quad (4)$$

The initial layers of VGG16 detect low-level features, such as edges and textures, and as the network deepens, it captures more complex patterns and structures. The maximum pooling layers reduce the spatial dimensions and retain the most important features while reducing the computational complexity. Given the limited availability of labelled medical images, transfer learning using VGG16 is particularly effective. Once trained, the VGG16 model can classify fresh blood images into two categories: anaemic and normal. A schematic of the proposed model is shown in Figure 5.

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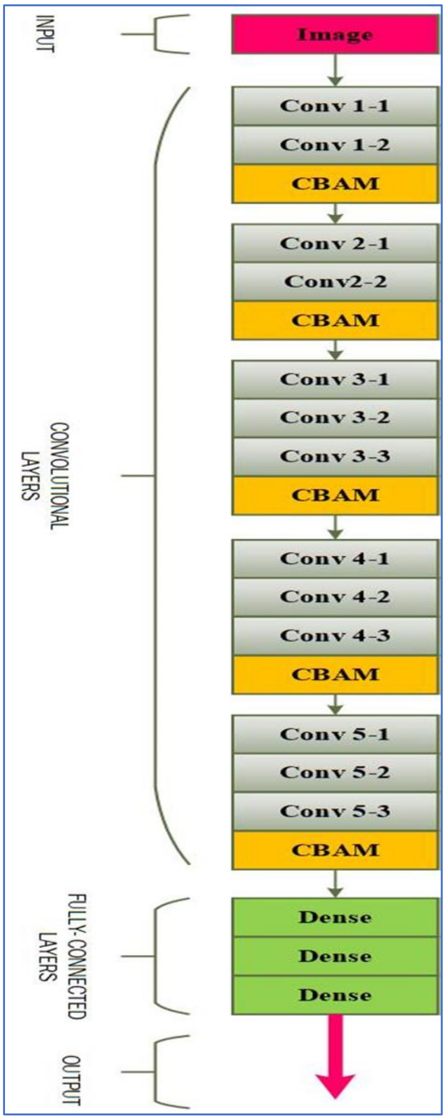

Figure 5: *Proposed VGG16 Model Architecture*

5. Performance Evaluation Matrices

To evaluate the model, the following metrics were used: recall, precision, and accuracy.

To illustrate the accuracy of anemia detection using VGG16 in classification task, True Positives (TP) are calculated as the number of anemic samples that were correctly predicted as anemic. False Positives (FP) are the number of healthy (non-anemic) samples that were incorrectly predicted as anemic. True Negatives (TN) are the number of healthy samples that were correctly predicted as healthy. False Negatives (FN) are the number of anemic samples that were incorrectly predicted as healthy.

To calculate the metrics that help evaluate the performance of the VGG16 model in anemia detection,

Accuracy: The percentage of samples that were correctly classified out of the total samples, according to Equation (5).

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \quad (5)$$

Recall: The percentage of anemic samples that were correctly detected according to Equation (6).

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \quad (6)$$

Precision: The percentage of samples predicted to have anemia according to equation (7).

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \quad (7)$$

6. RESULT AND DISCUSSIONS

The VGG16 architecture was used to detect anemia in blood films using Python and its libraries, Keras, sci-kit, and Tensorflow. Image preprocessing and augmentation prior to classification improved the accuracy of the model. Hyperparameters such as the number of epochs, hidden layers, nodes, activation functions, discontinuities, learning rates, and batch sizes were adjusted to affect the performance. The dataset was split using a test split function with 70% for training and 20% for testing. The pre-trained VGG16 algorithms were used, using 224 × 224 input images, 100 epochs, 16 batch sizes, a learning rate of 0.0001, early stopping mode, and the Adam optimizer. Each pooling layer performs a maximum pooling operation with a modified set size by using the RELU function. A sigma activation function was used for the two output classes, and the hyperparameters, including the learning rate and epoch size, were adjusted during training. Learning rate optimization and adjustments to epochs and batch sizes were based on the total number of images to improve accuracy. The hyperparameters used are listed in Table 2.

Table 2: *Hyperparameter settings.*

Parameter	Value
Image size	224x224 pixels
Learning rate	0.00001, 0.0001
Epochs	100
Activation function	Relu, Sigmoid
Dropout rate	0.20, 0.25

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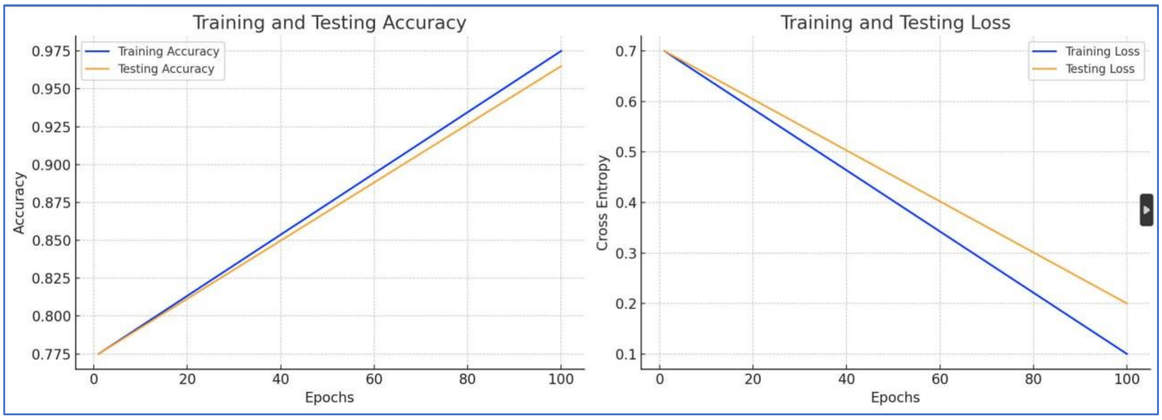

***Figure 6:** Training and Testing, accuracy and loss of Vgg16*

Shown Figure 6 The left graph illustrates training and validation accuracy, with the x-axis indicating epochs and the y-axis showing accuracy. The blue line denotes the training accuracy, whereas the orange line indicates the testing accuracy. As epochs increased, both accuracies improved, approaching 97% by the end of training, indicating an enhanced model accuracy over time. The right graph presents the training and testing loss, with the x-axis representing epochs and the y-axis showing cross-entropy loss. The blue line represents the training loss, and the orange line denotes the testing loss. Both the losses decreased with more epochs, indicating effective learning and improved predictive accuracy.

The confusion matrix illustrated in Figure 7 provides a visual representation of the performance of the classification model across three classes, which were classified into five major categories: RBC, WBC, and Platelets. The diagonal cells in the matrix show the normalized accuracy of the predictions made by the model. The diagonal cells show the correct prediction accuracy for each class with a value of 0. 84 for RBC, 0. 93 for WBC, and 0. 92 for Platelets.

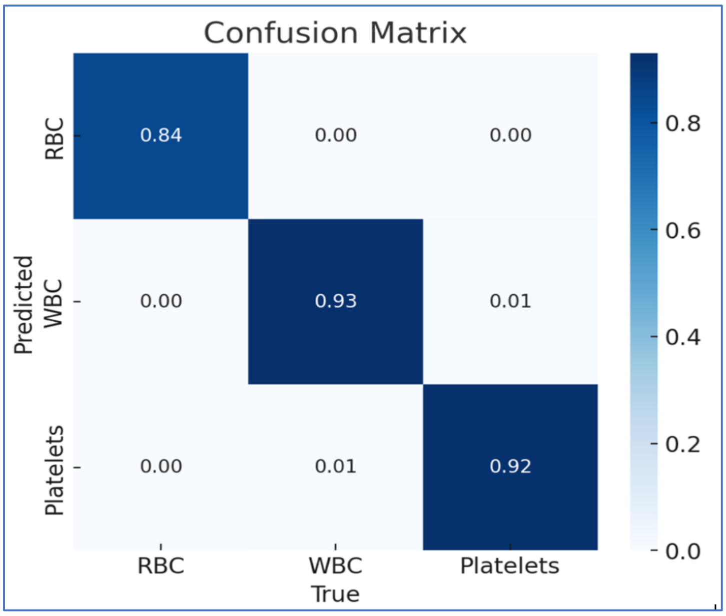

***Figure. 7:** Confusion Matrices.*

Table 3 (a,b,c) shows a comparison of the improved model with different models of convolutional neural network architectures, where the CNN models (AlexNet, ResNet 18, VGG-16, VGG-19) were run. The results were compared across three blood cell types: RBCs, WBCs, and platelets. The evaluation metrics used included mean average precision (mAP 0.5) and accuracy.

The VGG-19 model achieved a high accuracy for red blood cells with values of 0.81, while the Fast-RCNN model achieved an accuracy of 0.91 for white blood cells. In addition, the VGG-16 model achieved an accuracy of 0.90 for platelets. In contrast, the proposed VGG-16-CBAM model showed competitive performance and high accuracy for RBCs, WBCs, and platelets, with values of 0.84 and 0.93, and 0.92, respectively, demonstrating the effectiveness of attention mechanisms in improving the model's focus on relevant features.

Table 3: *compassion result* ***(a)***

Type	Red Blood Cell	
	mAP 0.5	Accuracy
AlexNet	0.69	0.63
Fast-RCNN [17]	0.76	0.72
ResNet 18	0.83	0.80
VGG-16	0.86	0.78
VGG-19	0.82	0.81
VGG-16 -CBAM (proposed)	0.85	0.84

(b)

Type	White Blood Cell	
	mAP 0.5	Accuracy
AlexNet	0.72	0.72
Fast-RCNN [17]	0.85	0.85
ResNet 18	0.90	0.90
VGG-16	0.85	0.85
VGG-19	0.91	0.91
VGG-16 -CBAM (proposed)	0.95	0.93

(c)

Type	Platelets	
	mAP 0.5	Accuracy
AlexNet	0.67	0.67
Fast-RCNN [17]	0.80	0.80
ResNet 18	0.84	0.84
VGG-16	0.89	0.89
VGG-19	0.86	0.86
VGG-16 -CBAM (proposed)	0.90	0.92

7. Conclusions

Red blood cells accounted for the majority of the BCCD dataset. Red blood cells become more difficult to detect when they are dense and overlapping. With proper preprocessing and upscaling of the input images, our model performs remarkably well. It has high accuracy for detecting red blood cells, and white blood cells are larger than red blood cells and platelets. White blood cells are usually more easily counted. With proper preprocessing, even the white blood cells were adjacent. While platelets are few and small. Platelet detection is the most difficult task in blood cell counting. The improved VGG16 architecture for blood-cell detection achieved impressive results. The feature maps generated by VGG16 were enriched using feature fusion and CBAM for blood-cell detection. The BCCD dataset of blood smear images was used to evaluate the performance of the proposed architecture. The original images were preprocessed using upscaling, sharpening, and blurring. Thus, an accuracy of 98% is achieved. Our results highlight the potential of deep learning as a valuable diagnostic tool for type 2 diabetes, offering superior outcomes and time efficiency compared with other techniques. This study advances clinical image analysis and underscores AI's role of AI in improving the diagnostic processes.

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