Mustansiriyah Journal of Pure and Applied Sciences, Print ISSN: 2957-9910. Online ISSN: 2957-9929, Vol. 4, No. 2, 2026, Pages 136-148
DOI: 10.47831/mjpas.v4i2.358

MJPAS

MUSTANSIRIYAH JOURNAL OF PURE AND APPLIED SCIENCES

Journal homepage:
https://mjpas.uomustansiriyah.edu.iq/index.php/mjpas

RESEARCH ARTICLE – MATHEMATICS

Hybrid Whale Optimization Algorithm and CNN for White Blood Cell Image Classification

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Article Info.

Article history:

Received
27 November 2024

Accepted
13 January 2025

Publishing
30 June 2026

Abstract

Blood cells include red blood cells, white blood cells, and platelets. In blood, leukocytes play an important role in human immune function, so they are also called immune cells. In medicine, white blood cells play an important role in the human immune system. Therefore, studying the classification of white blood cells is important for medical diagnosis. Various abnormalities of white blood cells are related to various diseases, so the total number and classification of white blood cells are crucial for clinical diagnosis and treatment. However, the traditional method of white blood cell classification is to segment cells, extract features, and then classify them. Such a method depends on good segmentation and does not have high accuracy. In addition, insufficient data or unbalanced samples using deep learning in medical diagnosis, in addition to reducing the classification accuracy of the model, cannot fully exploit the dependency relationship between some key features of images and image labels. To solve these problems, this research proposes a blood cell image classification framework WOA-CNN, which, based on the combination of Convolutional Neural Network (CNN) and Whale Optimization Algorithm (WOA), can deepen the understanding of image content and learn the structured features of images, and initiate the training leading to big data in medical image analysis. According to experimental data, the suggested WOA-CNN system outperforms more conventional techniques like Decision Trees, Random Forests, Support Vector Machines, and Proposed Method (WOA-CNN) in terms of classification accuracy 98.6%.

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The official journal published by the College of Education at Mustansiriyah University

Keywords: Machine Learning; DT; Detection; classification; image processing; convolutional neural networks; Whale Optimization Algorithm.

Nomenclature & Symbols

ML	Machine Learning	KNN	K-nearest Neighbors
DT	Decision Tree	CNN	Convolutional Neural Networks
RF	Random forest	WOA	Whale Optimization Algorithm
SVM	Support Vector Machine	WBC	White Blood Cell

1. Introduction

The human body's immune system and physiological well-being depend on blood cells, which are vital for delivering nutrition and oxygen to organs, preventing infections, and aiding in clotting. Since every type of blood cell has distinct traits and functions, it is essential to accurately identify and categorize them. Leukocytes support the immune system and combat infections, whereas red blood cells carry oxygen to organs and play a critical role in oxygen balancing processes[1]. In addition to studying physiological and pathological alterations in blood for early disease detection and treatment efficacy, accurate blood cell type identification can aid in the diagnosis and treatment of blood diseases such as leukemias and blood cancers. Biomedical research and the advancement of diagnostic and treatment approaches for people with blood disorders depend on this[2]. But Because blood samples contain a huge number of cells and their structures are complex, accurately classifying blood cells is a big difficulty. Deep learning methods and sophisticated data analysis are required for quicker and more precise diagnosis[3].

Leukocytes, another name for white blood cells (WBCs), are an essential component of the human immune system that protects the body from infections, foreign invaders, and aberrant cells like cancer. They can react swiftly to dangers because they are produced in the bone marrow and distributed throughout the bloodstream and lymphatic system. In a healthy person, WBCs make up around 1% of the total volume of blood, but during infections or immunological reactions, their numbers may rise. WBCs are crucial for preserving immunity and general health, despite their tiny number[4].

There are five main categories of white blood cells, and each has distinct characteristics, roles in immune defense, and architectures. With 55-70% of the total WBC count, neutrophils are the most prevalent kind. By phagocytosing and swallowing pathogens, they serve as the initial line of defense against microbial diseases. In adaptive immunity, lymphocytes are essential because they generate antibodies that specifically target infections. T-cells eliminate malignant or contaminated cells, B-cells generate antibodies, and Natural Killer (NK) cells find and eliminate aberrant cells without causing sensitization. Monocytes remove dead cells and start immunological reactions by differentiating into dendritic or macrophage cells. Eosinophils play a role in allergic reactions and fight multicellular parasites. During allergic reactions, basophils contribute to inflammation by releasing histamine and other substances. These cells are vital for enduring immunity and pathogen memory. Tissue healing, immunity, infection prevention, and cancer surveillance all depend on white blood cells. They identify and kill bacteria, viruses, and fungus; they facilitate quicker reactions; they remove damaged or dead cells; and they eradicate aberrant or malignant cells[5].

White blood cells, or WBCs, are essential for both diagnosing and treating a number of illnesses. Low WBC levels suggest bone marrow problems, autoimmune diseases, or viral infections, whereas high counts suggest infections, inflammation, or leukemia. Classification aids in directing focused therapy, while blood smear analysis identifies morphological abnormalities connected to diseases. conventional techniques for analyzing white blood cells are laborious, arbitrary, and prone to mistakes. Since speed and accuracy have increased due to developments in deep learning and image processing, automated methods are essential for contemporary diagnoses.

A metaheuristic optimization method called whale optimization (WOA) mimics the bubble-net hunting technique of humpback whales. It involves launching a bubble-net attack, encircling the prey, and initiating a set of whale solutions. The algorithm balances exploration and exploitation, shrinks the search space, and explores new regions using spiral motion. WOA is frequently used in image processing to improve classification accuracy and computational efficiency by optimizing hyperparameters and selecting features [6]. A deep learning architecture called convolutional neural network (CNN) is used to process image data, especially for classification tasks. This architecture consists of convolution layers, pooling layers, fully connected layers, and activation functions. Because CNNs can recognize abnormalities in white blood cells and aid in medical diagnosis by learning structured features from blood smear images, they are particularly useful for white blood cell classification. WOA and CNN together provide a powerful framework for image analysis tasks such as white blood cell classification. WOA improves the efficiency of the model by reducing redundant data and optimizing feature selection. It also modifies the CNN hyperparameters to increase accuracy. After processing the optimal input data, the CNN classifies blood cells according to their types and disorders through feature extraction . This combination ensures strong performance and good classification accuracy. Convolutional neural networks (CNN) and whale optimization algorithm (WOA) are used in medical diagnosis to classify white blood cells. WOA ensures that only relevant features are used by optimizing feature extraction and selection. CNN recognizes the characteristic patterns of different types of white blood cells by learning hierarchical features from images. This combination makes it possible to accurately classify cell abnormalities, which helps in early recognition and detection of diseases. The combination of WOA and CNN greatly improves diagnostic accuracy while reducing computational complexity. This method helps in early diagnosis and detection of diseases such as immune disorders and blood cancer [7].

Blood cell classification is the main topic in this paper, which addresses problems such the high number of cells in blood samples, their high degree of size and characteristic variability, and the laborious nature of manual categorization. Advanced approaches are required to identify the various types of blood cells in blood samples in order to increase efficiency and accuracy. Red blood cells, platelets, and white blood cells are the three different types of blood. White blood cells are the body's primary line of defense against illnesses and infections, whereas red blood cells make up half of the blood volume. Granulocytes and agranulocytes are the two types of white blood cells. Blood cells are made in the lymphatic system, which is where leukemia, a malignant tumor, forms. Usually, white blood cells develop in accordance with the body's requirements. However, they develop abnormally and become defective in leukemia. It is challenging to do additional analysis and processing because of the variation

in shape and texture. White blood cells must be surrounded by other blood components, such as red blood cells and platelets, and detected by an intelligent system that uses machine learning techniques .
The application of feature selection techniques, such as the Whale Optimization Algorithm (WOA), to enhance blood cell image analysis and recognition is the main focus of this paper. The WOA-CNN model is presented as a novel method that reduces cross-entropy by using topological representation transformations and preserving both local and global structures in images. The accuracy and data analysis capability are greatly enhanced by this method[8].
There are several benefits to using automated blood cell classification systems: Improved accuracy: Manual analysis by humans can be error-prone, especially when dealing with large data sets. Automated technologies increase accuracy and ensure consistent results. Time efficiency: By reducing the amount of time required to analyze blood cells, advanced algorithms allow for faster diagnosis and treatment. Savings: Automation reduces the need for a lot of manual labor, reducing laboratory operating expenses. Better disease monitoring: Monitoring the course of a disease and assessing the effectiveness of treatment are easier with routine blood analysis. Helping healthcare workers: Automated technologies improve accuracy and efficiency, allowing healthcare workers to focus on important decision-making tasks.
The proposed method combines convolutional neural networks and the whale algorithm to improve WBC classification and identification in medical settings. By precisely collecting and evaluating features from blood images, this method improves classification accuracy and reduces processing time. The method can improve the accuracy and speed of classification in other diagnostic procedures and provide a basis for future research into medical applications of artificial intelligence.
Thus, the rest of the paper is organized. Section II explains some related work, Section III explains the data analysis, feature extraction, and classification processes, and describes the proposed machine learning framework. Section IV presents the experimental results and discussion. Section V compares the proposed model with previous studies. Finally, Section VI presents the conclusion.

2. RELATED WORK

A common blood condition called anemia is defined by a reduction in red blood cells, or hemoglobin. For treatment to be effective, accurate detection is essential. The Whale Optimization-Driven Generative Convolutional Neural Network (WO-GCNN) is a novel structure designed to identify anemia from blood smear images. To increase accuracy, the system integrates convolutional neural networks and generative models. The system's functionality is enhanced by the application of the Whale Optimization Algorithm (WOA). By finding the ideal combination of CNN weights, the WOA balances exploration and exploitation. A sizable dataset of blood smear images is used to assess the WO-GCNN system, which shows an exact and successful method for early anemia detection. This paradigm may greatly impact patient care and medical image analysis[9].
White blood cell (WBC) counts can be identified from an image database using the Deep Features based Convolutional Neural Network (DFCNN) shown in this paper. Feature extraction, feature selection, and classification are the three stages of the process. Three thousand key features are extracted from the database by the Combined CNN structure, and key features are chosen by the hybrid Mayfly Algorithm with Particle Swarm Optimization (HMA-PSO). In order to categorize WBC types such as neutrophils, eosinophils, monocytes, and lymphocytes, the chosen features are subsequently fed into a Recurrent Neural Network-Long Short-Term Memory (RNN-LSTM) classifier. MATLAB is used to implement the approach, and its accuracy, precision, recall, specificity, and F_Measure are assessed. Accuracy of 0.97, precision of 0.9, and recall of 0.98 are the top performance measures attained[10].
The deadly blood condition known as acute lymphoblastic leukemia (ALL) is typified by an overabundance of immature white blood cells. Although deep convolutional neural networks (CNNs) have demonstrated potential in the field of digital pathology, their inability to distinguish between many subtypes stems from their modest morphological differences. An enhanced pipeline for the binary detection and subtype categorization of ALL using blood smear pictures is proposed in this work. The suggested method makes use of a customized 88-layer deep CNN that was trained with GoogleNet and transfer learning. Using publically accessible datasets, the study confirms the methodology and attains

the highest average accuracy of 99.15% for binary classification and 98.69% for B-ALL sub-type classification[11].

In this paper [12],A two-module weighted optimized deformable convolutional neural network (TWO-DCNN) is proposed in this paper for the categorization of white blood cells (WBCs). For increased resilience, the technique makes advantage of deformable convolutional layers and two-module transfer learning. Classical machine learning techniques such as VGG16, VGG19, Inception-V3, ResNet-50, support vector machine, multilayer perceptron, decision tree, and random forest were compared to the approach. For low-resolution and noisy data sets, the TWO-DCNN performed the best, achieving precisions (PREs) of 95.7%, recalls (RECs) of 95.7%, F1-scores (F1s) of 95.7%, 94.5%, and 91.6%, and area under curves (AUCs) of 0.98, 0.97, and 0.95.

The bone marrow produces white blood cells, which are essential for the immune system and shield the body from infectious diseases and outside intruders. Leukopenia, which lowers resistance to infections, can result from insufficient white blood cell counts. Image processing techniques have been employed in biomedical diagnosis, however identifying and treating this condition is a specialized undertaking. With the use of quadratic discriminant analysis as a classifier, AlexNet, GoogLeNet, and ResNet-50 as feature extractors, Maximal Information Coefficient and Ridge feature selection techniques, and Convolutional Neural Network models, this study sought to enhance the classification performance of deep learning models in white blood cell classification. Convolutional neural network models with feature selection techniques greatly increased the classification success of white blood cell kinds, as seen by the overall success rate of 97.95% [13].

In this paper[14], deep convolutional neural networks are used to propose a revolutionary white blood cell (WBC) identification system. The approach extracts deep activation features from pre-trained networks by fine-tuning existing deep networks and using transfer learning. A limited balanced WBCs dataset classification is carried out using a brand-new end-to-end convolutional deep architecture named "WBCsNet" that is constructed from the ground up. The system outperforms conventional identification systems and other transfer learning strategies with an overall system accuracy of 96.1%. The suggested system can be used as a network that has already been trained.

In this paper[15], this work proposes an automatic technique for segmenting white blood cell nuclei in peripheral blood smear images. The technique fuses color components from CMYK and HSV color spaces using an adaptive fusion based on principle components analysis. This technique offers enhanced contrast because of PCA-based fusion, independence from color and brightness change, and nuclei extraction without morphological processes. When evaluated on three distinct public image datasets, the algorithm outperformed other available techniques. CellaVision, BloodSeg basis, and JTSC databases have dice similarity coefficients of 97.06%, 94.75%, and 90.79%, respectively.

For the identification of Acute Lymphoblastic Leukemia (ALL), a computer-aided ALL detection technique utilizing a Whale Optimization Algorithm-based Support Vector Machine (WOA-SVM) has been developed. The plan tackles issues like WBC classification, discriminant feature extraction, and WBC segmentation. The mean intensity of Cyan of the CMYK color model, the sum of rotation invariant Local Binary Pattern with a uniform pattern, and the 2D-Discrete Orthonormal S-Transform with weighted Principal Component Analysis are among the suggested features. Using the feature set, WOA-SVM's performance was assessed; on the ALL-IDB1 dataset, it achieved an accuracy of 98.42%. The experimental results show that the suggested methodology outperforms other comparing methodologies[16].

For the purposes of cell segmentation, feature extraction, and cell classification, this study contrasts deep learning and conventional machine learning models. For the CellaVision and BCCD datasets, traditional machine learning produces accuracies of 94.36% and 98.75%, respectively. Accuracies of 81.18% and 97.82% for BCCD and 91.31% and 100% for CellaVision are attained via deep learning, which includes AlexNet, VGG16, and ResNet18. With cell-type classification of ALL-IDB2 and PCB-HBC datasets reaching high accuracies of 100% and 98.49%, respectively, the study also showed the potential of deep neural networks in leukocyte classification, confirming the deep learning model employed[17].

A deep neural network architecture is proposed in this paper to recognize and detect entire blood cells in blood smear images. To get around the challenge of distinguishing between various cell types because of overlap, the method makes advantage of YOLOV8, a deep neural network. To acquire full-

dimensional attention value and aid in the differentiation of various blood cell types, ODConv is utilized in place of standard convolution. For more in-depth features, BiFPN is introduced. On the BCCD dataset, the approach produces improved mAP50 values of WBC 0.972 and WBC 0.893[18].

In This paper [19],proposes an improved YOLOv5 (AYOLOv5) based on the attention mechanism to address the low recognition rate of cell detection in dense and complex cell distribution. The attention mechanism is introduced to improve the features of the convolutional neural network in areas with a high feature density. The transformer encoder block and the convolutional block attention module (CBAM) are used in the development of the attention mechanism. The YOLOv5 integrated convolutional block attention module increases the weight of cell-dense regions in blood cell pictures, allowing the network to tolerate input other than cells. The experiment using the BCCD dataset showed improved mAP results for cell detection and an average recognition accuracy of 98%. More effectively, the proposed AYOLOv5 may extract feature information from cells, significantly improving recognition performance and cell pictures [19].

Leukemia cases are difficult to diagnose medically because samples must be carefully examined under a microscope to determine the quantity, form, size, and morphological characteristics of white blood cells. Pathologists' expertise and professional abilities can affect this process, and machine and deep learning techniques have been shown to improve accuracy and productivity. Segmentation systems have been divided into four primary categories by recent research on leukemia identification and classification conducted between 2015 and 2023: supervised machine learning techniques, unsupervised machine learning techniques, deep learning approaches, and conventional image processing techniques. Classification techniques fall into one of three categories: deep learning, traditional machine learning, or a mix of the two. Conventional CNN, transfer learning, and other CNN advancements are further subcategories of CNN-based classification systems[20].

In this study, silver nanoparticles (AgNPs) are made using a green synthesis process, and their structural characteristics are examined using atomic force microscopy (AFM), scanning electron microscopy (SEM), and X-ray diffraction (XRD). According to the findings, AgNPs are spherical in shape, have an average particle size of 52.532 nm, and are polycrystalline with a grain size of 6.73 nm. Organic chemicals are identified to make up AgNPs' chemical signature. Escherichia coli-related illnesses in humans have been discovered to be lessened by the AgNPs' ability to eradicate the bacteria[21].

The review articles are analyzed in this section and compared in Table 1.

Table 1 compares blood cell image classification methods.

Study	Year	Disadvantages	Advantages	Methodology	Dataset	Accuracy
[16]	2024	Limited to specific features; may not generalize well to other datasets.	Achieved high accuracy for ALL detection; reduced computational time.	Whale Optimization Algorithm (WOA) and SVM	ALL-IDB1	98.42%
[11]	2024	Difficulty in differentiating subtypes due to morphological similarities.	High accuracy for binary classification and sub-type identification using a customized 88-layer CNN.	Deep CNN with Transfer Learning	Public Datasets	99.15% (Binary) and 98.69% (Subtypes)
[17]	2024	Traditional models less accurate on complex datasets.	Deep learning achieved 100% accuracy on ALL-IDB2 and 98.49% on PCB-HBC.	CellaVision is powered by deep learning, which includes AlexNet, VGG16, and ResNet18.	BCCD	91.31%
[18]	2024	Overlap between cell types remains a challenge.	High mAP50 values and better differentiation of overlapping cells.	Improved algorithm based on YOLOV8. We use ODConv	BCCD	97.2%
[19]	2024	Complexity of attention mechanism integration.	Improved recognition in dense cell regions; high average recognition accuracy.	Augmented (AYOLOv5). To enhance the features of the convolutional neural network in regions with high feature density.	BCCD	98%

Common weaknesses in medical models include lack of validation on diverse or imbalanced datasets, computational costs, limited interpretability, and limited use of advanced optimization techniques, leading to suboptimal performance.
Shortcomings in previous research include small or outdated datasets and overly simplified models that may not translate to practical uses and may miss complex data relationships. Low classification accuracy, inability to handle large datasets efficiently in real time, manual feature extraction, and lack of sophisticated feature selection optimization algorithms are examples of performance difficulties.

3. Methodology

A crucial component of transfusion therapy and medical diagnostics is blood cell classification. Conventional manual WBC detection techniques take a lot of time, are prone to human error, and call for qualified personnel. In order to overcome these obstacles, we suggest a novel automated blood cell recognition system that combines the capabilities of Convolutional Neural Networks (CNN) for classification and Whale Optimization Algorithm (WOA) for feature selection. The four main steps of our approach are preprocessing, which improves the quality of blood sample images; feature selection, which uses WOA to find the most pertinent features; classification, which uses a CNN to process the chosen features to precisely identify blood cell and evaluation, which uses standard metrics to gauge the system's performance and guarantee dependability and efficacy. The arrangement of the Figure 1 shows the proposed algorithm for the methodology architecture.

Figure 1 Methodology steps.

1. Dataset

BCCD Dataset[1] 12,500 improved JPEG images of blood cells with cell type labels (CSV) are included in this dataset. Each of the four distinct cell types has about 3000 photos, which are arranged into four folders based on the cell type. These cell types include neutrophils, monocytes, lymphocytes, and eosinophils. An extra dataset that includes 410 pre-enhanced original images, two more subgroup labels (WBC vs. WBC), and bounding boxes for every cell in each of these 410 photos (JPEG + XML information) is included with this dataset. Is. In particular, the 'dataset-master' folder has 410 blood cell images with bounding boxes (JPEG + XML) and subgroup labels, whereas the 'dataset2-master' folder has 2500 additional photos with 4 labels. JPEG and other subcategories (CSV + JPEG). In contrast to the 88, 33, 21, and 207 photographs in the 'dataset-master' folder, there are over 3000 additional images for each of the four classes. Examples of the dataset's photos are displayed in Figure 2.

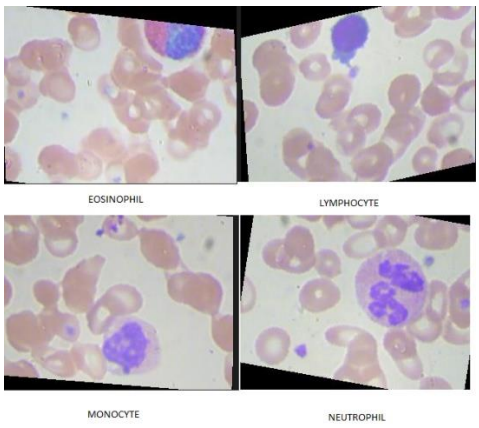

Figure 2 Example of images dataset

The table 2 shows the distribution of the white blood cell (BCCD) data into four classes: Eosinophil, Lymphocyte, Monocyte, Neutrophil. The data is split 70% for training and 30% for testing, with the training section containing 8551 images and the testing section containing 3665 images.

[1] https://www.kaggle.com/datasets/paultimothymooney/blood-cells

Table 2 WBC distribution (BCCD) data between training and testing

Dataset BCCD (image)	EOSINOPHIL	LYMPHOCYTE	MONOCYTE	NEUTROPHIL	Total
Train	2162	2156	2079	2154	8551
Test	892	951	864	958	3665

The Figure 3 represent samples of the white blood cell images used in training and testing, with the different classes for each cell shown.

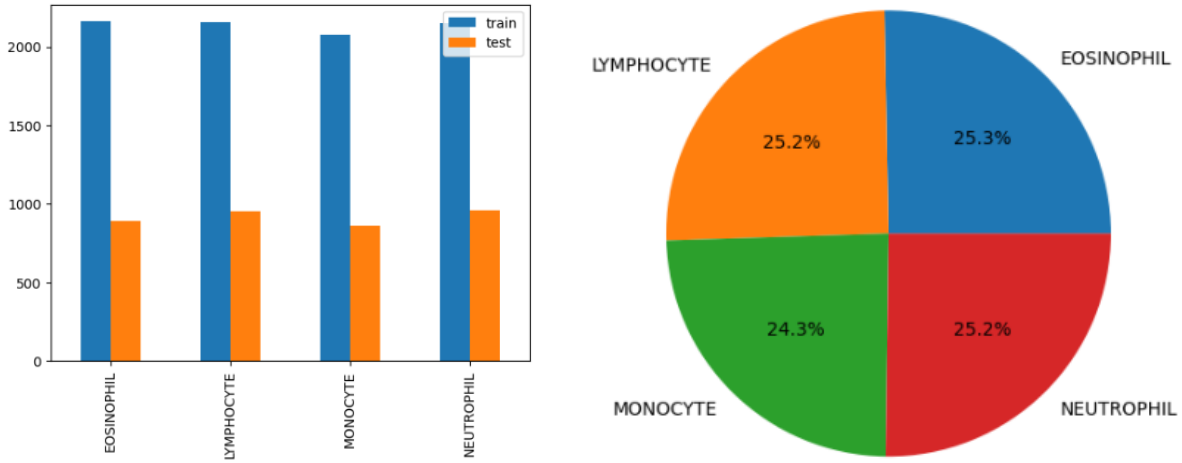

Figure 3 Number of WBC image samples classified by category

2. Preprocessing

Image preprocessing for blood cell extraction and classification is performed automatically. Images are loaded from the training and test folders, then a frame is added to the image to improve cell detection at the edges. Target cells are identified using thresholding based on color values, then the image is enhanced using erosion and dilation. Edges are detected automatically using Canny Edge Detection as in the figures 4 and 5, then cell boundaries are extracted using Contours. Next, the smallest bounding rectangle for each cell is determined using minAreaRect, and the cell is cropped from the original image based on the bounding box coordinates. The image is resized to a fixed dimension (120x120), and the processed images with labels are stored in two arrays (images and labels) for use in training and testing.

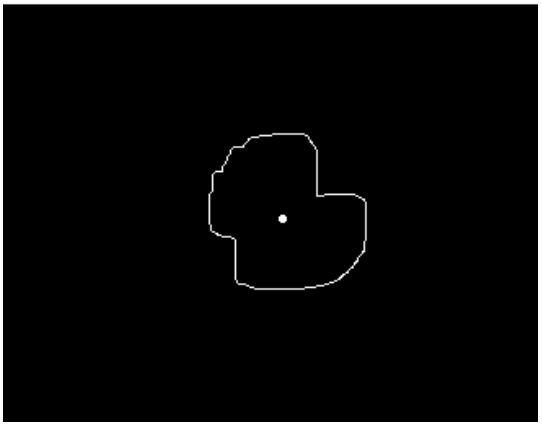

Figure 4 Edge detection with Canny filter on input image

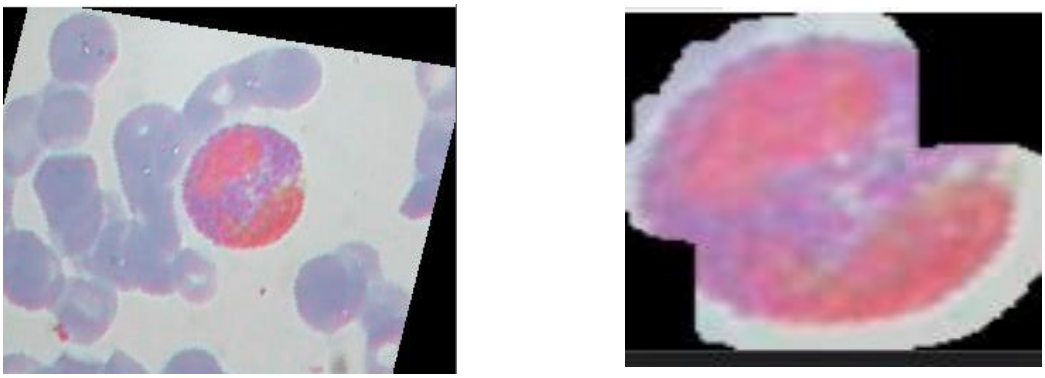

Figure 5 Canny filter on the input image

3. Proposed WOA-CNN Structure

Feature selection using WOA. When using a larger dataset, the issue of scalability arises with the increase in the size of the feature vector. This problem can be solved by optimizing the feature vector by minimizing its size while maintaining accuracy. This issue is raised in this section and its solution is proposed using the WOA method. Figure 6 shows the combined WOA-CNN algorithm and the calculation fit function (ff) using CNN models to find a set of features with high accuracy.

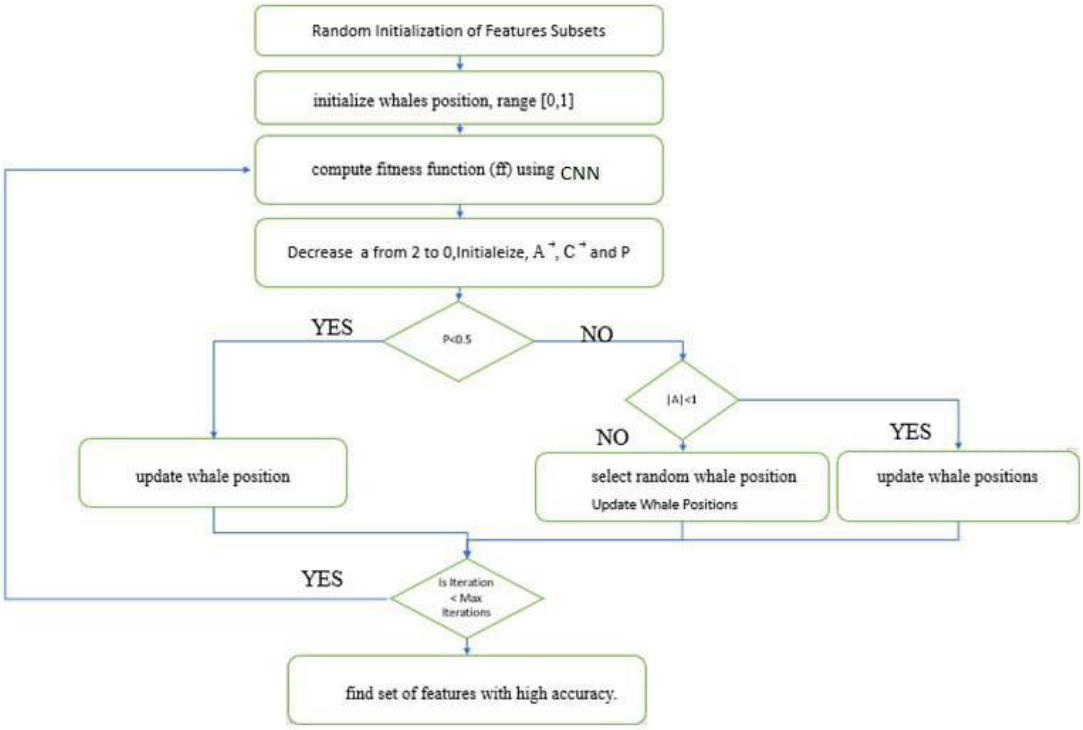

Figure 6 Flow chart of the operation of the proposed WOA-CNN mode.

Algorithm 1: Feature selection with WOA and CNN classifier

Output: Features Selection

initialize whales population (x_i , i = 1,2,3, … n)
initialize whales position, range [0,1]
if position value > 1 then
feature selected
else
feature is not selected
compute fitness function (ff) using CNN models
find set of features with high accuracy.
While maximum iteration < iteration
for each whale in the swarm
update $\vec{A}$, $\vec{C}$, l, p

```
                    if p < 0.5
                        if |A|<1
                            update whale positions
                    else if  |A|> 1
                            select random whale position
                            update whale positions
                        end
                    else if p>0.5
                        update whale position
                    end
                end
            end
        end
```

In this proposed system, after the first three steps, it moves to the feature selection step. In this step, the goal is to obtain the best features using the whale optimization algorithm. First, the parameters related to this algorithm are determined. Then the fitness function is determined, which evaluates the performance of artificial neural network models in sentiment analysis, and the accuracy criterion is used as the fitness function. The next step is to generate an initial population of feature states (0 or 1) that are randomly selected. Then the parameters of the whale algorithm are set, including the population size (10), the number of generations (100), the linear decrease of the parameter a from 0 to 2, the calculation of A, the calculation of C, and the random generation of the parameter p, which is a number in the interval [0, 1] evolution begins and in the first stage the fitness of each whale is calculated. Then the values of a, A, C and p are randomly generated and if p is less than 0.5 and the value of |A| is less than 1, the position of each whale is updated and the feature states of each whale are changed. In the evaluation and selection phase, the new features are evaluated using the fitness function, and the best features are selected for the next generation. Evolution continues until a certain condition is reached. For example, the number of evolution periods is maximum or enough improvement in the fitness function is reached, it continues. After the completion of the algorithm, the selected features are used as important features for sentiment analysis using a neural network model, and the accuracy and performance of the model in sentiment analysis are improved. After selecting the appropriate features by the whale algorithm, these features are They are used as input to neural network models. In the neural network architecture selection stage, it should be determined how the neural network architecture to be used is determined, including the number of layers and the number of units. In this research, three layers of neural network are used.

The parameters of the neural model must also be specified. These parameters include the learning rate (0.001), the number of training cycles (100 Epoch), the softmax function for the final layer, and activation functions of the ReLU type for all layers.

Using the chosen features, the neural network model is trained during the training phase. In this step, the network's weights are updated and the error (Loss) is calculated. Using evaluation data and evaluation criteria including accuracy, recall, and precision, the neural network model is assessed during the evaluation step. These actions enhance the neural network model's performance and accuracy in sentiment analysis and yield more precise findings.

4. Evaluation Mattress

That is, out of all the positive classes that we have correctly predicted, how many are actually positive. As shown in equation (1).

$$\boldsymbol{precision} = \frac{\boldsymbol{TP}}{\boldsymbol{TP} + \boldsymbol{FP}} \qquad (1)$$

Classification accuracy is an important metric for evaluating classifier performance. This scale shows how accurate data will be classified using a particular classification model, as shown in equation (2). The best classification accuracy is one, while the worst is zero.

$$\boldsymbol{Accuracy} = \frac{\boldsymbol{TP} + \boldsymbol{TN}}{\boldsymbol{TP} + \boldsymbol{TN} + \boldsymbol{FP} + \boldsymbol{FN}} \qquad (2)$$

It refers to the concept of how many correct predictions we made out of all the positive classes. It should be as high as possible, as shown in equation (3):

$$\boldsymbol{Recall = \frac{TP}{TP + FN}} \quad (3)$$

If we want both Precision and recall criteria to be involved in the evaluation of the model, we use this criterion ,as shown in equation(4).

$$\boldsymbol{F1 - score \; = \; 2 \times \frac{Recall \times precision}{Recall + precision}} \quad (4)$$

4. RESULTS ANALYSIS

1. PARAMETERS

The table 3 outlines the parameters for the WOA used in blood cell categorization. It includes:

- **Number of Search Agents: 10**
- **Maximum Iteration: 100**
- **P: Randomly initialized between 0 and 1**

These parameters guide the feature selection process, enhancing the model's accuracy.

Table 3: Parameters WOA For Feature Extraction

Parameters	**WOA**
Number of search agents	10
Maximum iteration	100
P	Random [0,1]

Along with additional characteristics like pooling size and dropout rate, the second table displays the CNN's parameters, which include the input shape, number of filters, filter size, and activation function. These parameters are essential to the neural network's architecture because they affect how well the network can identify intricate patterns in the input data and classify blood types.

Table 4: Parameters CNN

Parameters	**CNN**
Epoch	1000
LR	0.001
activation function	Relu
output layer activation	Softmax
The number of neurons in the output layer	4

2. RESULTS

The performance of our method was compared with that of several popular machine learning algorithms (Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), and K-Nearest Neighbors (KNN)) using the same dataset, the BCCD dataset. The performance of each algorithm was evaluated using four main metrics: Accuracy, Precision, Recall, and F1 Score. As shown in Table 5, our method showed a clear superiority over all other algorithms in terms of all metrics.

Table 5 shows the results obtained on the BCCD dataset

Method	Accuracy	Precision	Recall	F1 Score
DT	91.43%	87.87%	94.94%	91.01%
RF	86.80%	86.81%	83.86%	84.84%
SVM	95.96%	94.64%	72.73%	81.76%
KNN	88.46%	85.72%	86.76%	84.72%
Our method	98.6%	97.88%	97.50%	98.18%

The performance of several classification techniques, including DT, RF), SVM, KNN and the suggested WOA-CNN, is shown in a bar chart in Figure 7. F1 Score, Accuracy, Precision, and Recall are the performance measures displayed. When compared to the other approaches, the WOA-CNN method performs better on all parameters, especially accuracy.

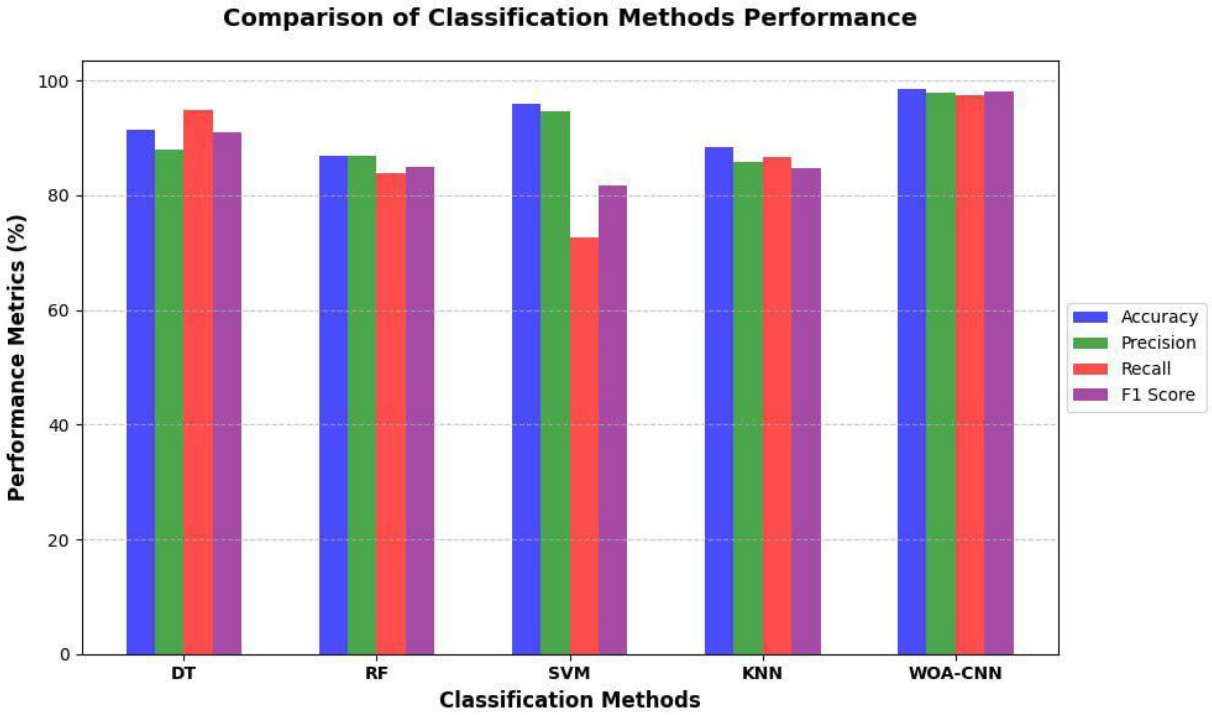

Figure 7 Comparison of classification methods

Figure 8's confusion matrix shows how well the model classified the four different types of blood cells: neutrophils, monocytes, lymphocytes, and eosinophils. With 289 Eosinophils, 305 Lymphocytes, 299 Monocytes, and 287 Neutrophils correctly identified, the diagonal numbers show accurate classifications. Misclassifications are shown by off-diagonal numbers; for example, 12 Eosinophils are categorized as neutrophils and 17 neutrophils as eosinophils. This implies that although the model functions well overall, it has some difficulty differentiating between neutrophils and eosinophils.

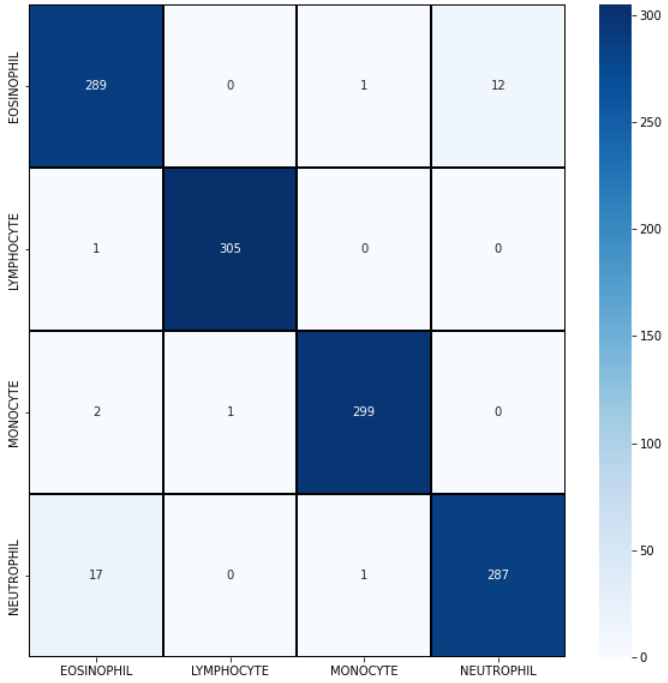

Figure 8 The figure displays matrix confusion.

3. Comparison with Previous Works

Many approaches have made significant progress in the long-term study of blood cell classification and its associated disorders. With an accuracy of 98.6% on the BCCD dataset, our proposed approach—which combines grey wolf optimization and convolutional neural networks, or WOA-CNN performs

the best. Table 6 shows how our approach can improve classification results and optimize feature selection, outperforming other state-of-the-art approaches and comparing previous studies.

Table 6 comparison with previous works

Study	Year	Methodology	Dataset	Precision	Recall	F1 Score	Accuracy
[12]	2021	DCNN	BCCD	95.7%	95.7%	95.7%	98%
[17]	2024	CellaVision is powered by deep learning, which includes AlexNet, VGG16, and ResNet18.	BCCD	-	-	-	97.82%
[18]	2024	Improved algorithm based on YOLOV8. We use ODConv	BCCD	91.2%	98.6%	-	97.2%
[19]	2024	Augmented (AYOLOv5). To enhance the features of the convolutional neural network in regions with high feature density.	BCCD	-	-	-	98%
Our method	2024	Method (WOA-CNN)	BCCD	97.88%	97.50%	98.18%	98.6%

4. limitations

Although they have limits, CNN and image processing techniques are useful tools for identifying and categorizing human WBC. CNN accuracy depends on high-quality, well-annotated picture data, yet computational complexity is significant, particularly for large datasets or real-time applications. System reliability can be decreased by variations in lighting, picture quality, and environmental conditions that can impact categorization findings. Accurate identification may also be hampered by the CNN classifier's generalizability to unknown or unbalanced data. Resolving these issues might increase the precision and dependability of the system

5. Conclusions and Future Work

The proposed system's integration of CNN and WOA demonstrates significant improvements in the accuracy and efficiency of WBC classification. By reducing processing time and simplifying feature selection, the approach addresses significant problems in medical diagnosis. Future studies will focus on improving the generalizability of the dataset, accelerating processing for real-time applications, and exploring potential uses of the system for other medical diagnostics, such as the diagnosis of anemia and leukemia. Using state-of-the-art AI techniques will significantly enhance the system's performance and lay the groundwork for future medical applications.

Future Work Upcoming Projects Future research will expand the dataset to include larger and more diverse samples, improve it for real-time applications, and examine its applicability for diagnosing other illnesses like anemia and leukemia. Modern artificial intelligence algorithms and hybrid optimization approaches will also be integrated with the system to increase accuracy and reliability and pave the way for more comprehensive healthcare diagnostics applications.

Acknowledgement

I am profoundly thankful to my dear parents, who have always stood by me in every stage of my life. Their unwavering support and encouragement have been a constant source of strength and motivation.

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