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Multiclass Classification of Heterogeneous Blood Cells Using Deep Learning and contourlet Transform

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Abstract

The classification of human blood cells is very important in the diagnosis of inflammation, infection and blood disorders such as leukemia. Diagnosis of blood malignancies requires identification and classification of white blood cells in peripheral blood smear. The pathologist spends a lot of time analyzing blood cells to determine the minor differences between blood subsets. Due to the high similarity of blood types, human error is sometimes possible. Manual procedures for diagnosing blood diseases are time-consuming, subjective and prone to human error. Therefore, we need machine analysis of microscopic images. Usually, methods based on image processing contain limitations. On the other hand, with the increase in computational processing power in computer-based clinical diagnosis systems, it has enabled the use of machine learning methods. In this article, we will use the combination of deep learning; Gabor filter and wavelet transform to provide a high accuracy blood cells classification model while extracting features from macroscopic images. The basis of the current research is the classification of blood smear images using the combination of contourlet transform, recurrent neural network and optimization method. Feature extraction is based on the combination of wavelet transform and recurrent neural network and feature selection is based on the African vulture optimization method. Finally, an innovative classifier based on clustering is presented to classify different blood cells. Based on the results obtained on the set of Jiangxi Tecom images, the proposed design has achieved an acceptable accuracy and has been able to increase the precision, recall and F-Measure.

Keywords: White blood cell, classification, contourlet transform, recurrent neural network, precision

1. Introduction

Blood is a vital component of the human body, consisting of cells suspended in plasma that circulate continuously to maintain life. Among the various cell types, white blood cells (WBCs) play a crucial role in the immune system by defending the body against infections, bacteria, and fungi. Accurate identification of WBC subtypes such as eosinophils, lymphocytes, neutrophils, monocytes, and basophils is essential for the diagnosis of disorders including acute lymphoblastic leukemia (ALL), a malignant disease caused by abnormal proliferation of immature leukocytes.

Traditionally, pathologists examine peripheral blood smear (PBS) images under microscopes to classify WBCs. However, this manual process is time-consuming, subjective, and prone to human error, especially due to the subtle morphological differences among WBC subtypes. Therefore, automated and reliable classification systems are required to assist hematologists in clinical decision-making.

In recent years, machine learning and deep learning techniques have gained significant attention in medical image analysis, offering powerful tools for feature extraction and classification. Conventional image processing methods such as Fourier transform, wavelet transform, or handcrafted morphological features were among the first attempts at automated WBC classification. However, these approaches often suffer from limitations, including sensitivity to image rotation, noise, and illumination conditions.

Deep learning, particularly convolutional neural networks (CNNs), has shown remarkable success in medical image classification, achieving high accuracy in WBC detection and subtype identification. Nevertheless, CNN-based methods typically require large-scale training data and high computational cost, and they may not fully capture sequential dependencies or domain-specific features. Moreover, limited robustness to noisy clinical data remains a significant challenge in practical applications.

Contribution of this paper:

To address these challenges, we propose a novel hybrid framework for multiclass classification of heterogeneous blood cells. The main contributions of this work are as follows:

1. Frequency-domain feature extraction using contourlet transform to capture directional edges and structural information beyond conventional wavelet-based methods.
2. Deep sequential feature learning through recurrent neural networks (RNNs), enabling the model to retain contextual dependencies in microscopic images.
3. Efficient feature selection using the African Vulture Optimization Algorithm (AVOA), a recent nature-inspired metaheuristic, to reduce dimensionality and computational complexity.
4. Innovative clustering-based classifier that improves classification accuracy and robustness, even under uncertain or noisy conditions.
5. Extensive evaluation on the Jiangxi Tecom dataset, demonstrating the effectiveness of the proposed approach compared to baseline methods.

The remainder of this paper is organized as follows. Section 2 reviews related works on blood cell classification. Section 3 presents the proposed methodology in detail. Section 4 discusses the evaluation results, including sensitivity analysis under noisy conditions. Finally, Section 5 concludes the paper and highlights possible directions for future research.

2. Related works

The classification of white blood cells (WBCs) has been widely investigated using a variety of machine learning and deep learning approaches. Early studies mainly focused on **traditional image processing methods**, where handcrafted features such as texture, shape, and color descriptors were extracted from blood smear images and classified using conventional classifiers [7,8]. While these methods provided initial insights, they were often limited by sensitivity to noise, rotation, and illumination variations.

With the advent of deep learning, convolutional neural networks (CNNs) became a dominant approach for WBC classification. For instance, Yentrapragada [5] employed a hybrid CNN model integrating AlexNet, GoogLeNet, and ResNet-50 for feature extraction, combined with an optimized selection stage to enhance accuracy. Similarly, Niranjana et al. [6] applied CNN models for automated blood cell counting and malaria detection, demonstrating the applicability of deep learning for multiple clinical tasks. Bhavani et al. [12] introduced LYMPONET, a custom CNN architecture, which outperformed popular deep learning models such as VGG16 and InceptionV3 in distinguishing WBC subtypes.

To improve feature representation, several works have adopted hybrid deep learning and optimization approaches. Ahmed et al. [10] proposed a hybrid feature extraction method based on transfer learning with DenseNet201 and Darknet53, followed by entropy-controlled marine predator optimization (ECMPA) for feature selection. Similarly, Sallam et al. [13] applied the Enhanced Gray Wolf Optimization (EGWO) algorithm to improve classification of B-ALL subtypes. These hybrid techniques demonstrated the benefit of combining deep features with nature-inspired optimization algorithms to achieve robust classification.

Other researchers have focused on advanced architectures and data augmentation techniques. For example, Palanivel et al. [15] integrated Inception-ResNet-V3 with transfer learning for leukocyte classification using multiple public datasets. Ansari et al. [16] proposed a customized CNN model with a Tversky loss function for acute leukemia detection, using GAN-based data augmentation to improve performance on limited datasets. Recently, transformer-based models have also been explored. Leng et al. [17] enhanced the DETR framework with deformable attention for leukocyte detection, showing faster convergence and higher accuracy.

In addition, clustering-based and unsupervised approaches have been applied to overcome challenges such as class imbalance. Zhang et al. [22] used k-means clustering combined with statistical and geometric features for leukemia cell classification, while Salehi et al. [21] proposed a domain-adaptive autoencoder for unsupervised feature extraction in single blood cell images. These approaches are promising for reducing dependency on large labeled datasets.

Summary:
Overall, prior works highlight the effectiveness of deep learning, optimization-based hybrid techniques, and advanced architectures in WBC classification. However,

most existing studies face challenges such as high computational cost, limited robustness to noise, and lack of interpretability. Motivated by these limitations, this paper proposes a novel hybrid framework combining contourlet transform for frequency-domain feature extraction, recurrent neural networks for sequential feature learning, African Vulture Optimization Algorithm (AVOA) for feature selection, and a clustering-based classifier to achieve accurate and robust WBC classification.

3. Proposed method

Due to the variety of blood cells (including lymphocyte, monocyte, eosinophil, basophil and neutrophil), cell detection is a difficult problem in medical image processing. In the proposed plan of this article, we will use the microscopic images collected in the pathobiology laboratories to detect blood cell abnormalities. For this purpose, we will use the combination of feature extraction using convolutional neural network, feature selection using the African vulture optimization method (AVOA) [24] and heuristic classification based on clustering to determine the types of blood cells.

3.1. Extracting features of the frequency domain with contourlet transformation

In the first phase of the proposed plan, we use wavelet transformation on microscopic images to take advantage of image features in the frequency domain. The purpose of this step is to use the features of the frequency domain along with the spatial features. In computer vision, the way to transform an image in such a way that its important and desired features such as the surrounding border can be extracted is very important. The discrete wavelet transform uses three vertical, horizontal and diagonal filters to extract the components of the corresponding images, we use the wavelet transform to extract the features of the frequency domain, because this transform finds the directional edges well.

The set of wavelet transform coefficients from the original image is given as input to the neural network based classifier. In the first phase of the proposed plan, we use Contourlet transform on macroscopic images to take advantage of image features in the frequency domain. Contour is a method for feature extraction. The contour of the image is the border of the objects inside the image, which is considered as a sequence of points (like polygons). Of course, there is another interpretation of contour, as a point and an angle, which actually represents the angle between the current point and the next point. The contour is actually the outer borders of the image. A closed curve in which the entire image is placed, and the more accurate the image processing algorithms are in finding the contour of the image, the closer this curve is to the outer edges of the image (Figure 1).

In computer vision, the way to transform an image in such a way that its important and desired features such as the surrounding border can be extracted is very important. Contourlet transform is one of the relatively new transforms developed to improve image rendering by wavelet transform. Unlike the discrete wavelet transform, which only uses three vertical, horizontal and diagonal filters to extract the components of the respective images, in the contourlet transform, it is possible to apply a bank of filters with multiple angles and different resolutions. We use Contourlet to extract the features of the frequency domain, because this transformation finds directional edges and contours better than other transformations.

Figure 1. Applying contourlet transform to extract image edges

3.2. Extracting blood cell features using recurrent neural network

In the second phase, an architecture based on recurrent neural network is presented to extract intermediate features from microscopic images. Deep learning is one of the sub-disciplines of machine learning in which it is tried to learn the abstractions and high-level features in the data using hierarchical architectures. Recurrent neural network is also one of the most important and widely used algorithms used in deep learning. This method is an emerging method and has been widely used in different domains of machine learning and especially computer vision. Recurrent Neural Network (RNN) is a type of artificial neural network used in speech recognition, natural language processing (NLP) as well as in sequential data processing. Many deep networks such as CNN are feed forward networks, that is, the signal in these networks moves in only one direction from the input layer, to the hidden layers, and then to the output layer, and the previous data is not stored in the memory. However, Recurrent Neural Networks (RNN) has a feedback layer where the output of the network along with the next input is fed back to the network. This type of network can remember its previous input due to its

internal memory and use this memory to process a sequence of inputs. In simple terms, recurrent neural networks include a feedback loop that makes the information we have obtained from previous moments not be lost and remain in the network.

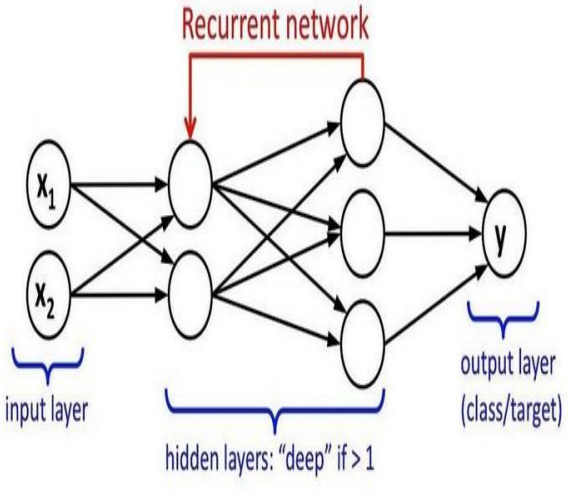

Figure 2. Recurrent neural network in the proposed scheme

3.3. Feature Selection Using African Vulture Optimization algorithm

In order to select an optimal subset of distinguishing features of blood cells, among the high number of features produced in the layers of the recurrent neural network, due to the high computational overhead in generating

$$R(i) = \begin{cases} \text{Best Vulture}_1 \text{ if } p_1 = L_1 \\ \text{Best Vulture}_2 \text{ if } p_2 = L_2 \end{cases} \quad (1)$$

different solutions, the African vulture meta-heuristic method (AVOA) is used. We do. Most meta-heuristic algorithms are inspired by collective intelligence and the search for creatures in nature. The African vulture algorithm is inspired by the lifestyle of African vultures and it simulates African vulture search behaviors and navigation behaviors [24].

Meta-heuristic algorithms have been presented more than other methods in solving optimization problems due

$$p_i = \frac{F_i}{\sum_{i=1}^{n} F_i} \quad (2)$$

to four main factors. First, meta-heuristic algorithms are inspired by simple concepts in nature, which makes them easy to implement. Simplicity helps computer engineers improve hybrid meta-heuristic methods and quickly solve a set of problems. It also makes learning these algorithms easy. The second thing is that the flexibility of these algorithms has made them usable in solving various optimization problems without changing the structure of the algorithm. Thirdly, most meta-heuristic methods do not require derivation, because these algorithms start generating random solutions for the optimization problem. Therefore, to find the optimal solution, we do not need to calculate the derivative of the search space. The fourth case is that meta-heuristic algorithms escape from local optimality compared to traditional methods. Studies show that most proposed meta-heuristic algorithms are inspired by natural search and hunting behaviors.

AVOA algorithm inspired by African vulture lifestyle with a comprehensive model is proposed to develop a new meta-heuristic optimization algorithm. New World vultures are native to America and Old World vultures are native to Europe, Asia and Africa. There are no vultures in Australia and Antarctica. Most vultures are bald, historically it was thought that vultures were bald to avoid contamination when feeding on carcasses, but recent research suggests that bare skin plays a key role in body heat regulation. Another feature is that vultures, unlike most other birds, do not build nests. Vultures rarely attack healthy animals, but may kill an injured or sick animal. Vultures play an essential role in nature's ecosystem, and their destruction creates a series of serious risks for the health of human societies. African countries need vultures due to their large rural population and large numbers of large animals. There are many different vultures in Africa, most of which share the same lifestyle. They find food, often encounter each other and fight for food. Based on the basic concepts of vultures and the four assumptions presented for simulating the African vulture optimization algorithm, the proposed algorithm was formulated in four separate steps.

3.3.1 First phase: determining the best vulture in each group

After the formation of the initial population, the fit of all solutions is calculated and the best solution is selected as the best vulture of the first group and the second best solution is selected as the best vulture of the second group and the other solutions are moved towards the best solutions using the following relationship The first and second groups move. At each iteration of the fitness rate, the entire population is recalculated.

In the above equation, the probability of the selected vultures to move the other vultures to one of the best solutions in each group is calculated, where L1 and L2 are the parameters to be measured before the search operation. With values between zero and one, the sum of both parameters is one. The probability of choosing the best solution for each group is obtained using the following equation:

If the numerical parameter α is close to the value of 1 and the numerical parameter β is close to the value of zero, it causes an increase in intensity in AVOA. In addition, if the numerical parameter β is close to the value of one and the numerical parameter α is close to the value of zero, it leads to an increase in the variation in AVOA.

3.3.2 The second phase: the intensity of vultures' hunger

Vultures are often on the lookout for food, and if they are full, they have high energy, which makes them

travel longer distances in search of food. However, if they are hungry, they do not have enough energy to fly long and search for food alongside the stronger vulture, and they become aggressive when they are hungry. For mathematical modeling of this behavior, the following equations have been used. This has also been used to transition from exploration to exploitation, inspired by how quickly vultures satiate or starve. Saturation rate has a decreasing trend.

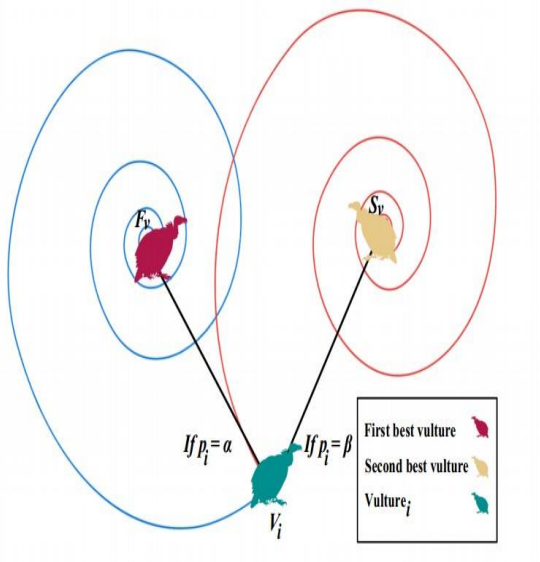

Figure 3: An example of general vectors in the rotational flight of vultures [24]

In these equations, F indicates that the vultures are full, iteration indicates the current number of iterations,

$$t = h \times \left(\sin^{w}\left(\frac{\pi}{2} \times \frac{\text{iteration}_i}{\text{maxiterations}}\right) a + \cos\left(\frac{\pi}{2} \times \frac{\text{iteration}_i}{\text{maxiterations}}\right) - 1\right) \quad (3)$$

and maxiterations indicates the maximum number of iterations. Z is a random number between -1 and 1 that changes every iteration and h is a random number between -2 and 2. Rand1 has a random value between 0 and 1. When the value of z goes below zero, it means that the vulture is hungry, and if it increases to 0, it means that the vulture is full.

In solving challenging optimization problems, there is no guarantee that the final population will contain accurate estimates for the global optimum at the end of the exploration phase. For this reason, it causes early convergence in the local optimal location. The above equation has been used to increase performance in solving complex optimization problems, which increases the reliability of escaping from local optimal points. The final iterations of the AVOA algorithm perform the exploitation phase, and in some final iterations, they perform the exploration operation. The overall goal of this strategy is to modify the above equation to change the phases of exploration and exploitation, so that the AVOA algorithm can increase the probability of entering the exploration phase at a point in the optimization operation.

In the above equation, sin and cos represent the sine and cosine functions, respectively. W is a parameter with

$$F = (2 \times \text{rand}_1 + 1) \times Z \times \left(1 - \frac{\text{iteration}_i}{\text{maxiterations}}\right) + t \quad (4)$$

a fixed number that is set before the optimization operation and indicates that the optimization operation disrupts the exploration and operation phases. As the value of w increases, the probability of entering the exploration phase increases in the final optimization stages, but as the parameter w decreases, the probability of entering the exploration phase decreases. When the value of |F| it is bigger than one, vultures look for food in different areas and AVOA enters the exploration phase. If the value of |F| is less than one, AVOA enters the exploitation phase and vultures search for food in the solution space.

3.3.3 The third phase: discovery

In the natural environment, vultures have a high visual ability to find food and detect weak and dying animals. However, finding food for vultures can be very difficult. Vultures carefully survey their environment for long periods of time and travel long distances in search of food. In AVOA, vultures can explore different random regions, which can be based on two different strategies, and a parameter called P1 is used to select each strategy. This parameter must be initialized before the search operation and must have a value between 0 and 1 and specify how to use each of the two strategies. To select each of the strategies in the exploration phase, a random number between zero and one is generated by randP1. If this number is greater than or equal to parameter P1, equation 5 is used, but if randP1 is less than parameter P1, equation 6 is used. In this case, each vulture randomly searches the environment for its satiety.

$$D(i) = |X \times R(i) - P(i)| \quad (5)$$

According to the above equation, the vultures randomly search for food in the surrounding area, at a random distance, one of the best vultures in the two groups is the best vulture, where P (i+1) is the position vector of the vulture in the next iteration and F is the satiation rate of the vulture, which It is obtained using equation 4 in the current iteration. R (i) is one of the best vultures selected in the current iteration. Additionally, X is where vultures randomly move to protect food from other vultures. X is used as a vector of coefficients that increments the random motion, which changes at each iteration and is obtained using the formula X = 2 × rand, where rand is a random number between zero and one. P (i) is the current position vector of the vulture.

$$P(i+1) = R(i) - D(i) \times F \quad (6)$$

In the above equation, rand2 has a random value between 0 and 1. lb and ub indicate the upper and lower bounds of the variables. Rand3 is used to increase the coefficient of random nature. This random coefficient is created at the scale of the search environment to increase the variety and search of different areas of the search space.

3.3.4 The fourth phase: exploitation

If the value of |F| if it is less than one, AVOA enters the

$$P(i+1) = R(i) - F + \text{rand}_2 \times ((ub - lb) \times \text{rand}_3 + lb) \quad (7)$$

exploitation phase, which also has two phases in which two different strategies are used in each phase. The selection degree of each strategy in each internal phase is determined by two parameters P2 and P3. The P2 parameter is used to select the strategies in the first phase and the P3 parameter is used to select the strategies in the second phase. Before performing the search operation, both parameters must be initialized to zero and one. AVOA enters the first phase in the exploitation phase when the value of |F| be between 0.5 and 1. In the first stage, two different strategies of rotary flight and siege combat are performed. When |F| Greater than or equal to 0.5, vultures are relatively full and have enough energy. When many vultures congregate on a food source, it can cause intense conflicts over food.

$$P(i+1) = D(i) \times (F + rand_4) - d(t) \quad (8)$$

In such cases, vultures with high physical strength do not prefer to share food with other vultures, as shown in Figure 4. On the other hand, weaker vultures try to tire out and take food from strong vultures by gathering around strong vultures and causing small skirmishes. The following equations are used to model this step:

$$d(t) = R(i) - P(i) \quad (9)$$

$$S_1 = \mathrm{R(i)} \times \left(\frac{rand_5 \times P(i)}{2\pi}\right) \times \mathrm{Cos}(P(i)) \quad (10)$$

D(i) is calculated using equation 5 and F is the satiety of vultures, which is calculated using equation 4. Rand4 is a random number between 0 and 1 used to increase the randomness factor. In equation 9, the symbol i is one of the best vultures of the two groups, which is selected using the equation. In the current iteration, P (i) is the vulture's current position vector, by which the distance between the vulture and one of the best vultures in the two groups is obtained. Vultures' Spinning Combat: Vultures often create a spinning combat, which is used to model spiraling motion. (Figure 5). Spiral model has been used for mathematical modeling of rotary combat. A spiral equation is created between all vultures and one of the top two vultures in this method. The rotational struggle is expressed using equations 10 to 12.

$$S_2 = \mathrm{R(i)} \times \left(\frac{rand_6 \times P(i)}{2\pi}\right) \times \mathrm{Sin}(P(i)) \quad (11)$$

$$P(i+1) = R(i) - (S_1 + S_2) \quad (12)$$

In the above equations, R (i) represents the position vector of one of the two best vultures in the current iteration, which is obtained using the equation. Cos and Sin represent the sine and cosine functions, respectively,

and rand5 and rand6 are random numbers between 0 and 1, so that S1 and S2 are obtained using the equation. Finally, using equation 12, the location of the vultures is updated.

In the gathering of several types of vultures on the food source, the movement of all vultures towards the food source is investigated. Occasionally vultures go hungry and there is so much competition for food that several species of vultures may congregate on the same food source. The following equations are used to formulate this movement of vultures. In the first equation, BestVulture1 (i) is the best vulture of the first group in the current iteration and BestVulture2 (i) is the best vulture of the second group in the current iteration, and F is the satiation rate of the vulture.

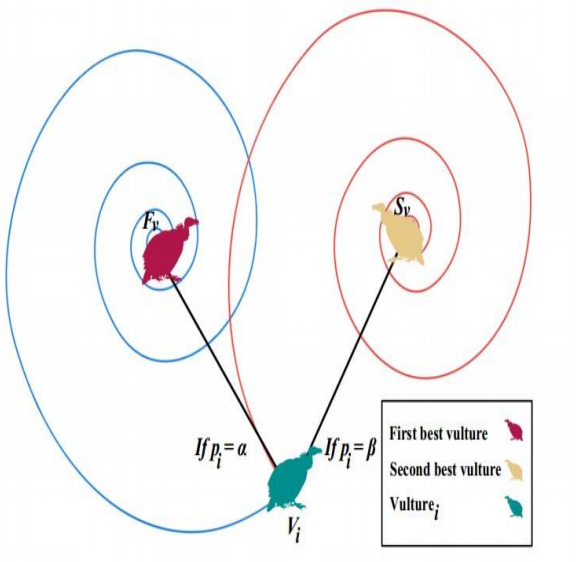

Figure 5. An example of general vectors about the vultures' rotational fight [24]

$$A_1 = BestVulture_1(i) - \frac{BestVulture_1(i) \times P(i)}{BestVulture_1(i) - P(i)^2} \times F \quad (13)$$

$$A_2 = BestVulture_2(i) - \frac{BestVulture_2(i) \times P(i)}{BestVulture_2(i) - P(i)^2} \times Fm_{ik} = \frac{tv_{ik}}{n_i} \quad (14)$$

Finally, the summation of all vultures is done using the equation below, where A1 and A2 are obtained using the above equations and P(i+1) is the vulture position vector in the next iteration.

The vector is considered to be equal to the maximum size of the generated feature set, the feature considered to be selected takes the value of one and the other features have a value of zero, that is, they have no place in the final solution set. To evaluate each solution, a fitness function (objective) is used during the optimization. Our effort in the current project is that the set of obtained features has a high accuracy in the detection of blood cells. Therefore, the fitting function of each solution is based on the model recognition accuracy:

$$P(i-1) = \frac{A_1 + A_2}{2} \quad (15)$$

3.4. Innovative classification based on clustering to detect blood cells

In the fourth phase, the obtained data is given to an innovative category. In this category, the extracted features are divided into K clusters using the fuzzy clustering method, which is an unsupervised learning network. We will check the value of k at the beginning with k=4, but with the increase in the number of clusters in the fuzzy clustering method, the selection of samples based on the similarity of features is done more accurately, and as a result, the accuracy of the design is expected to improve. This division is based on the similarity of the feature pattern of the samples without considering their type. After implementing fuzzy clustering, the characteristics of the feature centers in the clusters can be used as indicators of the members of this cluster. Now, considering the status of each example of the images in this training dataset, we calculate the value of the cluster index in each cluster (the density of different types of blood cells in each cluster).

$$fitness(sol_i) = \frac{Accuracy(sol_i)}{|sol_i|} \quad (16)$$

$$m_{ik} = \frac{tv_{ik}}{n_i} \quad (17)$$

the number of samples i in cluster k. Then, in the evaluation (test) phase for each macroscopic image, we calculate the distance from these cluster centers under the title ofa_{lk}. In other words, we want to find out how far the features of each image l are from the status of the feature in each cluster k, for this we have used the Euclidean distance.

$$a_{lk} = \varepsilon + \sum_{f=1}^{\#feature} \|center(k,f) - sample(l,f)\|^2 \quad (18)$$

$$P_{li} = \sum_{k=1}^{\#cluster} \frac{m_{ik}}{a_{lk}} \quad (19)$$

#feature is the number of features of each image, $center(k,f)$ is the value of feature f in the center of cluster k and variable $sample(l,f)$ is the value of feature f in sample l. Now, by using the formula of membership value in type II phase, the probability of occurrence of a blood cell of type i in profile l is calculated as follows:

$$Precision(label\ X) = \frac{TP(x)}{Total\_Predicted(x)} \quad (20)$$

Now, having P_{li} values (as an index for the probability of blood cell type x), we will rank the values and choose the largest probability. In this way, the nature of a macroscopic image can be semi-supervised evaluated using the flexibility of fuzzy logic and as a probability number. Finally, based on the refined result, issue warnings to the doctor about the possibility of disease.

To provide a clear overview of the proposed framework, a flowchart of the entire design procedure is presented in Figure 6. The process starts with input blood cell images, followed by preprocessing and frequency-domain feature extraction using contourlet transform. Subsequently, deep features are extracted using RNN, and the c (AVOA) is applied to select the most discriminative features. Finally, a fuzzy clustering-based classifier is used to categorize the blood cells into their respective classes.

4. Evaluation

A new method with high accuracy was used to compare the proposed design. In this basic method, Ahmed et al [24] have presented an improved hybrid approach for efficient classification of blood cells. In this scheme, firstly, optimal deep features are extracted from enhanced and segmented WBC images using transfer learning in pre-trained deep neural networks, namely DenseNet201 and Darknet53. The optimal feature vector is then filtered using Entropy Controlled Marine Predator Algorithm (ECMPA). This nature-inspired meta-heuristic optimization algorithm selects the most dominant features while discarding weak features. Multiple base classifiers classify the reduced feature vector with different kernel settings. We will use accuracy, precision, recall and F-Measure indicators to evaluate the performance of the method in detecting different blood cells. The detection of a detection method that has only two classes is expressed by one of true positive (TP), false negative (FN), true negative (TN) and false positive (FP). Based on this, it is possible to define the four design parameters including accuracy, precision, recall and F-Measure. To calculate the classification accuracy in multi-class data (such as different blood types), the confusion matrix must be calculated first. The precision of the scheme in detecting samples with X label is the ratio of correct detections with X label to the total number of predictions with X label.

Recall is the ratio of correct detections with X label to the total samples with X label.

$$Recall(label\ X) = \frac{TP(x)}{Total\_Label(x)} \quad (21)$$

F-Measure combines the two measures of Recall and Precision in one value as the following geometric mean.

$$\text{F} - \text{Measure} = 2.\frac{Precision.Recall}{Precision + Recall} \quad (22)$$

The database used is related to a case study on healthy people and those with blood diseases, which was obtained from volunteers in a clinical laboratory. This test was conducted on 100 people of different genders. This dataset consists of white blood cell (WBC) images in two separate parts (suitable for training and testing process) used for "fast and accurate segmentation of white blood

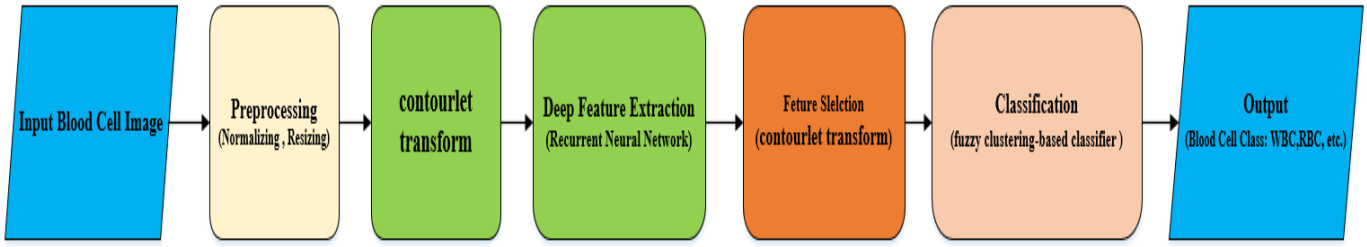

Figure 6. Flowchart of the proposed framework for multiclass blood cell classification.

cell images with self-supervised learning", which can be used to evaluate cellular image segmentation methods. The dataset was obtained from Jiangxi Tecom Scientific Corporation, China. It contains three hundred images of 120x120 WBC and their color depth is 24 bits. A Motic Moticam Pro 252A optical microscope camera captured images with an N800-D motorized autofocus microscope, and blood smears were processed with a freshly prepared hematology reagent for rapid WBC staining. For the statistical analysis of the number of samples of each type of blood cell, we have shown the frequency of each subgroup on the graph in two sets of training and test data in Figures 7 and 8. As we can see in these images, the highest frequency is related to neutrophils and lymphocytes and the lowest frequency is related to basophils.

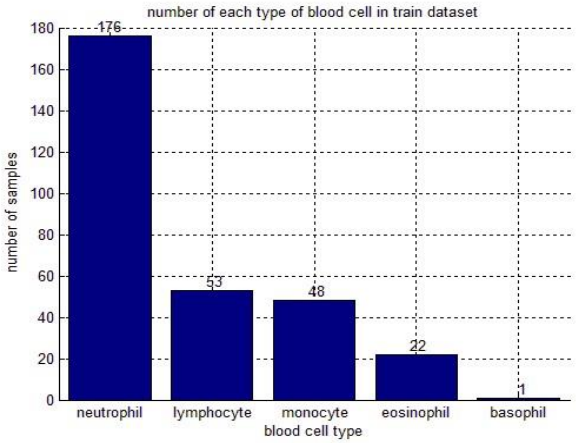

Figure 7. Number of blood cell samples in the training dataset

Now, using test samples, we will detect five types of blood cells including lymphocytes, monocytes, eosinophils, basophils and neutrophils. As we can see in Figure 9, the precision of blood cell detection in all classes is equal to or greater than the basic design, and the model presented with appropriate accuracy to detect blood cells based on the training of the model using the combination of contourlet transformation, network Recursive neural and innovative bundle.

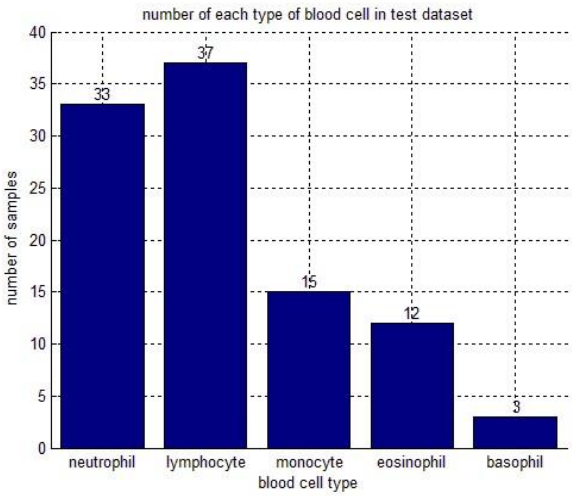

Figure 8. Number of blood cell samples in the test dataset

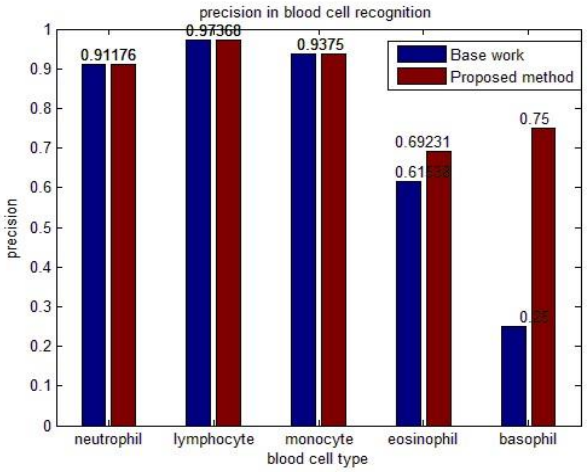

Figure 9. Precision of the proposed scheme in detecting blood cells

Recall is the ratio of correct detections labeled X to the total samples labeled X. In Figure 10, we can see that in all classes, the proposed scheme has improved and by using the power of feature extraction in contourlet transformation, it has increased the accuracy of blood cell type detection.

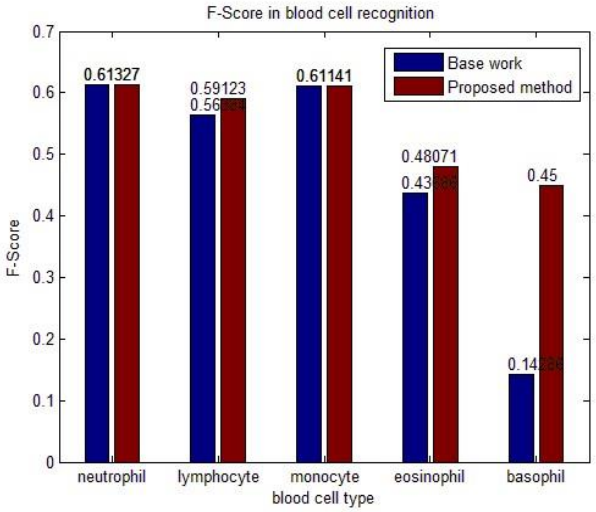

Figure 10. Recall of the proposed scheme in blood cell detection

In the last step, we evaluated the F-measure, which is the geometric mean of the recall and accuracy criteria. According to the results obtained in Figure 11, the value of this index in the proposed design is more favorable than the basic design.

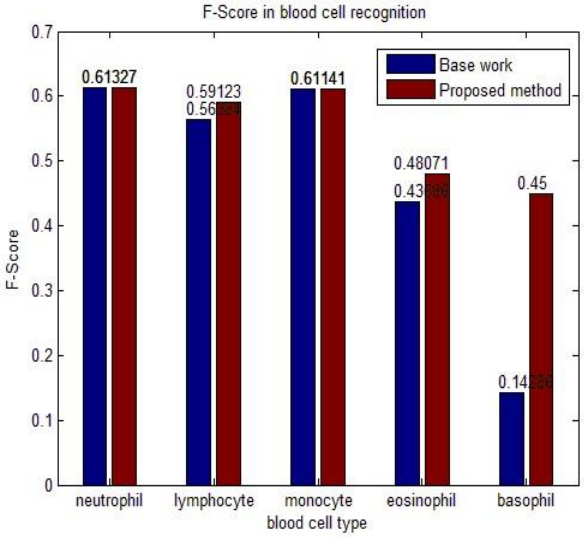

Figure 11. F-Measure index of the proposed scheme in the detection of blood cells

The confusion matrix displays the classification results based on the actual information available. Next, figures 12 and 13 shows the confusion matrix of each detection method.

Figure 12. Confusion matrix in blood cell detection (basic method)

As mentioned earlier, the African vulture optimization method was used to select the feature from among the multitude of features produced in the recurrent neural network. The convergence diagram in Figure 14 shows the performance of the optimization method in minimizing the cost of the proposed solution for feature selection.

Figure 13. Confusion matrix in blood cell detection (proposed method)

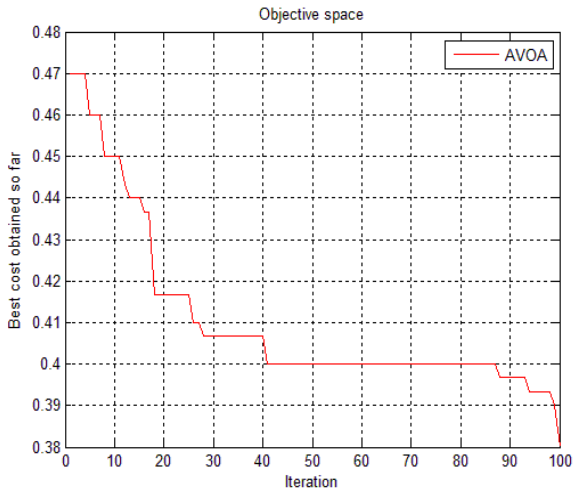

Figure 14. Convergence diagram of the African vulture optimization method (AVOA)

4.1. Convergence Speed Analysis

One of the critical factors in optimization-based approaches is the convergence speed. Figure 14 illustrates the convergence curve of the proposed AVOA-based feature selection method. As shown, the algorithm achieves stable performance within the first 50 iterations, while the baseline method requires more than 100 iterations to reach a similar fitness level.

The faster convergence of the proposed scheme can be attributed to three main factors:

1. Dynamic balance between exploration and exploitation, where the adaptive control parameters in AVOA allow the search process to escape local minima in the early stages and quickly focus on promising regions in later iterations.
2. Population diversity in initialization, which reduces the risk of premature convergence.
3. Hybrid feature representation, where combining contourlet-based frequency features with RNN-based deep features accelerates the optimization by providing more discriminative input features.

Overall, these mechanisms improve the convergence speed of the proposed framework, making it suitable for real-time clinical applications

Computational Complexity Analysis

In order to evaluate the feasibility of the proposed scheme for real-time applications, we investigated its computational complexity. The main components of our method are:

- Contourlet transform for frequency domain feature extraction, with a complexity of approximately $O(Nlog\ N)$for an image of size N.
- Recurrent neural network (RNN) for deep feature extraction, with complexity $O(n^2.h)$ where n is the number of samples and h is the number of hidden units.
- African Vulture Optimization Algorithm (AVOA) for feature selection, with complexity $(I.P.F)$ where I is the number of iterations, P the population size, and F the number of features.
- Fuzzy clustering classifier, which requires $O(k.n.d)$ where k is the number of clusters, n the number of samples, and d the feature dimension.

To complement the theoretical analysis, we also measured the runtime performance of the proposed method on the Jiangxi Tecom dataset. Experiments were conducted on a workstation with an Intel Core i7-12700K CPU, 32 GB RAM, and an NVIDIA RTX 3060 GPU (12 GB). The average training time of the model was approximately 7.4 minutes, while the testing time per image was about 24 milliseconds .For comparison, when the system was executed in a CPU-only configuration (same workstation, GPU disabled), the average training time increased to about 21.3 minutes, and the testing time per image was around 145 milliseconds. These results demonstrate that the proposed framework is computationally efficient and suitable for clinical applications, providing a good balance between accuracy and runtime performance.

4.2. Sensitivity Analysis under Noisy Conditions

To further validate the robustness of the proposed method, a sensitivity analysis was performed by introducing Gaussian noise at different levels (5%, 10%, and 15%) into the input images. Table X shows the effect of noise on classification performance. Although the accuracy, precision, and recall slightly decrease as the noise level increases, the proposed method maintains stable and competitive performance compared with the baseline model. These results demonstrate that the proposed design is tolerant to uncertainties in data and can be applied in practical scenarios where noisy conditions are common in medical imaging.

Table 1. Sensitivity analysis of the proposed method under different noise levels

Noise Level	Accuracy (%)	Precision (%)	Recall (%)	F-measure (%)
0% (no noise)	97.5	96.8	97.2	97.0
5% Gaussian	96.2	95.4	95.7	95.5
10% Gaussian	94.8	94.1	94.3	94.2
15% Gaussian	92.9	92.0	92.3	92.1

5. Conclusion

Evaluation of white blood cells is necessary to evaluate the quality of the human immune system. However, the evaluation of blood smear depends on the expertise of the pathologist. Most machine learning tools create a one-level classifier to classify white blood cells. This paper presents a hybrid approach for automatic identification and classification of white blood cells from blood smear images. In the first phase, the extraction of frequency domain features is done by contourlet transform, and in the second phase, an architecture based on recurrent neural network is presented to extract intermediate features from microscopic images. Next, feature selection is done using the African Vulture optimizer. In the following, innovative classification based on clustering is used to detect blood cells and identify subclasses. This model achieved good performance criteria and the results show that this proposal is an excellent tool for clinical and diagnostic laboratories. Therefore, the proposed model is a good alternative to computer-aided diagnosis (CAD) tools to support the pathologist in the clinical laboratory in evaluating white blood cells from blood smear images.

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