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PAPER

Study of AI-Based Solutions for Automatic Detection of Some Diseases Related to Red Blood Cells in West Africa

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ABSTRACT

The majority of hematology laboratories in the West Africa does not have equipment dedicated to the automatic classification of blood cells. The integration of artificial intelligence (AI) in hematology improves diagnostic accuracy, reduces the burden on healthcare systems, and provide timely interventions in regions with limited access to medical resources. This paper discusses the development and implementation of AI-based tools designed to automatically detect diseases related to red blood cells (RBC) in West Africa. These tools leverage advanced machine learning algorithms to analyze blood cell morphology and identify abnormalities indicative of diseases such as sickle cell anemia, elliptocytosis and other blood disorders. An analysis of previous techniques shows that models based on artificial neural networks (ANNs) and convolutional neural networks (CNNs) are the best systems for automatically detecting pathologies, with performance over 80%. When these models are combined with classifiers such as support vector machine (SVM) and k-nearest neighbor (KNN), they achieve better performance, with values between 91% and 98%.

KEYWORDS

artificial intelligence (AI), automatic detection, red blood cells (RBC), hematology, West Africa, white blood cells (WBC), gray level co-occurrence matrix (GLCM)

1 INTRODUCTION

Hematology is the branch of medicine that studies blood, the hematopoietic organs, and their diseases [1]. One of its main components is cytology, which plays an essential role in hematology laboratories and requires qualified staff [2]. In Benin, hematological cytology is primarily conducted at the Centre National Hospitalier Universitaire (CNHU-HKM) in Cotonou, serving a population of nearly 14 million [3]. The CNHU also houses the only blood disease management service in the country [4]. When data from automated systems are qualitatively or quantitatively abnormal or require confirmation, the study of blood smears becomes essential [5]. Cutté reports that 15 to 30% of hemograms still need to be verified using stained smears examined

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under a microscope, despite improvements in automated systems [6]. At the CNHU-HKM, the ultimate reference center in Benin, 1,800 hemograms are performed every month [4]. Blood smears are routinely conducted for any indication, as a continuation of automated counting.

Blood is made up of blood cells in plasma. These cells are made in the red bone marrow from a stem cell, which, by dividing and differentiating, gives rise to one of three categories of blood cells [5]. Red blood cells (RBC), also known as erythrocytes, which are anucleate cells and are the most numerous, around 5 million/mm^3. White blood cells (WBC) or leukocytes, around 8000/mm^3 and include polynuclear cells or granulocytes (neutrophils, basophils, eosinophils) and mononuclear cells (lymphocytes, monocytes). Platelets (PLT), which are anucleate fragments and occur at a rate of 150,000 to 450,000/mm^3 [5].

Each of these constituents play a crucial role in the body. The shape, color, size, or even the number of these cells are important characteristics in defining a patient's state of health. For example, the shape of RBC can indicate whether a patient has sickle cell anemia; an excessive number of WBC can be indicative of a specific type of blood cancer. This study focuses on RBC, which are essential for transporting oxygen throughout the body. They are shaped like a biconcave disc, which allows them to move easily through the blood vessels. The manual manipulation of blood smears to count and classify blood cells was, for a long time, the only technique in use.

Although automated equipment can quickly determine the number of different types of blood cells and provide information on the size and shape of RBC and the types of WBC, examining a blood sample under a microscope can provide additional information (blood smears) [7]. The traditional learning method consists of several steps: image segmentation, feature extraction, and optimal classification [8].

At the CNHU-HKM, blood slides are read remotely using an existing tele-hematology-cytology system. This system consists of a microscope that allows specialists to read slides and a computer with software for capturing and storing images. The practical method is as follows: preparation, staining and reading of blood and marrow smears, and acquisition of digitized images [9].

What is the contribution of artificial intelligence (AI) to the identification of qualitative hemogram abnormalities in West Africa? Artificial intelligence involves replicating human intelligence through the creation and application of algorithms in a dynamic computing environment [10]. To make things easier for technicians and help doctors save lives, we designed a model based on a convolutional neural network (CNN) that was able to recognize and classify different types of WBC. This CNN model, consisting of 12 layers with convolution layers and Maxpooling layers, was trained on a database of images of patients taken for blood samples in the hematology laboratory at the CNHU-HKM in Benin. It achieved a training performance of 99% and test data accuracy of over 90% [11]. This model then enabled us to automatically detect diseases linked to abnormalities in the shape of RBCs, such as sickle cell anemia and schizocytosis and elliptocytosis, with a performance of 86% [12]. To improve these already satisfactory results for the laboratory technicians who did not have such a technique, we compared its performance with those of other existing models.

The aim of this study is to make a comparative analysis of the performance obtained using existing CNN models in order to assess the results of the CNHU-HKM hematology laboratory-designed model.

This paper is organized as follows. In the materials and methods section, we detail the tools and techniques used for this study. The results section presents the collected data and observations. Then, the discussion section analyzes these results, comparing them with previous studies and offering interpretations. Finally, the conclusion section summarizes the main findings of the study and suggests directions for future research.

2 MATERIAL AND METHODS

2.1 Sample obtention process

The centrifugation method, which separates blood cells from plasma, is used to isolate RBC for analysis once the sample is taken from patients. The cells are fixed with methanol and stained with specific dyes (MGG in this case) to facilitate microscopic observation of morphological abnormalities. Thanks to the existing tele-hematology-cytology system, digitized photographs of blood and marrow smears are easily obtained. These images are manually annotated to identify specific morphological characteristics of RBCs. Healthy RBCs are biconcave in shape, sickle cell disease is manifested by sickle-shaped RBCs, elliptocytosis by elliptical RBCs, and schizocytosis by RBC fragments. These annotated images are stored in a database to serve as a reference for training automatic detection algorithms.

Image processing and ML algorithms are used to automatically detect and classify morphological anomalies in RBCs. The results of this detection are compared with manual annotations to assess the accuracy and reliability of the automatic system.

2.2 Sample description

This work included 100 images of each type of cell (healthy cells, sickle cells, elliptocytes, schizocytes) i.e., a total of 400 images captured on blood slides from healthy and sick patients collected in the hematology laboratory of CNHU-HKM between August 2022 and October 2023.

These patients were selected according to specific inclusion criteria: absence of chronic diseases other than those studied (sickle cell disease, elliptocytosis, and schizocytosis), non-smokers, and no history of recent blood transfusions. These 400 images are classified according to the following percentages: 60% for training data, 25% for validation data, and 15% for test data. Exclusion criteria included any condition that could affect blood parameters, such as recent infections or the use of immunosuppressive drugs.

2.3 Classification process of RBC

RBC classification followed a well-defined process to distinguish between healthy and diseased cells. Figure 1 below shows the different techniques used on images, from acquisition to classification. Input images are digital images obtained from the patient's blood slides using the optical microscope. Once diseased RBCs are identified, they are classified into three categories using the same process: sickle cells, elliptocytes, and schizocytes. Sickle-shaped RBCs are classified as sickle cells, half-moon, or helmet-shaped RBCs as schizocytes, and oval or ellipsoid-shaped RBCs as elliptocytes.

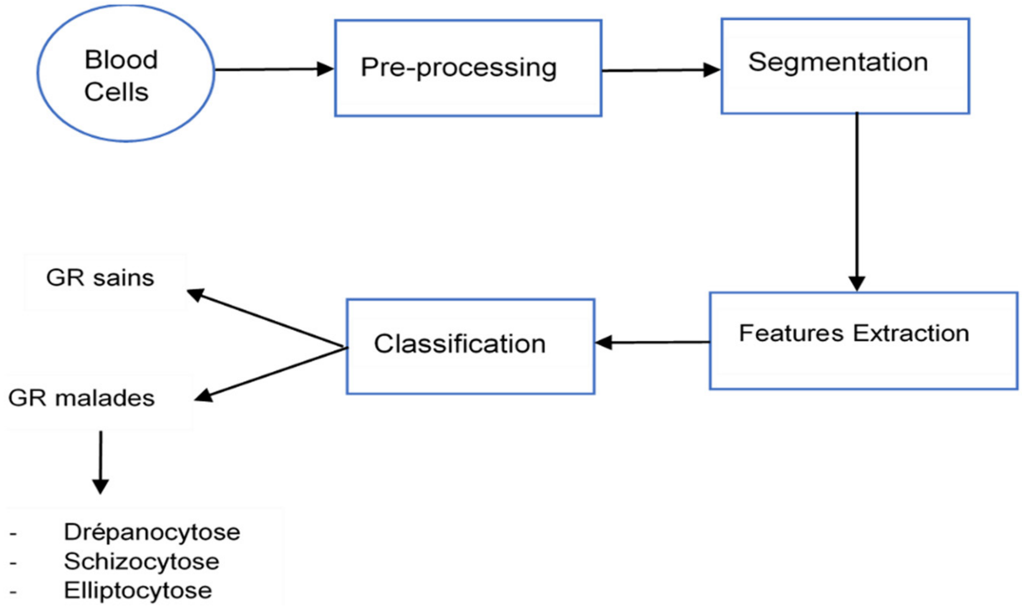

Fig. 1. Classification process of healthy and diseased RBCs

- **Pre-processing technique of blood images:** This step is very important in image classification. Its aim is to improve image quality to reduce training time and obtain better results. It is done automatically by programming filters to initially reduce or even eliminate noise due to sensors or caused by data conversion and to correct distortions induced by the transmission medium and acquisition optics. Size adjustments, orientation, and lighting are used to standardize images, ensuring they are ready for analysis.
- **Segmentation technique:** This automatic technique involves isolating individual cells in an image. There are several segmentation methods, but the one used here is edge segmentation using the U-Net model. Using the Canny filter, this method detects the edges of objects in the image.
- **Features extraction:** To enable classification, features are extracted from these images. Invariant moments are used to extract shape features (such as circularity, ellipticity, etc.), and the gray level co-occurrence matrix (GLCM) is applied to extract texture features (analyzing texture patterns within cells). The mean, standard deviation, and skewness of pixel values are used to extract color from the three RBC color planes. Edges are determined using the Canny edge detector.
- **Cell classification:** Cells are classified based on extracted characteristics. The model used is based on a CNN in addition to a machine learning classifier (K-NN and SVM).
  - Convolutional neural networks: Use of CNNs for more accurate image-based classification.
  - Machine learning algorithms: Use of techniques such as SVM, K-NN, or random forest (RF) to classify cells into categories such as sickle cells, elliptocytes, schizocytes, etc.

  Once images are properly classified, we move on to validation to assess the performance of the designed model.
- **Validation:** The classification results are validated by comparing them with manual diagnoses made by hematology experts. This methodology automates

the detection and classification of blood cells abnormalities, making it easier to diagnose diseases such as sickle cell disease, elliptocytosis, and schizocytosis.

3 RESULTS

3.1 Description of the architecture of the CNN model designed for the hematology laboratory at CNHU-HKM

The model used is a 12-layer convolutional neural network (CNN), consisting of one input layer, three convolutional layers, two MaxPooling layers, one flatten layer, three fully connected (FC) layers, and two dropout layers with a dropout rate of 0.5. The first two convolutional layers detect basic features such as curves, lines, and colors, which are common to all types of image classification. The intermediate layer focuses on specific features for classification, using the rectified linear unit (ReLU) activation function similar to the earlier layers. This is followed by the FC layers, with the final layer being the output layer, which uses the softmax activation function to enable efficient classification. The architecture is optimized to achieve a high positive prediction rate.

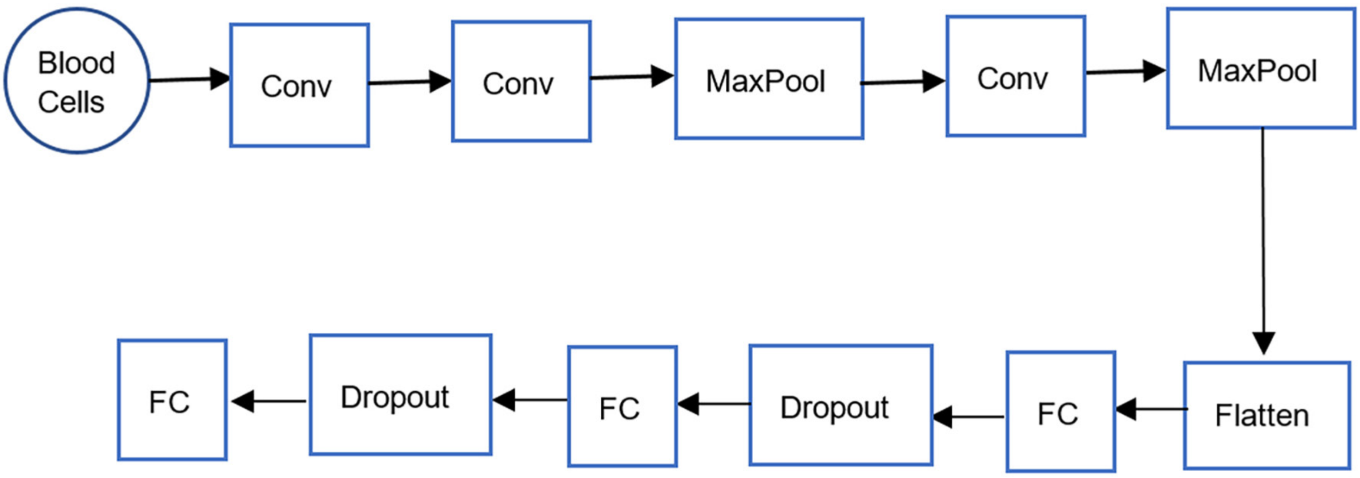

Fig. 2. CNN model architecture [11]

The CNN receives an image tensor as input and converts it into a feature map, an array of concatenated pixels with extracted features. The values of the feature map depend on the image resolution and the number of features extracted. For the input tensor, we used RGB images, combined with the Canny edge detector and the GLCM for enhanced feature extraction (see Figure 2).

3.2 Performances of the designed model

Results are obtained using an 11th generation Intel i7 2.30 GHz processor with 32GB RAM and a 64-bit operating system. The source code environment is Python 3.7.

Figure 3 shows the performance obtained in the automatic classification of RBCs (sick or not). After running the model, we achieved 98.78% for training and 90.11% for validation with a dataset of 400 images [11].

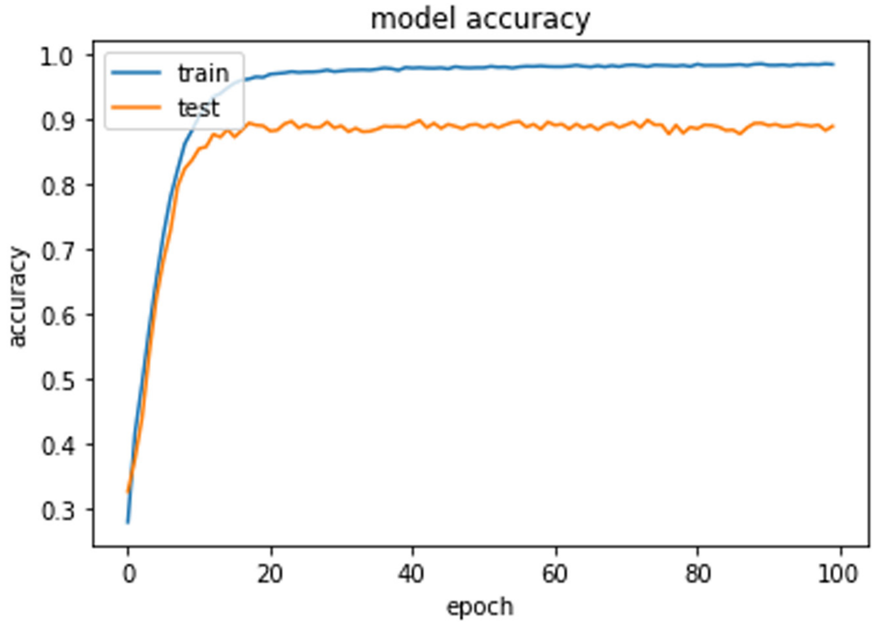

Fig. 3. The accuracy curve for classifying healthy red blood cells from the sick ones

Figure 4 shows the performance obtained in the automatic detection of sickle cell disease, elliptocytosis, and schizocytosis. After running the model, we achieved 100% for training and 86% for validation for a dataset of 300 images [12].

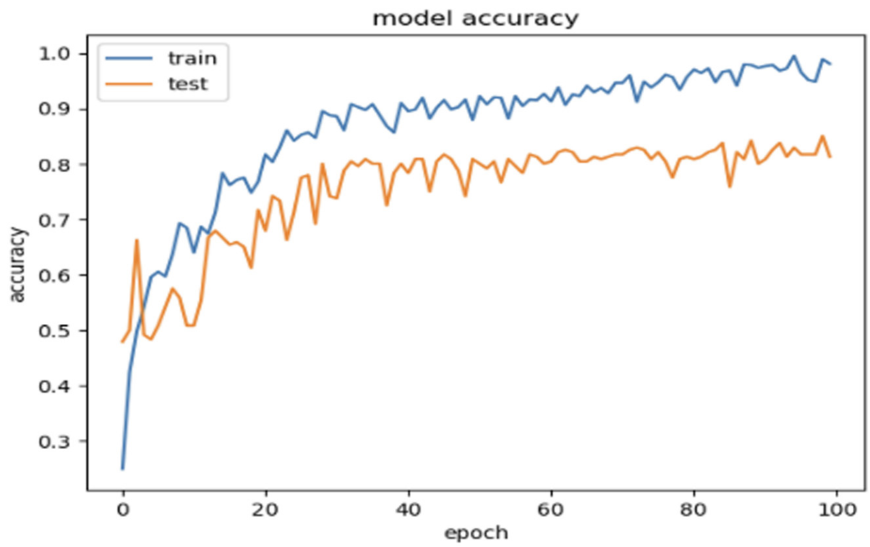

Fig. 4. The accuracy curve for the classification of sickle cell disease, schizocytosis, and elliptocytosis

3.3 Other works on the automatic detection of diseases related to RBC

Many researchers have focused on the early detection of RBC diseases. Rakshit et al. emphasized the detection of sickle cells, achieving 95.8% accuracy using a wiener filter, sobel edge detector, and morphological operator [13]. Sharma et al. classified normal and abnormal cells with an accuracy of 80.6% using the KNN classifier and watershed segmentation technique. Their dataset consisted of 100 images of healthy and diseased RBCs samples divided into four classes: sickle cells, dacrocytes, ovalocytes, and erythrocytes [14]. Dalvi et al. compared an artificial neural network (ANN) with a decision tree for classifying abnormal RBCs into four categories, including elliptocytes, finding the neural network to perform better with an accuracy of 91.3% compared to 90.91% for the decision tree [15].

Xu et al. proposed a deep CNN model that classifies RBCs into eight shapes, achieving 87.9% accuracy in classifying sickle cells [16]. Acharya et al., using a computer-aided system, successfully detected 11 sub-classes of RBCs, including sickle cells, with 98% accuracy [17]. Aliyu et al. applied AlexNet to blood sample data from 130 patients, obtaining 95.92% accuracy [18].

Chy et al. employed an image processing technique with an efficient SVM classifier to identify healthy RBCs and sickle cells, achieving 95% accuracy [19]. The following year, they compared three models—extreme learning machine (ELM), SVM, and KNN—finding ELM to perform best with 87.73% accuracy [20].

In a study by Hortinela et al., an ANN architecture classified normal and abnormal RBCs with 90.54% accuracy. Combining this with an SVM classifier improved performance to 93.3% for seven categories of abnormal RBCs, including elliptocytes [21]. Mohamad et al. used a sobel edge detection algorithm and blob measurement for shape detection in 2D images, achieving 95% accuracy. This low-cost technique is particularly beneficial for remote areas with limited medical facilities [22].

Table 1 shows the number of samples used by different authors, including the model designed for the CNHU-HKM hematology laboratory, and the various performances obtained according to the techniques used. All the studies considered here focus on the automatic detection of diseases related to RBC.

Table 1. Summary of techniques used for automatic detection of RBC diseases

Authors, Years	Number of Samples	Performances (%)	Model Used
BF Bio Nigan et al. [12]	300	86	CNN
Rakshit and Bhowmik [13]	–	95.8	Image processing + Sobel Edge Detector
Sharma et al. [14]	100	80.6	KNN
Dalvi and Vernekar [15]	1500	91.3	ANN
Xu et al. [16]	7000	87.9	CNN
Acharya and Kumar [17]	96	98	CAS
Aliyu et al. [18]	130	95.92	AlexNet
Chy and Rahaman [19]	–	95	Image processing + SVM
Chy and Rahaman [20]	–	87.73	ELM
Hortinela et al. [21]	1500	93.3	ANN + SVM
Mohamad et al. [22]	7000	95	CNN + Sobel Edge Detector

Performances in Table 1 are shown in the graph below (see Figure 5). The blue line with 86% represents the performance obtained in our study for the automatic detection of sickle cells, elliptocytes, and schizocytes. The performances range between 80.60% and 98%.

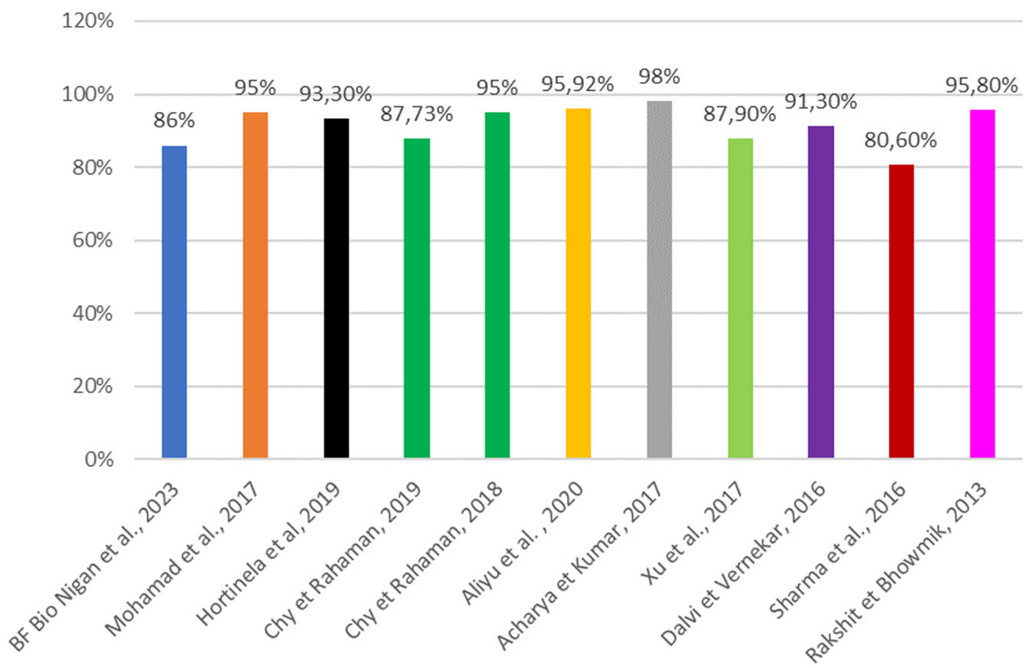

Fig. 5. Performance of the different models across the various studies

4 DISCUSSION

The results obtained from this study highlight several key findings in the automatic detection of RBC diseases using AI-based models, specifically ANNs and convolutional neural networks.

Studies reviewed indicate that ANNs and CNNs are highly effective for automatic RBC classification and disease detection, achieving accuracy rates between 80% and 90%. This effectiveness is due to their ability to capture complex patterns and features in blood cell images. When these models are supplemented with classifiers such as SVM and KNN, performance often exceeds 90%. This is because these classifiers further refine the decision boundaries and improve the model's ability to distinguish between different cell types. For example, Chy et al. [19] employed SVM to classify healthy and sickle cells, achieving 95% accuracy, while Xu et al. used a CNN to classify RBC categories with 87.9% accuracy [16].

Effective segmentation is crucial for isolating individual cells from blood smear images. The use of U-Net models and filters such as the Canny edge detector has proven instrumental in enhancing segmentation accuracy. Segmentation facilitates the extraction of detailed shape and texture features through techniques such as invariant moments and the GLCM. These extracted features are critical for accurate classification.

The CNN model for the CNHU-HKM hematology laboratory demonstrated robust performance [12], achieving 86% accuracy for detecting RBC diseases such as sickle cell anemia, elliptocytosis, and schizocytosis. The simplicity of this model, using fewer layers, resulted in shorter processing times and fewer parameters, making it practical for real-world applications. The performance, although slightly lower than some state-of-the-art models, is competitive, especially given the constraints of the dataset size.

The dataset size, comprising 300 images, is a significant factor influencing models' performance. Larger datasets generally lead to better model generalization and improved accuracy. The results are promising but could be enhanced with a more extensive dataset. For instance, expanding this dataset could increase the robustness of the model, making it better at generalizing across different types of RBC abnormalities.

To enhance the results of the designed model, expanding the image database is a primary goal. Increasing the number and diversity of images would provide a more comprehensive training set, leading to improved model accuracy and reliability. Additionally, incorporating more advanced classifiers such as SVM and KNN, as well as sophisticated techniques such as morphological operators and Sobel edge detectors could further enhance feature extraction and classification accuracy. For example, Dalvi et al. found that combining ANN with decision trees improved classification accuracy for abnormal RBCs [15].

5 CONCLUSION

Recognition and counting of different blood cells are crucial for medical purposes. Historically, the manual manipulation of blood smears was the primary method for counting and classifying blood cells. While semi-automated procedures are now available; characteristic extraction is often done manually before automatic classification, which remains time-consuming, tedious, and sometimes prone to errors.

This paper investigates AI-based solutions, concluding that ANNs and CNNs are the most effective models for blood cell analysis, achieving performance levels over 80%. Using the PRISMA model approach, various ML techniques were reviewed for the automatic detection of RBC diseases and found ANNs and CNNs are superior in blood cell classification.

We have demonstrated the efficient and effective contribution of AI to hemograms through the identification of morphological anomalies characteristic of certain blood cells pathologies (WBC, RBC). However, there are a number of limitations to the model used, particularly with regard to the size of the dataset, which could be extended to improve the generalization of the model. We also propose incorporating additional classifiers such as SVM and KNN, as well as advanced techniques like the Sobel edge detector to further improve results. Taking these limitations in consideration represent our team's future research prospects.

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