AI to minimise human errors in the detection of hematological diseases[*]

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Abstract

Hematology is a branch of medicine that relies on accurate diagnosis and appropriate treatment of blood-related diseases. However, human errors, whether due to technician fatigue, inattention or technical limitations, can have serious consequences for patients. Artificial intelligence offers a solution to these problems. By integrating advanced machine learning and deep learning algorithms, AI offers innovative solutions for reducing diagnostic and treatment errors. With its ability to analyse big data with high accuracy, AI promises to transform hematology practice, ensuring safer and more effective care for patients. This article reviews the different AI techniques used in the recognition of blood cells and the detection of related diseases, while highlighting its benefits in minimising human errors in diagnosis.

Keywords

AI, errors, hematology, minimise.

1. Introduction

Artificial intelligence (AI) is defined as a process of imitating human intelligence, based on the creation and application of algorithms executed in a dynamic computer environment [1]. It is therefore the ability of a machine to imitate human behavior (analysis, interpretation, decision-making based on an image) via algorithms and to make predictions based on data already acquired [2]. AI is faster and makes fewer errors than humans when it comes to achieving results. Its importance is growing by the day. It has developed and is now present in almost every sector of human activity: transport, agriculture, commerce, medicine, ...

The use of AI in medicine began in the 20th century in developed countries for the rapid management of patients and the accurate diagnosis of certain diseases [3]. Today, AI is commonly used in the detection of rare genetic diseases (Cornelia de Lange syndrome, Angelman syndrome, etc.) [4], heart disease and cancer [5], blood diseases, ... It is transforming many areas of medicine, including hematology. Hematology is a medical speciality that studies blood, the hematopoietic organs (bone marrow, lymph nodes and spleen being the main ones) and their diseases [6].

Blood includes blood cells in plasma which are made in the red bone marrow from a stem cell. By dividing and differentiating, this cell gives rise to one of three categories of blood cells [7]:

- Red blood cells (RBC), also known as erythrocytes, which are anucleate cells and are the most numerous, around 5 million/mm3.
- White blood cells (WBC) or leukocytes, around 8000/mm3:
    - Polynuclear cells or granulocytes (neutrophils, basophils, eosinophils);
    - Mononuclear cells (lymphocytes, monocytes).
- Platelets (PLT), which are anucleate fragments and occur at a rate of 150,000 to 450,000/mm3.

Each type of cell has its own distinguishing features, whether in terms of shape, colour or even size.

In most of our hematology laboratories in Africa and in Benin in particular (CNHU-HKM), our technicians carry out this recognition work manually using a microscope. In addition to the long wait by patients before obtaining results, these results are sometimes exposed to human errors of inattention. This is justified by the large number of blood slides to be analysed by these technicians.

By using advanced algorithms and massive data processing capabilities, AI offers unprecedented opportunities to improve the diagnosis, treatment and management of hematological diseases and sometimes reduce the cost of analysis. This is the case of an AI model used by some authors to help practitioners identifying different hematological diseases with inexpensive hemogram tests. This binary and multi-class classification model achieved up to 96% accuracy [8]. This article explores the different applications of AI in hematology, highlighting the potential benefits of this revolutionary technology.

We first present the litterature review on recognition and classification of blood cells and automatic detection of blood diseases. Then, we present the CNN model designed for the CNHU-HKM hematology laboratory and performances obtained. Finally, we discuss the benefits of AI in minimising human error in hematology diagnosis.

2. Litterature Review

2.1. Recognition and Classification of Blood Cells

2.1.1. White blood cells (WBC)

For cell recognition, authors used different ML/DL methods for cell segmentation, classification, and counting.

S Khan et al. (2021) used both traditional learning methods (manual extraction of features + classification cells by ANN) and DL-based methods (characteristic extraction + classification cells by CNN) to classify WBCs. This study reveals that they achieved the same performance in all 02

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cases [9]. RB Hegde et al. (2019) also compared traditional and DL methods and arrived at the same results with 99% of accuracy for WBCs classification [10].

AS Ashour et al. (2021) used a neural network associated with the SVM algorithm on a database combination and achieved a segmentation performance of 94.9counting accuracy for both cells is 97.4Ruberto et al. (2015) created a multi-classifier system for WBC segmentation using ANN + Nearest Neighbor and SVM algorithms and obtained a segmentation accuracy of 99% [12].

S Manik et al. (2016) used an ANN-based system with MAT-LAB capabilities to detect and classify WBC. The accuracy of the entire system is 98.9% with 100for eosinophils and neutrophils, 96.7% for lymphocytes [13]. Using the Faster R-CNN (Fast R-CNN + Region Proposal Network (RPN)) method on the BCCD dataset to recognize and classify different blood cells, S Raina et al. (2020) obtained the following results: RBC 55.83%, PLT 68.36% and WBC 92.10% [14].

J Basnet et al. (2020), using a Deep CNN-based method, improved classification accuracy from 96.1% to 98.92% and reduced processing time from 0.354 to 0.216 s [15]. MJ Macawile et al. (2018) created a CNN- based system to classify and count WBCs using the HSV (Hue Saturation Value) saturation component on the ALL-IDB database. They compared several models (Alexnet, GoogleNet, and ResNet-101). AlexNet appears to be the best, with a sensitivity of 89.18%, a specificity of 97.85% and an accuracy of 96.63% [16].

With a model based on the Deep RN and using the characteristics of the convolutional layers of the AlexNet architecture, A Khan et al. (2021) were able to identify the different types of WBCs with a training accuracy of 99.99% and the test of 99.12%. This model is named MLANet-FS-ELM [17].

A Malkawi et al. (2020) set up a CNN-based hybrid system to extract WBCs characteristics and classify them. They evaluated the performance of 3 classifiers (SVM, k-NN, RF) on the LISC WBC and the RF performed better with a test accuracy of 98.7% [18]. A. Şengür et al. (2019) used a system based on image processing and ML in particular Deep CNN to classify WBCs according to their shape and other deep characteristics. This system achieved an accuracy of 80% in relation to the shape and 82.9% in relation to the deep characteristics; combining these 02 parameters, the overall accuracy is 85.7

2.1.2. Red blood cells

Differents ML/DL techniques have been used for automatic cell recognition [20].

Maity et al. (2012) employed an efficient supervised-decision-tree C4.5 to classify RBCs into six sub-classes including sickle-cells with 98.2% precision and 99.6% specificity [21]. They also proposed another method which emphasizes the extraction of crucial shape-based features for RBC classification into nine classes including healthy cells in 2017. This method achieved 99.71% specificity and 97.81% accuracy [22].

Acharya and Kumar (2017) employed a technique capable to classify RBCs into 11 sub-classes including sickle-cells with 98% precision [23]. Using the Hough Circular Transform (HCT) method, Mazalan SM et al. (2013) were able to count the total number of RBCs in a peripheral blood smear image. Results showed that from ten sample peripheral blood smear images, accuracy was 91.87% [24]. Using the same method, Chadha GK et al. (2020) were able to count and classify RBCs according to four types of abnormality (ellip-

tocytes, echinocytes, lacrimal cells and macrocytes) with an accuracy of 91.667% over a period of 0.81432 seconds for different blood samples [25].

Namata et al (2021) proposed an image processing method using a convolution neural network for classification of RBCs. The algorithm used extracts features from segmented images and classifies in nine categories with an overall accuracy of 98.5% [26].

2.2. Automatic detection of blood cells diseases

2.2.1. White blood cells

The excessive presence of certain immature cells in the peripheral blood reveals that the patient has a disease, the case of blasts for leukemia [27].

M Jiang et al. (2018) developed a WBCNet model to fully extract WBC characteristics by combining a batch normalisation algorithm, residual convolution architecture and the enhanced activation function to diagnose leukemia and reduce the misdiagnosis rate. This model obtained an accuracy of 77.65% and 98.65% for Top-1 and Top-5 respectively in training and 83% in testing for Top-1 [28]. To improve these results, Sheikh IM Chachoo, MA. (2020) used an advanced ML-based method to segment the GBs. This segmentation is based on grey level and consists of eliminating the other cells and the cytoplasm of the WBCs and extracting only their nuclei. It achieved a nucleus extraction accuracy of 91%. This method is only applicable to WBCs [29].

An automatic CNN system has been designed by Anwar S, Alam A (2020) for the detection of acute lymphoblastic leukemia (ALL) without preprocessing or segmentation. It has achieved 99.5% accuracy [30]. Boldú L et al. (2021) used a LD model to firstly recognise lymphocytes, monocytes, blasts and activated lymphocytes and then classify blasts found. Authors ran several architectures (VGG16, ResNet101, DenseNet121, SENet154, ALNet (02 CNNs in series)). The ALNet model performed better: Myeloid leukemia (accuracy 93.7%, specificity 92.3%, sensitivity 100%) and Lymphoid leukemia (accuracy & specificity 100sensitivity 89%) [31].

An ML model based on digital image processing techniques and the RF classifier has enabled Mohamed H et al. (2018) to diagnose WBC-related diseases. The model achieved an accuracy of 94.3% [32]. Similarly, another study conducted by Sheng B et al. (2020), used the Faster R-CNN method combined with the VGG16 technique to classify WBCs and detect the presence of lymphoma in the blood. It obtained a lymphoma detection rate of > 96% [33].

Agrawal R et al. (2019) developed a CNN model for diagnosing all types of cancer. Its operation is based on image processing techniques. The system is 97.3% accurate [34]. A decision support system based on ANNs was used by Negm AS (2018) to identify blasts. Several classifiers (k-Means, LBG, KPE) were evaluated and k-Means performed better with an accuracy of 99.74% and a sensitivity of 100% [35].

2.2.2. Red blood cells

The literature is full of studies on the detection of diseases caused by RBCs.

Normal and abnormal cells were classified into four classes: sickle cells, dacrocytes, ovalocytes and erythrocytes by Sharma V (2016) using the KNN classifier and Watershed

segmentation technique with an accuracy of 80.6% [36]. Xu M et al. (2017) focused on the RBC shape detection using different techniques. A Deep CNN was used to find their region of interest (ROI) using an automatic seed generation technique and a mask based on patch normalization to obtain images of uniform size. This method is not widely used because it requires a very large database [37].

Sobel's edge detection algorithm is used by Mohamad A et al. (2017) for detecting RBC shape with blob measurement. This inexpensive technique is beneficial for people living in remote areas and achieveded 95% accuracy but only for 2D images [38]. Zhang M et al. (2020) adopted a semantic segmentation framework based on deep learning to solve the GR classification task. The performance obtained was 97% for the dU-Net model and 94.7% for the classical U-Net model [39].

A transfer learning technique that automatically extracts features and is specific to small databases has also been proposed by Alzubaidi L et al. (2020). Thanks to data augmentation, it achieved 99.98% [40]. Chy T et al. (2019) used different techniques (fuzzy C mean clustering algorithm, KNN, SVM and ELM) to automatically detect sickle cell disease. ELM classifier performed better, with an accuracy of 95.45% [41]. AlexNet was also used by Aliyu H. et al. (2020) to classify red blood cells in sickle cell anemia. The accuracy obtained was 95.92% [42]. Another technique using a smartphone microscope has also been used on blood smears for the same purpose by De Haan K. et al. (2020). It comprises two distinct and complementary deep neural networks and achieved an accuracy of around 98% [43].

3. Performances of the proposed model for the CNHU-HKM hematology laboratory

The model designed for CNHU-HKM hematology laboratory is a CNN architecture of 12-layers. It allows to recognize blood cells (WBC, RBC) and detect blood cells diseases like sickle cell anemia in CNHU-HKM hematology laboratory [44]. These layers are optimized for the maximum positive prediction rate. Figure1 and 2 show performance obtained in automatic classification of blood cells for 32*32 images and 16*16 images respectively with accuracy of 98.78% for training and 88.11% for test and 86.59% for cross validation for 32*32 images, and 90.11% for test and 88.53% for cross validation with 16*16 images [44].
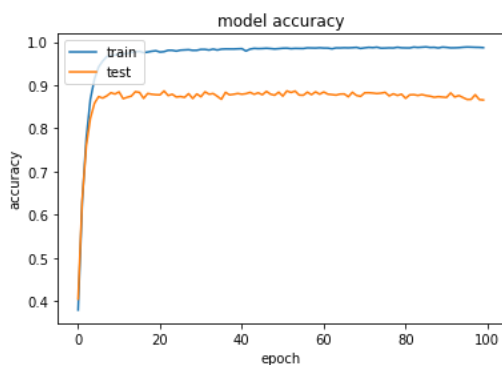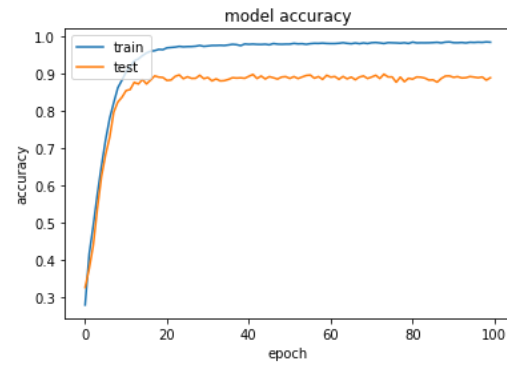

Figure 1: Accuracy curve 32*32

Figure 2: Accuracy curve 16*16

The loss curve evaluates how well our algorithm models the dataset. The lower the loss, the better is. Figure3 and 4 show performance obtained in the automatic classification of blood cells for 32*32 images and 16*16 images respectively. We notice that while the training curve tends towards zero (0), the validation curve is a bit high [45].
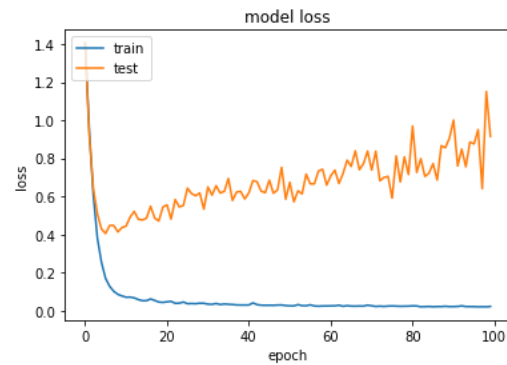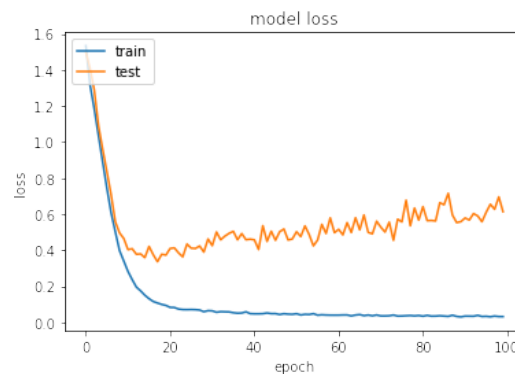

Figure 3: Loss curve 32*32

Figure 4: Loss curve 16*16

Figure5 and 6 show performance obtained in automatic detection of sickle cells disease, elliptocytosis and schizocytosis for 32*32 images and 16*16 images respectively. After running the model, we obtained 100% for training and 82% for validation with 32*32 images, and 86% for validation with 16*16 images [45].
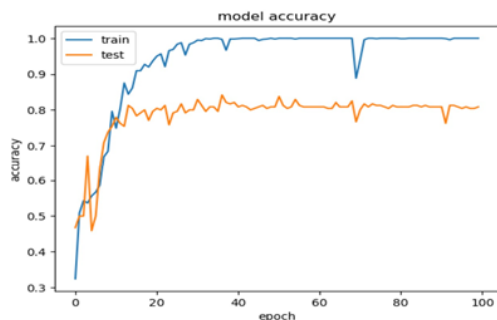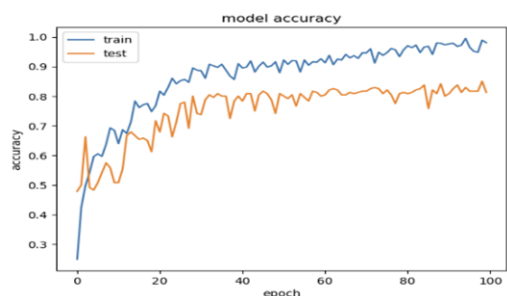
Figure 5: Accuracy curve 32*32

Figure 6: Accuracy curve 16*16

4. Discussion

AI has remarkable potential to reduce human error in hematology. It is beneficial in several ways:

- Data analysis: ML algorithms can analyse big medical data, including blood test results, to detect anomalies or patterns that humans might miss. This can help diagnose hematological diseases more quickly and accurately.
- Clinical decision support: AI systems can provide recommendations based on clinical data and best practice, helping doctors to make more informed decisions. For example, in hematology, AI can suggest optimal treatments for diseases such as leukemia or anemia.
- corresponding author mark : \cormark[<num>]Automation of repetitive tasks: AI can automate administrative and clinical tasks, reducing the risk of human error. For example, the transcription of test results or the management of medical records can be carried out by AI systems, which relieves healthcare professionals.
- Continuous monitoring: AI systems can continuously monitor patients and alert doctors to significant changes in health parameters. This is particularly useful for patients with chronic diseases or who require constant monitoring, such as certain hematological diseases.

5. Conclusion

In conclusion, AI integration in hematology represents a major advance that promises to transform clinical and research practices. Although challenges remain, particularly

in terms of regulation, ethics and acceptance by healthcare professionals, the potential benefits of AI are immense. By improving diagnostic accuracy, optimizing treatments, and facilitating data management, AI has the potential to reduce human error and improve patient outcomes. The future of hematology, enriched by AI, looks promising and will bring significant innovations.

6. Acknowledgments

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