Hematological Classification of White Blood Cells by Exploiting Digital Microscopic Images

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ABSTRACT

A blood test is an essential examination process for evaluating body functions. Blood cell classification is an important laboratory process for detecting blood diseases. Microscopic evaluation by experts is a slow process, and the outcome depends on skill and experience. In addition, the process can be tedious and time-consuming. Therefore, an automated medical diagnostic system is essential in recognizing diseases in a short time and providing information about blood-related diseases such as leukemia. White blood cells are one of the most important types of blood cells associated with the immune system, as their forms are important and necessary for diagnosing blood diseases. In this study, a new Deep Learning (DL) network model called White Blood Cell Hematological Diseases Classification (WBC_HDC) is proposed. The classification was based on a convolution neural network (CNN) scheme for classifying hematology. A dataset containing 2800 images of white blood cells has been used, which were obtained with a CellaVision DM96 analyzer in the laboratory of the Barcelona Hospital Clinic (BHC). The data set is organized into the following four groups: Lymphocytes, Monocytes, Immature Granulocytes (IG), and Erythroblasts. The images' sizes are 360 x 363x 3 pixels in Joint Photographic Group (JPG) format and have been annotated by clinical pathology experts. Images were taken from individuals without infection, hematology, or neoplasia and free of any drug treatment at the moment of blood collection. The WBC_HDC network has recorded an accuracy of 90.86% after going through numerous tests of network layer parameters for eight different stages.

Keywords: White Blood Cells, Classification, Deep Learning

1. Introduction:

The immune system is the third line of protection for the human body against diseases, including viruses and bacteria. This innate defense identifies and eliminates abnormal cells as cancer cells. Immune systems, immune cells, and immunological chemicals make up the immune system. White blood cells (WBCs) are the building blocks of immune cells. The concentration of white blood cells in human blood is usually stable. Health problems may arise if the level of white blood cells exceeds the standard limit. One of the essential operations in the pathological investigation of blood is the morphological study of WBCs.

Even for professionals, doing morphological analysis manually is tedious and time-consuming. Furthermore, morphological analysis is limited to the expertise and vision of the pathologist. In recent years, automated approaches have been developed to address the shortcomings of human diagnostic methods, which can lead to inaccurate results [1]. There are five types of white blood cells: neutrophils, lymphocytes, eosinophils, and monocytes [2,3]. The last two categories are non-granular. There is difficulty in diagnosing these types manually. Therefore, image analysis networks have been adopted to address this problem as they may lead to evaluations equal to human assessment. Image analysis can identify abnormal cells and apply pathologists' expertise in pathologic diagnosis [4-5]. There are recent studies related to this work. The automated categorization of blood cells is frequently accomplished by utilizing sophisticated feature extraction and picture preprocessing techniques. White blood cell pictures were preprocessed in [6], employing minimum intensity homogenization, contrast stretching, opening, edge detection, dilation, filling, and contrast stretching. In the study [7], WBCs were separated from obtained pictures using k-means clustering, features were extracted, feature selection was carried out using an Artificial Neural Network (ANN), and principal component analysis (PCA) and classification were performed. The Fast Relevance Vector Machine (F-RVM) is a technique for segmenting and classifying WBCs introduced in [8]. The F-RVM requires less time for inference and is easier to train than the Extreme Learning Machine (ELM) and standard RVM. This study aims to create a system that can automatically recognize and classify WBCs from blood images. This technology takes advantage of the high-resolution and customizable extracted qualities of the White Blood Cell Hematological Diseases Classification (WBC_HDC) network to enhance classification productivity and accuracy.

The following are some highlights of this work's goals and contributions:

- Proposing, evaluating, and implementing an effective WBC_HDC network.
- Several experiments are applied to enhance confidence in the classification decision by verifying the suggested model parameters.
- This study presents in-depth research that offers a comprehensive system for classifying WBC. This can help in diagnosis easier and take less time for doctors, researchers, healthcare professionals, and medical laboratory staff.

2. The Methodology and Materials:

2.1 Clinical dataset

The suggested WBC_HDC network is designed to classify four types of blood diseases related to white blood cells. This program has used the diagnosis of diseases easily with less time means. 2.800 images of WBCs have been used. A dataset that employed the Cell _ Vision DM96 analyser in the Barcelona Hospital Clinic's (BHC) Laboratory has been used. The dataset is divided into four categories: Erythroblasts, Immature Granulocytes (IG), Lymphocytes, and Monocytes. Expert clinical pathologists classified the images, to a resolution of 363x360x3 pixels. The individuals didn't have any hematologic disorders, infections, or other diseases at the time of blood collection. They were also not receiving any medication.

2.2 Classification models

The WBC_HDC model was used to classify the four blood diseases based on white blood cells in a new way. High classification accuracy is the goal of designing and implementing the WBC_HDC network. In essence, this task is divided into several logical steps. First, a comprehensive hematopoietic picture examination is compiled and presented. In addition, both the training test phases use a different set of discrete images. Basically, at this stage, the model is checked. All network parameters are evaluated using the tested collection of images after being trained using the trained set of images. This can improve classification accuracy and account for the output of the WBC_HDC network layers. As shown in Figure 1.

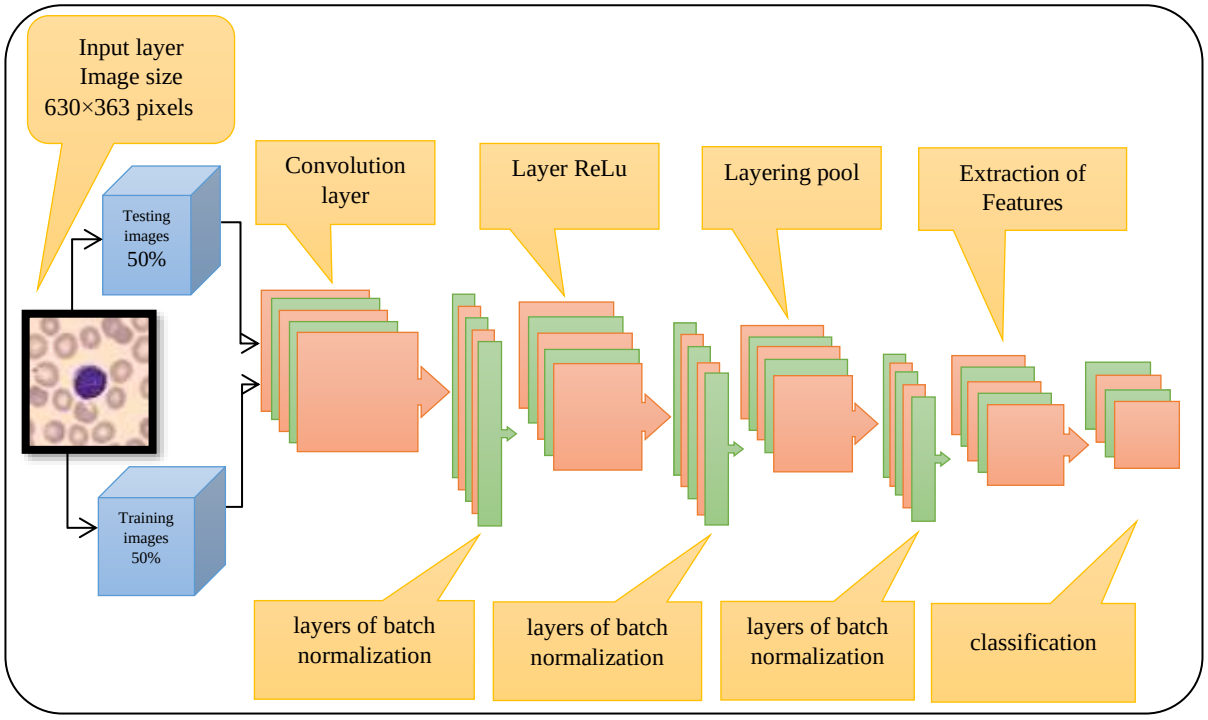

Figure 1: the importance, necessary processing steps are shown, along with a completely recommended system.

The following formula [9] is used to determine the feature map values:

$$F_{u,v,c^l} = U_{c^l} + \sum_{i=-H_h^l}^{H_h^l} \sum_{j=-H_w^l}^{H_w^l} \sum_{c^{l-1}=1}^{c^{l-1}} W_{i+H_h^l, j, H_w^l, c^{l-1}}^{c^l} F_{u+i,v+j,c^{l-1}} \quad (1)$$

F_{u,v,c^l} is the convolution layer's output, (u,v) is the pixel's coordinate, U_{c^l} is the channel bias, $W_{i,j,c^{l-1}}^{c^l}$ is the kernel weights, c is the channel number, H_w^l and H_h^l are the width and height of the convolution layer kernel, respectively, l is the current layer, and $l-1$ is the previous layer.

Each channel picture can be filtered using preset kernel values, also known as weights. By utilizing several kernels for each channel, numerous feature maps may be produced. Various filtering analyses may be provided in this case for each channel picture. Convolution operations can be implemented using a variety of filter sizes, filter numbers, padding, and stride parameters [10].

$$R_{u,v,c^l} = \max(0, F_{u,v,c^l}) \quad (2)$$

Where: Max is the maximal operation, F_{u,v,c^l} is a positive input value to the ReLU activation function, and R_{u,v,c^l} is the output of ReLU [10].

Information gets down-sampled when it is pooled. This layer can further reduce the spatial dimensions but not the depth. It is introduced following convolution operations, more especially following ReLU's nonlinearity. It uses every feature map independently and generates a fresh set of feature maps [11]. A pooling operation's size must be less substantial than a feature map's. This causes each prior feature map's pixel count to decrease eliminating overfitting. The pooling layer can aid in lowering the size of feature maps and improving performance [12] within the model. There are two popular pooling types:

❖ **Maximum Pooling (MP):**

In every preceding feature map, it determines the down sampling values of tiny matrices

(windows). The corresponding equation [13] indicates that the MP performance is wise:

$$T_{n^l,m^l,q\ Max} = \underset{0 \le n < ph, 0 \le m < p_w}{\text{MAX}} R_{n^l \times ph+n, m^l \times p_w + m, q} \quad (3)$$

Place: $k\,n^l, m^l, q\ Max$ is an output of the pooling layer with maximum type, where $0 \le n^l < p_h^l$, p_h^l, $0 \le m^l < p_w^l$, p_w, $0 \le q < q^l = q^{l-1}$, p_h is the height of each pooled window, and p_w is the width of each pooled window.

- **Average Pooling (AP):**

It determines the down-sampling feature map. In accordance with the simultaneous equation [14], the AP pretence is practical:

$$f_{ave}(R) = \frac{1}{S \times S} \sum_{i=1}^{s} k_i \quad (4)$$

Where S is the size of the pooling area, k_i is the output ReLU, and f_{ave} is an output of the average or max type pooling layer.

Each node from a previous layer is connected to every node in this layer via the FC layer. It adjusts between a DL model's feature extraction part and the classification part's respective node counts. The following equation will determine the composition of the layer's output:

$$Z_r = \sum_{n=1}^{n_1^{l-1}} \sum_{m=1}^{n_2^{l-1}} \sum_{q=1}^{n_3^{l-1}} U_{n,m,q,r}^{l} (T_s)_{n,m} \quad \forall 1 \le r \le n^l \quad (5)$$

$n_1^{l-1}$is the previous pooling channel width, $n_2^{l-1}$is the previous pooling channel height, $n_3^{l-1}$is the number of previous pooling channels, and Z_r is the output of the FC layer. A pooling layer output is $(T_s)_{n,m}$ and $U_{n,m,q,r}^{l}$Between the pooling and FC layers, there is a weight called l, and the necessary number of classes is n^l.

Typically, the softmax layer is put right before the classification layer, which is the final layer. The softmax offers the corresponding probability distributions for all output classes for a given input [15]. The softmax function is represented mathematically as stated in the following equation:

$$N_r = \frac{exp\,(Z_r)}{\sum_{s=1}^{n^{l-1}} exp\,(Z_s)} \quad (6)$$

Where: The softmax layer's output is N_r. The softmax function, in other words, normalizes the output values of each node to lie between 0 and 1. Each output value is divided by the sum of all the other output values.

The last layer is the classification layer. It assigns a specified input to the class that is the closest. It generates the result [6]. This layer's functionality may be explained as follows:

$$X_r = \begin{cases} 1 & if\ N_r = max \\ 0 & otherwise \end{cases} \quad (7)$$

The highest value of X_r represents the winning class for the classification of WBCs for the four diseases of the WBC_HDC network.

4.Results and Discussions

4.1 Real clinical data classify

Classification of the real clinical dataset for four groups (Erythroblast, Lymphocytes, Monocytes, and Immature IG) has been done with the WBC_HDC network in MATLAB. Data were processed using grid WBC_HDC. The data set includes 2800 images containing all the mentioned diseases. Each slide is 360×363×3 pixels, is in JPE format, and includes a collection of color images. Figure 2 displays hematology samples for WBCs. In this work, the training sets of images are first used to train the WBC_HDC network. Second, the tested image sets are used to test the trained networks. The parameters of each network's layers are used to gauge how accurate the network is. The following computer specifications were used to develop, train, and test the proposed network: Intel Core (TM) i5, 3 GHz, and 8 GB of RAM in an HP laptop. Every program runs using the CPU as its foundation. To sum up, the WBC_HDC network that has been suggested may be compared to various AI models found in [16-17]. They may be applied to significant tasks like [8][18].

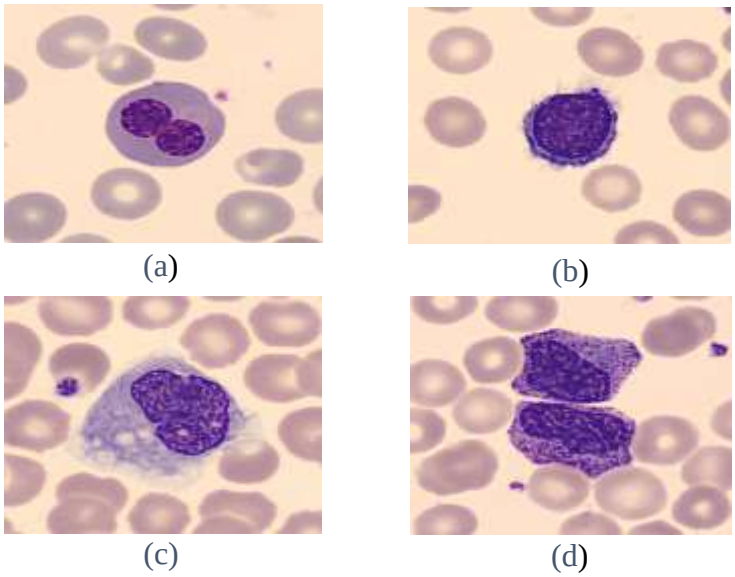

Figure 2: Haematology samples for white blood cells (a) Erythroblast, (b) Lymphocyte, (c) Monocyte, (d) Immature Granulocyte (IG)

4.2 White Blood Cell Hematological Diseases Classification (WBC_HDC) network

Every layer in the proposed WBC_HDC network is a detection of WBCs features. The convolution and pooling layers of the WBC_HDMC network are the main layers that hold the crucial factors that might affect the outcomes. For the convolution layer, we examine several choices for the filter/kernel size, filter count, stride, and padding parameters. Different settings for the pooling layer's type, window size, stride, and padding parameters are assessed. Fig. 3 displays the results of WBC_HDC testing after adjusting or altering the relevant parameters to make the recommended WBC_HDC network work with Hight efficiently as possible.

In the first case, Fig. 3 illustrates that switching the filter size from 3 x 3 pixels to 13 x 13 pixels, 3 x 3 pixels recorded the highest accuracy obtained 81.43%, after analyzing the image by WBC_HDC network [19]. This value is taken into account while evaluating the second convolution layer parameter. The second case involves testing the number of filters, which ranges from 2 to 14. It has been observed the network reached the best result with 6 filtrations and recorded an accuracy of 88.00%. In the third case, the stride convolution layer of the filter was examined, with its values reduced from 1 pixel to 5 pixels (both horizontally and vertically). The maximum accuracy record was 88.36%. It has been obtained with the best number of strides equal to 2. Case 4 focuses on altering the convolution layer's padding procedure. In convolution processes, that are conducted for particular widths of the kernel and the input channel. Its value might range from 1, 2,..., or Same (S) pixels. In other words, S indicates a boundary size of pixels that is automatically calculated by copying the latest values, whereas any integer number represents a border size of pixels with zero values. Every padding value other than 0 pixels has a detrimental impact on performance by lowering accuracy percentages, with the maximum accuracy measured at 88.79%. Case five involves switching between the pooling layer's Maximum (Max) and Average (Ave) types. Applying the Ave type causes the accuracy to drop to 86.43%, as can be seen. As a result, the Max type is used as a benchmark since it provided the highest figure, 88.79%. This is the result of Max pooling's capability to extract the most significant components required to choose the best features for

classifying WBCs. In case six, the pooling filter's size is modified. The accuracy is evaluated using a range of window sizes, from 3 x 3 pixels to 13 × 13 pixels. It can be concluded that a resolution of 13 x 13 pixels yields the best outcome, which is 89.79%. The previous dimension of feature maps appears to be reduced with this pooling window size, but the patterns of employed feature extraction are maintained. Case seven changes the pooling stride from one to seven pixels (horizontally and vertically). This procedure can specify how many pixels in a feature map overlap between the pooling windows. The 2 pixels have been recorded highest accuracy. This stride value provides the proper overlaps between the occurrences of the features. The padding settings of 0 to S pixels are examined in case eight. The padding 3-pixel value, the appropriate accuracy of an instrument in this situation, is said to provide the best accuracy. The width of a feature map grows overall when increasing padding values, and width frequently contains unwanted information. As a result, this can make the WBC_HDC network perform worse. After the applied experiments, the following parameters produced the highest accuracy: Max pooling type; 3 x 3 pixels for the convolution filter size; 6 convolution filters; 2 stride pixels for the convolution kernel; 0 padding pixels for the convolution and pooling slayers; and 13 x 13 pixels for the size of the pooling window.

The WBC_HDC can be considered one of the suggested techniques in [20-23]

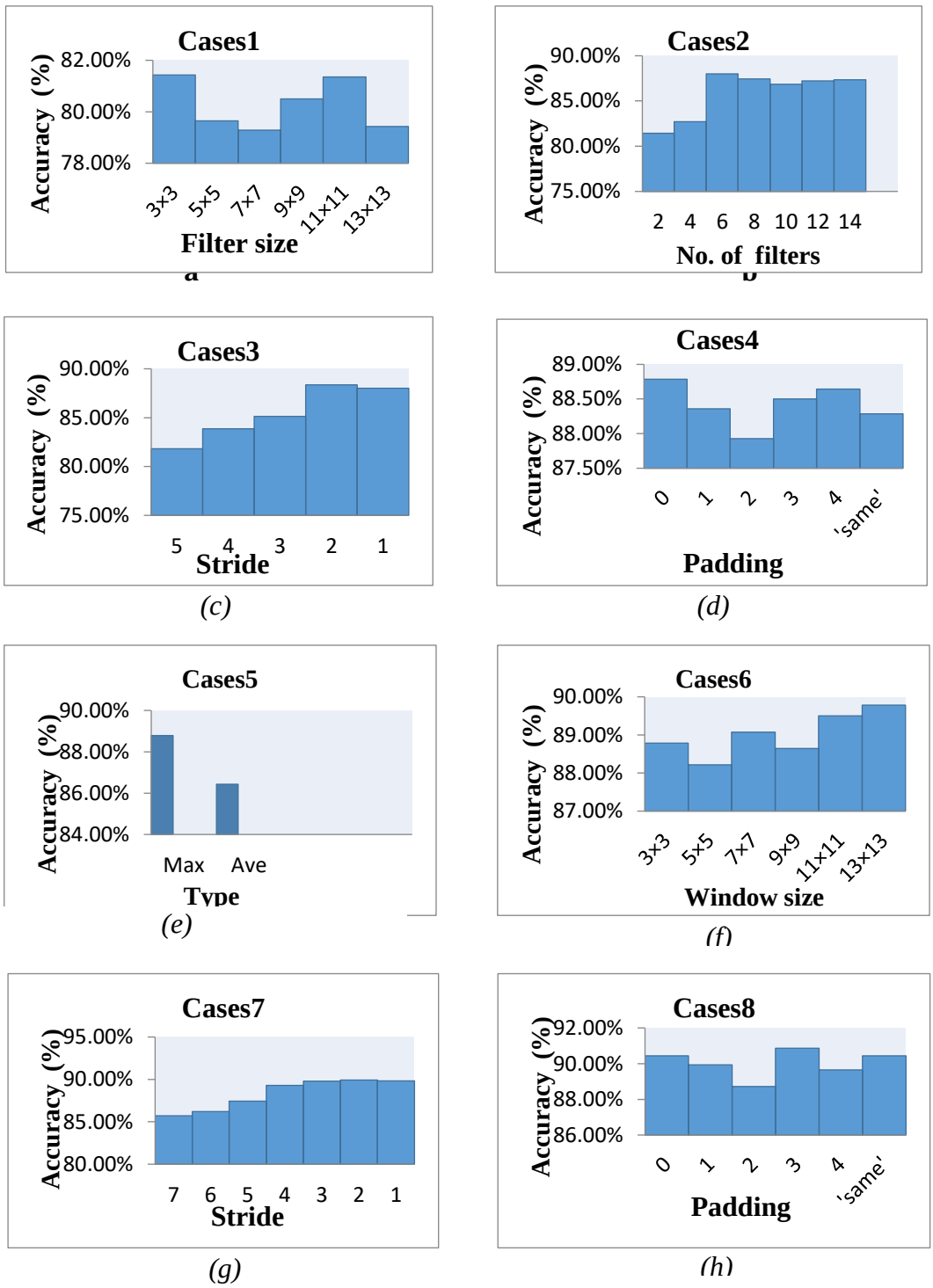

Figure 3: Additional demonstrations to evaluate the performances of changing different WBC_HDC parameters the parameters are for the convolution layer: (a)filter size, (b) number of filters, (c) stride and (d) padding, and for the pooling layer: (e) type, (f) window size, (g) stride and (h) padding

5. Conclusion

A brand-new, comprehensive classification WBCs with a WBC_HDC network is developed in this study. The planned structure has several processing steps: First, WBCs images have been collected from four groups. Then, based on deep learning, the WBC_HDC network classifies the images after splitting the images into training and testing phases. Then, all the parameters between the layers have been examined to record the best result. The network recorded an accuracy of 90.86%. The

topic of this study can assist medical practitioners, researchers, and lab staff in and simpler classifying WBCs.

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