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Identification of White Blood Cells using Convolutional Neural Network: A Review

Miss. S. D. Maske[1] and Prof. V. K. Shah[2]

Research Scholar, Electronics and Communication, M. S. Bidve Engineering College Latur,India[1]

Professor, Electronics and Communication, M. S. Bidve Engineering College Latur,India[2]

Abstract: *A blood sample usually contains red blood cells, white blood cells, and platelets. White blood cells, also called white blood cells, are cells of the immune system. White blood cell measurements are very important for doctors diagnosing various diseases such as leukemia and tissue damage. Therefore, white blood cell count plays an important role. Manual counting of white blood cells in medical laboratories is done using a device called a hemacytometer. However, this process is very tedious, time consuming and gives inaccurate results.*

This study uses image processing and deep learning mechanisms to locate leukocytes and classify them based on their categories. The typed white blood cells are counted and compared to a standard range of types available in human blood samples. By comparing the availability of leukocyte types, normal and abnormal blood samples are predicted accordingly. The dataset of normal blood samples was obtained from the laboratory of the Faculty of Biotechnology, and the dataset used for training the convolutional neural network was obtained from his website for Leukocyte Images for Segmentation and Classification (LISC). increase. This increases efficiency and reduces the burden on clinicians, as traditional manual counting can be tedious, monotonous and subjective.

Keywords: RBC (Red Blood Cell), WBC (White Blood Cell), Leukocyte, leukemia etc

I. INTRODUCTION

Image processing involves manipulating an image to achieve certain aesthetic standards or to support a desired representation. It also serves as a means of converting between the human visual system and digital imaging devices. Notable disparities exist between human and digital detectors, necessitating translation techniques. To ensure reproducibility, image processing should adhere to the scientific method. Human blood comprises three types of cells: red blood cells (RBCs), white blood cells (WBCs), and platelets. WBCs, also known as leukocytes or leucocytes, play a crucial role in the immune system's defense against infectious diseases and foreign invaders. They are derived from hematopoietic stem cells in the bone marrow. WBCs encompass five subcategories: monocytes, lymphocytes, eosinophils, basophils, and neutrophils. In a normal adult, the differential WBC count is as follows:

- Neutrophils: 40 – 70%
- Lymphocytes: 20 – 30%
- Monocytes: 2 – 15%
- Eosinophils: 1 – 7%
- Basophils: 1 – 3%

The count of leukocytes in the blood often serves as an indicator of disease, and the WBC count is an important subset of the complete blood count. The typical range for WBC count is between 4 x 10^9/L and 11 x 10^9/L. Counting WBCs can be performed manually or automatically. Automatic methods are employed for counting large numbers of cells but can be expensive due to specialized equipment. Manual methods involve the use of a conventional light microscope setup, which is more challenging, prone to errors, and cost-effective.

The percentage ranges provided for each WBC subtype represent typical values found in the blood of a healthy individual. Deviations from these ranges can indicate various diseases. For instance, an elevated monocyte and eosinophil count may suggest a bacterial infection. An increased lymphocyte count could indicate AIDS (Acquired

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Immune Deficiency Syndrome), while a high neutrophil count may suggest cancer. Therefore, developing an accurate method for classifying and counting WBCs according to their subtypes is of significant importance.

Traditionally, WBC classification and counting have been performed manually by hematology experts using microscopes. However, this procedure is time-consuming and prone to errors due to its complexity. In the field of image processing, various research and alternative methodologies have been proposed for WBC classification and counting. While some of these methods achieved accurate results in WBC counting by utilizing techniques such as fuzzy c-means and snake for WBC segmentation, color space conversion with Otsu's algorithm, machine vision systems, and k-means clustering, their primary focus was on determining the number of WBCs. Other research aimed to develop methodologies that could perform both counting and classifying of WBCs by their subtypes. Although these methods show promise, there is still room for improvement in achieving more accurate results.

This research aims to introduce an innovative approach that can simultaneously segment, classify, and count WBCs in microscopic blood images. The proposed method builds upon the authors' previous study, which successfully segmented WBCs using the saturation component of the HSV color model and blob analysis. It also incorporates convolutional neural networks (CNNs) for classification and counting.

In summary, white blood cells (WBCs) play a crucial role in the immune system, defending the body against infections and foreign materials. Different types of WBCs have distinct functions, such as recognizing intruders, killing harmful bacteria, and producing antibodies to protect the body against bacteria and viruses.

II. LITERATURE REVIEW

Rosyadi et al. conducted a research that is able to classify WBC from blood cell images taken from blood smear samples using digital microscope. The researchers utilized Otsu threshold method for segmentation and K-Means clustering method for classification. Based on their research it was concluded that upon execution of k-means clustering to classify and count WBC, the most significant geometry feature is its circularity generating an accuracy of 67%

Alternatively, Gautam et al. proposed a method which utilizes Naïve Bayes classifier and morphological features to classify WBC. The features which the researchers used to train their system were; area, eccentricity, perimeter and circularity. The proposed method was able to generate 80.88% accuracy [11]

In the pursuit to further improve the accuracy of previous papers, Yu et al. proposed a method which uses CNN to automatically classify WBCs. The researchers utilized the network architectures; ResNet50, Inception V3, VGG 16, VGG 19, and Xception. The proposed method was able to generate an accuracy of 88.5% [10].

Recently, the study on the field of CNN showed to be increasingly significant in the advancement of image classification. There have been various types of CNN that was used by previous researchers. However, recent models proved to be more efficient on the improvement of image classification accuracy specifically on tasks such as object detection and segmentation. Thus, the proposed method in this paper utilized the models AlexNet, ResNet101, and GoogleNet for WBC classification. AlexNet was a winning model in the ILSVRC 2012 (ImageNet Large Scale Visual Recognition Challenge), GoogleNet is the winner of ILSVRC 2014 [13], and ResNet with 152 layers won ILSVRC 2015 [14].

Yuehua Liu, Feilong Cao, Jianwei Zhao, and Jianjun Chu [1] introduced a new approach for locating the WBC and sub image segmentation. It is noted that almost all the WBCs have two characteristics 1) The compactness of edges in the edge map produced using the Canny detector is always concerted I regions with WBCs.

III. PROPOSED SYSTEM

This section provides the detailed description of the proposed Estimation of White Blood cells using image processing techniques. The microscopic image of the blood sample is taken as the input where blood samples contains RBCs, WBCs and platelets. The first step involved is preprocessing where the RBCs and platelets are removed.

The proposed system works as follows.

A. Preprocessing : Preprocessing step involves

1. Removal of RBCs
2. Removal of Platelets

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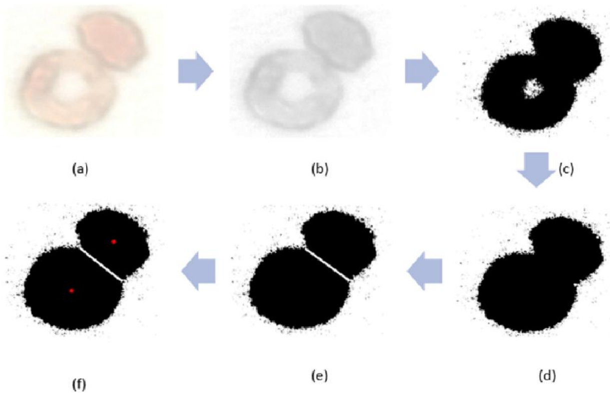

Figure 3.1 Removed RBC image and Located WBC

B. Classification of WBC

The classification of WBC is performed by Convolutional Neural Network. The 5 types of WBC images are trained by the layers available in CNN and the features are extracted accordingly

The located WBC in a window is given as the input to the trained CNN and the particular type located is classified.

Layers used in CNN are

1. Input Layer
2. Convolution Layer
3. Batch Normalization Layer
4. Rectified Linear Unit Layer
5. Max Pooling Layer
6. Fully Connected Layer
7. Softmax Layer
8. Classification Layer

IV. DESIGN OF CNN-BASED CLASSIFIERS

CNNs use feedforward methods to feed neurons and backpropagation to train parameters. A major advantage of the CNN approach is that it can automatically extract topological features from raw grayscale images and generate predictions for classifying high-dimensional patterns. A CNN consists of two distinct parts. The first part consists of several layers that extract features from the input image pattern through a combination of convolutional and subsampling layers. Conceptually, visual features are extracted from the local receptive field [15] by an extended 2D convolution approach to obtain the corresponding spatially local correlations present in the input image. Since the exact location of the extracted features is not important or essential, the subsampling layer only reduces the resolution of two of the features. The second unique part classifies patterns into classes.

CNNs generally consist of three different layers: a convolutional layer, a subsampling layer (maximum pooling), and an ensemble of fully connected layers. In our current work, we use a CNN with the architecture of LeNet5 [15] (see Fig. 5).

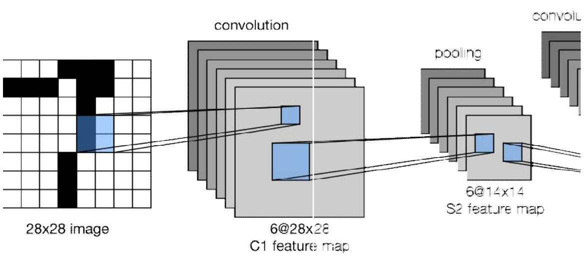

Fig. 5. LeNet-5 structure in modelling *CNN* for a 28×28 input image

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In the first layers (properties extractors) convolutional filters in a 5×5 pixels window are applied over the image. It is highly recommended to add two blank pixels at each four directions to avoid missing real data at each border in convolution computations.

The number of alternative three main layers depends on input database and can be varied between different input size to get better performance and confidence. In this work a LeNet5 with eight layers is used (including first layer as input gray-scale image and also output layer). Each convolution layer (C-layers) has different feature maps, C1 is composed of 6 units while C3 has 16 and C5 has 120 units. Also because of convolution windows size (5×5) and input size (28×28), the size of each convolution layer is defined as shown in Fig. 3: C1 is 28×28, C3 10×10, and C5 is 1×1, a single neuron.

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