White Blood Cell Classification Based on Shape and Deep Features

Abdulkadir Şengür[1]
Electrical & Electronics Eng.
Firat University
Elazığ, Turkey
ksengur@gmail.com

Yaman Akbulut[2]
Electrical & Electronics Eng.
Firat University
Elazığ, Turkey
yamanakbulut@gmail.com

Ümit Budak[3]
Electrical & Electronics Eng.
Bitlis Eren University
Bitlis, Turkey
umtbudak@gmail.com

Zafer Cömert[4]
Software Engineering
Samsun University
Samsun, Turkey
comertzafer@gmail.com

***Abstract*—Classification of the white blood cells (WBCs) in blood smear images is essential for providing important information to the physicians. In addition, manual analyzing of the blood smear images for determining the various WBCs is a time-consuming issue for the physicians. In this paper, a hybrid method is proposed for the classification of the WBCs. Image processing (IP) and machine learning (ML) are used to determine and classify the WBCs in blood smear images. In the IP perspective, various IP algorithms are used to segment the WBCs and in ML perspective, feature extraction and classification are employed. RGB to HSV transformation, color to gray tone conversion, filtering operations, thresholding, and morphological processes are used for determining the WBCs. Median filtering and adaptive histogram equalization are used for filtering and image enhancement and Otsu thresholding is considered for thresholding due to its simplicity. Shape based features and deep features are used for characterization of the WBCs and long-short term memory (LSTM) network is employed for classification. A dataset containing totally 349 blood smear images is considered in the evaluation of the proposed method. 10-fold cross validation is used in experiments and classification accuracy is calculated accordingly. While the shape based features produce 80.0% accuracy, deep features obtain 82.9% accuracy. When both shape and deep features are concatenated, 85.7% accuracy score is obtained.**

***Index Terms*— WBCs, shape features, deep features, LSTM network.**

I. Introduction

White blood cells (WBCs) recognition is an important topic for the diagnosing of many diseases in peripheral blood. There are five different types of WBC in blood. Their names are Basophil, Eosinophil, Lymphocyte, Monocyte, and Neutrophil [1]. The number of WBCs in peripheral blood gives us clues about disorders. The shape and the size of those cells also help us to diagnose the disorders.

In the open literature, there have been so many works about the WBCs classification. Gupta et al. [2] proposed an optimized binary bat algorithm for classification of WBCs. Researchers were optimized the algorithm by using some of the well-known machine learning classifiers. The most discriminative features were efficiently selected in the proposed method; therefore, it achieves the high accuracy rate for diagnosis of the disorders. Wang et al. [3] proposed a spectral and morphological method based on blood images for identification of WBCs. The proposed method reached a higher accuracy of more than 90% since it combines both spatial and spectral features. Lopez-Puigdollers et al. [4] proposed a method that recognizes the WBCs on blood images by using local image descriptors and bag of words. The researchers investigated local image descriptors and sampling strategies. Tiwari et al. [5] developed a deep learning algorithm based method to automatically classify the WBCs. As a Deep Learning (DL) algorithm, Convolutional Neural Networks (CNN) was used due to its ability to handle a huge number of images. The proposed CNN based method called Double Convolution Layer Neural Networks (DCLNN). The researchers compared the proposed DCLNN method with Support Vector Machines (SVM) and Naive Bayes (NB). The proposed DCLNN method outperformed higher accuracy and precision than SVM and NB. Researchers claim that the proposed DL model may implement on a large dataset. Shahin et al. [6] proposed a DCNN based approach to identify the WBCs. As they used transfer learning methodology, pre-trained networks were used to extract deep activation features. Experiments were carried out on three public datasets. The overall system accuracy was achieved higher accuracy than the other transfer learning based methods and traditional identification systems. Nazlibilek et al. [7] proposed a system, which is automatically segmented, and classify the WBCs into five types. Neural network based classifiers were employed for classification. As an advantage of the proposed system, traditional methods need the operator's expertise and blood specimen but the proposed system uses the blood smear images. The principal component analysis (PCA) was applied to reduce the dimension of the dataset therefore; the classification performance of the proposed system was increased. Silva et al. [8] proposed a radial feature descriptor (RFD) to classify the blood cells as normal or abnormal. To evaluate the cell classification, two datasets were considered for experiments. 14 different descriptors including RFD were compared by using the same two CNN classifiers. Zheng et al. [9] proposed a method to segment the WBCs. It has a feature vector by using topological structure and enhancement of boundaries. To evaluate the performance of the proposed method, extensive experiments have been carried out on different real datasets. Ghosh et al. [10] designed an automatic system, called analyzer,

to count WBCs in blood smear images. The analyzer system does not need a blood specimen and the operator's expertise. After preprocessing, the analyzer system uses four classification approaches based on color feature, size feature, shape feature, and texture feature. Then, the system combines four classification results into the final classification.

In this paper, a hybrid method is proposed for the classification of the WBCs. IP is used to segment the WBC as a foreground object. To this end, RGB to HSV color space transformation, color to gray tone conversion, filtering operations, thresholding, and morphological processes are used. Median filtering and adaptive histogram equalization are used for filtering and image enhancement and Otsu thresholding is considered for thresholding due to its simplicity. Shape-based features and deep features are used for characterization of the WBCs. Hierarchical centroid features and deep features are extracted. The hierarchical centroid features are also known as the binary shape descriptors that are built with the centroid coordinates extracted from a binary image. kd-tree decomposition technique is used in hierarchical centroid feature extraction. ResNet model is considered as the pre-trained CNN model [11]. The fc1000 fully connected layer is used to acquire 1000-dimensional feature vector. Deep features both contain texture and color information. A dataset containing totally 349 blood smear images is considered in the evaluation of the proposed method. 10-fold cross validation is used in experiments and classification accuracy is calculated accordingly. While the shape based features produce 80.0% accuracy, deep features obtain 82.9% accuracy. When both shape and deep features are concatenated, 85.7% accuracy score is obtained.

The rest of the paper is organized as follows. Next section introduces the proposed method. The details about the proposed method are described and illustrated. Section 3 gives the experimental works and results. The concluding remarks are given in Section 4.

II. Proposed Method

The proposed WBCs classification method is composed of three layers. The first layer is developed to extract the region of interest (ROI) as shown in Fig. 1. In other words, the WBCs region determination is carried out in the first layer of the proposed method. In ROI extraction, the RGB blood smear image is read initially and then converted to the HSV color space. The S channel of the HSV color space is kept for further processes. The S channel of the HSV color space is chosen because the contrast between WBC region and the other regions is quite high. The contrast in S channel is further adjusted and then median filtered, respectively. These processes make the S channel more convenient before thresholding operation. The ROI extraction is handled with simple thresholding. The unwanted binary noises are removed with morphological processes.

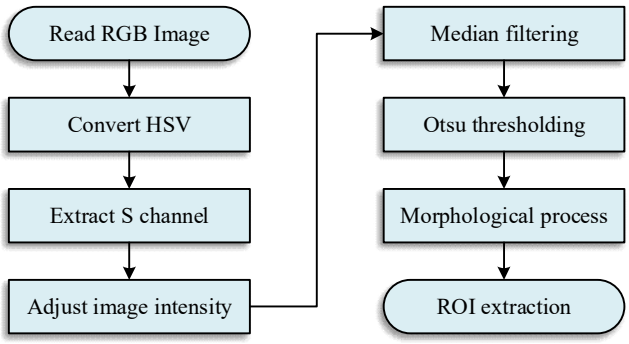


Fig. 1. The ROI extraction layer of the proposed method.

After ROI is detected, hierarchical centroid features and deep features are extracted. The feature extraction is in the second layer of the proposed method. The hierarchical centroid features are also known as the binary shape descriptors that are built with the centroid coordinates extracted from a binary image. kd-tree decomposition technique is used in hierarchical centroid feature extraction. For hierarchical centroid feature extraction, the binary image is recursively decomposed into sub-images by the kd-tree method. Readers may refer to [12] for detailed information about hierarchical centroid feature extraction method. The hierarchical centroid features are 60 dimensional. Besides shape descriptors, the color and texture based features are extracted by using deep feature extraction. More specifically, a fully connected layer of a pre-trained CNN model is used for deep feature extraction. Deep features both contain the texture and color information and are quite efficient in object recognition. To this end, the ResNet model is considered as the pre-trained CNN model. The fc1000 fully connected layer is used to acquire 1000-dimensional feature vector for each blood smear image. The PCA is then used to reduce the dimension of the deep features. In the classification layer of the proposed scheme, the LSTM network is considered. The LSTM network is used classifier of the proposed scheme. LSTM network is quite efficient in the classification of the complex systems. It can be seen as a type of recurrent neural networks (RNNs). The memory block, which is a new structure, is the difference between the LSTM model and the RNN model. The memory block consists of four main elements, namely, input gate, memory cell, forget gate and output gate. The memory cell element contains a self-recurrent connection. Gates of the memory cells which change the state of the signal while allowing or blocking the output gate prevents the state of the memory cell to have an effect on the rest of the network or avoided. The forget gate allows the memory cell to forget its previous state when the information stream is out of date. Fig. 2 shows the second and third layers of the proposed method.

It is worth mentioning that the determined binary ROI is used for hierarchical centroid feature extraction and the ROI region that is superimposed on RGB image is used for deep feature extraction.

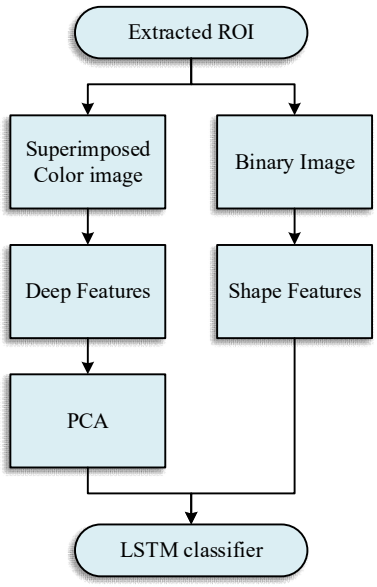


Fig. 2. The second and third layers of the proposed method.

III. Experimental Works and Results

The WBCs dataset, which was used in our experiments, was downloaded from the Kaggle web site [13]. The dataset contains two folders where folder 1 contains 410 original blood smear images and folder 2 contains 12,500 augmented blood smear images. There are 4 different WB cell types namely Eosinophil, Lymphocyte, Monocyte, and Neutrophil. In our experiments, we opted to use original dataset (410 images) and after elimination of the non-labeled and degraded images, we have totally 349 blood smear images. 207 blood smear images contain Neutrophil cells, 88 blood smear images contain Eosinophil cells, 33 blood smear images contain Lymphocyte and 21 blood smear images contain Monocyte cells. Fig. 3 shows sample WBCs.

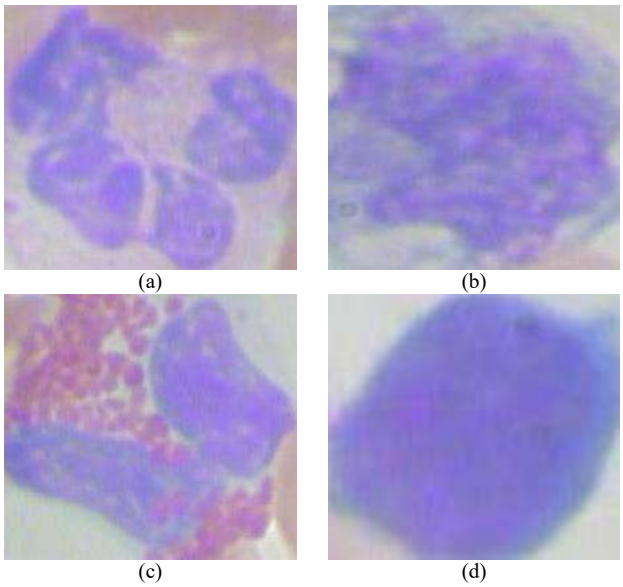


Fig. 3. Sample WBCs, a) Neutrophil, b) Monocyte, c) Eosinophil and d) Lymphocyte.

As it was mentioned earlier, shape, texture and color features are extracted from the WBCs and LSTM network is used for classification. For shape feature extraction, the hierarchical centroid approach is used and for texture and color feature extraction, a pre-trained deep CNN model is considered. The shape features are 60 dimensional and the CNN features are 1000 dimensional. The dimensions of deep features are reduced to 60 by PCA for the sake of convenience with shape features. These feature vectors are fed into the LSTM network. The input sequence size of the LSTM is set to 60. The bidirectional LSTM layer with an output size of 150 is used. The fully connected layer of LSTM network was set to 4, and a softmax layer is used after fully connected layer. "ADAM" solver was chosen as a training method for LSTM. The gradient threshold of the LSTM network is set to 1. The mini-batch size of the LSTM network is used as 10. The initial learning rate of the LSTM network is chosen to 0.01. The learning rate is dropped with a dropped factor 0.001 during the training with 50 epoch periods. Classification accuracy, which is defined as the ratio of number of correctly classified samples to the number of total samples, is calculated as following;

$$Accuracy(\%) = \frac{N_c}{N_t} \times 100 \qquad (1)$$

where N_c indicates the number of correctly classified WBCs and N_t is the number of total WBCs. 10-fold cross validation is used in experiments and classification accuracy is calculated accordingly. While the shape based features produce 80.0% accuracy, deep features obtain 82.9% accuracy. When both shape and deep features are concatenated, 85.7% accuracy score is obtained. The shape features achievement (confusion matrix) is shown in Table 1. As seen in Table 1, while 5 of the 9 Eosinophil cells are classified correctly, 4 of the 9 Eosinophil cells are classified as Neutrophil cell. Similar, 1 of the 3 Lymphocyte cell is classified as Eosinophil cell. The classification accuracy for Monocyte cells is 50%. The best classification accuracy of 95.2% is obtained for Neutrophil cells. Only 1 Neutrophil cell is wrongly classified.

TABLE I. Performance Prediction of Shape Features

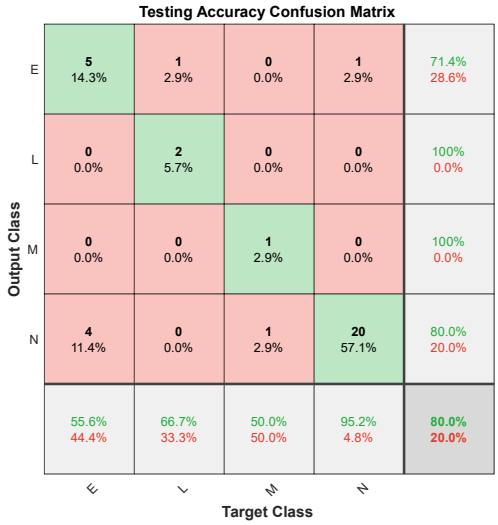


Table 2 shows the confusion matrix for deep features. The overall classification accuracy for deep features is 82.9%. Eosinophil cells are classified with 100% accuracy and none of the Monocyte cells are classified correctly. 3 of the Neutrophil cells are classified as Eosinophil cell. The classification accuracy for Lymphocyte cells is 66.7%.

TABLE II. PERFORMANCE PREDICTION OF DEEP FEATURES

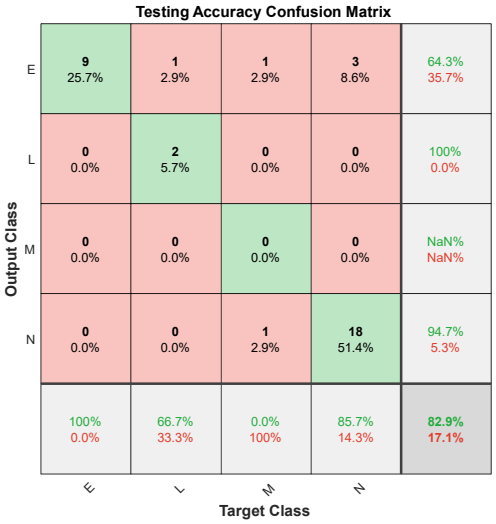
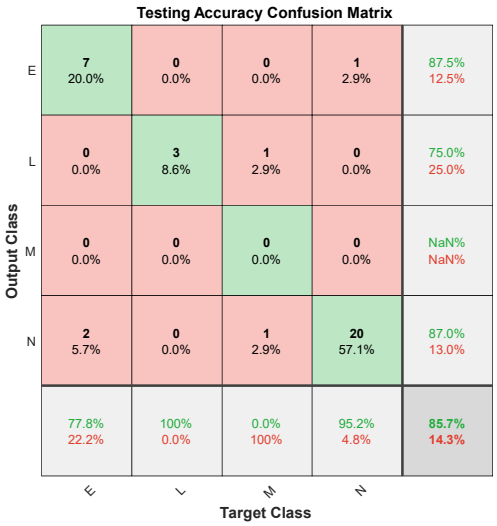


Table 3 shows the confusion matrix for concatenated features. The overall classification accuracy for deep features is 85.7%. Eosinophil cells are classified with 77.8% accuracy and none of the Monocyte cells are classified correctly. All Lymphocyte cells are classified correctly and the classification accuracy for Neutrophil cells is 95.2%.

TABLE III. PERFORMANCE PREDICTION OF CONCATENATED FEATURES



IV. CONCLUSIONS

Automatic classification of WBCs is important for the determination of the various diseases. Researchers generally used shape and texture features for the characterization of the WBCs. In this paper, WBCs classification is achieved with a hybrid approach. Shape and reduced deep features are combined. LSTM network is used for classification. A dataset containing totally 349 blood smear images is considered in the evaluation of the proposed method. 10-fold cross validation is used in experiments and classification accuracy is calculated accordingly. While the shape based features produce 80.0% accuracy, deep features obtain 82.9% accuracy. When both shape and deep features are concatenated, 85.7% accuracy score is obtained.

REFERENCES

[1] Hegde, R. B., Prasad, K., Hebbar, H., & Singh, B. M. K. (2019). Comparison of traditional image processing and deep learning approaches for classification of white blood cells in peripheral blood smear images. Biocybernetics and Biomedical Engineering, 39(2), 382-392.

[2] Gupta, D., Arora, J., Agrawal, U., Khanna, A., & de Albuquerque, V. H. C. (2019). Optimized Binary Bat Algorithm for classification of White Blood Cells. Measurement.

[3] Wang, Q., Chang, L., Zhou, M., Li, Q., Liu, H., & Guo, F. (2016). A spectral and morphologic method for white blood cell classification. Optics & Laser Technology, 84, 144-148.

[4] Lopez-Puigdollers, D., Traver, V. J., & Pla, F. (2019). Recognizing white blood cells with local image descriptors. Expert Systems with Applications, 115, 695-708.

[5] Tiwari, P., Qian, J., Li, Q., Wang, B., Gupta, D., Khanna, A., ... & de Albuquerque, V. H. C. (2018). Detection of subtype blood cells using deep learning. Cognitive Systems Research, 52, 1036-1044.

[6] Shahin, A. I., Guo, Y., Amin, K. M., & Sharawi, A. A. (2017). White blood cells identification system based on convolutional deep neural learning networks. Computer methods and programs in biomedicine.

[7] Nazlibilek, S., Karacor, D., Ercan, T., Sazli, M. H., Kalender, O., & Ege, Y. (2014). Automatic segmentation, counting, size determination and classification of white blood cells. Measurement, 55, 58-65.

[8] Silva, R. R., Araujo, F. H., Ushizima, D. M., Bianchi, A. G., Carneiro, C. M., & Medeiros, F. N. (2019). Radial Feature Descriptors for Cell Classification and Recommendation. Journal of Visual Communication and Image Representation.

[9] Zheng, X., Wang, Y., Wang, G., & Liu, J. (2018). Fast and robust segmentation of white blood cell images by self-supervised learning. Micron, 107, 55-71.

[10] Ghosh, P., Bhattacharjee, D., & Nasipuri, M. (2016). Blood smear analyzer for white blood cell counting: a hybrid microscopic image analyzing technique. Applied Soft Computing, 46, 629-638.

[11] He, Kaiming, Xiangyu Zhang, Shaoqing Ren, and Jian Sun. "Deep residual learning for image recognition." In Proceedings of the IEEE conference on computer vision and pattern recognition, pp. 770-778. 2016.

[12] A. Sexton, A. Todman, and K. Woodward, “Font recognition using shape-based quad-tree and kd-tree decomposition,” in Proceedings Of The Joint Conference On Information Sciences, vol. 5, no. 2, 2000, pp. 212 – 215.

[13] https://www.kaggle.com/paultimothymooney/blood-cells