# A DEEP LEARNING ENHANCED TECHNIQUE FOR CLASSIFICATION OF BLOOD CELL IMAGES

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**Abstract**

The problem of identifying and counting blood cells within the blood smear is of both theoretical and practical interest. The differential counting of blood cells provides invaluable information to pathologist for diagnosis and treatment of many diseases. In this paper we propose an efficient hierarchical blood cell image identification and classification method based on multi-class support vector machine. In this automated process, segmentation and classification of blood cells are the most important stages. We segment the stained blood cells in digital microscopic images and extract the geometric features for each segment to identify and classify the different types of blood cells. The experimental results are compared with the manual results obtained by the pathologist, and demonstrate the effectiveness of the proposed method.

***Keywords:*** *Artificial Intelligence, Convolutional Neural Network, Machine Learning.*

## I. INTRODUCTION

It is notable that platelets principally incorporate red blood cells, white platelets and platelets. In blood, leucocyte assumes an essential job in the human insusceptible capacity, so it is likewise called the safe cell. More often than not, hematologists use granulated data and shape data in leukocytes to isolate white platelets into granular cells: neutrophil, eosinophil, basophil and non-granular cells: monocyte and lymphocyte. The extent in the blood of these five types of cells is diverse for the sick and non-ailing bloods. Specialists regularly utilize these fundamental information as criteria for deciding the sort and seriousness of this ailment. In this manner, the investigation of white platelet classification has critical significance and esteem for restorative conclusion. In light of the significance of platelet classification in the conclusion, scientists have proposed numerous calculations to order platelets. In 2003, Sinha and Ramakrishnan [1] classified cells utilizing SVM with an acknowledgment rate of 94.1%. In 2006, Yampri et al. [2] utilized 100 pictures to play out the same trials. They actualized the programmed edge also, versatile shape to fragment cells, and utilized the littlest blunder strategy to group them, and the acknowledgment rate was 96% [2]. Yampri et al. [2] used the KNN calculation.

Be that as it may, the KNN calculation does not deal with uneven tests well. In the event that the example limit of a class is vast, while the example limit of different classes is little, a few issues emerge. For instance, when another example is contribution to the analytic framework, it might result in a class with a vast limit of being overwhelming in the K closest neighbors of this example. What's more, the calculation is computationally costly on the grounds that each example should be sorted in request to compute its separation from every single referred to test so as to get its K closest neighbors.

## II RELATED WORK

Previously related blood cell classification algorithms mainly include the KNN algorithm, Bayesian classifier, SVM classifier, etc. We briefly review and discuss in this section. The core idea of the KNN algorithm is that if most of the k most adjacent samples in a feature space belong to a certain category. Note that the sample also has the characteristics of all the other samples in this category. This method determines the class in which the sample is to be classified based on the category of the nearest samples in determining the classification decision. The KNN method is only relevant to a very small number of neighboring samples in the category decision. Based on this theory, Young (1972) experimented with 199 cell images. He first used histogram thresholds to segment white blood cells and classified them using a distance

classifier. The recognition rate was 92.46% [24]. Bikhet *et al.* [25] used entropy based and iterative thresholding methods to divide cells and classify them with a distance classifier, with a recognition rate of 90.14%. Bayesian classification is based on statistical classification and uses its knowledge of probability statistics to classify data. In many classifications, naive Bayes algorithm can be compared with decision tree and neural network algorithm. Sinha and Ramakrishnan [1] used Bayesian classifiers to classify cells and the recognition rate was 82.3%. The era-Umpon and Dhompongsa (2007) used a Bayesian classifier to classify the bone marrow images of the Ellis Fisher Cancer Center at the center of Missouri (only one cell per picture), and the recognition rate was 77% [26], [27]. Ghosh *et al.* [28] used a watershed algorithm to segment 150 cell images and classify them using a Bayesian classifier, and the recognition rate was 83.2%. The classification idea of SVM is essentially similar to the linear regression LR classification method. It is to obtain a set of weight coefficients that can be classified after linear representation. SVM _rst trains a separation hyper-plane, and then the plane is the decision boundary of the classification. Classical SVM algorithm is only suitable for two types of classification problems. After improvement, SVM can also be applied to multiple classification problems. In the actual application of white blood cell classification, it is generally necessary to solve the problem of multiple classifications. For example, the five-classification problem of leukocytes we studied can be solved by combining multiple binary SVM. Rezato_ghi and Soltanian-Zadeh [29] used the Gram-Schmidt Orthogonal and Snake algorithm to segment 400 blood smears and classified them using SVM. Their recognition rate was 90% [29]. Recently, convolutional neural networks have been widely implemented in various image classification fields. In particular, convolutional neural networks (ConvNets) [11] achieved unprecedented results in the 2012 ImageNet large-scale visual recognition challenge, which included classifying natural images in the ImageNet dataset into 1000 _ne-grained categories [3]. They also significantly improve the performance of various medical imaging applications [30], [31], such as classification of lung diseases and lymph nodes in CT images [32], [33], segmentation (pixel classification) of brain tissues in MRI [34], vessel segmentation based on fundus images [37], and detecting cervical intraepithelial neoplasia (CIN, particularly CIN2C) at patient level based on Cervigram images or Multimodal data [36]. In addition, ConvNets showed superior performance in cell image classification such as pleural cancer [38] and human epithelial cell images [39]. Although these methods can be used to generate good classification engines, they still have some drawbacks. Traditional machine learning methods (such as SVM) need to extract features manually. The acquisition of features mainly depends on the designer's prior knowledge. This feature extraction method is difficult to make full use of the information contained in the image, and will increase the designer's workload. The deep learning algorithm effectively solves this problem. It can automatically learn the effective features of the image. Deep learning algorithms such as deep residual network also have good performance in image classification tasks. However, these neural network classification algorithms cannot fully utilize some features of the image that have a long-term dependency relationship with image labels, and thus these classification methods cannot classify cell images like people with memory. For this purpose, we introduce a recurrent neural network and fuse it with a convolutional neural network to perform the task of blood cell image classification.

## III PROPOSED SYSTEM

### Convolutional Neural Networks

Both the 2-dimensional and 3-dimensional structures of an organ being studied are crucial in order to identify what is normal versus abnormal. By maintaining these local spatial relationships, CNNs are well-suited to perform image recognition tasks. CNNs have been put to work in many ways, including image classification, localization, detection, segmentation and registration. CNNs are the most popular machine learning algorithm in image recognition and visual learning tasks, due to its unique characteristic of preserving local image relations, while performing dimensionality reduction. This captures important feature relationships in an image (such as how pixels on an edge join to form a line), and reduces the number of parameters the algorithm has to compute, increasing computational efficiency. CNNs are able to take as inputs and process both 2-dimensional images, as well as 3-dimensional images with minor modi_cations. This is a useful advantage in designing a system for hospital use, as some modalities like X-rays are 2-dimensional while others like CT or MRI scans are 3-dimensional volumes. CNNs and Recurrent Neural Networks (RNNs) are examples of supervised machine learning algorithms, which require significant amounts of training data. Unsupervised learning algorithms have also been studied for use in medical image analysis. These include Autoencoders, Restricted Boltzmann Machines (RBMs), Deep Belief Networks (DBNs), and Generative Adversarial Networks (GANs)

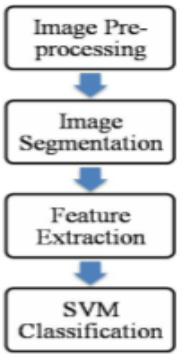


Fig 3 : The Flow Chart of automatic recognition of blood cells

## IV METHODOLOGY

### Color Split Channel

The blood smear may be stained by different color dyes. To avoid being influenced by dye color, all blood smear images were first transformed into gray level. A typical peripheral blood smear image consists of four components, which are the background, erythrocytes, leukocytes, and thrombocytes. Leukocytes appear rather darker than the background, and erythrocytes appear in an intermediate intensity level. To segment the desired object from the background, it is found that the green component of the RGB input image gives the best contrast between the background and the blood cells components, as shown in Fig. 4. As a result, the green channel is used to segment the blood cells in our proposed method.

### Image Segmentation

Image segmentation consists basically on partitioning an image into a set of disjoint and homogeneous regions which are supposed to correspond to image objects that are meaningful to a certain application. Thus, the segmentation process is based on using thresholding, morphology, and watershed to enclose every element in the blood slide in a distinct area.

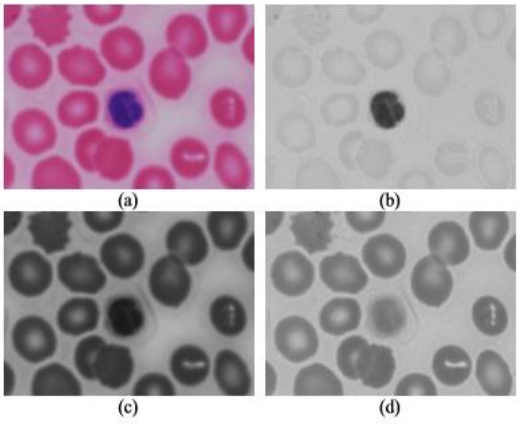


Figure 4. Color channel. (a) Original blood cell image. (b) Red channel. (c) Green channel. (d) Blue channel.

### Binary

In order to segment the desired object from the background, we need to generate a binary image that separates foreground and background image pixels. To produce a representative binary image, Otsu's adaptive threshold algorithm [7] is applied on the green channel to classify all the pixels into two classes. Otsu's method exhaustively searches for the threshold Tc that minimizes the within-class variance, defined as a weighted sum of variances of two classes:

$$T_c = Arg\left(min_{0\le t<L}\left(p_1(t)\sigma_1^2(t) + p_2(t)\sigma_2^2(t)\right)\right),$$

Where the weight pi is the probability of a pixel in the i-th class separated by a threshold t and$^r$ the variance of pixels' gray level intensities in the i-th classes. Fig. 5 shows the output binary image produced corresponding to that shown in Fig. 4(c).

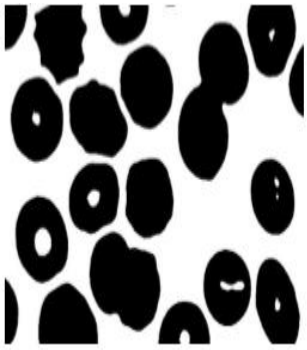

Figure 5 The binary blood cell image generated by Otsu's threshold algorithm.

**Mathematical Morphology** Mathematical morphology operations [8] are nonlinear, translation invariant transformations. The basic morphological operations involving an image S and a structuring element E are where denote the set intersec respectively. E + s denote the translation of a s. The opening and closing derived from dilation are defined by Mathematical morphology operations are holes in blood cells and to remove the unwanted blood cells and background. Watershed The objective of watershed segmentation of the highest gray levels, which are called The simplest way to explain watershed seggimmersion approach." Imagine that a hole minimum of the surface, and we flood was catchment basins from the holes. If the w catchment basins is likely to merge due to fu a dam is built to prevent the merging. This will eventually reach a stage when only the watershed lines) is visible above the water order to separation of overlapping cells, water is applied on distance transform of binary having larger area. Fig. 6 shows the watersh result for the blood cell image.

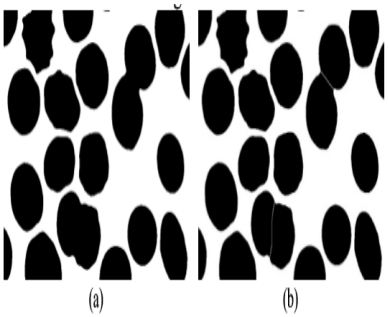


Figure 6. Image segmentation. (a) The binary image of Fig. 4(c). (b) The watershed segmentation result of (a).

### Feature Extraction

**MATERIALS AND METHODS**

stages Image Data Collection: The blood specimens were obtained from different patients with sickle cell anemia, sickle cell disease and normal volunteers.

Each blood cell image contains number of normal and abnormal cells. Blood Cell Segmentation: Image segmentation is used to detect the entire blood cells (Dougherty, 1994; Wroblewska et al., 2003). in a segmented image, the picture elements are no longer the pixels, but connected set of pixels, all belonging to the same region. An object can be easily detected in an image if the object has sufficient contrast from the background. We use edge detection and basic morphology tools to detect a cell.

The individual cells are close to each other and the borders among them are not well defined. The morphological operations aim at extracting relevant structures of the image by probing the image with another set of a known shape called structuring element, chosen as the result of prior knowledge concerning the geometry of the relevant and irrelevant image structures.

The most known morphological operations include erosion, dilation, opening and closing. The morphological approach to image segmentation combines regions growing and edge detection techniques (Serra, 1984; Ponsen et al., 2009). The applied procedure of the image segmentation and cell separation consists of the following: Transformation of the original image into gray scale. Detect the entire cell using edge detection technique Application of dilation and erosion operations to smooth the object and to eliminate the distortions Feature Extraction: Twenty seven features were extracted from each cell image (Table 1). This included 4 geometrical features, 16 statistical features and 7 moment invariant features (Osowski et al., 2004; Santinelli et al., 2002). Geometrical Features Description: We use the following geometrical features to study characteristics of the cells:

Area A-the number of pixels on the interior of the cell

Perimeter P-the total distance between consecutive points of the border

Compactness C-given by the formula: perimeter2 /area • Form factor F-4*3.14*Area/Perimeter2

**SVM Classification**

Support vector machine (SVM) [10] is a concept for a set of related supervised learning methods that analyze data and recognize patterns, used for classification and regression analysis. The main advantage of the SVM network used as a classifier is its very good generalization ability and extremely powerful learning procedure, leading to the global minimum of the defined error function. Given instances xi, i=1, …, l with labels 8$ !K2K3, the main task in training SVMs is to solve the following quadratic optimization problem [11]:

$$\min_{\alpha} f(\alpha) = \frac{1}{2}\alpha^T Q\alpha - e^T\alpha$$
$$\text{subject to} \quad 0 \le \alpha_i \le C, i = 1, \dots, l,$$
$$y^T\alpha = 0.$$

where e is the vector of all ones, C is the upper bound of all variables, Q is an l by l symmetric matrix with Qij = yiyjK(xi, xj), and K(xi, xj) is the kernel function. The most known kernel functions are the radial Gaussian basis, polynomial, spline, or sigmoidal functions. The final learning problem of the SVM is transformed to the solution of the so-called dual problem defined with respect to the Lagrange multipliers [12]:

$$\max Q(\alpha) = \sum_{i=1}^{l} \alpha_i - \frac{1}{2}\sum_{i=1}^{l}\sum_{j=1}^{l} \alpha_i \alpha_j y_i y_j K(x_i, x_j)$$

with the constrains $(i=1, \dots, l)$

$$\sum_{i=1}^{l} \alpha_i y_i = 0, \quad 0 \le \alpha_i \le C.$$

The output signal s(x) of the SVM after learning is described in the form [11],

$$s(x) = \sum_{i=1}^{l} \alpha_i y_i K(x_i, x) + b,$$

where b is the bias and the vector x represents the class when s(x) is positive and the alternative class when s(x) is negative. The hyperparameter of the kernel function and the regularization constant C have been adjusted by repeating the learning experiments for the set of their predefined values and choosing the best value on the validation data sets. Their optimal values are those for which the classification error on the validation data set was the smallest.

The one-against-one method [13] is applied to deal with the problem of multiple classes. The maximum voting of the multiple classes is used to find the final classification results. During the training phase, the models of the multiple classes SVMs are learned from training data. In the testing phase, the learned models are employed to generate multiple sets of predictions for each test sample. The one having the largest prediction is the final decision.

From earlier literatures, we found that it is hard to accurately distinguish blood cells into seven classes by using the single-stage SVM classification. Thus, we propose the hierarchical SVM classification to improve the recognition ratio. Fig. 8 illustrates our proposed hierarchical strategy. For fast and efficient classification, five features, area, histogram, circularity, cytoplasm ratio, and color of cytoplasm, are extracted for the following SVM training. For the first level,

blood cells can be distinguished into two types, thrombocytes and erythrocytes, leukocytes by the feature "area." Next, we can use the feature "histogram" to identify erythrocytes and leukocytes. For leukocytes, we can use the

feature "circularity" to identify granulocytes and agranulocytes due to agranulocytes belong to the mononuclear cell group. In the following, we use the feature "color of cytoplasm" to distinguish granulocytes into neutrophils, eosinophils, and basophils. Finally, monocytes and lymphocytes can be recognized by the feature "cytoplasm ratio."

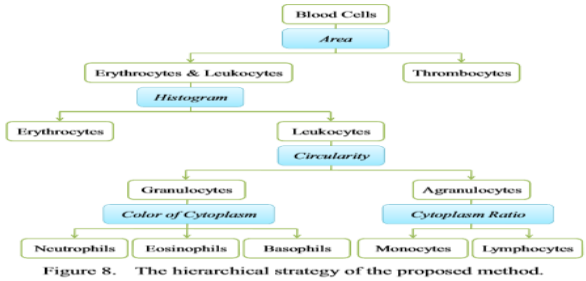

Figure 8. The hierarchical strategy of the proposed method.

## V CONCLUSION

This study demonstrated an efficient hierarchical blood cells classification method using the geometric features from the nucleus and the cytoplasm and a multi-class SVM classification scheme. Classification using the proposed hierarchical strategy outperformed classification using only the single-stage SVM because the cytoplasm of some leukocytes presents a very weak difference against the background and touches neighboring cells. In addition, experimental results showed that using the hierarchical multi-class SVM classification with hierarchical features could indeed improve the classification performance compared to the single-stage SVM method.

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