Classification of White Blood Cells Using L-Moments Invariant Features of Nuclei Shape

1st Khamael AL-Dulaimi
School of EECS
[*]Queensland University of Technology
QLD, Australia
khamaelabbaskhudhair.aldulaimi@hdr.qut.edu.au
[**]AL-Nahrain University, Computer Science Dept., Iraq

2nd Kien Nguyen
School of EECS
Queensland University of Technology
QLD, Australia
k.nguyenthanh@qut.edu.au

3rd Jasmine Banks
School of EECS
Queensland University of Technology
QLD, Australia
j.banks@qut.edu.au

4th Vinod Chandran
School of EECS
Queensland University of Technology
QLD, Australia
v.chandran@qut.edu.au

5th Inmaculada Tomeo-Reyes
Electrical Engineering & Telecommunications
University of New South Wales
NSW, Australia
i.tomeoreyes@unsw.edu.au

***Abstract*—Automated classification of white blood cells from microscope images is still challenging, particularly in terms of feature representations choice considering its complexity, compactness and efficiency. Particularly, in this scenario, the feature representations have to be invariant to non-uniform illumination, shape of the nuclei, stage of maturity, change in topology due to rotation, scale and shifting. This paper proposes a new white blood cell feature representation which aims at increasing robustness to those challenges. The proposed feature representation is designed based on L-moments (L-skewness, L-mean, L-scale and L-kurtosis) of the Radon projection of segmented nuclei shape. Coupled with Linear Discriminant Analysis, the proposed feature representation has been shown to be highly effective at encoding the discriminative properties of the white blood cells, and invariant to intra-class cell variations. Support Vector Machine (SVM) based (ones-vs-all) schema and a classification tree are applied to separate the multiple classes of cells. The proposed approach is evaluated for a 10-class problem. It achieves an average classification accuracy of 97.23% and outperforms all other feature representations, including bispectral invariant, local binary pattern, and histogram of oriented gradients using the same classifier on the same dataset. The proposed method is also compared and benchmarked with the other 12 existing techniques for classification of white blood cells into 10 classes over the same datasets and the results show that the proposed method achieves high accuracy in comparison with other approaches. The proposed method is also highly competitive in terms of computation and efficiency in comparison with other approaches.**

***Index Terms*—Classification, White Blood Cells, L-moments, Linear Discriminant Analysis, Support Vector Machines.**

I. Introduction

White blood cells (WBCs) classification plays a key role in the diagnosis of several blood disorders, such as leukaemia and certain types of cancer. The traditional procedure, which requires manually classifying and segmenting WBCs with the help of a microscope, has difficulties: (a) it is time consuming; (b) it requires more than two experts to make a decision; and (c) as a result it takes a substantial effort to classify large numbers of cells. Furthermore, manual classification of WBCs may produce inaccurate results due to human error in classifying different shapes of WBCs, large numbers of cells, different staining methods and overlapping cells [1]. In contrast, automated classification of WBCs can process larger numbers of cells and different shapes, and therefore, can potentially produce better accuracy if the algorithm used for classification is trained well. The important steps of WBC classification are segmentation, feature extraction, and classification [2], [3]. Segmentation of the WBC nuclei and the feature extraction procedures play a significant role in the classification of WBCs, and it is key that they yield useful information while being invariant to intra-class variations of the cell nuclei shape, non-uniform illumination, staining, and changes in the cell topology due to stage of maturity, rotation, scale and shifting. The most useful information for cell classification comes from morphological features of WBC nuclei. WBCs can be classified into three main types and seven subtypes, as shown in Fig.1. An overview of types and subtypes of WBC nuclei shape information and the morphological characteristics can be found in [3], [4].

This paper is organized as follows: Motivation and contribution are presented in Section-II, Section-III presents a literature survey, Section-IV describes the proposed methodology, Section-V provides experimental results and Section-VI presents the conclusions of the work.

II. Motivation and Contribution

The accuracy of WBC classification is directly influenced by the quality of the segmentation and feature extraction steps. The discriminative capacity of the feature representation is still questionable because of several challenges, including time complexity of the method, the large number of features, and intra-class variations, including the shape of cells, shifting, scale and rotation, and stage of maturity. Many

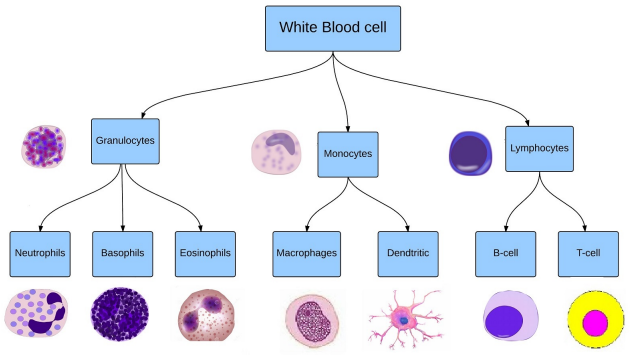


Fig. 1: WBC taxonomy from bone marrow, including main types (Granulocytes, Monocytes and Lymphocytes) and subtypes (Neutrophils, Basophils, Eosinophils, Macrophages, Dendritic, B-lymphocytes and T-lymphocytes) [2], [3].

feature extraction representations have been proposed although none of them address all challenges of WBCs classification simultaneously. The motivation of this paper is to investigate an effective feature representation for WBCs and to propose an automated classification based on this representation. The original contribution of this work is the use, for the first time, of L-moments invariant features (skewness, scaling, mean and kurtosis) and Linear Discriminant Analysis (LDA) to classify WBC into 10-classes with better accuracy than similar work. The novelty of this paper is that the L-moments features (skewness, scaling, mean and kurtosis), which are extracted from Radon projections, are based on the shape information of the segmented WBC nuclei from microscope images. This feature extraction scheme generates a small-sized feature representation for each WBC, produces feature types that are invariant to shifting, rotation and scale, and eliminates traditional dimensionality reduction requirements. Support Vector Machines (SVMs) and the classification tree subsequently used to perform classification, and the method has performed well with large or small training data sets. In this paper, a Radial Basis Function (RBF) with (SVMs) is used to achieve high accuracy by minimizing overlapping of features from different classes that cause classification errors.

III. Literature Survey

A. Application to WBC Classification

In the last decade, different approaches have been proposed and adopted to extract the following features from WBC images: Geometrical features, Textural features and Colour features. These features have been used with different machine learning techniques to classify WBCs into five types: neutrophil, eosinophil, basophil, lymphocyte, and monocyte. Table-I summarizes existing techniques of WBC classification, including: segmentation technique, number of classes, databases, feature extraction representations and accuracy. However,issues the affect the classification results for the techniques in Table-I include: a) they are computationally intensive; b) cell types are poorly/insufficiently represented in the data sample; c) some techniques used flow cytometry data which is not image based; and d) errors occurred during the segmentation and feature extraction stages due to cells having different orientation of nuclei, shape and size.

The feature extraction process plays a significant role in WBC classification. Despite numerous work having been undertaken in this field, automatic WBC classification in terms of feature representations is still challenging, particularly in the presence of different structures within WBC types, non-uniform illumination, low resolution of images, changes in the cell topology (including translation, rotation, scaling, and phase of maturation). L-moments can be useful to extract new features to address the WBC classification problems. For classification techniques, DL has attracted great attention in computer vision and medical imaging tasks due to the breakthroughs it has achieved in automatic feature learning by mimicking the structure and operation of the human brain, and it has also used to diagnose diseases such Alzheimer's disease in [5]. DL has als been explored in classification of WBCs In [6], [7]; however, DL requires a huge amount of training data if training from scratch. In addition, DL is extremely computationally expensive. For these reasons, DL is not within the scope of this work. In the WBC scenario, human-expert knowledge from this domain could achieve highly-accurate performance with interpretable evidence for the reasoning process, this process is amenable to implementation in a classification tree, as used in this work.

B. Moments: Background and Application

Moments have been used for decades. They are scalar quantities used to describe a function and to capture its significant features. In image processing and computer vision, the first order moment measures the center of mass, where the mass of a pixel means intensity; the second order moment gives the variation of the mass around the center of mass; etc. [15]. L-moments have been proposed by [16] as an alternative method to other types of moments. L-moments are considered to be a key tool of wide-ranging practical advantage in signal processing. Computation of L-moments for a data set can summarize useful information about the location, dispersion, and distribution of the shape from which the data sample has been drawn. To date, it is apparent that few works have used moments in medical imaging and blood fields. In WBC classification, few works have used moments to extract features in [17], [18]. To date, state-of-the-art of classification of WBCs based on L-moment features has not been used in terms of feature extraction representation.

IV. Proposed Method of WBCs Classification

The proposed method of WBCs classification process is shown in Fig.2:

A. Segmentation of WBCs Nuclei

The segmentation method uses A level set curvature force via edge-based Geometric Active Contours (GACs) to obtain the shape of WBC nuclei, as shown in Fig.3. This previous work was presented and benchmarked in [4], [19].

TABLE I: Summary of WBC classification methods (since 2005) up to current state-of-the-art, including number of classes, segmentation approaches, feature extraction representations, classification methods, databases, and accuracy.

Research	Classes	Segmentation	Features extraction	Classification	Database	Accuracy
Adjouadi *et al.*(2005) [8]	4	-	Flow cytomery blood cell	SVMs	Beckman-coulter corporation data	87%
Ghosh *et al.*(2010) [9]	5	Watershed	Geometrical features	Naïve Bayes	Midnapur Hospital	83.2%
Rezatofighi *et al.*(2011) [10]	5	GramSchmidt Orthogonal-snake	LBP	SVMs & ANN	BMT Research Center	86.10%
Habibzadeh *et al.* (2013) [11]	5	Manual segmentation	K-PAC and DT-CWT	SVMs & K-PCA	—	84-86.17%
Sue *et al.* (2014) [6]	5	Discriminating region	LDP	HCNN, MPLs & SVMs	CellaVision Databases	77–97%
Schneider *et al.* (2015) [12]	3	–	flow cytometer	Optical neural network	Flow cytometer database	89%
Ravikumar *et al.* (2016) [13]	5	ELM	Discriminative features	ELM & Fast-RVM	Hospital database	82.45–90%
Habibzadeh *et al.* (2018) [7]	4	Inception and ResNet architecture	Hierarchy topological	Deep Learning	Hospital database	—-
Jiang *et al.* (2018) [14]	-	-	Batch normalization	CNN WBCNet model	–	83%

B. L-moments Based on Radon Projection

L-moments analyze and estimate the distributions of data using linear combinations of order statistics, and can be used to compute quantities analogous to standard deviation, skewness and kurtosis, which are known as the L-scale, L-skewness and L-kurtosis, respectively (the L-mean is identical to the conventional mean). Standardised L-moments are called L-moment ratios and are analogous to standardise moments [16]. In this paper, L-moments statistics are used to calculate sample statistics, including L-scale, L-skewness, L-mean and L-kurtosis for image data after taking multiple and parallel-path projections of the image from various angles θ by rotating the source around the centre of the cell nucleus $f(x, y)$. A Radon projection is used to convert a two-dimensional image to a one-dimensional vector. The Radon function $R[\theta]$ is written as in [20]:

$$R[\theta] = \int\int f(x,y)\delta(x\sin\theta - y\cos\theta - r) \tag{1}$$

where r represents a vector containing the radon transform of the intensity image $f(x, y)$ for each θ between $[0, 90]$ degrees. The projection result $R[\theta]$ is the summation of the intensity of the pixels from the segmented image in each direction.

The L-moment measure of location, and L-moment ratio measures of scale, skewness and kurtosis are adapted using Radon projection $R[\theta]$ and written as [21]:

$$\begin{aligned} L\text{-}Mean &= L1 \\ L\text{-}Scale &= L2/L1 \\ L\text{-}Skewness &= L3/L2 \\ L\text{-}Kurtosis &= L4/L2 \end{aligned} \iff \begin{aligned} L1 &= \beta_0 \\ L2 &= 2\beta_1 - \beta_0 \\ L3 &= 6\beta_2 - 6\beta_1 + \beta_0 \\ L4 &= 20\beta_3 - 30\beta_2 + 12\beta_1 - \beta_0. \end{aligned} \tag{2}$$

where the data $R[\theta]$ is in ascending order from 1 to n and n is the size of individual projections (the length of the vector which collects the results of each line integral). L-moments features is adapted using Radon projection of $R[\theta]$ for θ from 0 to 90 to measure the variation nuclei shape as follows :

- L-Mean will consider location features of cell nuclei.
- L-Scale measures variation in scaling of the cell nuclei.
- L-Skewness measures the concavity of cell nuclei.
- L-Kurtosis measures the sharpness of cell nuclei.

$$\beta_0 = \frac{1}{n}\sum_{j=1}^{n} R_j \tag{3}$$

$$\beta_1 = \frac{1}{n}\sum_{j=2}^{n} R_j[(j-1)/(n-1)] \tag{4}$$

$$\beta_2 = \frac{1}{n}\sum_{j=3}^{n} R_j[(j-1)(j-2)/(n-1)(n-2)] \tag{5}$$

$$\beta_3 = \frac{1}{n}\sum_{j=4}^{n} R_j[(j-1)(j-2)(j-3)/(n-1)(n-2)(n-3)] \tag{6}$$

C. Linear Discriminant Analysis (LDA)

LDA is considered a concept of Fisher's linear discriminant analysis, and has been used for data classification and dimensionality reduction in different disciplines, such as pattern recognition, machine learning and statistics. It helps to find a linear combination of features that discriminates or separates two or more classes of objects or events [22]. In order to find good features, L-skewness, L-scaling, L-mean and L-kurtosis are collected from more than one class into one matrix x, and each column in the matrix represents one sample referred to as y. A measure of separation between two classes or more should be calculated as follows:

$$\mu_i = \frac{1}{N_i}\sum_{x\in\omega_i} x, \ and \ \overline{\mu_i} = \frac{1}{N_i}\sum_{y\in\omega_i} y \tag{7}$$

The LDA measures the distance between the projected means normalized by the projected samples. Therefore, the data from the same class are projected very close to each other. The LDA projection (good features) is then obtained as the solution of the generalized eigenvector λ. More details about LDA procedure can be found in [23].

$$S_W^{-1} S_B = \lambda w \tag{8}$$

V. Experiments and Results

A. Databases

Three databases are used for the evaluation of the proposed methodology, have all WBC types images, and have been used in previous work on WBC segmentation [4] and classification [2]: Cellavision Database [24] Acute Lymphoblastic Leukemia

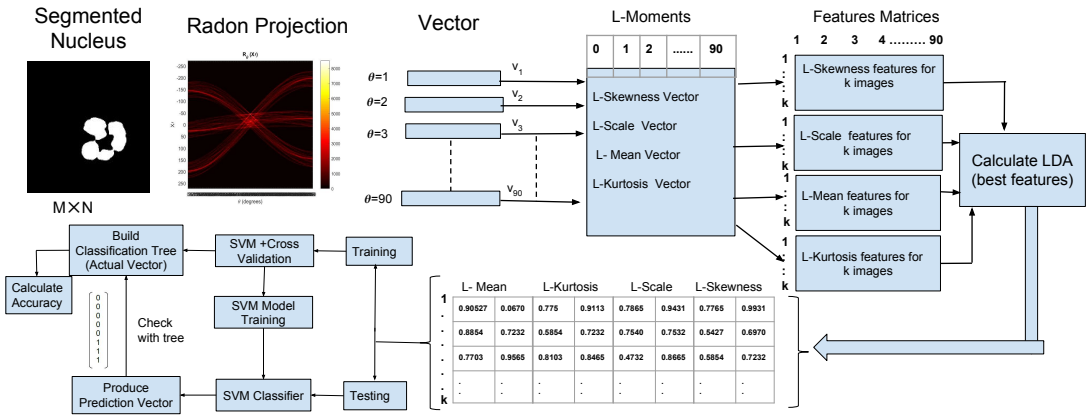


Fig. 2: Diagram of WBCs classification process includes segmentation of nuclei; steps of feature extraction to calculate L-moments, features; Calculating LDA, where k is number of images and 8 features; WBCs classification.

Image Database (ALL-IDB) [25] were collected by the Department of Information Technology Universit'a degli Studi di Milano and Wadsworth Centre [26].

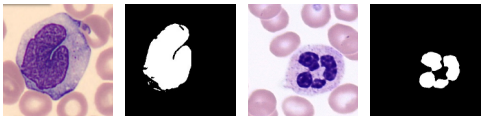
B. Proposed Method Implementation

The proposed method of WBC classification is implemented using MATLAB 2017a. Fig.2 shows the process of the proposed method. The proposed technique is tested using 460 labelled digital images of different WBCs. In this paper, level set based curvature forces via edge-based GACs is first used to detect the shape of the nucleus for each type of WBCs, as shown in Fig. 3 [4]. Then, the $N \times M$ segmented nucleus cell image is converted to a 1D vector using the MATLAB Radon projection function. The Radon projection produces a Radon vector R for each θ from 0 to 90 degrees in 1 degree increments. L-moments are then used to calculate L-scale, L-skewness, L-kurtosis and L-mean features for each Radon vector R to obtain useful information (features) of the location, scale, concavity, and sharpness of the segmented nucleus shape. LDA is then implemented to find good features, and produces one matrix of size $(k \times 8)$ where k is number of images and 8 is number of features which are two feature vectors for each L-scale, L-skewness and L-kurtosis and L-mean features. The set is then split randomly into train and test subsets in the ratio of $1/3$ (train) and $2/3$ (test) for each type of cell. SVMs classifier (ones vs all) learning schema and classification tree are used to classify WBC into multi classes. The accuracy is calculated based on parameters: True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN) [27].

C. Experiment Results and Benchmark

1) Building Classification Tree

An SVM classifier is trained for each type and sub-type of cell to create a classification tree. 151 images randomly chosen are used for training the SVM with 5-fold cross validation to calculate the accuracy. The experiment is repeated 15 times to obtain consistency of the classification accuracy, as shown in Table-II, Table-III.



(a) (b) (c) (d)

Fig. 3: WBC nuclei segmentation [4]: (a) monocyte cell, (b) segmented nucleus, (c) neutrophil cell, (d) segmented nucleus.

TABLE II: Average accuracy after 15 repetitions to order WBC main types in the classification tree.

Order	Actual class	Accuracy
1	Granulocyte	97.08
2	Lymphocyte	95.33
3	Monocyte	94.36

TABLE III: Average accuracy after 15 repetitions to order WBC sub-types in the classification tree.

Main class	Sub-types class	Accuracy
Granulocyte	Neutrophil	96.61
	Basophil	93.53
	Eosinophil	90.04
Lymphocyte	T-cell	92.63
	B-cell	91.21
Monocyte	Macrophage	97.30
	Dendritic	95.87

2) Classification Results

SVMs using RBF function based (ones-vs-all) schema are implemented to classify 460 labelled images. Both training and testing are performed using 151 and 309 images, respectively. This experiment is repeated 100 times to obtain predictive labels each time. The predictive labels are created for each type of WBC as 0's for one class and 1's for other classes. These predicted labels of the test set can be compared to the actual labels in the classification tree to get TP, FP, FN, TN parameters, as shown in Table- IV. Table-V shows a confusion

matrix to calculate classification accuracy.

TABLE IV: Average accuracy of classification 100 repetitions of WBC types and sub-types.

Actual class	TP	TN	FP	FN	Accuracy
Neutrophil	67	107	0	1	99.43%
Basophil	52	54	2	2	96.12%
Eosinophil	52	0	1	1	95.03%
Macrophage	47	27	2	0	97.36%
Denditric	26	0	0	1	96.29%
T-cell	28	32	1	1	96.96%
B-cell	28	2	0	2	94.22%

TABLE V: Confusion matrix after 100 repetitions to classify labelled images.

Class	Neutro.	Baso.	Eosino.	Macro.	Dendi.	B-cell	T-cell
Neutro.	67	0	0	0	0	0	0
Baso.	1	52	1	0	0	0	0
Eosino.	0	1	52	1	0	0	0
Macro.	0	0	0	47	0	0	0
Dendi.	0	0	0	1	26	0	0
T-cell	0	0	0	0	0	28	1
B-cell	0	1	0	0	0	1	28

3) Comparison With Other Methods and Benchmarking

The average accuracy is computed for the proposed feature extraction method with the SVM classifier and compared with other feature extraction methods using the same segementation method and SVM classifier. These methods of feature extraction are: Local Binary Pattern (LBP), Histogram of Oriented Gradients (HOG), bispectral invariant integrated from Higher Order Spectra (HOS) [2] and Speeded Up Robust Features (SURF). 460 images of WBCs over the same databases have been used to evaluate the performance of all methods. Table-VI shows that 8 L-moments features with the SVMs classifier results in higher accuracy than the other methods.

TABLE VI: Comparison of performance between LDA based on L-moments invariant features (the proposed method) with other feature extraction representations using the same segmentation method and SVMs classifier.

Actual class	**Proposed method**	HOS	LBP	HOG	SURF
Granulocyte	**100.00%**	99.67%	85.07%	80.12%	83.02%
Neutrophil	**99.01%**	98.18%	83.64%	79.99%	75.12%
Basophil	**96.12%**	94.33%	86.50%	90.43%	77.14%
Eosinophil	**95.03%**	94.54 %	67.71%	77.78%	74.19%
Lymphocyte	**99.00%**	98.82%	81.23%	92.23%	81.71%
T-cell	**96.66%**	96.29%	75.11%	82.54%	79.12%
B-cell	**94.25%**	93.10%	90.15%	84.88%	82.66%
Monocyte	**98.28%**	97.76%	76.05%	83.12%	70.15%
Macrophage	**97.36%**	96.18%	83.03%	82.55%	81.92%
Denditric	**96.77%**	92.13%	84.53%	78.24%	88.12%
Average	**97.23%**	96.13%	82.01%	83.19%	80.08%

Table-VII has shown a comparison of the classification accuracy of the proposed method with other existing methods. Average accuracy is computed for the proposed classification technique and compared with average accuracy values of other existing methods using the 460 WBC images of 3 databases presented in Subsection-V-A. The evaluation performance of the proposed WBC classification technique is benchmarked versus 12 other existing techniques: Fast-RVM, ELM [13], FCM, Fast Fuzzy C Mean (FFCM) [28], ANN [10], HHCN , MLPs [6], random forest and regression tree [29], PCA [30] and K-PCA [11]. The results show that the proposed method based on LDA on L-moments invariant features with SVMs and classification tree method, for classifying WBC into 10-classes, has higher accuracy than all other techniques except bispectral invariant features [2] where LDA on L-moments invariant features has slightly better accuracy. Other techniques do not work well with those databases due to variation in shape, rotation, scaling, shifting and maturity stage. ELM and Fast-RVM methods were designed to classify 5-classes of WBCs. An ANN technique could not classify WBCs and produces results because it requires a huge data training set for this task. Other techniques have also not performed as well as the proposed method, due to issues in segmentation of WBC nuclei technique, feature exaction representations and processing time.

TABLE VII: Comparison accuracy of different WBC classification techniques. The average accuracy of the proposed method are compared with other existing techniques (the fisrt twelve rows) using the same databases from Subsection-V-A. The best result for existing methods are highlighted in blue, and the proposed method (the last row), which highlighted in green, outperforms it.

Existing Methods	**No.Class**	**Accuracy**
Discriminative features + Fast-RVM [13]	5	84.13%
Discriminative features + ELM [13]	5	79.94%
DT-CWT features + K-PCA [11]	10	84.53%
SURF features + PCA [30]	10	74.05%
Colour Features via histogram + FCM [28]	10	84.15%
Colour Features via histogram + FFCM [28]	10	90.18%
Prominent features + Random forest [29]	–	82.13%
Prominent features + Logistic regression [29]	–	74.02%
LDP features + MPLs [6]	10	78.51%
LDP features + HCNN [6]	10	67.58%
LBP and Discriminative features + ANN [10]	-	-
Bispectral invariant features of nuclei + SVMs [2]	10	96.13%
L-moments invariant features of nuclei + SVMs	10	97.23%

4) Time Performance

The proposed method was tested using a processor Intel(R) Core(TM) i7-4600U CPU 2.70 GHz and MATLAB 2017a. The computation time for techniques listed in Table-VII are: random forest and logistic regression techniques are implemented using Python and require a longer computation time than the other methods. A computation time in (sec) for the whole system of other methods (Fast-RVM, ELM, FCM, FFCM, PCA,K-PCA, bispectral invariant features and L-moments invariant features) are respectively: 2230, 6967, 6359, 1190, 8750, 6500, 15800, 85.

VI. Conclusion and Discussion

In this paper, new features relying on L-moments features (skewness, mean, scaling and kurtosis) adapted using a Radon projection and coupled with linear discriminant analysis, support vector machines and classification tree, are used to classify white blood cells into ten classes (three main types and seven sub-types). The proposed method addresses the challenges of automated white blood cell classification, including variation in cell shape and illumination, time complexity and changes in topology due to rotation, shifting, scale, staining and maturity stage. The proposed method is evaluated using three public databases to demonstrate the capability of the method to account for diverse intra-class variations. A confusion matrix has been used to calculate classification accuracy. The results of the proposed method are compared with other 4 feature extraction representations. The overall accuracy of using eight L-moments features is 97.23%, which is higher than other feature extraction representations. The proposed method is also benchmarked and compared to 12 other methods. The proposed method achieves an accuracy of 97.13%, while the best accuracy results for the other methods are 96.13% and 90.18%, obtained for bispectral invariant and FFCM method, respectively. The results are shown that L-moments features are invariant to shifting, scaling, and rotation. These features are shown to have the ability to distinguish between different types of white blood cells accurately and quickly. The L-moments features produce improved results in comparison to other features because the L-moments method can take advantage of a well segmented nucleus, more than other feature representations. This is because the nucleus captures information about skewness, scale, mean and kurtosis, while remaining invariant to shift, rotation and scale. L-moments can also produce features with little overlap. This means that LDA gives high discrimination of features when used with L-moments. In terms of computational time, the proposed method is significantly faster than other methods.

References

[1] K. D. McClatchey, *Clinical laboratory medicine*. Lippincott Williams & Wilkins, 2002.

[2] K. AL-Dulaimi, V. Chandran, J. Banks, I. Tomeo-Reyes, and K. Nguyen, "Classification of white blood cells using bispectral invariant features of nuclei shape," in *International Conference on Digital Image Computing: Techniques and Applications (DICTA)*, IEEE, 2018.

[3] K. AL-Dulaimi, J. Banks, V. Chandran, I. Tomeo-Reyes, and K. Nyugen, "Classification of white blood cell types from microscope images: Techniques and challenges," in *Microscopy Science: Last Approaches on Educational Programs and Applied Research*, vol. 8, Formatex Research Center, 2018.

[4] K. AL-Dulaimi, I. Tomeo-Reyes, J. Banks, and V. Chandran, "White blood cell nuclei segmentation using level set methods and geometric active contours," in *International Conference on Digital Image Computing: Techniques and Applications (DICTA)*, pp. 1–7, IEEE, 2016.

[5] P. Bhatkoti and M. Paul, "Early diagnosis of alzheimer's disease: A multi-class deep learning framework with modified k-sparse autoencoder classification," in *International Conference onImage and Vision Computing New Zealand (IVCNZ)*, IEEE, 2016.

[6] S. Mu-Chun, C. Chun-Yen, and W. Pa-Chun, "A neural-network-based approach to white blood cell classification," *The Scientific World Journal*, 2014.

[7] H. Mehdi, J. Mahboobeh, R. Zahra, B. Hossein, and T. Mehdi, "Automatic white blood cell classification using pre-trained deep learning models: Resnet and inception," in *10th International Conference on Machine Vision (ICMV 2017)*, vol. 10696, 2018.

[8] M. Adjouadi, N. Zong, and M. Ayala, "Multidimensional pattern recognition and classification of white blood cells using support vector machines," *Particle & Particle Systems Characterization*, vol. 22, 2005.

[9] G. Madhumala, D. Devkumar, M. Subhodip, C. Chandan, P. Mallika, M. A. K, P. S. K, and R. A. K, "Statistical pattern analysis of white blood cell nuclei morphometry," in *Students' Technology Symposium (TechSym)*, pp. 59–66, IEEE, 2010.

[10] R. S. Hamid and S.-Z. Hamid, "Automatic recognition of five types of white blood cells in peripheral blood," *Computerized Medical Imaging and Graphics*, vol. 35, 2011.

[11] H. Mehdi, K. Adam, and F. Thomas, "Comparative study of shape, intensity and texture features and support vector machine for white blood cell classification," *Journal of Theoretical and Applied Computer Science*, vol. 7, 2013.

[12] S. Bendix, V. Geert, S. Richard, L. Liesbet, D. Joni, and B. Peter, "Neural network for blood cell classification in a holographic microscopy system," in *International Conference on Transparent Optical Networks (ICTON)*, pp. 1–4, IEEE, 2015.

[13] S. Ravikumar, "Image segmentation and classification of white blood cells with the extreme learning machine and the fast relevance vector machine," *Artificial cells, nanomedicine, and biotechnology*, vol. 44, 2016.

[14] M. Jiang, L. Cheng, F. Qin, L. Du, and M. Zhang, "White blood cells classification with deep convolutional neural networks," *International Journal of Pattern Recognition and Artificial Intelligence*, vol. 32, 2018.

[15] J. Flusser, T. Suk, and B. Zitová, "Introduction to moments," *Moments and Moment Invariants in Pattern Recognition*, pp. 1–11, 2009.

[16] J. Hosking, "L-moments: analysis and estimation of distributions using linear combinations of order statistics," *Journal of the Royal Statistical Society.*, 1990.

[17] N. Theera-Umpon, "White blood cell segmentation and classification in microscopic bone marrow images," in *International Conference on Fuzzy Systems and Knowledge Discovery*, pp. 787–796, Springer, 2005.

[18] S. Shivhare and R. Shrivastava, "Automatic bone marrow white blood cell classfication using morphological granulometric feature of nucleus," *International Journal of Scientific & Technology Research*, vol. 1, 2012.

[19] K. AL-Dulaimi, J. Banks, I. Tomeo-Reyes, and V. Chandran, "Automatic segmentation of hep-2 cell fluorescence microscope images using level set method via geometric active contours," in *23rd International Conference on Pattern Recognition (ICPR)*, pp. 81–83, IEEE, 2016.

[20] C. Solomon and T. Breckon, *Fundamentals of Digital Image Processing: A practical approach with examples in Matlab*. John Wiley & Sons, 2011.

[21] J. R. M. Hosking and J. R. Wallis, *Regional frequency analysis: an approach based on L-moments*. Cambridge University Press, 2005.

[22] M. Welling, "Fisher linear discriminant analysis," *Department of Computer Science, University of Toronto*, vol. 3, 2005.

[23] S. Fengxi, M. Dayong, and L. Hongfeng, "Feature selection based on linear discriminant analysis," in *International Conference on Intelligent System Design and Engineering Application (ISDEA)*, vol. 1, IEEE, 2010.

[24] Cellvision-Database, "Cellavision leading the way in digital cell morphology." http://www.cellavision.com/, 2011.

[25] ALL-IDB, "Acute lymphoblastic leukemia image database for image processing." http://crema.di.unimi.it/fscotti/all/, 2005.

[26] Wadsworth-Center, "White blood cell images." http://www.wadsworth.org.

[27] C. M. Bishop, "Pattern recognition," *Machine Learning*, vol. 128, 2006.

[28] A. M. P. G. Vale, A. M. G. Guerreiro, A. D. Dória Neto, G. B. Cavalvanti Junior, V. C. L. T. d. Leitão, A. M. Martins, *et al.*, "Automatic segmentation and classification of blood components in microscopic images using a fuzzy approach," *Revista Brasileira de Engenharia Biomédica*, vol. 30, 2014.

[29] M. Saraswat and K. Arya, "Feature selection and classification of leukocytes using random forest," *Medical & biological engineering & computing*, vol. 52, 2014.

[30] S. Nazlibilek, D. Karacor, K. L. Ertürk, G. Sengul, T. Ercan, and F. Aliew, "White blood cells classifications by surf image matching, pca and dendrogram," *Biomedical Research*, vol. 26, 2015.