Ilkogretim Online - Elementary Education Online, 2021; Vol 20 (Issue 3): pp. 4193-4205
http://ilkogretim-online.org
doi: 10.17051/ilkonline.2021.03.433

A Deep Learning Method Of White Blood Cell Identification In Peripheral Blood

Kumud Pant Department of Biotechnology, Graphic Era Deemed to be University, Dehradun, Uttarakhand India, 248002 kumud.pant@geu.ac.in

Devvret Verma Department of Biotechnology, Graphic Era Deemed to be University, Dehradun, Uttarakhand India, 248002 devvret@geu.ac.in

Richa Gupta Department of Computer Science & Engineering Graphic Era Hill University, Dehradun, Uttarakhand India, 248002 richagupta@gehu.ac.in

ABSTRACT

By monitoring leukocyte ratios, computerized leukocyte detection and classification aids in the diagnosis of numerous blood-related disorders. Different methods developed by various researchers use conventional learning to categories multiple kinds of leukocytes. Deep learning, as opposed to traditional learning, which doesn't retain any knowledge that may be carried over from one modeling to the next, is used for categorization and segmentation in our proposed method. Standard learning doesn't have any of these capabilities. The pipeline of the recommended algorithm consists of two stages: the first is semantic separation, and the second is basis for evaluating on domain adaptation. We used DeepLabv3+ for leukocyte division and Alex Net to classify five different types of leukocytes found in peripheral circulation from the whole blood smears microscopy photos by making use of information obtained from previously completed jobs. In order to conduct the experiment, a data set consisting of 245 cells was taken from a series of microscopy pictures. These cells represented five distinct types of leukocytes. When compared to other methods, the suggested methodology achieved a classification performance of 98.90% and a mean precision of 97.37% (with an IoU value of 0.7) when locating white blood cells. This was achieved in locating the cells.

KEYWORD Classification, Semantic division, Deep Lab construction

1. INTRODUCTION

Image processing techniques are used in clinical diagnosis to observe and analyse cells to pinpoint blood cell abnormalities. The accuracy of conventional blood cell recognition systems relies on the operator's skill, is time-consuming, and calls for medical professionals. This inspired researchers to create a computer-aided technique for blood

cell analysis that makes utilisation of blood micrographs made up of platelets, RBC, and WBC. The use of blood micrographs for the analysis of blood cells has the benefit of being inexpensive and not requiring expensive equipment. WBC analysis can be used to diagnose a variety of blood cell problems, including infections, allergic reactions, inflammation, and blood malignancies including leukaemia and lymphoma. Leukocytes, sometimes referred to as white blood cells, aid the body in battling illnesses and infections. WBCs are more massive, have a nucleus, and are much less common than RBCs. There are two main kinds of leukocytes: granulated and agranular. There is a wide range in the percentage of granular and agranular leukocytes present in the blood (examples of each are basophils, eosinophils, and neutrophils, and monocytes and lymphocytes, respectively) [1]. In Fig. 1, the different types of leukocytes are represented; it can be seen that macrophages have a nucleus with several lobes, whereas eosinophils have only two. The theoretical and practical features of leukocytes are evaluated using automated machines in the lab; however, these devices are not reliable enough to detect morphological abnormalities. Improved reproducibility in picture classification is made possible by computer-aided erythrocytes categorization methods [2] in comparison to manual methods. The three types of blood cells can be distinguished by their appearance to the naked eye [3]. By streaking the blood, the white blood cells go from being clear to being opaque, and we can take pictures of the smeared blood with a high-definition camera mounted to a light microscopy. Computer vision like fragmentation, semantic segmentation, extraction of features, and classification are used to build an automated machine for analyzing white blood cells. Categorization is used to get rid of red blood cells, macrophages, as well as the background before WBCs can be taken out of the smear images. Segmentation of WBCs is followed by retrieval of morphological characteristics. Many of these characteristics are used by hematologists, for example those based on hue, shape, and surface roughness.

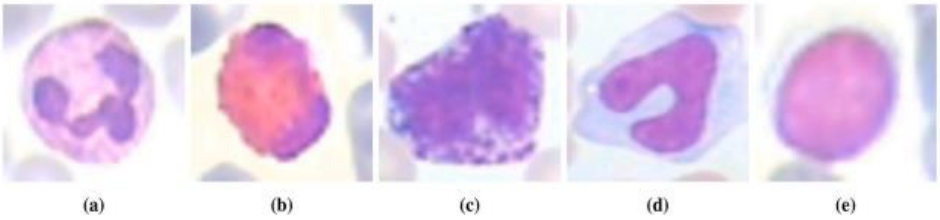

Fig 1: (a) Neutrophil (b) Eosinophil (c) Basophil (d) Monocyte (e) Lymphocyte.

After features have been picked to bring down the dimensionality of the feature vectors, a machine learning technique can be used to perform the classification. The purpose of classification is to determine which category a given thing best fits into. [4]. Feature extraction comes first in the conventional machine learning method before categorization. Various features have been employed for classification by numerous researchers [5]. The

primary components of the suggested methodology are transfer learning-based categorization, semantic segmentation, & database updating.

Our study is unique because it incorporates fragmentation with this kind of transition having to learn categories to find a way to use deep learning to find the five subcategories of WBC in images over whole blood smears. The rest of this article is broken up into the sections below. In Section 2, we talk about the works that go with them. In Section 3, the recommended plan is laid out. Section 4 talks about the result, Section 5 talks about the evaluation, and Section 6 gives the conclusion.

2. RELATED WORKS

Many scientists have come up with computerised ways to look at dermoscopic examination of cells. A few really studies show algorithms that divide eukaryotic cells only along the borders of their nuclei, whereas in others, the both core and the cytosolic are split apart. Yiping Cao et al. [6] wrote about a fast method for thalamic fragmentation that separates the A and H elements and then filters out whatever residual platelets. They also suggested adding Otsu chromaticity thresholding [7] to a different method for separating nuclei, but only after making the absorption component more noticeable. R. S. Gomalka et al. [8] give an automated system for accurately detecting nuclei in Rgb space from microscopic examination of dyed specimens taken from individuals with dispersed large B-cell leukaemia. F. Cao et al. [9] said that to detach WBC nuclei and cytosolic, they used a method based on a moving window.Specifically, they used an adaptive threshold-based approach to partition the nucleus, and the window-initiated GrabCut technique to partition the cytoplasm.

In numerous studies, the total number of leukocytes was calculated following careful segmentation of the cells. N. Ritter et al. detailed a histogram-based method for structures that make up in blood smear images. They weren't able to get great accuracy because they only evaluated the algorithm on a small dataset. When dividing WBCs, Y. Liu et al. use the continuous GrabCut algorithm with a geographical window as an initialization. Instead of manually selecting a rectangle to use as the starting point for automatic segmentation with the GrabCut method, the position windows can be used instead [10]. Although F. Zhang et al[11] .'s suggestion of a deep learning approach that uses pixel information for supervised training to locate the leukocyte zone is promising, it is still constrained to input photographs featuring a single WBC. Scientists have developed a battery of tests that use microscopic images of blood to separate leukocytes and identify any abnormalities, allowing for the early diagnosis of leukaemia and its variants. C. Reta et al. [12] recommended white blood cell (WBC) analysis as a means of classifying leukaemia subtypes. When they modelled the segmentation problem as a MAP estimation and used a recursive conditional model to solve it, they were able to attain a 92% accuracy rate and a

96% evaluation of the future. J. Rawat et al. [13] employed a genetic technique to classify normal acute regarding the biological and acute myeloblast cells. Once the image was thresholded, we employed morphology analysis and categorization based on colour and texture appearances to get to the meat of the matter. Thanks to the rapid development of AI, early and speedy detection of a variety of diseases is now feasible using automated procedures that make use of deep learning approaches. CNNs are being used more and more for diagnosis and treatment in the field of diagnostic imaging.

Examples include a skeletal bone age work referred to in the classroom [14] and a machine learning approach once again for detecting leukaemia in blood photos that employs transfers requiring the learning of methods for extracting features and support vector machine (SVM)-based classification. In this article, the authors showed that the effectiveness of medical training with a reduced sample size can be improved by employing transferable learning techniques. They also demonstrated that adding more neural network to a system doesn't always make the results better.

A slight number of papers have been written about how deep learning methods can be used to sort monocytes subsets. F. Qin et al. [15] came up with a classification model using a deep residue left neural network. They showed that it could correctly divide leukocytes into 40 different groups. P. Tiwari et al. [16] was using a CNN-based architectural features to divide the mitochondria into 4 categories and got average recall, accuracy, and F1 scores below 93% while leaving basophils out of their investigation. Using the structure of WBCNet [17], Y. Using deep convolutional neural network, Guo et al. created a system for identifying white blood cells that works very well (95.1% of the time). B. Hegde et al. [18] used a computational intelligence algorithm to classify six different types of WBC, which include malignant growth, with excellent precision by introducing additional data preprocessing methods. Using a deep neural network, they also devised a way for dividing WBC into 5 distinct categories. Y. Baydilli et al. demonstrated 97.50% accuracy using a capsule network to classify five subtypes of leukocytes. However, these analyses rely on trimmed versions of WBC datasets. However, when analysing a blood smear at a microscopic level, we must take into account the full blood spread image, which comprises RBC and numerous WBC. Methods for sorting leukocytes in a blood smear image can be broken down into two categories: segmentation followed by classify (two-stage) techniques, and categorization entity monitoring devices.

3. PROPOSED WORK

Two phases of pipelining are used in the suggested procedure. WBC localization is performed in the initial stage employing semantic segmentation, that is then proceeded by images cropping. To better isolate WBCs from the overall blood smears image, our study aims to apply segmentation to find all WBCs with higher overlap over union and mean

average accuracy, which then in turn results in more accurate classification. These are covered in more detail below. Fig. 2 depicts the proposed method's general layout.

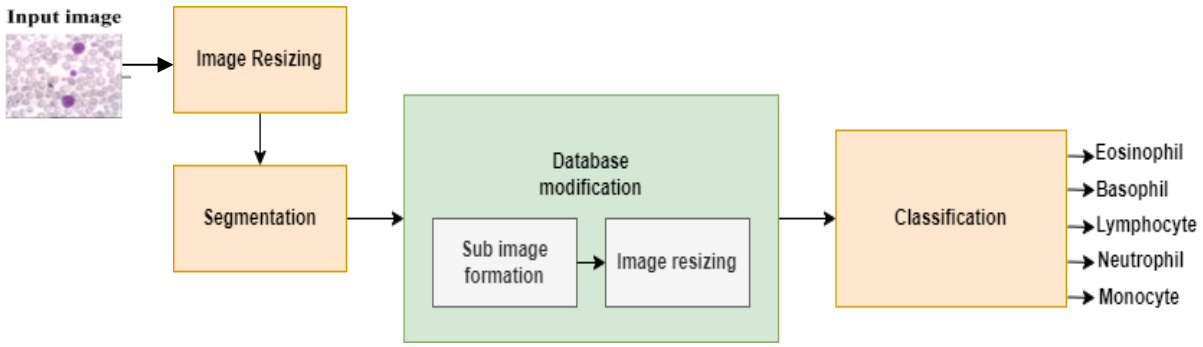

Fig 2: Overview of the Proposed system

3.1 WBC LOCALIZATION

Images of human blood that were manually sorted into five categories serve as input, and they can be obtained from the publicly available database LISC (Monocytes Imaging for Segment and Classification). Semantic segmentation is the first step in the localization of White blood, which is proceeded by image cropping. Following semantic segmentation, the preprocessed image is subjected to an area widening procedure to eliminate duplicate items with fewer than 200 pixels.

3.2 SEMANTIC SEGMENTATION

Semantic segmentation classifies every image pixel into one of many groups. This classification method is also known as "classification at the pixel level." Semantic segmentation has indeed been posed as a binary classification problem throughout our proposed work, with each pixel being labelled as belonging either to the WBC or the background. To make such a dense forecast, a NN with many convolutional layers should be used, with same buffering. Maintaining the original quality throughout the process with this implementation approach, however, requires a high degree of computing complexity. So, an encoder-decoder design that uses downsampling in the encoding phase and upsampling in the decoding phase is a typical approach. Separating WBCs from the blood smear images is the focus of this research, and to do so, we employ semantic segmentation based on DeepLab architecture.

3.3 DEEPLAB BUILDING DESIGN.

Plans for the DeepLab, as they are called. For text categorization, DeepLab uses a two-step process using machine learning: encode and decoder. In the encoding phase, a trained deep neural network (CNN) is used to extract information from the images. The decoder takes

the inputs and generates a new output of the same dimensions. The bulk of decoders employ bilinear upsampling, despite its inability to reconstitute finer features [20]. Our suggested research uses the DeepLabv3+ segmentation model; its architecture is shown in Fig. 4. As part of the encoding process, it employs input image able convolutions [21] to ensure complete coverage. In the decoder stage, the 4-factor extract features rendition of the encoded features is joined with the limited attributes that were retrieved in the encoding stage. The image obtained is upsampled by a factor of four, and then a couple 3*3 convnets are performed so that it has the same proportions as the original images.

The recommended training algorithm as well as the alternative training methods are discussed. Stochastic descending with velocity, a common optimization approach with quick convergence, is used to train the planned network. Assuming you've set your system up such that it learns at a pace of 103 per second at first, you should have it learn at a rate of 100.3 per second.. For this period, let's say we reduce the total amount by a ratio of 10. The speed ratio, which is set to 0.9 [41], determines the amount of time needed to learn how to use the transfer mechanism. In order to avoid overfitting, training is performed with weights started at 0.02 and L2 regularisation [22]. To construct the improved images for the classification task, the input images were duplicated left-right, shifted vertically and horizontally by up to 10 pixels, and twisted by up to 20 degrees. Using the technique, we can see the specific steps involved in WBC localization.

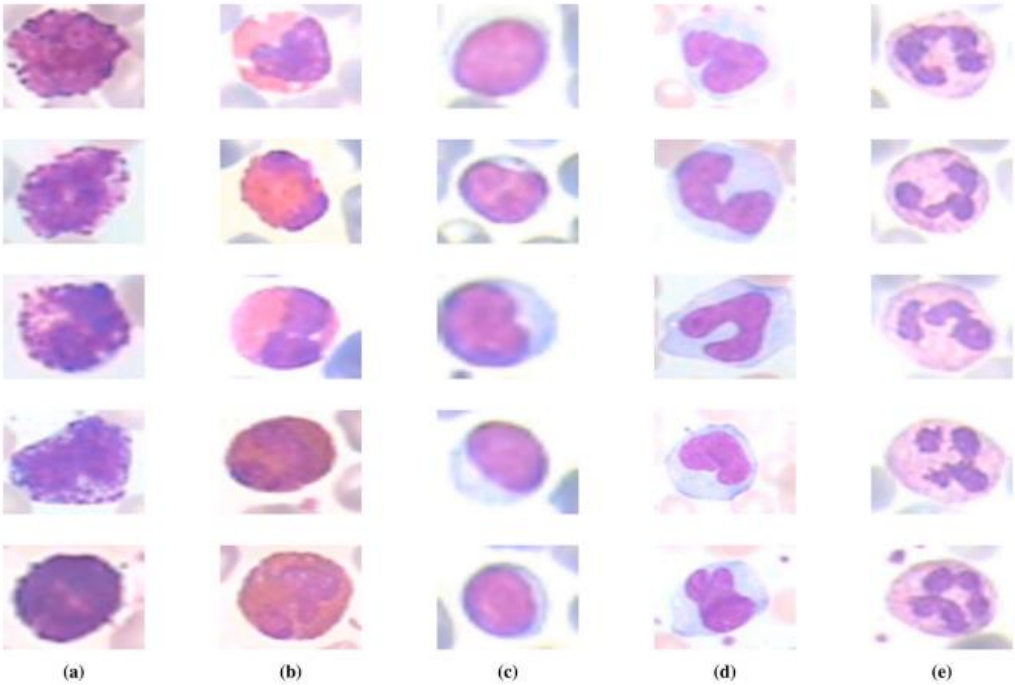

Fig 3: Dataset samples. (a) Basophil (b) Eosinophil (c) Lymphocyte (d) Monocyte (e) Neutrophil.

Algorithm 1: WBC segmentation method

Input: Regression coefficients images in gray scale image and a blood smear image in RGB format are the inputs.

Output: Mask Image is the result.

1. Scale up all input photos to 215 x 215.

2. Select the RGB images within the database and create an image data store.

3. Decide to have 2 classes.

4. Based upon ground truth pictures, assign the labels "WBC" and "background" to each pixel in the input image to create a labeling storage service.

5. Using the already-trained network ResNet50, create layers for the DeepLabv3+ network.

6. Substitute a supervised classification layer with values initialised with average periodic class weight for the classification layer in the DeepLabv3+ network.

7. Assign 12 groups to the photographs in the data storage.

8. Choose one group for testing and the other groups for instruction.

9. Apply training data to create enhanced images.

10. Using test photos as input, obtain the segmentation results.

11. Binarize the result of segmentation.

12. Complete the gaps in the source images, and if there are any small items there, do an area clearing operation to get rid of them.

Algorithm 2: WBC cropping

Input: Cover image input.

Output: Leukocyte sub-images are the result.

1. The enclosing box's beginning point (x,y), width, and height should be determined. Do the following for each object: x = Minmumvalueofrow 0.3; y = Minimumvalueofcolumn 0.3; width = Max.ValueOfRow + 1; height = Max.ValueOfColumn + 1;
2. Use bounding boxes to crop the WBCs from the entire blood smears image, then resize the sub-images to 215*215*2

Using a frame, which refers to the lowest rectangle that includes the area of interest, an automatic vehicle cropping is done to make a new dataset composed of half of the WBCs. Using key - point labelling, we locate each object's frame and identify the items in the input images. Three variables are required to establish the enclosing box's original position: its box's beginning position (x, y), breadth, and heights. Here, the object in the source images is 0.3 px towards the left of the primary section and 0.3 px next to the first queue. The width of the box at the beginning is set by the difference in between block's most and least values plus 1. In a similar way, the starting altitude is the discrepancy between column's maximum and lowest values times 1. The recommended Automatic system 2 and Training methodologies both demonstrate the exact steps for resizing the WBC in order to update the database. They also show how the input image's frame is utilized in the crop growth operation. The cropped image is then resized to match the size set in the action recognition network so that it can be sorted into categories in the image data repository.

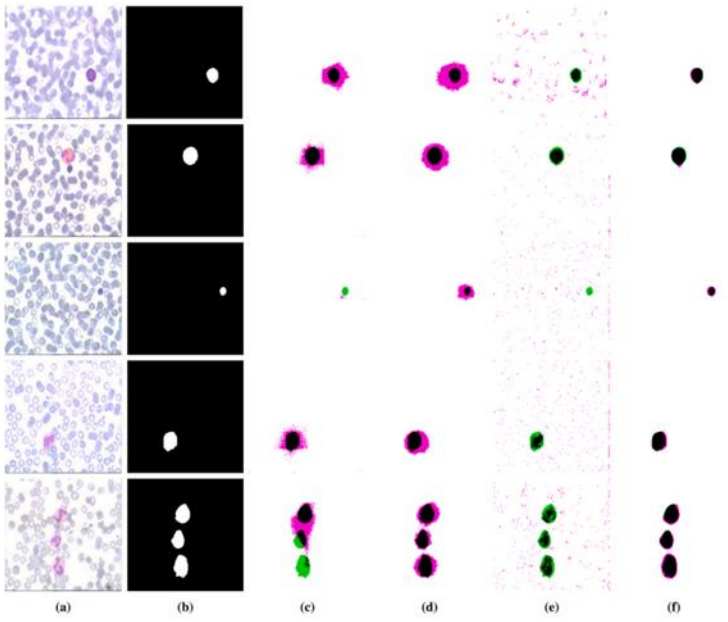

Fig 4: (a) Input image (b) Ground truth (c) Results of FCN (d) Results of SegNet (e) Results of U-Net (f) Results of the proposed method. Top to bottom: Basophil, Eosinophil, Lymphocyte, Monocyte, and Neutrophil image.

4. EXPERIMENTAL ASSESSMENT

4.1 THE DATABASE

The 715 x 550-pixel photographs in the publicly accessible LISC database have been the subject of experiments. Hematological photos from peripheral smears stained using the Gismo-Right method are included. All of the photographs were shot with a hd camera mounted on a microscope with a grayscale lens at a resolution of 120 and they were all saved in the BMP file format. 45 photographs of basophils, 45 images of neutrophils, 38 images of eosinophils, 49 images of lymphocytes, and 45 images of monocytes are included in the database.54 images of basophils, 38 photographs of eosinophils, 59 images of lymphocytes, 48 images of monocytes, and 54 images of neutrophils are included in the modified database that contains clipped images of leukocytes needed for classification.

4.2 EVALUATION AND RESULTS

All of our test results for MATLAB R2019b are carried out on a computer with a CORE i5 processor running at 1.85 Gigahertz, 8 GB of RAM, and an Integrated Intel Visuals 620 GPU. To find WBCs in electron micrographs, we use one feature extraction relying just on DeepLabv3+ model to identify them. Then, we are using a frame to delete only the WBCs we want to get rid of. A 10-fold cross-validation was used to show how well the classification method worked. During in the system testing of a segmented image, we had an accuracy rate of 97.39%, a mean IoU of 84%, and an approximated precision of 97.89%.

The segmentation of several leukocyte subtypes yielded average IoUs, which are displayed in Tables 1 and 2. Researchers were able to localised all WBCs thanks to the high IoU (over 76%) achieved by our suggested approach across all pictures. Correctness is a useful indicator for classification problems when working with symmetric sets of data. We have calculated the specificity, recall, and sharpness of our identification to back up the Accuracy level. F1 score has been regarded as an effective discriminator in place of accuracy in improved classification techniques. We propose a strategy in which the F1 score can reach 100 for eosinophils and eosinophils and a noteworthy value for the other 3 types of cells. Mini and meta techniques, as well as the F1 score, Precision and recall, were utilised to prove the classification system's worth. The proposed legislation has scores of 98.12 percent on the micro-F1, micro-precision, and micro-recall measures, and of 98.97 percent, 97.75 percent, and 97.92 percent on the macro-F1, macro-precision, and macro-recall measures, respectively. Performance metrics for each class inside the classification job are shown in Table 1.

Table 1: Evaluated performance metrics for classification

Parameters	SegNet	FCN-AlexNet	U-Net	Proposed
Mean accuracy	98.14	98.53	80.01	99.04
Mean IoU	65.42	62.85	77.61	80.57
Mean BF-Score	0.532	0.4521	0.689	0.786

Types of WBC	Precision	Recall	F1 Score	Specificity
Basophil	99	99	99	99
Monocyte	99.5	100	98.2	100
Lymphocyte	96.8	100	98.8	97.5
Eosinophil	99.5	99.5	99.5	100
Neutrophil	100	97.8	100	99.4

Table 2: Comparison of segmentation result with the proposed model

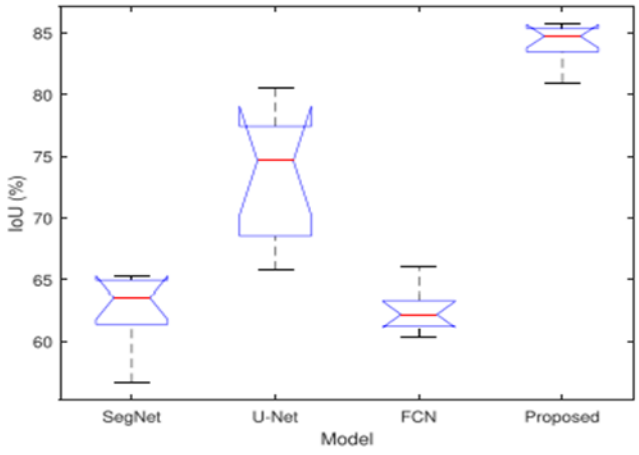

Fig.5. Comparsion of model

Using one-way analysis of variance, we examined the average reliability (@IoU = 0.6) achieved by our conceptual scheme to that achieved by category-based object recognition.

Here, we employ 10 minor datasets to test our hypothesis there was no statistically valid distinction between the results accuracy of the developed system as well as those generated by classification methods for object recognition, such as Faster R-CNN and YOLOv2. The resultant boxplot is shown. The achieved p-value of 3.839e 11 is small enough to indicate that the null hypothesis can be rejected. where the dataset contains cells that touch, while simultaneously improving processing time.

5. CONCLUSION

The five subtypes of leukocytes in peripheral blood are categorized using an analysis of RGB-format blood microscopy pictures. Semantic segmentation is used to pinpoint the location of white blood cells (WBCs), and transfer learning is used to classify samples using previously-trained connections, with the top three layers of which are modified to fit our specifications. Cropped and scaled versions of the WBCs that were detected make up the database used for classification. Accuracy, specificity, and F1 Score for each class are calculated as performance metrics to show how well the proposed recognition system works. Several metrics show that the proposed algorithm outperforms state-of-the-art methods: accuracy (average 97.35%), IoU (85.62%), average precision (average 97.74%) (@IoU = 0.7), and classification accuracy (99.021%). Another limitation of our investigations is the current paucity of data regarding leukocyte clustering and cell-cell contact. The processing time is slightly longer than with anchor box identification because we've created two-stage pipelines. To remedy this, future work will center on increasing processing performance and improving the scenario when the dataset comprises touching cells.

References

[1] Haichao Cao, Hong Liu, Enmin Song, A novel algorithm for segmentation of leukocytes in peripheral blood, Biomed. Signal Process Contr. 45 (2018) 10–21.

[2] Xin Zheng, Yong Wang, Guoyou Wang, Jianguo Liu, Fast and robust segmentation of white blood cell images by self-supervised learning, Micron 107 (2018) 55–71.

[3] Lorenzo Putzu, Giovanni Caocci, Cecilia Di Ruberto, Leucocyte classification for leukaemia detection using image processing techniques, Artif. Intell. Med. 62 (3) (2014) 179–191.

[4] N.Z. Supardi, M.Y. Mashor, N.H. Harun, F.A. Bakri, R. Hassan, Classification of blasts in acute leukemia blood samples using k-nearest neighbour, in: IEEE 8th International Colloquium on Signal Processing and its Applications, IEEE, 2012, pp. 461–465, 2012.

[5] Jakkrich Laosai, Kosin Chamnongthai, Classification of acute leukemia using medical-knowledge-based morphology and cd marker, Biomed. Signal Process Contr. 44 (2018) 127–137

[6] Yapin Wang, Yiping Cao, Quick leukocyte nucleus segmentation in leukocyte counting, Comput. Math. Methods Med. 1–10 (2019) 2019.

[7] Yapin Wang, Yiping Cao, Leukocyte nucleus segmentation method based on enhancing the saliency of saturation component, J. Algorithm Comput. Technol. 13 (2019), 1748302619845783..

[8] Ryszard S. Gomolka, Korzynska Anna, Krzysztof Siemion, Karolina Gabor Siatkowska, Wlodzimierz Klonowski, Automatic method for assessment of proliferation index in digital
images of dlbcl tissue section, Biocybern. Biomed. Eng. 39 (1) (2019) 30–37.

[9] Feilong Cao, Yuehua Liu, Zhen Huang, Jianjun Chu, Jianwei Zhao, Effective segmentations in white blood cell images using ε-svr-based detection method, Neural Comput. Appl. 31 (10) (2019) 6767–6780.

[10] Yuehua Liu, Feilong Cao, Jianwei Zhao, Jianjun Chu, Segmentation of white blood cells image using adaptive location and iteration, IEEE J. Biomed. Health Inf. 21 (6) (2016) 1644–1655.

[11] Haoyi Fan, Fengbin Zhang, Xi Liang, Zuoyong Li, Guanghai Liu, Yong Xu, Leukocytemask: an automated localization and segmentation method for leukocyte in blood smear images using deep neural networks, J. Biophot. 12 (7) (2019)e201800488.

[12] Carolina Reta, Leopoldo Altamirano, Jesus A. Gonzalez, Raquel Diaz-Hernandez, Hayde Peregrina, Ivan Olmos, Jose E. Alonso, Ruben Lobato, Segmentation and classification of bone marrow cells images using contextual information for medical diagnosis of acute leukemias, PloS One 10 (6) (2015), e0134066.

[13] Jyoti Rawat, Annapurna Singh, H.S. Bhadauria, Jitendra Virmani, Jagtar Singh Devgun, Computer assisted classification framework for prediction of acute lymphoblastic and acute myeloblastic leukemia, Biocybern. Biomed. Eng. 37 (4) (2017) 637–654.

[14] Concetto Spampinato, Simone Palazzo, Daniela Giordano, Marco Aldinucci, Rosalia Leonardi, Deep learning for automated skeletal bone age assessment in x ray images, Med. Image Anal. 36 (2017) 41–51.

[15] Feiwei Qin, Nannan Gao, Yong Peng, Zizhao Wu, Shuying Shen, Artur Grudtsin, Fine-grained leukocyte classification with deep residual learning for microscopic images, Comput. Methods Progr. Biomed. 162 (2018) 243–252.

[16] P Tiwari, J Qian, Q Li, B Wang, D Gupta, A Khanna, Joel JPC. Rodrigues, Victor Hugo C. de Albuquerque, Detection of subtype blood cells using deep learning, Cognit. Syst. Res. 52 (2018) 1036–1044

[17] A.I. Shahin, Yanhui Guo, Khalid M. Amin, Amr A. Sharawi, White blood cells identification system based on convolutional deep neural learning networks, Comput. Methods Progr. Biomed. 168 (2019) 69–80.

[18] B Hegde Roopa, Keerthana Prasad, Harishchandra Hebbar, Brij Mohan Kumar Singh, Comparison of traditional image processing and deep learning approaches for classification of white blood cells in peripheral blood smear images, Biocybern. Biomed. Eng. 39 (2) (2019) 382–392.

[19] B Hegde Roopa, Keerthana Prasad, Harishchandra Hebbar, Brij Mohan Kumar Singh, Feature extraction using traditional image processing and convolutional neural network methods to classify white blood cells: a study, Australas. Phys. Eng. Sci. Med. 42 (2) (2019) 627–638.

[20] Panqu Wang, Pengfei Chen, Ye Yuan, Liu Ding, Zehua Huang, Xiaodi Hou, Garrison Cottrell, Understanding convolution for semantic segmentation, in: IEEE Winter Conference on Applications of Computer Vision (WACV), IEEE, 2018, pp. 1451–1460, 2018.

[21] Liang-Chieh Chen, Yukun Zhu, Papandreou George, Florian Schroff, Hartwig Adam, Encoder-decoder with atrous separable convolution for semantic image segmentation, in: Proceedings of the European Conference on Computer Vision, ECCV), 2018, pp. 801–818.

[22] Twan Van Laarhoven, L2 Regularization versus Batch and Weight Normalization, 2017 arXiv preprint arXiv:1706.05350

[23] Vivienne Sze, Yu-Hsin Chen, Tien-Ju Yang, Joel S. Emer, Efficient processing of deep neural networks: a tutorial and survey, Proc. IEEE 105 (12) (2017) 2295–2329