Blood Cell Images Segmentation using Deep Learning Semantic Segmentation

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Abstract – **Segmentation of red blood cells (RBCs) and white blood cells (WBCs) in peripheral blood smear images plays an important role in the evaluation and diagnosis a vast of disorders, including infection, leukemia, and some types of cancer. Generally, various image processing techniques are used to enhance the quality of images before the segmentation step. Therefore, the segmentation of blood cells is still a challenge. However, in this research, deep learning semantic segmentation - cutting-edge technology is applied for segmentation red blood cells and white blood cells in blood smear images. The experiment result shows that the global accuracy of our model yielded 89.45%. Besides, the accuracy of the segmentation of white blood cells, red blood cells, and the background of blood smear image reached 94.93%, 91.11%, and 87.32%, respectively.**

Keywords-CNN; deep learning; segmentation; SegNet; Vgg-16

I. INTRODUCTION

Peripheral blood smear image analysis is used to early diagnose various diseases such as leukemia, anemia, and disorders of blood. There are three main types of blood cells, including red blood cells (RBCs), white blood cells (WBCs), and platelets. Medically, a complete blood count (CBC) is conducted to measure the number and quality of these components in blood cells images. Any abnormal CBC valued may be due to medical problems. The first illustration is from an extraordinary-increased WBC value may be led to some diseases, for example, allergies, tissue injury, infection, bronchogenic, and leukemia. Similarly, a high RBC count may be a sign of kidney tumours, polycythemia vera, or lung diseases [1].

A CBC is usually executed manually by a specialist in the strict laboratory environment under the microscope. Besides, the specialist may feel extreme fatigue as they have to count a large number of blood cells in a blood smear image. Hence, a computer-aided system is a necessary demand for supporting blood cell count. Meanwhile, segmentation of white blood cells and red blood cells in an image is an essential step on this system.

Some recent works related to WBCs and RBCs segmentation are based on color space such as HSI color space, L*a*b*. The other method utilizes conventional machine learning methods and image processing technique, for instance, K-Means clustering, Fuzzy C-Means clustering

and Watershed Segmentation. Because the blood cells have a diversity of shape and color, the segmentation exactly red blood cells and white blood cells in blood images still is a challenge. In this work, we ultilize a convolutional neural network (CNN) called SegNet to efficiently segment both WBCs and RBCs. SegNet architecture classifies all pixels in an image. The result is an image that is segmented by class.

The rest of this paper is organized as follows. A survey of recent works in literature is introduced in section 2. Our proposed method is presented in section 3. In the next section, the experiment result and discussion section are shown. Finally, section 5 illustrates the conclusion and future works.

II. RELATED WORK

In literature, various segmentation techniques were used to segment leucocytes and erythrocytes in images. Most recent segmentation methods utilize color space segmentation, clustering, and region growing. Due to peripheral blood smear images is affected by the acquisition condition and the light in the laboratory, these images can contain some noise. Consequently, in the past, most researches employ image processing algorithm to strengthen the quality of images.

In [2], the authors used Gram-Schmidt orthogonalization to enhance nuclei color, then localized the nuclei using morphological enhancement. To segment the cytoplasm the author utilized clustering-based seed extraction and marker-controlled watershed. The authors are not only segment white blood cells in an image but also they segment nucleus and cytoplasm of the white blood cells. The limitation of this paper only focuses on segmenting white blood cells in images.

In [3], the author integrated a shift-invariant complex wavelet transform into watershed segmentation for leukocyte segmentation.

Research in [4] segmented abnormal white blood cells in leukemia image using k-means, fuzzy c-means and moving k-means clustering. The authors made a comparison between three clustering algorithms and figured out that the moving k-means clustering reached the best performance for leukemia segmentation.

In [5], they proposed using image processing techniques for white blood cell segmentation. The author used CMYK color model for processing. Then, histogram equalization is

applied to images before thresholding images based on the triangle method.

In contrast to previous methods, our method reduces complex image processing steps for image enhancement purpose. In addition, this method reveals the good result in semantic segmentation cells. The detail of our method is introduced in the next section.

III. PROPOSED METHODOLOGY

A. Dataset Processing

Peripheral blood smear images from ALL-IDB1 database is used for our research purpose. Unfortunately, images available in this dataset lack corresponding segmentation ground truth images for segmentation purpose. Consequently, GNU Image Manipulation Program (GIMP 2.10.2) is used to label red blood cells and white blood cells in images for the purpose of segmentation. A part of an image in each blood smear image is cropped for creating the corresponding ground truth image. Totally, 42 cropped images were carefully annotated as ground truth images. Figure 1 shows an example of a peripheral blood cell image and its ground truth in the dataset.
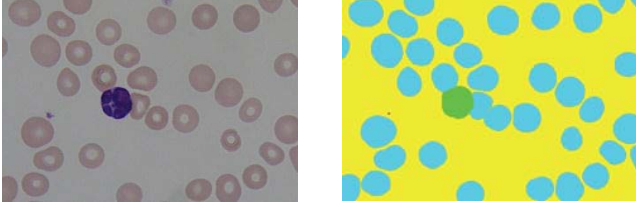

Figure 1. A peripheral blood smear image and its ground truth.

B. SegNet architecture

Semantic segmentation is a process of assigning each pixel of an image into a class label. For many years, semantic segmentation is widely used in various applications, especially road segmentation for autonomous driving and medical imaging analysis. In this paper, SegNet is utilized to segment blood cells in a peripheral blood smear image. SegNet is proposed in [2] for semantic segmentation tasks. This architecture utilizes pairs of encoder and decoder to create feature maps for segmentation, as illustrated in Figure 2.

Encoder architecture of SegNet stacks convolutional layer, batch normalization and using ReLu for activation function. After that, max-pooling is used to reduce the feature map size. This also leads to blurring the boundaries of the object in images. To solve this problem, before sub-sampling, boundary information is stored in the encoder feature maps.

It is necessary for the output image has the same size as the input image. Therefore, the decoder stage of SegNet includes upsampling. Memorized max-pooling indices, which is stored in each encoder map, is used to upsample the feature map. Each decoder has corresponded with an encoder.

The last decoder is connected to a softmax classifier to classify each pixel in an image.
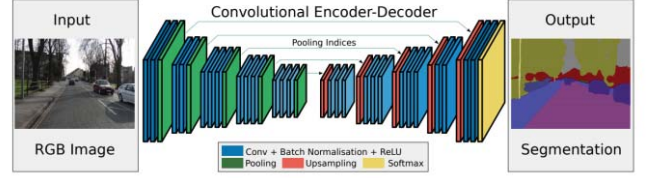

Figure 2. SegNet architecture [2].

In this work, SegNet network is created with weight initialized from the VGG-16 network. The last pooling layer for classification from the pre-trained VGG-16 is removed. Then the additional layers required for semantic segmentation is added.
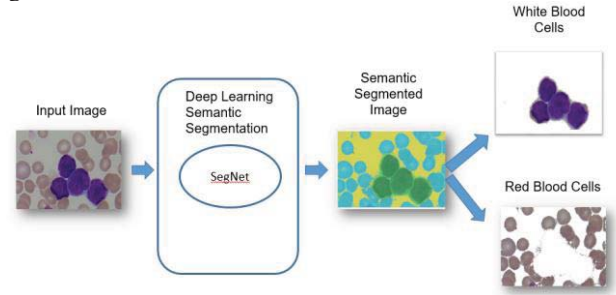

Figure 3. Our proposed procedure.

An overall framework of our method is shown in Figure 3. The first step of our proposed method is labeling all of red blood cells, and white blood cells in input images with different colors. This step utilizes SegNet to label each pixel with its corresponding class. Then, all leucocytes and all erythrocytes are separated into two individual images. Finally, the result images can be used for various purpose. For instance, the image contains only white blood cell can be used as the input of a neural network to early detect leukemia – a type of white blood cell cancer. Complete blood cell count is also another application of our work.

IV. EXPERIMENT RESULT AND DISCUSSION

In this paper, an experiment was conducted on a collection of images including 42 images and its corresponding collection of 42 pixel labeled images. Each pixel in a pixel labeled image has a value represents the categorical label of that pixel. The images in our dataset have different size. The size of images and corresponding pixel label images in the dataset are reduced to [360x480x3] to decrease the memory usage and training time. We use 70% images (29 images and 29 pixel label images) for training and 30% images (13 images and 13 pixel label images) for testing. To increase the size of dataset, original images are augmented by random reflection and random translation belong x-axis and y-axis 10 pixels. After augmentation training dataset, the number of training images is 145 images and 145 label images. The more dataset we handle, the more accuracy of the model reaches.

This research focuses on the segmentation of three classes in an image. For visualization, a pixel-labeled image is overlaid on top of an original image, as illustrated in Figure 4. In Figure 4, red blood cells are labeled as the blue color, white blood cells are annotated as the green color, and the background of the image is yellow. The areas with no color overlay which indicated by red arrow do not have pixel labels. These areas are not used during training.
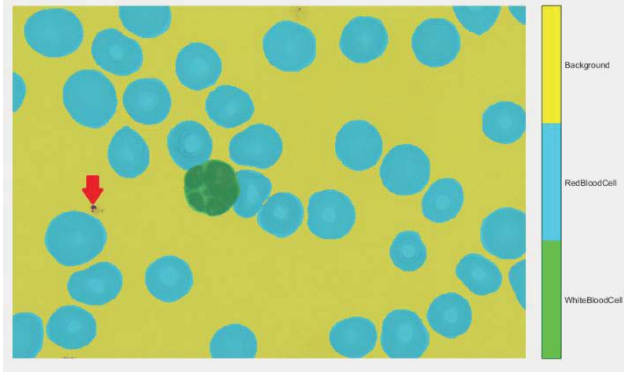

Figure 4. Overlaying a pixel-labeled image on top of an original image; blue color represents red blood cells; green color represents white blood cells, and yellow color represents the background. The red arrow indicates the area does not have pixel labels.
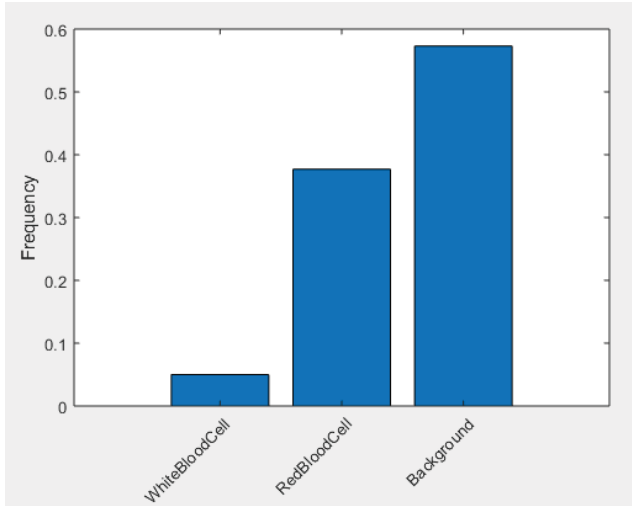

Figure 5. Histogram of the frequency of the number of pixels in each class.

As illustrated in Figure 5, images have more red blood cells, background pixels than white blood cells pixels. This imbalance of the number of pixels in each class can affect to the learning process of SegNet model on the training phase. In order to deal with this problem, class weighting is utilized to balance the classes [2].

Table 1 shows the semantic segmentation metrics to evaluate the quality of our model on testing dataset. The mean accuracy takes an average accuracy of three classes in our dataset ((white blood cells, red blood cells, and background). The model has a mean accuracy of 91.12%

when run on the testing dataset. We also use weighted IoU metric, an average IoU of each class, weighted by the number of pixels in that class. Weighted IoU metric decrease the impact of error in white blood cell class because the number of pixel in classes are imbalance.

TABLE 1. SEMANTIC SEGMENTATION METRICS OF THE MODEL

Global accuracy	0.89447
Mean accuracy	0.91120
Mean IoU	0.79184
Weighted IoU	0.80901
Mean BF Score	0.77040

Class metrics for each class (including classification accuracy, the intersection over union (IoU), and the boundary F1 contour matching score) illustrated as in Table 2.

TABLE 2. THE CLASS METRICS FOR EACH CLASS

	Accuracy	IoU	Mean BF Score
White Blood Cells	0.94929	0.75042	0.62464
Red Blood Cells	0.91112	0.80025	0.84247
Background	0.87319	0.82485	0.84409

Figure 6. The confusion matrix of the proposed method for testing phase

IoU is a measure of the overlap between the ground truth labeled image in the dataset and the resulting image was generated by our model. This metric is calculated by dividing the area of the overlap between the ground truth image and the resulting image by the area of a union (the area which is combined with the ground truth and the resulting image). The threshold value of IoU larger or equal 0.5 to decide that the segmentation result is good. The value of boundary F1 contour matching score (mean BF score) is between [0, 1].

In Figure 6, a confusion matrix of the proposed method on testing dataset is shown. True positives for white blood cells, red blood cells, and background class corresponds with 94.93%, 91.11%, and 87.32%.
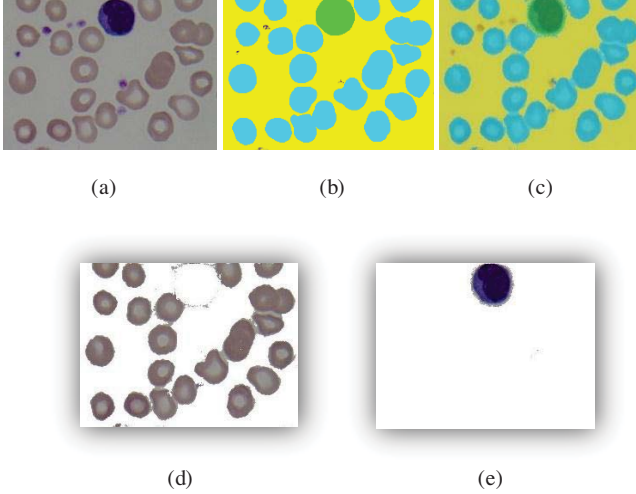
| (a) | (b) | (c) |

| (d) | (e) |

Figure 7. (a) The original image, (b) The ground truth image, and (c) The predicted result (IoU = 0.89966).

Figure 7(c) illustrates a results image in the test dataset with IoU reaches 0.89966. In Figure 7, the IoU for white blood cells, red blood cells, and the background class yields 85.50%, 82.9%, 84.88%, respectively. Figure 7 (d), (e) shows the final result of the segmentation phase, whereas the image in Figure 7 (a) is separated into 2 images. One of these includes all red blood cells, and another image contains white blood cell.

In the past, the vast majority of related works conduct their testing experiment with their own datasets. Most of them are private datasets. Thus, it is difficult to reproduce the state-of-the-art methods proposed in the literature for comparison purpose.

V.   CONCLUSION

In this paper, we propose using an innovative deep learning architecture for identification and segmentation of WBCs and RBCs in peripheral blood cells images. Our method proves the high accuracy when classifying WBCs and RBCs region in a blood image. This work promises to integrate as an initial step into a support system for counting blood cells in images. Besides, WBCs segmentation is an essential step to the prediction of some disease, such as leukemia. In the future, we would like to expand the size of the dataset in order to the model can learn the good features in the training phase of the model.

REFERENCES

[1] "www.cancer.ca," Canadian Cancer Society, [Online]. Available: http://www.cancer.ca/en/cancer-information/diagnosis-and-treatment/tests-and-procedures/complete-blood-count-cbc/?region=on#ixzz5JmJ8jOk9. [Accessed 20 08 2018].

[2] Afaf Tareef, Yang Song, Dagan Feng, "Automated multi-stage segmentation of white blood cells via optimizing color processing," in *2017 IEEE 14th International Symposium on Biomedical Imaging (ISBI 2017)*, 2017.

[3] Wei Gao, Yinggan Tang, Xiaoli Li, "Segmentation of Microscopic Images for Counting Leukocytes," in *2008 2nd International Conference on Bioinfomatics and Biomedical Engineering*.

[4] N. H. Harun, A. S. Abdul Nasir, M. Y. Mashor, R. Hassan, "Unsupervised Segmentation Technique for Acute Leukemia Cells Using Clustering Algorithms," vol. 9, 2015.

[5] Lorenzo Putzua, Giovanni Caocci, Cecilia Di Rubertoa, "Leucocyte classification for leukaemia detection using image processing techniques," *Artificial Intelligence in Medicine,* vol. 62, no. 3, pp. 179-191, 2014.

[6] Vijay Badrinarayanan, Alex Kendall, Roberto Cipolla, "SegNet: A Deep Convolutional Encoder-Decoder Architecture for Image Segmentation," 2016.

[7] Mateusz Budaab, Atsuto Makib, Maciej A. Mazurowskiac, "A systematic study of the class imbalance problem in convolutional neural networks," *Neural Networks,* vol. 106, pp. 249-259, 2018.