American Journal of
Biomedical Sciences
ISSN: 1937-9080
nwpii.com/ajbms

Classification of White Blood Cells using Convolutional Neural Network with Data Augmentation

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Received:31 March 2022; | Revised:29 May 2022; | Accepted:06 September 2022

Abstract

Nowadays, along with the development of science and technology, the classification of white blood cells (WBC) can assist in the diagnosis of leukemia. Manual blood cell classification is often not very accurate, time-consuming, laborious, and costly. Moreover, the risk of manual blood collection can be the transmission of infectious diseases such as HIV/AIDS, which causes unnecessary harm. Therefore, developing an automated system for blood cell classification will improve safety and save time and money. In this work, we proposed the classification method of white blood cells using Convolutional Neural Network (CNN) with Data Augmentation. To test the effectiveness of the proposed white blood cell classification system, a total of 10,299 white blood cells images from CellaVision was used. The experimented results of the proposed method have achieved 96% accuracy and compared to other published methods.

Keywords: White blood cells, Classification, Convolutional Neural Network, Data Augmentation, Blood disorder

1. Introduction

White blood cells play an important role in the body's immune system. They protect the body from harmful agents like viruses, fungi, etc. White blood cells are usually divided into 5 classes, which are basophil, neutrophil, eosinophil, monocyte, and lymphocyte as shown in Fig.1.

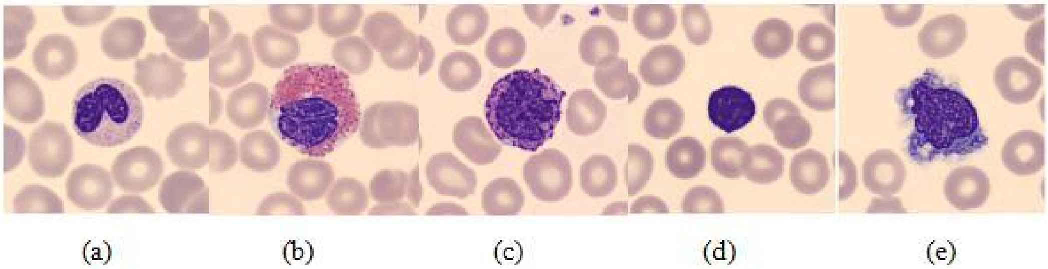

Figure 1: Five subtypes of white blood cell, (a) Neutrophil, (b) Eosinophil, (c) Basophil, (d) Lymphocyte, (e) Monocyte

The classification of white blood cells will help diagnose leukemia, thereby assisting doctors more in analyzing and diagnosing blood diseases. Traditional methods through microscopy are performed manually, it is laborious, time-consuming, and costly, especially when working with a large number of samples. Moreover, the low accuracy hinders the diagnosis and treatment process. Therefore, the automatic method of classifying white blood cells is being researched, developed, and widely applied because of its superior advantages compared to the manual method.

In studies reporting classification of WBC the accuracy is again the key aim for improvement. In 2013, Habibzadeh M. et al. [1] used SVM method to classify 140 WBC images and achieved 84.00% accuracy.

In 2016, Sajjad M. et al. [2] classified 1,030 leukocytes into 5 classes using SVM method. This method gave an average accuracy of 98.60%.

S. Ravikumar et al. [3] made a comparison between Fast-RVM method and ELM method in 2016 that achieved the accuracy of 84.13% and 79.94% respectively.

In the same year 2016, Zhao J. et al. [4] used a bigger dataset of 1,498 WBC images using the combination of 3 methods: SVM, random forest, CNN that provided an average accuracy of 92.80%.

T. Rosyadi et al. [5] applied K -Means Clustering on the classification of 100 leukocyte images. The average accuracy was roughly 60%.

In 2016, Anjali Gautam et al [6] used the Naive Bayes algorithm to classify WBCs into 5 layers. The simple thresholding technique is used for the segmentation of leukocytes by using Otsu thresholding. Only the nucleus region was considered for feature extraction. Thereafter, Naïve Bayes classification technique is used for the classification of leukocytes, the classification accuracy was about 80.88%.

In 2017, the project of M. I. Razzak et al. [7] utilized FRCN and ELM methods to classify a huge dataset of 64000 leukocyte images and reached an average accuracy of 95.10%.

Yu W.et al. [8] used CNN methods to classify a dataset of 2,000 WBC images into 5 classes in 2017. This method gave an average accuracy of 95.10%.

The project of Khamael A. et al. [9] in 2018 achieved the accuracy of 97.23% after using SVM model on 460 WBC images dataset.

In 2018, Macawile M. J. et al. [10] classified 100-500 WBC images using AlexNet CNN model that gave an average accuracy of 96.63%.

Wang Y et al. [11] ultilized a combination of CNN model with data augmentation to classify a dataset of 11658 leukocyte images from Sichuan Meisheng Biotech Company in 2019. The project performed at an average accuracy of 97.60%.

Kutlu et al. [12] used 6,250 WBC images dataset for the project. This project used VCG and RestNet50 of CNN model that provided an average accuracy of 97.52%.

In 2020, Truong, K.H et al. [13] published a study using a combination of CNN and SVM method to classify over 15000 WBC images that achieved an average accuracy of 97.52%.

Then, we have summarized these studies in Table 1.

Table 1: Published studies on WBC classification

Works	Year	No. Images	Method	Average Accuracy in %	Sources
Habibzadeh M. et al. [1]	2013	140	SVM	84.00	Unknown
Sajjad M. et al. [2]	2016	1,030	SVM	98.60	HMC Hospital
S. Ravikumar et al. [3]	2016	unknown	Fast-RVM	84.13	Hospital
			ELM	79.94	
Zhao J. et al. [4]	2016	1,498	SVM, random forest, CNN	92.80	Cellavison ALL-IDB Jiashan
T. Rosyadi et al. [5]	2016	100	K -Means Clustering	60.07	An engineered microscope
A. Gautam et al. [6]	2016	88	Naïve Bayes classifier	80.88	Unknown
M. I. Razzak et al. [7]	2017	64,000	FRCN+ELM	95.10	All-IDB + ;other
Yu W. et al. [8]	2017	2,000	CNN	95.70	Hospital
Khamael A. et al. [9]	2018	460	SVM	97.23	Cellavison ALL-IDB
Macawile M. J. et al. [10]	2018	100-500	AlexNet	96.63	All-IDB+other
Wang Y et al. [11]	2019	11,658	CNN +Data augmetation	97.60	Sichuan Meisheng Biotech Company +other
Kutlu et al. [12]	2020	6,250	VGG 16, RestNet50	97.52	BCCD LISC
Truong, K.H et al. [13]	2020	15,764	CNN+ SVM	97.80	Cellavison ALL-IDB BCCD Hospital

2. Methodology

Our method in this paper is to classify WBC using the images extracted from blood smear images. The proposed solution section describes the algorithms and methods that are used to build the proposed convolutional neural network model [14]. The first stage is Image Pre-processing which contains four methods: Load the dataset, Configure the dataset, Standardize the data. The second stage is to create a Convolutional Neural Network model. The final step is to Overfitting and Test the model. We implement our research on a PC based on core i5 11th gen, GPU GTX1650, software Jupyter Notebook, or Google Colab by Python programming language. The processing steps are shown in the following diagram.

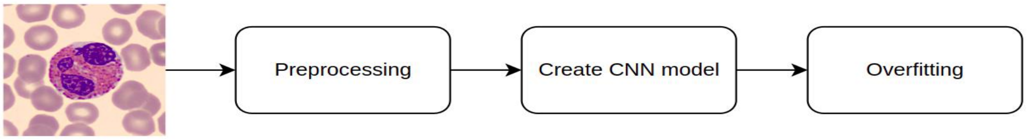

Figure 2: Diagram of the processing steps

2.1 Preprocessing

A. Load the dataset

We first define some parameters for the loader (batch_size, img_width and img_height). Then we split our data into 80% of the images for training, and 20% for validation.

B. Configure the dataset

We use buffered prefetching so you can yield data from the disk without having I/O become blocking. These are two important methods that could be used when loading data:

Dataset.cache: keeps the images in memory after they're loaded off disk during the first epoch. This will ensure the dataset does not become a bottleneck while training your model. If your dataset is too large to fit into memory, you can also use this method to create a performant on-disk cache.

Dataset.prefetch: overlaps data preprocessing and model execution while training.

C. Standardize the data

The RGB channel values are in the [0,255] range. This is not ideal for a neural network; in general, you should seek to make your input values small. Here, we will standardize values to be in the [0,1] range

2.2 Create CNN model

The sequential model consists of three convolution blocks with a max pooling layer in each of them. There's a fully-connected layer with 128 units on top of it that is activated by a ReLU activation function ('relu'). This model is a standard convolutional neural network model. Finally, we use “adam” optimizer and “Sparse Categorical Crossentropy” loss function from the Keras library to compile the model.

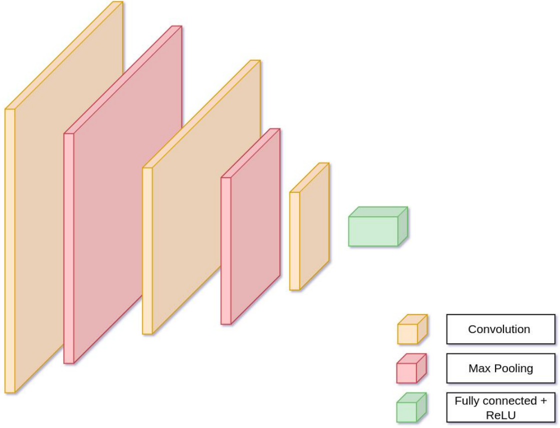

Figure 3: CNN model

2.3 Overfitting

When there are a small number of training examples, the model sometimes learns from noises or unwanted details from training examples—to an extent that it negatively impacts the performance of the model on new examples. This phenomenon is known as overfitting. It means that the model will have a difficult time generalizing on a new dataset. There are multiple ways to fight overfitting in the training process. In this tutorial, you'll use data augmentation and add Dropout to your model.

A. Data Augmentation

Data augmentation takes the approach of generating additional training data from your existing examples by augmenting them using random transformations that yield believable-looking images. This helps expose the model to more aspects of the data and generalize better. We will implement data augmentation using the following Keras preprocessing layers: RandomFlip, RandomRotation, and RandomZoom. These can be included inside your model like other layers, and run on the GPU.

B. Dropout

Another technique to reduce overfitting is to introduce dropout regularization to the network. When you apply dropout to a layer, it randomly drops out (by setting the activation to zero) some output units from the layer during the training process. Dropout takes a fractional number as its input value, in the form such as 0.1, 0.2, 0.4, etc.This means dropping out 10%, 20% or 40% of the output units randomly from the applied layer.

We create a new neural network with Dropout method before training it using the augmented images.

3. Dataset

The dataset contains a total of 10,299 images of individual normal cells, which were acquired using the analyzer CellaVision DM96 in the Core Laboratory at the Hospital Clinic of Barcelona [15]. The dataset is organized in the following five groups: neutrophils, eosinophils, basophils, lymphocytes and monocytes. The size of the images is 360 x 363 pixels, in format JPG, and they were annotated by expert clinical pathologists. The images were captured from individuals without infection, hematologic or oncologic disease and free of any pharmacologic treatment at the moment of blood collection. Dataset has 5 types of leukocytes: 1,218 images of basophil, 3,117 images of eosinophil, 1,214 images of lymphocyte, 1,420 images of monocyte and 3,330 images of neutrophil.

4. Results and Discussion

4.1 Results

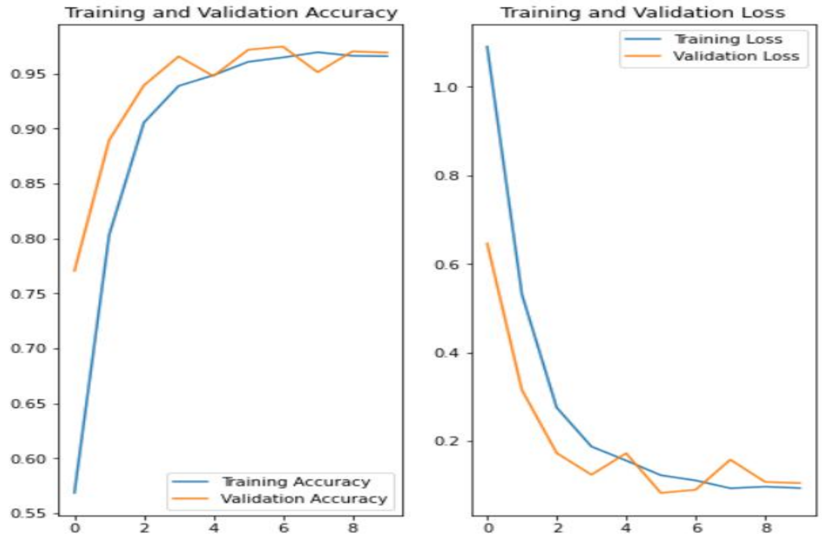

Figure 4: Training and Validation Accuracy Results

4.1.1 Validation data

Using the remaining 20% images in more 10,000 images for validation, we obtain the validation accuracy at 96.91%, as shown in Fig.4

4.1.2 Training data

Using 8,035 images to perform training, the author has achieved high accuracy with the accuracy rate of five layers of white blood cells. At the same time, the author compares some results of other methods, which are summarized in the table 2.

Table 2: Accuracy comparison (%) of our proposed classification method with other methods.

	Method	Basophil	Neutrophil	Eosinophil	Lymphocyte	Monocyte	Average accuracy
Kutlu H. et al. [12]	R-CNN VGG16	98.48	95.04	96.16	99.52	98.4	97.52
Zhao J. et al. [4]	SVM+ CNN, random forest	100	97.1	70	74.8	85.3	92.8
Our proposed	CNN+ Data augmentation	98.63	97.85	98.53	95.86	92.03	96.58

Kutlu H. et al. [12] utilizes the VGG16 and Resnet50 CNN and architectures trained with Transfer Learning showed the highest performance in all cells to be more successful in extracting features in the WBC images; cell types of Lymphocyte were detected with 99.52% accuracy rate, Monocyte with 98.40% accuracy rate, Basophil with 98.48% accuracy rate, Eosinophil with 96.16% accuracy rate and Neutrophil with 95.04% accuracy rate.

Zhao J. et al. [4] obtained PRICoLBP features for five types of WBC, they used SVM to classify them into three classes: eosinophil, basophil, and others. The applied learning algorithm for training CNN is the stochastic gradient descent method. Now a random forest is used to classify those extracted features with CNN to determine the left three types of WBCs: neutrophil, monocyte, and lymphocyte. A random forest is a classifier consisting of a collection of tree-structured classifiers, and each tree casts a unit vote for the most popular class at the input. Their classification method is not also perfect with an average accuracy of 92.8%, but they had the best classification of basophil.

While we proposed CNN for the classification of white blood cells into five subtypes and used data augmentation to improve the accuracy results and to avoid overfitting. Our accuracy results are basophil 98.63%, neutrophil 97.85%, eosinophil 98.53%, lymphocyte 95.86% and monocyte 92.03%, respectively.

4.1.3 Test data

Finally, in the test phase, we used 250 images into five classes of WBC and 50 images in each type. Cell types of Lymphocyte were detected with 97.52% accuracy rate, Monocyte with 96.40% accuracy rate, Basophil with 92.48% accuracy rate, Eosinophil with 85.16% accuracy rate, and Neutrophil with 90.04% accuracy rate.

4.2 Discussion

The classification of white blood cells into 5 subtypes has improved the process of analyzing and diagnosing diseases more quickly and accurately. We created a CNN model which is used to extract features at a high level, but the model will have a difficult time generalizing on a new dataset. To fight overfitting in the training process, we created a new neural network with the Dropout method before training it using the augmented images.The proposed method used CNN for the classification of white blood cells with data augmentation to avoid overfitting.

In this study, we achieved the classification of the result with a high average accuracy of 96.58%. Along with the previously used classification methods, as shown in Table 1, we have compared with other methods. As expected, the accuracy of eosinophil and neutrophil with our proposed method is 98.53% and 97.85%, respectively, which is higher than the results for Kutlu H. et al. [12] method and Zhao J. et al. [4] method. Moreover, our accuracy result of basophil is 98.63 %, which is not better than Zhao J. et al. [4] result but is also higher than Kutlu H. et al. [12] result. Although our classification results of lymphocyte and monocyte are 95.86% and 92.03%, respectively, which is not as accurate as of the above Kutlu H. et al. [12] methods, we have also achieved higher far from Zhao J. et al. [4] methods. The reason is that the number of our training images (8035 images) for training CNN is more than Kutlu H. et al. [12] methods (5000 images) and Zhao J. et al. [4] methods (1425 images). Moreover, the architecture of CNN is not the same. The ResNet-50 model of the method [12] consists of 5 stages each with a convolution and identity block; each convolution block has 3 convolution layers and each identity block also has 3 convolution layers and VGG-16 architecture consists of 13 convolutional layers, ReLU, Pooling, and 3 fully connected layers, all convolutional operation is done with 3x3 size filters while the method [4] used 5 convolutional layers and 2 pooling layers in their CNN architecture.

With the difference in the number and source of databases, the accuracy results of the methods are different, but all have achieved remarkable achievements. Of course, our classification method is also not perfect. Therefore, how to improve the classification of white blood cells based on our method is another direction of our study in the future.

5. Conclusion

The work presented in this paper describes a methodoloy for the diagnosis of WBC in blood images. We presented the method of white blood cell classification used CNN algorithm; this method has achieved quite promise results with high average accuracy over 96%. To avoid the problem of overfitting that some other methods encounter, in the implementation process, the author has used data augmentation to increase the database, improve the results better. In the near future, we might apply this method's results in hematology laboratory department, Hue Central Hospital, Viet Nam for counting and classifying of white blood.

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