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Detection, classification, and counting blood cells using YOLOv8

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***Abstract*: Distinguishing normal white blood cells from leukemia cells plays a role in assisting in the diagnosis of blood diseases. Up to now, many automated methods are applied to provide more time efficiency, timing, and accuracy such as YOLO, SVM, CNN, and Faster CNN. In this research, we propose to use YOLOv8 to detect, classify, and count normal white blood cells and leukemia cells. The result of the experiment method with accuracy is 95.1% using the first number of blood images is 1500 images from AML public source and Hanoi Medical University collected by ourselves, and after augmentation is 3629 images that are used for training, validation, and testing. At the same time, we compare the accuracy of this method with studies using different versions of YOLO.**

***Keywords*:** Normal White Blood Cells, Leukemia cell, classification, detection, WBC counting, machine learning.

I. Introduction

White blood cells, also called leukocytes or leucocytes, are important cells in the blood, in addition to red blood cells and platelets [1]. White blood cells perform the common task of protecting the body and preventing and destroying disease-causing factors that can weaken the immune system [2]. Usually, white blood cells are divided into 5 types: basophil, neutrophil, eosinophil, monocyte, and lymphocyte [3], as shown in Fig.1. In particular, each specific type of white blood cell takes on a specific function and role [4, 5], as follows:

A. Neutrophil

Has very strong motility and phagocytosis. This is a type of white blood cell that makes up the majority of white blood cells inside the body, responsible for killing bacteria, as well as fighting inflammation, and handling tissues in case of injury.

B. Eosinophil

Detoxifies proteins and foreign substances before they cause harm to the body. This type has a weaker phagocytic capacity than neutrophils.

C. Basophil

This is the least common type of white blood cell, making up less than 1% of white blood cells inside the body, unable to migrate and phagocytize. Functionally, they play an important role in some allergic reactions.

D. Monocyte

Exists in the blood in a transparent form. This type of white blood cell protects and repelling harmful agents, starting the production of antibodies.

E. Lymphocytes

Lymphocyte T: Recognizes and removes infection-causing cells.

Lymphocyte B: produces antibodies.

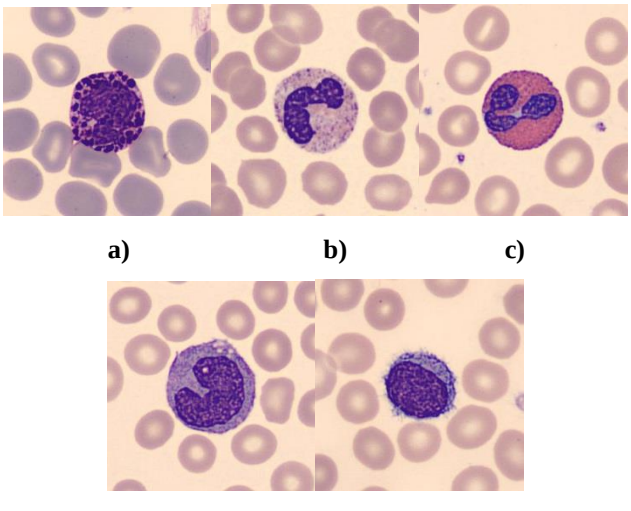

Figure 1. Five types of normal white blood cells (WBCs). a) Basophil, b) Neutrophil, c) Eosinophil, d) Monocyte, and e) Lymphocyte [28]

Because each type of white blood cell has its function and task, the process of counting, detecting, and classifying white blood cells by different methods will assist doctors in making a diagnosis and giving results, and discussing the patient's medical condition [6, 7].

During the analysis of data from the patient, in addition to the healthy white blood cells, there may also be the patient's diseased white blood cells. The diseased white blood cells are abnormally large, 3-4 times larger than normal cells, and have no cell nucleus. The most distinguishing feature is their size, in addition to their color and shape [8]. Leukemia is defined as a cancer of the blood (including the bone marrow and the lymphatic system) that is caused by abnormal cell hyperplasia of the bone marrow [9].

Acute leukemia is one of type diseased blood cells and is divided into 4 types: acute lymphoblastic leukemia (ALL) and acute myeloid leukemia (AML); Chronic leukemias include chronic lymphocytic leukemia (CLL) and chronic myeloid leukemia (CML) [10]. Acute myeloid leukemia (AML) is one of the white blood cells infected with acute leukemia that does not function like normal cells, and AML can rapidly increase in number [11], as shown in Fig.2. Therefore, the detection of AML blood cells has important implications for the protection of the human immune system.

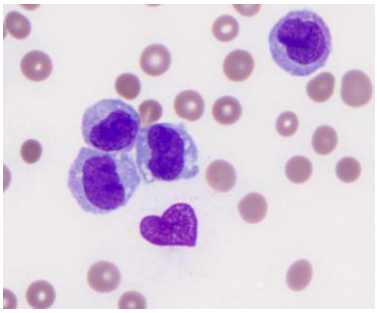

Figure 2. AML_M4 images: Leukemia cells [28]

The application of science and technology in the medical field is a common and well-received trend all over the world. In the field of blood tests in general and total white blood cell analysis in particular, the analysis of components of white blood cells is one of the methods to help doctors diagnose blood diseases, screen as well as detect blood diseases and disorders of the body affecting blood cells such as anemia, infections, inflammation, blood clotting disorders, blood cancers, and immune system disorders [12]. Therefore, counting white blood cells will help analyze the health status of people and limit the risk of infection with blood-borne diseases [13]. In addition, the detection and classification of diseased white blood cells from normal white blood cells play a role in the diagnosis of blood diseases, assessing the health condition of a person at a good level, or in the case of increased or decreased white blood cells.

In the previous, the analysis and classification of white blood cells by microscopic blood images is a manual process. This is the process of staining and counting white blood cells manually through a microscope and performed by expert blood analysts [14]. Performing this process for a long time causes a feeling of boredom, takes a lot of time, effort, and money, and is prone to human subjective errors, especially the inability to process the number of blood images large in a short time [14]. In addition, during the analysis, they also faced challenges such as not having enough training material on leukemic cell morphological changes to base their analysis and results on differentiating leukemic cells. Health leukocytes with diseased white blood cells [15].

Therefore, building a process of counting, detecting, and classifying white blood cells automatically brings many outstanding advantages. This helps to reduce costs, save time, and can process a large number of blood images in a short time [16]. Worth mentioning is the reduction of errors, high accuracy, and good results when testing with large amounts of data [17]. Therefore, the application of AI and deep learning, especially You Only Look Once (YOLO) in the process of analyzing blood images and classifying white blood cell types with diseased white blood cells helps to increase accuracy and reliability.

In this paper, we cover the use of You Only Look Once version 8 (YOLOv8) to detect, classify and count normal white blood cells with diseased white blood cells based on published and self-collected image data at the Hanoi Medical University, Vietnam. With this method, we achieve good results with high accuracy and are the basis for improving leukemia diagnosis and blood cell counting in the future.

II. Related Works

In the early stage of development of the automatic white blood cell sorting process, many researchers have introduced a method of blood cell classification using a sorting algorithm, which is performed through the following steps: Cell segmentation cytology, cell nucleus fractionation, feature extraction, cell classification [18-21]. This method has the advantage that it can achieve good accuracy and does not need large databases, or short training time, but the process of segmentation and feature extraction still faces many difficulties due to many variables different in color and size of normal and abnormal cell types and staining methods.

With the development of artificial neural networks, deep features of images are extracted from neural networks without going through preprocessing and segmentation. Some studies use a convolutional neural network model to classify white blood cells as shown in references [22-24]. Although this method does not need to perform cell segmentation, it requires the database to be large enough, about 3000 images for a cell class to give good classification results and avoid overfitting the model.

With the development of computer technology, the research and development of neural networks have led to the rapid application of deep learning models to detect and classify objects with high accuracy such as Support Vector Machine (SVM), Convolutional Neural Network (CNN), Region-Convolutional Neural Network (R-CNN), Fast Region-Convolutional Neural Network (Fast R-CNN), Faster Region- Convolutional Neural Network (Faster R-CNN), RetinaNet, and faster but very accurate method like Single Shot Detector (SSD) and YOLO network [25], [26], [31-33]. These methods do not need to use object segmentation and can detect objects in real-time, but this method still requires a large enough database and takes a long time to train the algorithm, it can be up to a few hours, or a few days.

Detecting small objects or dense areas is a challenge in object detection. Some white blood cells that are incomplete, immature, or located near the imaging boundaries are not detected [27-29]. Some large broken white blood cells can be mistaken for diseased cells. YOLOv8 is capable of classifying blood cells including normal cells and diseased cells in blood images with the same frame better due to bounding box and instance segmentation [34-43].

III. Methodology

In this paper, our purpose is detection, count, and classify WBCs using extracted images from blood smears of leukemia patients. In our paper, we use model Yolov8, the latest release of the famous model Yolov5 to classify and detect WBC. With the new features of Yolov8, we simply use CLI to train our custom dataset with Yolov8 weight. After 100 epochs of training, we obtain a new weight file to use the next time. We run our data on Google Colab, annotate data and deploy the model on RoboFlow.

A. Data Pre-Processing

Firstly, the Auto-orientation of pixel data (with EXIForientation stripping) was applied to the dataset. Then they are resized to 416x416 (Stretch).

B. Data-Augmentation

By adding random changes that produce realistic-looking photos to your current samples, data augmentation creates extra training data from them. This makes the model broader and exposes it to additional features of the data. We use: horizontal flip, rotate 90 degrees clockwise and counterclockwise, brightness between -25% and +25%, and applied mosaic.

C. Bounding-box Transformations

We use the following transformations of the bounding box: brightness between -25% and +25% and exposure between -25% and +25%.

D. Training the datasets

In the field of computer vision, the YOLO (You Only Look Once) set of models has achieved fame. The popularity of YOLO is due to its high degree of accuracy while retaining a tiny model size. A wide spectrum of developers can use YOLO models because they can be trained on a single GPU. On edge hardware or in the cloud, machine learning practitioners can deploy it for a reasonable cost. Since Joseph Redmond initially introduced YOLO in 2015, the computer vision community has fostered it. Versions 1-4 of YOLO were initially maintained in C code within Redmond's exclusive Darknet deep learning platform. Scaled-YOLOv4, YOLOR, and YOLOv7 are just a few of the models that have split off from the YOLOv5 PyTorch repository in the previous two years. Other models, such YOLOX and YOLOv6, have appeared all around the world as a result of their PyTorch-based implementations. Every YOLO model along the road has introduced fresh SOTA methods, pushing the model's precision and effectiveness. The most recent SOTA version of YOLO, YOLOv8, has been the focus of research by Ultralytics during the previous six months. Launched on January 10th, 2023, was YOLOv8, as shown in Fig. 3.

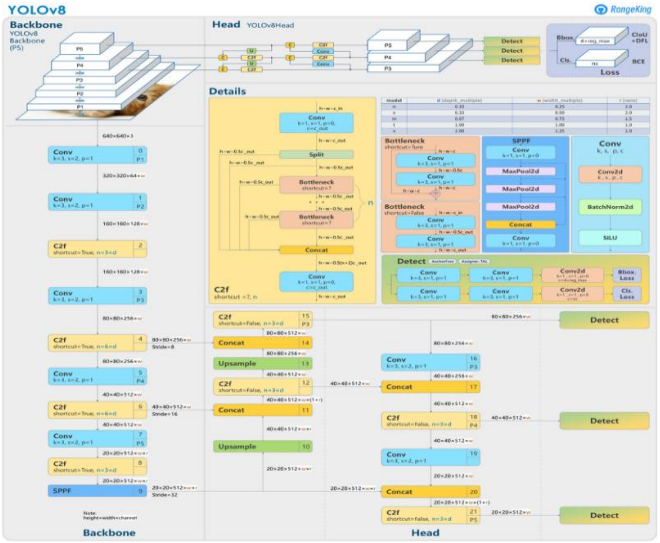

Figure 3. The network architecture of YOLOv8 [30]

In this paper, we choose the method using YOLOv8 with many advantages in research. According to COCO and Roboflow 100 measurements, YOLOv8 has a high accuracy rate.

A variety of developer-friendly features, including an intuitive CLI and a well-designed Python package, are included in YOLOv8.

Many experts in computer vision circles may be able to help you when you need advice because there is a sizable community around YOLO and a developing community around the YOLOv8 model, as shown in Table 1.

Model	Size (pixels)	mAP(val) 50-95	Speed CPU ONNX (ms)	Speed A100 TensorRT (ms)	Params (M)	FLOPs (B)
YOLOv8n	640	37.3	80.4	0.99	3.2	8.7
YOLOv8s	640	44.9	128.4	1.20	11.2	28.6
YOLOv8m	640	50.2	234.7	1.83	25.9	78.9
YOLOv8l	640	52.9	375.2	2.39	43.7	165.2
YOLOv8x	640	53.9	479.1	3.53	68.2	257.8

Table 1. Accuracy of YOLOv8 on COCO

IV. Dataset

Our data consists of 1071 images for the training set, 306 images for the validation set, and 123 images for the testing set. The original collection contains around 1500 pictures of blood samples taken from the public source that have Acute Myelomonocytic Leukemia (AML) images and our data that were taken from Hanoi Medical University and labeled by

qualified experts and doctors. 20% of the initial dataset was reserved for the validation phase, while the remaining 70% was used for training and the 10% rest is for testing The dataset now contains about 3629 photos after augmentation, with the number of images for training multi 3 and others not changed. The number of total images in initial data and augmentation data are shown in the Table 2.

	Dataset		
	Training data	**Validation data**	**Testing Data**
Initial data	1071	306	123
Augmentation data	3200	306	123

Table 2. Number of total images in initial data and augmentation data

V. Results

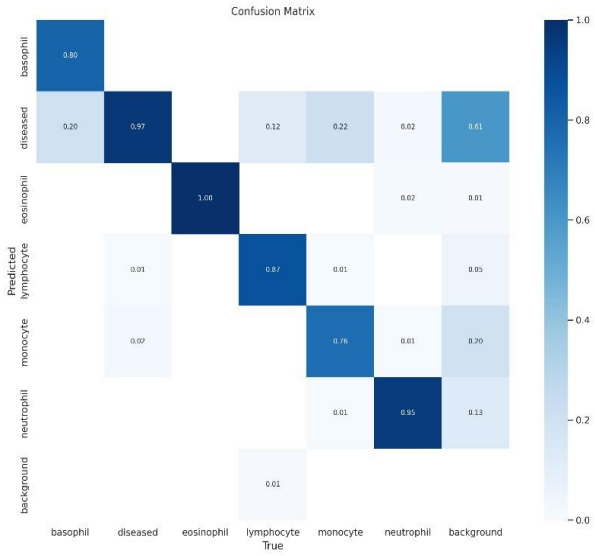

Figure 4. The results of the classification of blood cells

We used the YOLOv8 to detect, classify, and count both the normal WBCs and leukemia cells. And in our previous research, we also use YOLOv5 to experience but the result is not high, 93% [28]. YOLOv5 is easier to use, while YOLOv8 is faster and more accurate. However, for applications that require real-time object detection, YOLOv8 is the better choice in this research. Applying the new version 8 of YOLO, we develop, study, and achieve higher accuracy.

Following Fig.4, the correct prediction is basophil 80%, diseased 97%, eosinophil 100%, lymphocyte 87%, monocyte 76%, and neutrophil 95%. The reasons are quantity, labels, shape, and color. Once the blurred image or the error label, the classification is not true.

A. Training Data

One of the advantages of training data is large images. When the author trains about 3200 images of our data and the public sources, the result is good and can show 6 types, including 5 normal white blood cells and diseased cells.

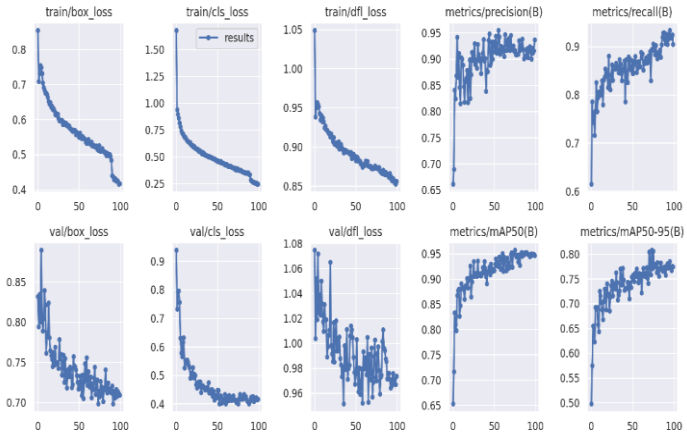

Figure 5. The results of the classification of blood cells

After training the data, the results are shown in Fig.5: bounding box regression loss (box_loss), classification_loss (cls_loss), distribution focal loss_loss (dfl_loss), precision (B), and recall (B).

We set the training to run for 100 epochs, and it converged after 100 epochs, so we stopped there. From 1-49 epochs, the results are not clear and not good. After 50 epochs, all results are the best, but after 50-95 epochs, the results decrease and have more loss than 50 epochs. So, we chose the result of 50 epochs to discuss prediction, recall, and mAP_50 results.

From Figure 5, the results of box_loss, cls_loss, and dfl_loss all converged after 100 epochs and decreased, which means that the smaller the total loss, the higher the accuracy.

B. Validation Data

When 100 epochs were completed in 3.237 hours, Ultralytics YOLOv8 in Python-3.8.10, the result is showed in the model summary with 218 layers, 25843234 parameters, 0 gradients, and 78.7 GFLOPs. Moreover, the speed is robust which is 1.4ms pre-process, 12.1ms inference, 0.0ms loss, and 1.4ms post-process per image.

By using YOLOv8 to validate 20% of the total images, we achieved an accuracy is 95.1%. In addition, the Precision, Recall, mAP50, and mAP50-95 results achieved good results, as shown in Figure 5 and Table 3.

Class	Images	Instances	Box_Precision	Box_Recall	Box_mAP50	Box_mAP50-95
All	306	908	92.5	89.5	95.1	80.7
Basophil	306	5	100	84.6	99.5	83.9
Diseased	306	587	92.0	97.4	97.0	79.7
Eosinophil	306	23	91.8	100	99.5	94.8
Lymphocyte	306	84	90.9	83.7	90.0	74.0
Monocyte	306	87	85.5	74.3	86.8	77.7
Neutrophil	306	122	94.5	96.7	97.9	74.1

Table 3. The BOX results(%) of the normal white blood cell (normal WBCs) and leukemia cells(Diseased)

To interpret the YOLOv8 prediction results in summary on a validation set, we focus on the results from Figure 5 and Table III such as mean Average Precision (mAP), precision, and recall. The mAP is a measure of the model's overall performance, while the Precision and Recall measure the model's accuracy in detecting different classes. Additionally, the class-wise performance of the model is the performance of the model for each class of white blood cells in the validation set. This will help to identify which classes are being correctly detected and which classes are being missed. So, basophil has the highest prediction while eosinophil has the highest recall, both 100%, and these two classes all have the highest accuracy, 99.5%. Moreover, the monocyte has the lowest prediction and recall result, so it has the lowest accuracy, 86.8%.

After 50 epochs, the results of mAP are the best, so we got it to discuss and analyze. The results of mAP_50 will be used and compared with other methods.

C. Testing Data

In the testing phase, we use randomly 123 blood sample images that obtain an average accuracy of 94.9%.

VI. Discussion

Each of version YOLO also has a main feature and helps the researchers study any method to detect, classify and count white blood cells. Sometimes, with small data, the result is not good or by the version YOLO itself, the accuracy results are not the same. Many previous versions of YOLO are used to detect and classify normal white blood cells but they have low accuracy of the results and need to go through the leukocyte segmentation process. Ramya et al. [27] trained YOLOv3, YOLOv4 and YOLOv5, they achieved the accuracy results are 91.0%, 89.0%, and 86.0% respectively. By comparing their methods, the YOLOv5 is the best accuracy but less than our result and not clearly what subtypes of white blood cells. With 14,700 annotated images, the highest images in this comparison, Wang et al. [29] classify 11 types of leukocytes and have good accuracy. Without significant modification, both SSD and YOLOv3 provide impressive performance in their study. With the new version of YOLOv8, our accuracy is the highest, 95.1%, as shown in Table 4.

Works	Year	No. Images	Sources	Method	Overall Accuracy (%)
Wang et al.[29]	2019	14,700	unknown	SSD300×300 YOLOV3	90.09 89.36
Ramya et al.[27]	2021	874	BCCD	YOLOv5 YOLOv4 YOLOv3	91.0 89.0 86.0
Our proposed	2023	3629	AML+ Hanoi	YOLOv8	95.1

Table 4. Comparison of accuracy (%) of our proposed method with other methods

VII. Conclusion

Detecting, classifying, and counting the normal white blood cells and diseased cells play a role in the diagnosis of blood diseases. With the differences in shape, color, or abnormal change cells, the manual method can be used, but have some drawbacks. The automatic process is applied and handles bulk conditions about large data. More and more methods are used in the automatic processing analysis of blood images. This method has good results in segmentation, and maintained a high classification accuracy, and others have robust time to detect and count subtypes of white blood cells. And the later version is developed, improved, and applied to be suitable for the different conditions of research. By using the YOLOv8 to detect, classify and count the normal white blood cells and leukemia, our accuracy is achieved good, 95.1%.

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