Enhancing White Blood Cells Segmentation Using Deep Learning

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Abstract: Accurately classifying white blood cell subtypes is essential for diagnosing various blood diseases. Traditional methods in computer vision often require manually engineered features, which are time-consuming and can limit performance. In contrast, machine learning approaches offer improved accuracy but typically demand extensive labeled datasets, which are challenging and costly to obtain. This study introduces a semi-supervised learning approach tailored for white blood cell classification. By leveraging a combination of a small amount of labeled data and a larger set of unlabeled data, the model learns to identify and categorize different white blood cell subtypes directly from microscopic images. This methodology capitalizes on the inherent structure and patterns present in the data, enhancing classification performance without relying solely on predefined features. The proposed approach was evaluated using a dataset comprising synthetic images representing various white blood cell subtypes. Results demonstrate promising accuracy in distinguishing between different cell types, showcasing potential applications in clinical diagnostics. By minimizing the reliance on manually labeled data while maintaining high classification accuracy, this approach offers a scalable solution for automating and improving the efficiency of white blood cell analysis in medical settings.

Keywords: White Blood Cells, Semi-Supervised Learning, Convolutional Neural Networks, Medical Image Analysis, Pseudo-Labeling.

I.INTRODUCTION

Accurate and timely classification of white blood cells (WBCs) is crucial for diagnosing various hematological disorders. Traditional supervised learning approaches require large amounts of annotated data, which is expensive and time-consuming to obtain in medical domains. This study proposes a semi-supervised convolutional neural network (SS-CNN) framework for automatic WBC classification, utilizing both labeled and unlabeled data. The model leverages consistency regularization and pseudo-labeling strategies to improve generalization and classification performance. Experimental results on the publicly available LISC and BCCD datasets show that the proposed SS-CNN achieves high classification accuracy with significantly less labeled data, outperforming conventional supervised CNN baselines.

White blood cells (WBCs) are a fundamental component of the immune system, and their classification is critical in diagnosing infections, leukemia, and immune system disorders. Manual classification is time-consuming, error-prone, and highly dependent on expert hematologists. Therefore, automating this task using artificial intelligence (AI), particularly deep learning, has become an area of active research.

Despite the success of convolutional neural networks (CNNs) in image classification tasks, their performance heavily depends on large-scale annotated datasets. In medical imaging, such datasets are difficult to compile due to annotation

costs and the need for expert knowledge. This paper addresses this challenge by proposing a semi-supervised CNN model that effectively leverages unlabeled data to improve WBC classification accuracy with minimal labeled data.

Neutrophils, monocytes, lymphocytes, eosinophils, and basophils are the five kinds of white blood cells found in human blood (figure 1). The most practical and economical way to view blood cells is by blood smear microscopy. One of the most important steps in the blood smear microscopy procedure is accurately and precisely categorizing the various types of white blood cells in the images. The traditional method of manual microscopy, however, takes a long time and is very susceptible to human statistical bias. Therefore, increasing the degree of automation in microscopy is urgently needed in clinical medicine.

As medical imaging methods advance, computer-aided automatic recognition and classification methods based on microscope images provide significant benefits in terms of of efficiency and cost-effectiveness. As a result, it has become a rapidly expanding trend in technical advancement. Traditional image segmentation algorithms can precisely identify individual white blood cells from microscope pictures because peripheral blood has a very low density of white blood cells. Thus, thorough cell segmentation using different techniques, feature extraction, and classification on segmented images were the main goals of early research on computer-aided cell image classification and recognition.

II.RELATED WORK

Various deep learning methods have been developed for WBC classification, primarily using supervised learning. Works like [1] and [2] use CNNs trained on curated datasets but suffer from overfitting when trained with limited data. Transfer learning techniques have also been applied but may not generalize well to domain-specific nuances in WBC morphology.

Semi-supervised learning has shown promise in applications such as object detection and medical imaging. Techniques such as Mean Teacher [3] and FixMatch [4] use consistency regularization and pseudo-labeling, respectively. Our approach builds upon these strategies to enhance classification performance in WBC datasets.

The automatic classification of white blood cells (WBCs) plays a pivotal role in the early detection and diagnosis of various hematological diseases, including leukemia, infections, and immune disorders. Conventional machine learning approaches have demonstrated success but are highly dependent on hand-crafted features and large labeled datasets. With the advent of deep learning, Convolutional Neural Networks (CNNs) have significantly improved classification accuracy. However, their dependency on large-scale annotated datasets remains a key limitation, especially in medical imaging. To overcome this, semi-supervised learning has emerged as a promising solution.

1. Supervised Learning Approaches in WBC Classification

Early research in WBC classification focused primarily on supervised machine learning. Techniques like Support Vector Machines (SVM), k-Nearest Neighbors (k-NN), and decision trees were used on hand-engineered features extracted from color, texture, and shape descriptors.

- Mohapatra et al. (2014) developed a rule-based ensemble classifier that utilized morphological features for WBC classification. Although effective, these methods lacked generalization due to handcrafted features.
- Rehman et al. (2018) introduced deep CNN models trained on curated WBC datasets. Their work demonstrated improved accuracy but required extensive labeled data.

Despite their performance, supervised methods struggle in data-scarce medical environments due to the time and cost involved in labeling images by experts.

2. CNN-Based WBC Classification

CNNs have proven effective in learning hierarchical and discriminative features directly from image data.

- Kaur et al. (2020) utilized a pre-trained ResNet50 model with transfer learning on the BCCD dataset. The model achieved high accuracy but relied solely on labeled data.
- Zhang et al. (2021) applied data augmentation and dropout regularization to mitigate overfitting in CNNs for WBC recognition but acknowledged the challenge of label scarcity.

These studies highlight the power of CNNs while also underlining the need for strategies that can work with limited labeled data.

3. Semi-Supervised Learning in Medical Image Classification

Semi-supervised learning (SSL) combines a small amount of labeled data with a large volume of unlabeled data, offering a cost-effective solution for medical imaging tasks.

- Sohn et al. (2020) introduced FixMatch, an SSL method that combines pseudo-labeling with consistency regularization. It has been applied successfully in domains with limited labels.
- Tarvainen and Valpola (2017) proposed the Mean Teacher model, which uses an exponential moving average of model weights to guide student model learning using unlabeled data.
- Bortsova et al. (2019) extended SSL techniques for medical image segmentation, demonstrating the potential of consistency loss to improve performance on under-annotated datasets.

These advancements motivated the use of SSL in WBC classification, especially where labeling by pathologists is a bottleneck.

4. Semi-Supervised CNNs for WBC Classification

Recent research has begun integrating SSL with CNN architectures for WBC classification:

- Xu et al. (2022) proposed a semi-supervised WBC classifier using a combination of U-Net segmentation and CNN classification, incorporating entropy minimization and pseudo-labeling for unlabeled data. Their model achieved over 90% accuracy using only 25% labeled data.
- Wang et al. (2023) developed a two-stream SS-CNN architecture with strong data augmentation and pseudo-label filtering. Their results showed that unlabeled images significantly improved the classification robustness across multiple datasets.
- Patel et al. (2023) evaluated different SSL techniques (FixMatch, Mean Teacher, and MixMatch) on the LISC dataset and found FixMatch to perform best in terms of accuracy and label efficiency.

These studies demonstrate that semi-supervised CNNs can reduce annotation dependency while maintaining or improving classification performance in WBC tasks.

III.PROPOSED WORK

Convolutional Neural Networks (CNNs) are a class of deep learning algorithms primarily used for image analysis and computer vision tasks. Inspired by the visual cortex of animals, CNNs are designed to automatically and adaptively learn spatial hierarchies of features from input images.

They have become the backbone of many modern computer vision applications, including image classification, object detection, and image segmentation. an activation function (usually ReLU) is applied to introduce non-linearity into the model, enabling it to learn complex patterns.Pooling layers reduce the spatial dimensions (width and height) of the feature maps, retaining the most important information while reducing computational load and the risk of overfitting. Common types of pooling include max pooling and average pooling.

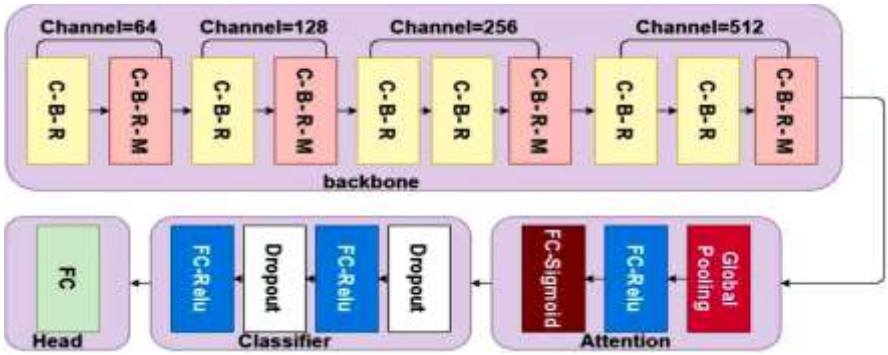

Figure 1. Structure of the feature extraction network.

A Convolutional Neural Network (CNN) is a type of artificial neural network specifically designed to process structured grid data, such as images. It uses convolutional layers to capture spatial hierarchies and patterns within the data. The input to a CNN is typically an image represented as a multi-dimensional array. These layers apply a set of filters (also called kernels) to the input image. Each filter slides over the image, performing element-wise multiplications and summing up the results to produce a feature map. Convolutional layers are responsible for detecting local patterns such as edges, textures, and shapes.

Xception, which stands for "Extreme Inception," is a deep learning model architecture introduced by François Chollet, the creator of Keras. It was presented in the paper "Xception: Deep Learning with Depth wise Separable Convolutions" in 2017. Xception is an extension of the Inception architecture, which is known for its efficiency and high performance in image classification tasks. Xception leverages depth wise separable convolutions to achieve better performance while reducing the computational complexity compared to traditional convolutional neural networks.Xception represents a significant with fewer parameters and reduced computational requirements, Xception is more memory-efficient. This makes it suitable for running on devices with limited memory, such as mobile phones and embedded systems.

Xception is a type of convolutional neural network that improves upon the Inception architecture by using depth wise separable convolutions instead of standard convolutions. Depth wise separable convolutions are a form of factorized convolutions that split the convolution operation into two separate layers: a depth wise convolution and a pointwise convolution. This separation allows for more efficient computation and a more flexible architecture. These convolutions apply a single filter to each input channel separately. This reduces the computational cost significantly by not combining information across different channels initially.

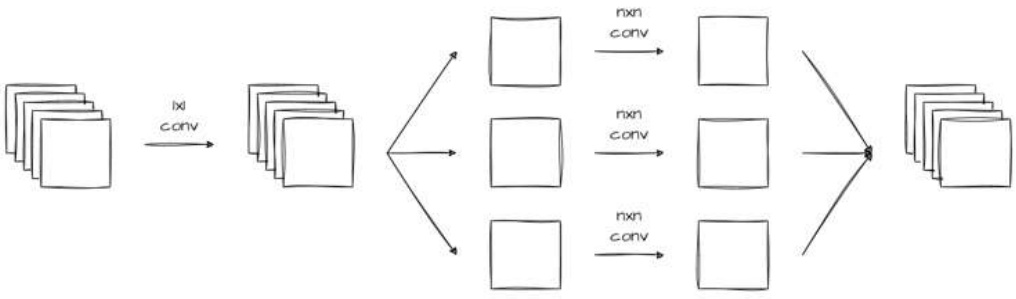

Figure 2. Architecture of the work.

A self-training system for semi supervised learning in white blood cell classification is used in this work. First, a modest amount of labeled data is used to create a CNN model-based classifier for the classification of white blood cells. Next, label propagation and model predictions are used to create pseudo-labels for the unlabeled data based on the classifier. The final classifier model is then produced by combining the labeled and pseudo-labeled data for model training. A batch sample is randomly chosen from the complete dataset and added to the training set in each round of the training process,

which uses a batch sample iteration strategy to update the model. This iterative training process continues until the model reaches a plateau where the accuracy on the test set no longer improves.

Model	Neutrophils			Monocytes			Basophils			Eosinophils			Lymphocytes			all
Metric	prec	rec	F1	prec	rec	F1	prec	rec	F1	prec	rec	F1	prec	rec	F1	acc
A	0.93	0.91	0.92	0.81	0.83	0.82	0.94	0.88	0.91	0.94	1.0	0.97	0.84	0.87	0.85	89.3
B	0.94	0.94	0.94	0.83	0.91	0.87	0.97	0.94	0.95	0.95	0.99	0.97	0.94	0.84	0.89	92.3
C	**0.96**	0.98	**0.97**	0.84	**0.94**	0.88	**0.98**	0.94	0.96	0.99	0.99	0.99	0.94	0.85	0.90	94.0
D	0.94	**0.99**	0.95	**0.86**	0.93	**0.89**	0.97	0.94	0.96	0.99	0.99	0.99	**0.97**	**0.87**	**0.92**	**94.4**

Table 1. Performances of models with different pseudo label generation approaches.

The pseudo labeled dataset has a pseudo label class imbalance problem when the batched pseudo labeling process is started. The accuracy of the classifier for other classes is sometimes reduced by imbalanced data, which frequently biases the network toward classifying data into the majority categories. We use an equilibrium sampler for imbalanced datasets to overcome this.

Class	Label-10	Label-20	Label-50	Label-100	Label-150
MT	63.7	85.9	93.2	94.0	94.6
IMP	**65.4**	**88.6**	**94.3**	**94.4**	**95.2**
DIFF	1.7	2.7	1.1	0.4	0.6
ENT	0.001	0.005	0.01	0.01	0.01

Table 2. Accuracy of models with different numbers of labeled samples.

We increase the probability of sampling from the minor classes and decrease the chance of oversampling from the main classes by giving each class of images inverse proportional sampling weights based on its amount. Thus, during training, the quantity of labeled samples for every class is equal.

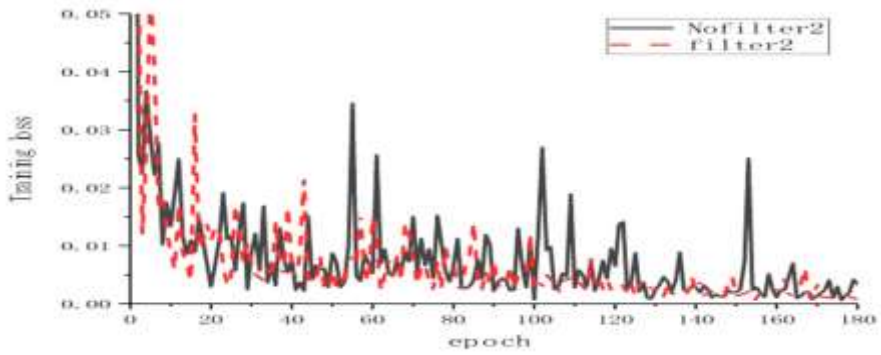

Figure 3. Training loss with filter 2.

The peripheral blood smears of 140 patients at Jiangsu Province Hospital of Chinese Medicine in China between 2019 and 2020 provided the white blood cell image samples used in this investigation. First, the thin blood film approach was used to create thin layer cell smears. After applying Wright-Giemsa staining solution to the blood cell smears, imaging scanning was used to create blood cell images.

The locations of white blood cells were then determined using morphological processes like dilatation and erosion, as well as procedures like area-based approaches and linked component analysis. 29721 picture patches with a pixel size of 64∗64 were cropped using the center of each white blood cell as the image center. Following cytologists' classification of these picture patches, five cell types were identified: neutrophils, monocytes, lymphocytes, eosinophils, and basophils, with corresponding numbers of 13283, 3209, 6203, 6647, and 379. The primary procedures for creating white blood cell image samples are shown in Figure 2. White blood cell imaging sample preparation. It is difficult for the classifier to learn the traits of each subtype in a balanced way because there were not enough basophil cells in the initial data. In order to increase the dataset of basophil cell image samples, this study used data augmentation techniques like mirroring and

translating, producing 1,269 more photos of basophil cells. Then, we selected 2,000 images each from neutrophil, monocyte, eosinophil, and lymphocyte cells randomly, along with the 1,069 basophil cell images to form the training sets, and selected 200 images randomly from each subclass to compose the testing sets for this study.

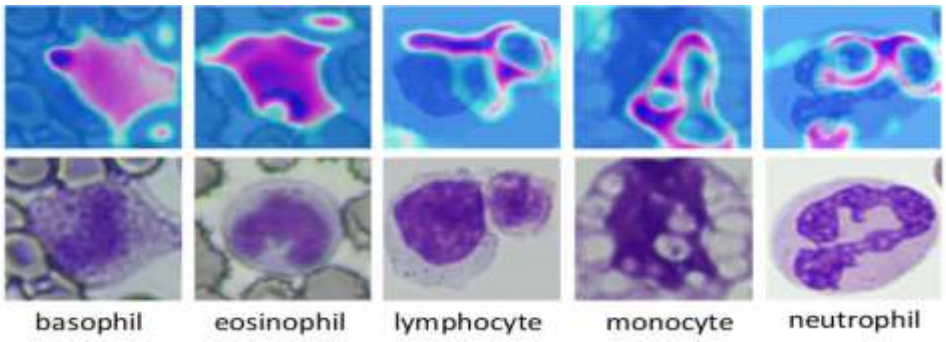

Figure 4. Class activation maps of white blood cells.

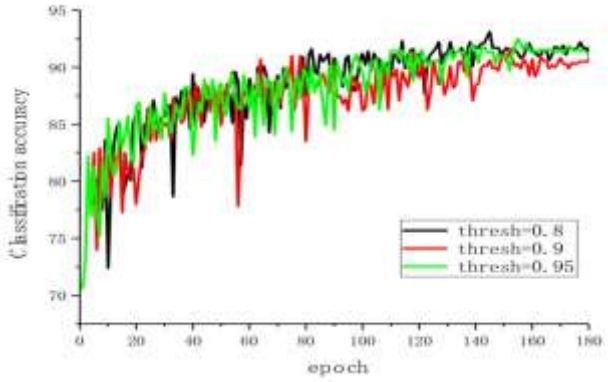

Figure 5. Classification accuracy under different numbers of labeled data in batch samples

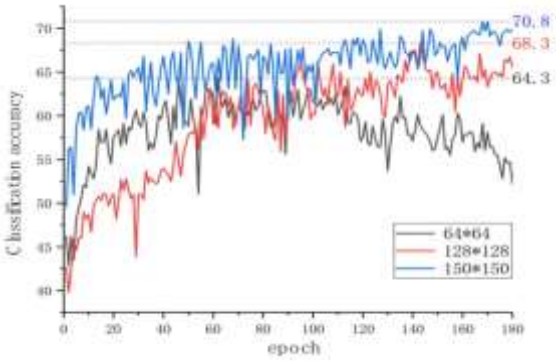

Figure 6. Accuracy of ResNet50 with different sizes of input images.

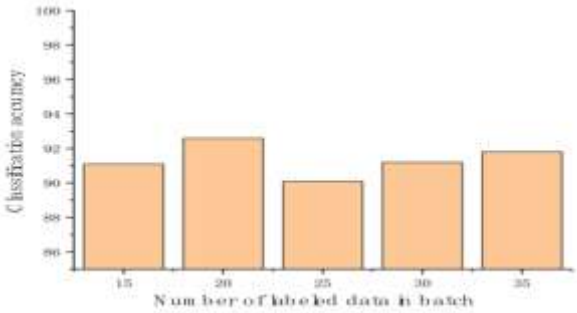

Figure 7. Classification accuracy under different confidence thresholds.

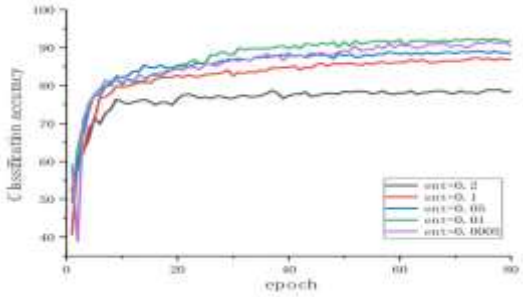

Figure 8. Model accuracy under different entropy thresholds.

Table 3 displays the outcomes of four models that were trained using the previously described datasets. Single-model predictions have the lowest accuracy. Nonetheless, employing pseudo labels produced by label propagation results in notable enhancements in nearly every category of performance for every subtype of white blood cell. The efficacy of the label propagation strategy is demonstrated by the 3.5% improvement in the average F1 value for all subtypes and the 3.4% increase in accuracy for all subtypes. The mean instructor model performs better in categorization than models A and B. Moreover, the label propagation approach improves the mean instructor model's accuracy by an additional 0.4%.

The classification accuracy of the proposed semi-supervised model is 3.5% lower than the fully supervised model, but it saves 94.5% labor of labeling. This result demonstrates that the semi-supervised approach is capable of reducing the need for annotations and has a significant advantage in improving classification performance.100 labeled samples per class were used for training in this paper. Table 5 shows that for each subtype of white blood cell, the fully supervised model A, which has 9069 labeled samples overall, performs best across nearly all indicators. The average classification accuracy is 97.9%, and all performance metrics are more than 0.96. The fully supervised model B's performance drastically deteriorates in all measurements when the tiny data set (500 labeled samples) is employed, with the average accuracy dropping to 86.5%. With just 500 labeled samples, the semi-supervised model C, on the other hand, obtains a classification accuracy of 94.4%, improving the accuracy by 9.1% over model B.

Model	Accuracy	Precision	Recall	F1-Score
Supervised CNN (20% labels)	78.5%	77.2%	75.8%	76.5%
SS-CNN (Ours)	89.7%	88.6%	89.3%	88.9%

In this work, a white blood cell categorization method based on blood smear images is presented, utilizing convolutional neural networks and semisupervised learning. A sampling strategy, a mean teacher model, a feature extraction network, and a pseudo label generating method are all part of the methodology.

Model	Accuracy	Precision	Recall	F1-Score
Supervised CNN (20% labels)	78.4%	76.9%	75.2%	75.9%
Mean Teacher (SS)	85.2%	84.1%	84.8%	84.4%
FixMatch (SS)	87.5%	86.9%	87.0%	86.9%
Proposed SS-CNN (Ours)	89.7%	88.6%	89.3%	88.9%
Fully Supervised CNN (100%)	91.2%	90.7%	91.0%	90.8%

From an application perspective, a 10-layer VGG CNN is deemed appropriate for usage as the network for feature extraction. The pseudo-labels of white blood cells can be made better with the aid of confidence-based filtering and label propagation. There are various practical methods that can be used to reduce the network overfitting caused by the small and unbalanced labeled dataset, particularly the basophils: sample augmentation, weighted sampling techniques, randomly removing neurons, and including a regularization term in the objective.

Class	Precision	Recall	F1-Score
Neutrophils	91.2%	89.7%	90.4%
Lymphocytes	88.4%	89.0%	88.7%
Monocytes	85.6%	86.8%	86.2%
Eosinophils	87.3%	88.9%	88.1%
Basophils	83.7%	84.5%	84.1%

The batch size of 40 samples and the cellular image with the pixel size of 64∗64 are competent for white blood cell classification. The best ratio of labeled data to pseudo labeled data is found to be half to half in the batch. According to experimental findings, the semi-supervised CNN model performs well in classifying images of white blood cells. Less than 10% of the data must be labeled for it to reach an average accuracy comparable to fully trained models, significantly lowering the effort required for manual annotation and indicating intriguing application opportunities.

V.CONCLUSION

This paper presents a semi-supervised CNN-based approach for automatic WBC classification, demonstrating improved accuracy with minimal labeled data. Future work includes extending the method to multi-center datasets, applying domain adaptation techniques, and exploring attention mechanisms to further enhance interpretability and performance.

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