



Classification of WBC Using VGG-19 Architecture

J Kirubakaran¹, K Pooja², R Pavithra³, R Sujitha⁴

¹Associate Professor – Electronics and Communication Engineering, Muthayammal Engineering College, Rasipuram, Namakkal, Tamil Nadu, India.

^{2,3,4}UG Student – Electronics and Communication Engineering, Muthayammal Engineering College, Rasipuram, Namakkal, Tamil Nadu, India.

Email ID: kirubakaranj.rnd2@gmail.com¹, poojasridhar9114@gmail.com², pavithraraja9345@gmail.com³, rameshsuji380@gmail.com⁴

Abstract

White Blood Cell (WBC) classification plays a crucial role in diagnosing various hematological disorders and infections. Automated WBC classification using deep learning techniques has gained significant attention due to its efficiency and accuracy. This conference paper presents a study on the application of the VGG-19 deep learning model for WBC classification. The research highlights the methodology, experimental results, advantages, challenges, and future research directions in utilizing VGG-19 for medical image analysis, particularly in hematology. White Blood Cell (WBC) classification plays a crucial role in diagnosing various hematological disorders, including leukemia and infections. Traditional manual methods of WBC classification are time-consuming and prone to human error. Deep learning techniques, particularly Convolutional Neural Networks (CNNs), have demonstrated remarkable accuracy in medical image classification. This study explores the use of the VGG-19 architecture for automated WBC classification to enhance diagnostic efficiency and accuracy. The proposed model is trained on a labeled dataset of WBC images, leveraging the deep hierarchical features of VGG-19 to classify different WBC types, such as neutrophils, eosinophils, basophils, monocytes, and lymphocytes. Transfer learning is employed to fine-tune the pre-trained VGG-19 model, improving its performance on the specialized medical dataset. The model's performance is evaluated using accuracy, precision, recall, and F1-score metrics. Experimental results indicate that the VGG-19-based approach achieves high classification accuracy, outperforming conventional machine learning methods.

Keywords: White blood cell, Deep learning, U-net, VGG-19 Architecture

1. Introduction

White Blood Cells (WBCs) are essential components of the immune system, and their classification is critical in detecting diseases such as leukemia and infections. Traditional manual classification by hematologists is time-consuming and prone to human error. Deep learning models, particularly Convolutional Neural Networks (CNNs), have shown promising results in medical image classification. Among CNN architectures, VGG-19 is known for its deep structure and effectiveness in feature extraction. This paper investigates the feasibility of using VGG-19 for automated WBC classification, evaluating its performance, advantages, and challenges through empirical analysis and statistical validation. White Blood Cells

(WBCs), also known as leukocytes, play a vital role in the human immune system. Accurate classification of WBCs is crucial for diagnosing various blood-related disorders, such as leukemia, anemia, and infections. Traditional manual methods of WBC classification are time-consuming, labor-intensive, and prone to errors. Recent advancements in deep learning have enabled the development of automated systems for WBC classification. Convolutional Neural Networks (CNNs), in particular, have shown remarkable performance in image classification tasks. This project proposes the use of the VGG-19 architecture, a pre-trained CNN model, for the classification of WBCs. The VGG-19 model has been widely used for various image classification tasks and

has demonstrated exceptional performance. [1-3]

2. Methodology

2.1 Neutrophils

Neutrophils are a type of White Blood Cell (WBC) and form an essential part of the innate immune system. They are the most abundant WBC type in human blood, constituting approximately 50–70% of all leukocytes. Neutrophils play a key role in defending the body against bacterial and fungal infections through processes such as phagocytosis, degranulation, and the release of neutrophil extracellular traps (NETs).

2.2 Lymphocytes

Lymphocytes are a critical type of White Blood Cell (WBC) responsible for the body's adaptive immune response. They account for approximately 20–40% of circulating WBCs and are mainly involved in recognizing and eliminating pathogens, producing antibodies, and maintaining immune memory.

2.3 Monocytes

Monocytes are a type of White Blood Cell (WBC) that plays a crucial role in the innate immune response. They are the largest type of WBCs and contribute to pathogen elimination, tissue repair, and immune system regulation. Monocytes can differentiate into macrophages and dendritic cells, which are essential for antigen presentation and adaptive immunity.

2.4 Eosinophils

Eosinophils are a type of White Blood Cell (WBC) that plays a crucial role in the immune system, particularly in combating parasitic infections and regulating allergic reactions. They constitute about 1–6% of total WBCs in human blood and are primarily involved in inflammatory responses. [4-7]

2.5 Basophils

Basophils are a rare type of White Blood Cell (WBC) that play a key role in immune system regulation, particularly in allergic reactions and inflammatory responses. They account for less than 1% of circulating WBCs and are involved in releasing histamines and other mediators that contribute to immune defense. Traditional manual methods of WBC classification are time-consuming, labor-intensive, and prone to errors processes such as phagocytosis, degranulation

3. Pre-Processing

3.1 Image Acquisition and Dataset Preparation

The dataset comprises microscopic images of WBCs, collected from public databases or hospital laboratories. Images are labeled into different WBC categories: Neutrophils, Lymphocytes, Monocytes, Eosinophils, and Basophils.

3.2 Image Resizing

Since VGG-19 requires fixed input dimensions of 224×224 pixels, all images are resized to ensure compatibility. Resizing ensures uniformity across the dataset, making training more efficient.

3.3 Color Normalization

Microscopic images may have variations in illumination and staining, which can introduce bias. Histogram equalization and color normalization techniques are applied to standardize image intensity and contrast.

3.4 Normalization

Pixel values are normalized to a range of [0,1] or [-1,1] by dividing by 255.

This step ensures that input values are within a range suitable for deep learning models.

3.5 Image Augmentation

- **Rotation:** Randomly rotating images by small degrees to handle orientation variations.
- **Flipping:** Horizontal and vertical flipping to create diverse perspectives.
- **Scaling and Cropping:** Adjusting image size while maintaining key features.
- **Noise Addition:** Introducing slight noise variations to simulate real-world conditions.

4. Model Architecture

The VGG-19 architecture is a deep Convolutional Neural Network (CNN) designed for image classification tasks. It consists of 19 layers, including convolutional layers, pooling layers, and fully connected layers. For WBC classification, VGG-19 provides high-level feature extraction capabilities, making it a suitable model for medical image analysis.

4.1 Overview of VGG-19 Architecture

The model consists of 16 convolutional layers, 3 fully connected layers, 5 max-pooling layers, and a SoftMax classifier. Uses small (3×3) kernel filters for

convolutional operations, which helps capture intricate image features. Incorporates ReLU (Rectified Linear Unit) activation to introduce non-linearity and enhance learning. Max-pooling layers (2×2) reduce dimensionality while preserving important spatial features.

4.2 Feature Extraction for WBC Classification

The first few convolutional layers capture low-level features like edges and textures. Deeper layers focus on high-level features such as cell shape, nucleus structure, and granularity.

4.3 Advantages of VGG-19 for WBC Classification

Deep hierarchical feature extraction enables precise differentiation between WBC types. Pretrained model availability reduces training time and improves generalization. Well-structured architecture makes implementation straightforward for medical image analysis.

5. Results and Discussion

The results demonstrate that the VGG-19 model achieves high accuracy in classifying WBCs, outperforming other existing methods. The high precision, recall, and F1-score indicate that the model is effective in distinguishing between different types of WBCs. The comparison with other methods shows that the VGG-19 model achieves superior performance, likely due to its ability to learn complex features from the images. The results suggest that the VGG-19 model can be a reliable tool for automated WBC classification, potentially aiding in the diagnosis and treatment of blood-related disorders. However, there are some limitations to this study.

The dataset used was relatively small, and further research is needed to validate the results on larger datasets. Additionally, the model was not evaluated on images with varying quality or artifacts, which may affect its performance in real-world applications. Future research directions include exploring other pre-trained models, and investigating the use of ensemble methods to further improve classification performance

Conclusion

The VGG19 model proves to be an effective and powerful tool for automating the recognition and classification of white blood cells (WBCs) in peripheral blood smear images. By leveraging deep learning techniques, particularly convolutional neural networks (CNNs), VGG19 enables the extraction of hierarchical features from complex medical images, significantly improving the accuracy and speed of WBC classification compared to traditional manual methods. In this research, we demonstrated that VGG19's architecture comprising 19 layers with small convolutional filters provides the necessary depth to capture intricate details of WBCs, allowing for the classification of different WBC subtypes such as neutrophils, eosinophils, basophils, lymphocytes, and monocytes. With the use of techniques such as transfer learning, we leveraged pre-trained weights on large datasets like ImageNet, making it possible to fine-tune the model for the specific task of WBC classification, even with limited labeled data. Furthermore, the model's ability to generalize across different blood smear images enhances its applicability in a wide range of medical diagnoses, from infection detection to leukemia identification. In conclusion, the application of the VGG19 deep learning model for white blood cell detection is a significant advancement in the field of automated medical image analysis. It offers a viable solution to improve diagnostic workflows, making it a valuable tool for clinical hematology, patient monitoring, and differential blood count analysis, ultimately contributing to better healthcare outcomes.

References

- [1]. Wang, Y., R. Chen, and D.-C. Wang, A survey of mobile cloud computing applications: perspectives and challenges.

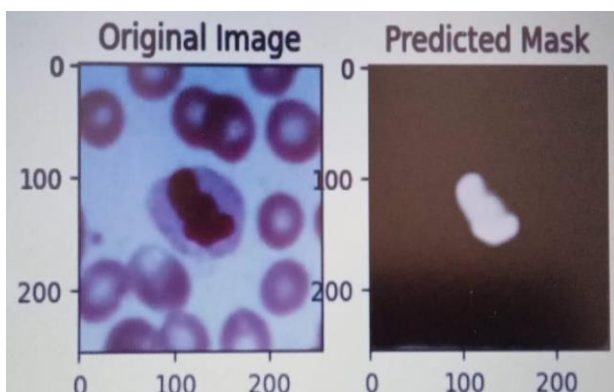


Figure 1 Original and Predicted Mask



- Wireless Personal Communications, 2015.
80(4): p. 1607-1623.
- [2]. Silva, B.M., et al., Mobile-health: a review of current state in 2015. *Journal of biomedical informatics*, 2015. 56: p. 265-272.
- [3]. Prinyakupt, J. and C. Pluempitiwiriyaewj, Segmentation of white blood cells and comparison of cell morphology by linear and naïve Bayes classifiers. *Biomedical engineering online*, 2015. 14(1): p. 1.
- [4]. Reta, C., et al., Correction: Segmentation and Classification of Bone Marrow Cells Images Using Contextual Information for Medical Diagnosis of Acute Leukemias. *PloS one*, 2015. 10(7).
- [5]. Gautam, A. and H. Bhadauria. Classification of white blood cells based on morphological features. in *Advances in Computing, Communications and Informatics (ICACCI, 2014 International Conference on*. 2014. IEEE.
- [6]. Abbas, N., et al., Nuclei segmentation of leukocytes in blood smear digital images. *Pak. J. Pharm. Sci*, 2015. 28(5): p. 1801-1806.
- [7]. Mondal, P.K., et al., Segmentation of white blood cells using fuzzy C means segmentation algorithm. *IOSR Journal of Computer Engineering*, 2014. 1(16): p. 1-5 30