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Automatic Detection of White Blood Cells in Clinical Laboratories with Recommend Vegetables

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ABSTRACT: The tests are analyzed by a doctor, all subtypes of WBCs are also examined. These procedures are performed manually and are, therefore, prone to errors and are time-consuming. Artificial intelligence techniques can help to solve these challenges. This study presented several analytical systems to diagnose microscopic blood sample datasets with high efficiency improving crop nutrient profiles crops grown under optimized conditions. Because the microscopic blood samples contain noise, the average and Laplacian filters were applied to increase the contrast of WBCs and remove the noise. The proposed methods are divided into three types, and each type contains more than one algorithm. The initial method proposed includes neural network algorithms (ANN and FFNN) based on the hybrid features extracted using the LBP and GLCM algorithms. These two algorithms achieved promising results for dataset diagnosis. In the second proposed method, the dataset was diagnosed using four pre-trained CNN models: AlexNet, ResNet-50, GoogLeNet, and ResNet-18. The dataset was diagnosed using the transfer learning method to extract deep features. All models achieved superior results for the early detection of WBC diseases with Dietary Recommendation Models are used to recommend vegetables with maximal anti-inflammatory benefits. Recommends vegetables optimized for anti-inflammatory benefits based on nutrient profiling models. In the third proposed method, the dataset was diagnosed using hybrid CNN models and SVM techniques, including AlexNet with SVM, ResNet-50 with SVM, GoogLeNet with SVM, and ResNet-18 with SVM. These techniques consist of two blocks, the first of which uses CNN models to extract feature maps.

KEYWORDS: CNN; neural networks; WBCs; Recommend Vegetables; SVM; LBP; GLCM

I. INTRODUCTION

Peripheral blood cells (PBCs) are crucial components of the human body. They perform a variety of essential tasks, including oxygen delivery, coagulation, immunity, and regeneration. These cells also carry and retain fundamental health data [1]. For example, a person's abnormal variations in the quantity, makeup, or morphology of their blood cells reveal vital details about their health. Increases or decreases in specific types of white blood cells have been related to a number of blood illnesses, including leukemia, infections, and inflammation. The morphological distinction of peripheral blood cell types serves as the basis for diagnosing hematological disorders. Over 80% of hematological disorders can be identified through morphological examination of several cell types in PBC. However, it is a challenging task that calls for expertise and skill to distinguish between many types of normal and pathological peripheral blood cells based on their morphology [2]. Despite being the gold standard in hematology, manual blood smear testing has many drawbacks, including high subjectivity and inconsistent outcomes. In order to reduce human interaction and deliver faster, more objective, and standardized analysis, automatic and semi-automatic methods have been created [3]. Human PBC can be divided into three classes: red blood cells (RBCs) erythrocytes, white blood cells (WBCs) or leukocytes, and platelets suspended in plasma. WBCs, also called leukocytes, play an important role in immunity and the formation of the body's first line of defense against pathogens and invaders. They protect the body against infections and foreign pathogens, including fungi, viruses, and bacteria [4]. The identification and quantification of white blood cells (WBCs) are crucial for clinical diagnosis. Medical professionals can identify the type, course, and prognosis of diseases by examining and measuring the quantity and ratio of various WBC types [5].

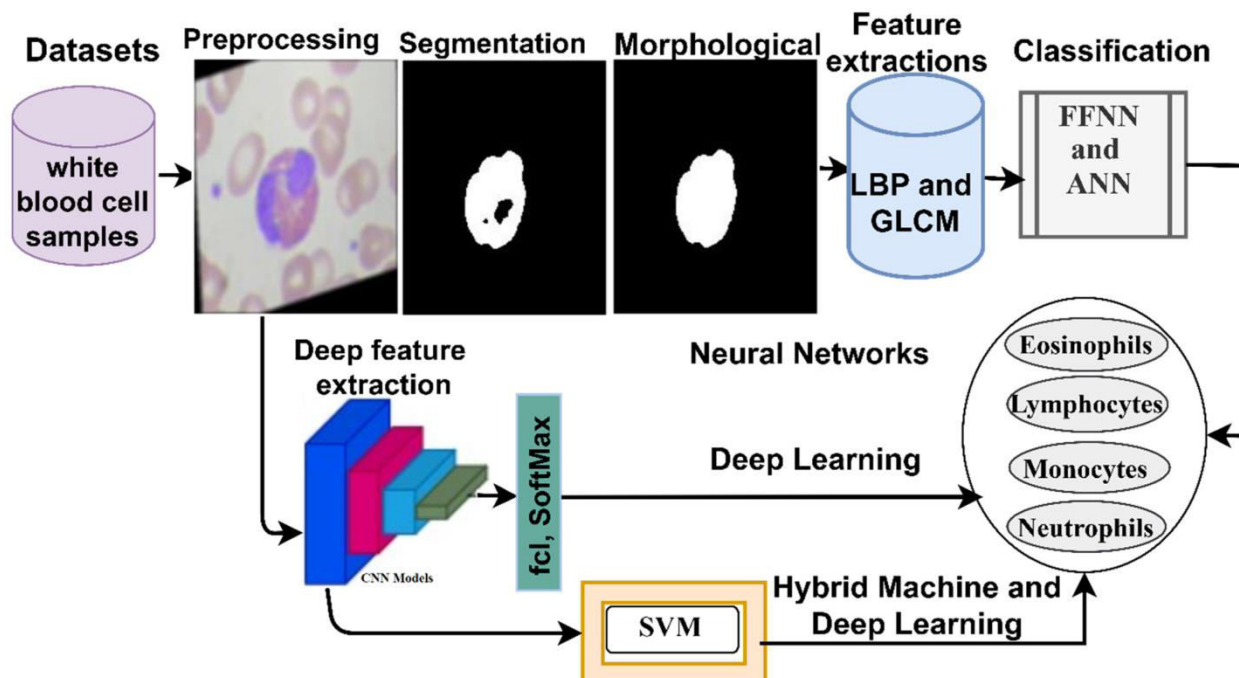


Fig1: Deep and Hybrid Learning Techniques for Diagnosing Microscopic Blood Samples

WBCs are divided into two groups: polynuclear (neutrophils, eosinophils, basophils) and mononuclear (monocytes, lymphocytes) [6]. WBCs exhibit variety in cell forms and types, in contrast to the homogeneity of form and shape observed in platelets and red blood cells. Due to this, WBCs have become the focus of numerous studies, particularly in the segmentation and classification of medical images [7]. The WBC count is used in the diagnosis of leukemia, AIDS, autoimmune illnesses, immunological deficiencies, and blood diseases. Neutrophils constitute 60% of WBCs. Thanks to their phagocytic capacity, neutrophils eliminate microbes and strengthen the body's defenses. They also help directly eliminate infectious agents by contributing to the inflammatory response [8]. The existence and physical characteristics of various inclusion types within neutrophils might give the clinical pathologist diagnostic details regarding specific clinical diseases that might be life-threatening for the patient. Eosinophils are pleiotropic multifunctional leukocytes that initiate and propagate various inflammatory responses and regulate innate and adaptive immunity. Peripheral blood eosinophil levels can be affected by corticosteroid therapy, autoimmune illnesses, medication responses, parasite infections, and allergies. Eosinophil percentages are employed in the diagnosis of illness [9]. Increased eosinophils may contribute to mucosal inflammation and tissue remodeling. Therefore, it is essential to count eosinophils accurately. Histopathology has been the gold standard for this diagnosis. Traditionally, counting eosinophils using light microscopy is time-consuming and prone to errors [10].

To count the different types of WBCs, a number of steps must be taken, including localizing the cells in the microscopic image and identifying their type. Even for an expert, this procedure is laborious and prone to mistakes. With the use of computer-aided automatic detection and diagnostic systems, one may decrease the likelihood of human mistake, speed up the diagnosis process, and get accurate results [11].

Analyzing human peripheral blood cells is crucial for the identification of numerous illnesses, including leukemia, anemia, and malaria [12].

These days, blood-related illnesses can be diagnosed with the use of quantitative and qualitative analysis of WBCs acquired from peripheral blood smears. Consequently, blood analysis can assist medical professionals in determining a patient's physiological state. Arterial thrombosis, a major contributor to myocardial infarction and stroke, can be brought on by platelets. They halt bleeding and promote wound healing during damage.

II. BACKGROUND OF WORK

Inflammation is a normal component of host defence; however, elevated unresolved chronic inflammation is a core perturbation in a range of chronic diseases [1]. Chronic inflammation and activation of immune cells are key mechanisms in the development of atherosclerosis with hypercholesterolemia-induced neutrophil recruitment promoting early atherosclerotic changes [2]. Moreover, inflammation is an important contributor to type 2 diabetes, via the processes of insulin resistance and islet β cell failure [3], and increased white blood cell (WBC) counts are predictive of incidence for type 2 diabetes [3, 4]. Neutrophils, which are the predominant circulating WBC in humans, kill and degrade microbes via the process of phagocytosis [5] and are major effectors of acute inflammation. They also contribute to chronic inflammatory conditions [6] including atherosclerosis [2] and adipose tissue inflammation [7]. Furthermore, chronic inflammation promotes lymphocyte infiltration into inflamed non-lymphoid tissues that do not recruit significant numbers of lymphocytes under normal conditions [8].

In the past decade, the composition of the gut microbiome has been identified as a key modifier of chronic inflammation and cardiometabolic risk [9]. Interactions between toll-like receptors (TLRs) and NOD-like receptors (NLRs) of the intestinal epithelium and bacterial pathogen-associated molecular patterns (PAMPs), the most common being lipopolysaccharide present on the membrane of Gram-negative bacteria, can result in the release of proinflammatory cytokines. This results in a balance between regulation of expression of epithelial receptors in the gut and stimulation by the gut microbiota. Independently of this direct interaction between the gastrointestinal epithelium and constituents of the microbiota, by-products of bacterial fermentation of components of the diet can also modulate the immune system. For example, short chain fatty acids produced via the fermentation of fibre will inhibit inflammation via suppression of monocyte and macrophage recruitment and cytokine production [10]. Conversely, trimethylamine-N-oxide, formed through the microbial breakdown of choline to trimethylamine after metabolism in the liver, will induce inflammation and atherosclerosis via inhibition of cholesterol transport and promotion of macrophage cholesterol accumulation by modulating scavenger receptor expression [11, 12]. As the main site of nutrient absorption, there is a clear interdependence between the gut microbiome and diet, with both of these factors interacting with the immune system [8].

A substantial amount of evidence suggests that many foods, nutrients and non-nutrient components modulate inflammation and immune function, both acutely and chronically [4–6]. In particular, a reduction in inflammatory markers (hs-CRP and TGF- β) has been observed in individuals adhering to a healthy plant-based diet [1, 8]. More specifically, a role has been proposed for dietary nitrate, the main source of which is leafy green vegetables such as spinach and lettuce [9]. In a 12-week placebo-controlled animal model, nitrate-fed mice had reduced systemic leukocyte rolling and adherence, circulating neutrophil numbers, neutrophil CD11b expression and myeloperoxidase activity (an enzymatic marker of neutrophil tissue infiltration, compared with wild-type littermates) [10]. Additionally, dietary nitrate administration was reported to reduce tissue level expression of myeloperoxidase [11] and oxidative stress [2], a pathophysiological process closely related to chronic low-grade inflammation [12].

III. METHODS

The proper and accurate recognition, counting, and classification of blood cells will help in diagnosing various blood disorders and diseases. Below are five images from each of the eight groups of blood cell nuclei in the same column, aligned in the same row. These images are randomly selected images from the eight cell groups. Some groups have subclasses: immature granulocytes (promyelocytes, myelocytes, and metamyelocytes) are one of these. These immature granulocytes were evaluated as a group. As can be seen in the images, the same cell nuclei in the column contain visible differences from the nuclei of the cell groups in the rows. When the column is examined downward, the same cell nuclei also contain similarities in terms of nucleus clusters. It is seen that there are also differences in different cell types to the right. Placing more than one of these blood cell nuclei images will help distinguish these similarities and differences. Different types of typical peripheral blood cells are currently used to train and evaluate deep learning and machine learning models. Machine learning (ML) is a subfield of artificial intelligence (AI). Convolutional neural networks (CNNs) are machine learning (ML) models. CNNs extract features from images and combine them.

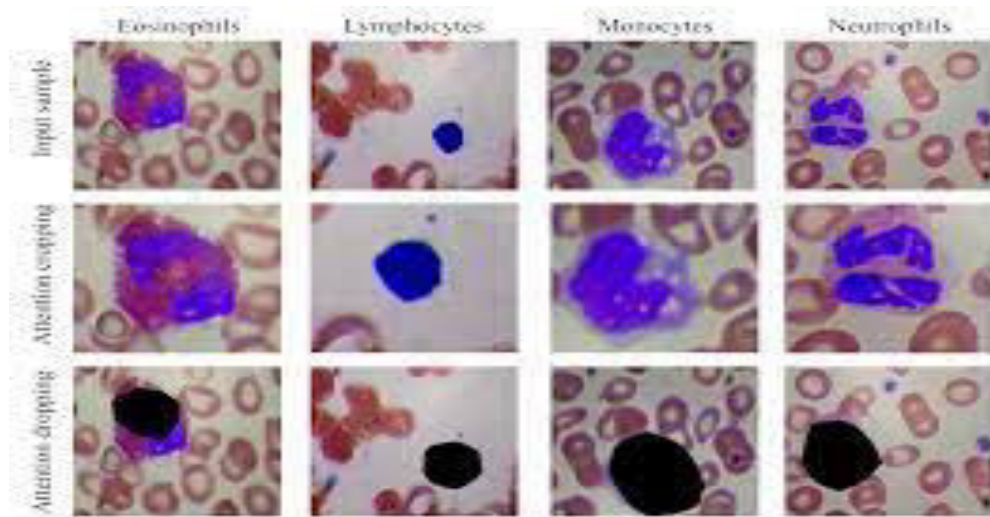


Fig 2: White Blood Cell Classification Using Multi-Attention Data Augmentation and Regularization

MobileNetV2 and EfficientNetb0 models, which achieved the highest success rate in the feature extraction process, were used in the proposed model. A total of 1000 features were extracted for each image in each architecture. Then, feature selection was performed with the NCA method for the proposed model to produce faster and more effective results. In total, 350 features were selected for each image from each feature map. Combining the features obtained in these two architectures created a feature map with different features. At this stage, unnecessary features were eliminated. At this stage, different features of the same image were brought together. As a result, 700 features were used in the proposed model for each image. Finally, the optimized feature map was classified into FT, LD, KNN, and SVM classifiers.

IV. RESULTS ANALYSIS

In order to categorize white blood cells, in this study, application results were obtained in the Matlab 2024a environment on a computer with an i7 processor and 16 GB RAM. In the study, preliminary results were obtained using six different pre-trained models and four different classifiers. In this way, it was shown that the performance of the proposed model was high. More than one performance measurement metric was used to measure the models' performance to classify white blood cell types. These parameters were accuracy, sensitivity, specificity, false discovery rate (FDR), false positive rate (FPR), false negative rate (FNR), and F1-score. While 80% of the images in the dataset were used for training, the remaining data were reserved for testing. In this way, the models used in the study were tested with 20% of the data in the dataset.

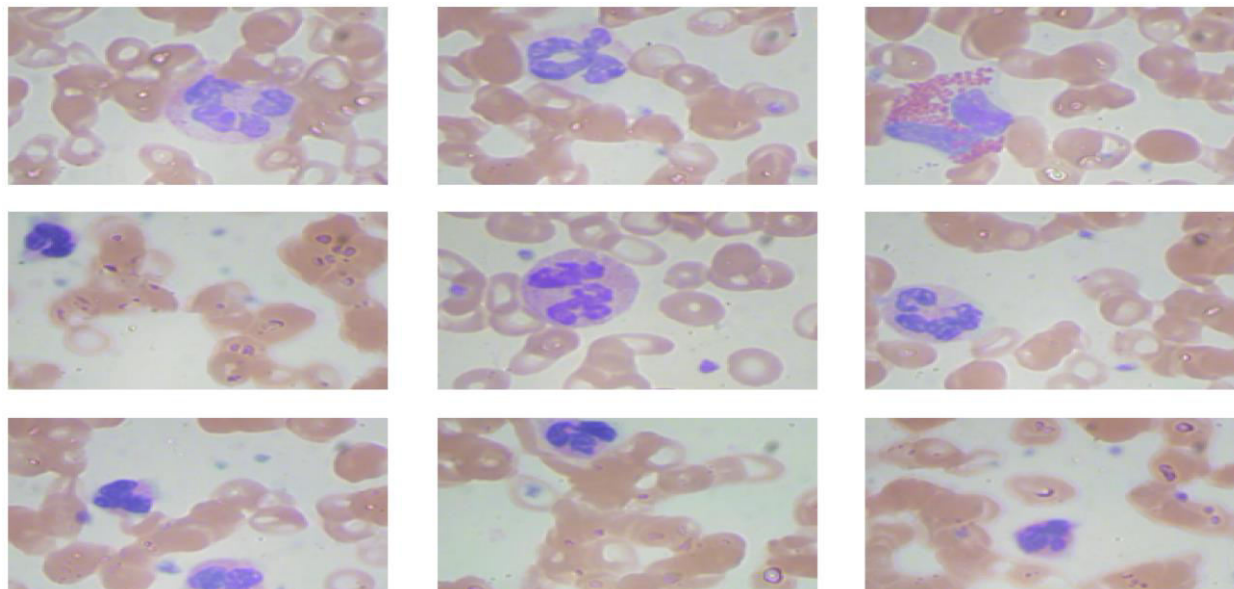


Fig 3: Automated Blood Cell Detection and Classification

WBCs are an important part of the immune system, and protect the body against infections and foreign substances. WBCs are produced in the bone marrow and are found in the bloodstream and lymphatic system. WBCs are found in different types, and each type has different functions. Automatic detection of these types with computer-aided systems is of great importance. In this study, a hybrid model was developed to detect WBCs. In the developed model, pre-trained models were used for feature extraction, and features obtained from two different models were combined to increase the model's performance. The NCA method was used for feature selection so that the proposed model could work faster. The optimized feature map was classified in the SVM classifier and achieved competitive results. With the developed method, WBCs can be detected automatically faster, reducing the workload of experts in the clinic, and minimizing traditional errors made by experts. In the future, we aim to collect data from different centers and implement an online program.

V. CONCLUSION

Here, we link the gut microbiome, cell counts and diet in a deeply phenotyped cohort, setting a foundation to generate specific hypotheses to be tested in dietary intervention studies aimed at reducing pro-inflammatory white cell profiles. Our data highlight the link between vegetable dietary intake, reduced abundance of a bacterial genus, which increases with the intake of processed foods, and higher levels of immune-response cells involved in inflammatory processes. Very recently, the direct functional links between gut microbiome composition and immune response in humans have been demonstrated in the 10-year follow-up of 2000 cancer patients. The next step, which our work contributes to address, is understanding the dietary patterns and specific nutrients involved in modifying the gut microbes that influence immune-response cells.

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