



Dense Net Algorithm for Blood Cell Image Classification

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Abstract: Deep learning algorithms for blood cell detection, aiming to improve diagnostic accuracy. White Blood Cells also known as leukocytes play an important role in the human body by increasing the immunity by fighting against infectious diseases. The classification of White Blood Cells plays an important role in detection of a disease in an individual. The classification can also assist with the identification of diseases like infections, allergies, anemia, leukemia, cancer, Acquired Immune Deficiency Syndrome (AIDS), etc. that are caused due to anomalies in the immune system. This classification will assist the hematologist distinguish the type of White Blood Cells present in human body and find the root cause of diseases. Currently there is a large amount of research going on in this field. Considering a huge potential in the significance of classification of WBCs, we will be using a deep learning technique Convolution Neural Networks (CNN) which can classify the images of WBCs into its subtypes namely, Neutrophil, Eosinophil, Lymphocyte and Monocyte. In this paper, we will be reporting the results of various experiments executed on the Blood Cell Classification and Detection (BCCD) dataset using Dense Net algorithm.

Keywords: BCCD, blood cells, cancer, classification, Dense Net, Filtering

I. INTRODUCTION

The introduction to deep learning models for the early detection and classification of skin cancer highlights the significance of leveraging advanced computational techniques to improve medical diagnosis. With skin cancer being one of the most common types of cancer globally, early detection is crucial for effective treatment and patient outcomes. Traditional diagnostic methods often rely on visual inspection by dermatologists, which can be subjective and prone to human error. The use of artificial intelligence (AI) algorithms, machine learning, and, in particular, deep learning methods in different medical and biological applications is quickly rising as the capacity of computer processors increases. These algorithms are utilized in several of disciplines, ranging from automated and semi-automated systems for analysing medical pictures to big data processing algorithms for processing human genome information [1].

The quantitative and qualitative evaluation and analysis of microscopic images of blood samples is one of the applications of artificial intelligence (AI) in medicine [2]. The goal of microscopic blood sample analysis is to count various cells in blood samples, like red-white blood cells, and platelets, or to assess their quality [3]. In the meantime, since WBCs are a key element of the immune system and demonstrate resistance to a variety of illnesses, quantitative and qualitative examination of various kinds of white blood cells is critical. Counting white blood cells can help doctors detect and treat illnesses like AIDS and leukaemia. As a result, one of the most important steps in analysing and testing blood samples is counting various types of white blood cells. Automatic and non-automatic methods can be used to analyse and count different kinds of white blood cells in blood samples. In non-automated methods, a blood sample is taken from a patient and examined by a specialist, in this method the analysis and counting of blood sample cells is a slow, tedious, time-consuming, and will be an inaccurate process. In contrast, there are several automated systems for the quantitative evaluation and WBC classification, based primarily on flow meters and the chemical properties of the



cells. These systems are often expensive and somewhat slow, providing only quantitative information about blood cells [4].

As a result, developing and implementing low-cost, quick, and reliable systems for evaluating, classifying, and counting various kinds of white blood cells are important. Processing microscopic images of blood samples are one of the most frequent approaches for building and implementing these systems. The main purpose of this study is to implement a CNN based model for processing of WBCs with the aim of classifying the type of these cells. In this study, our focus will be on detecting the type of WBCs in white blood cell images. Images of Kaggle white blood cells were utilized to do this. The collection contains microscopic images of eosinophils, monocytes, lymphocytes, and neutrophils. In this article, we built a CNN-based model for classifying white blood cell types.

II. RELATED WORKS

This part of the paper is allocated to several scholars who have discussed issues relating to white blood cell types classification.

Gurcan M et al. [6], in 2009, suggested a multi-level and hybrid model for WBC classification. They utilized a Faster R-CNN network in the first stage to identify the region of interest in white blood cells and to separate mononuclear cells from polymorphonuclear cells. After that, they employed two parallel convolutional neural networks with the MobileNet structure, in the second stage to detect WBC subtypes. Their proposed model shows a performance metric of around 98.4% (accuracy, recall, precision, and F1-score) in Kaggle blood cells dataset.

In 2013 Mohapatra S., [7] have classified WBC using the CNN Alexnet-Googlenet-SVM hybrid model. In this combined model, the feature vectors of the last pooling layer both architectures are integrated. The properties obtained are classified by the SVM technique. Their model has been tested with Kaggle and LISC datasets, the accuracy of both datasets is 99.73 and 98.23, respectively. The entire number of parameters and trainable parameters that can be utilized to train the developed model is not mentioned in their article.

In 2021[8] Classified white blood cells using convolutional features and Support Vector Machines. finally, their proposed model shows 85.95% accuracy. In 2020, [9] utilized three pre-trained models for feature extractor purposes, including GoogLeNet, AlexNet, and ResNet-50, and used the quadratic discriminant analysis (QDA) classifier to identify white blood cells. As a consequence, they were able to classify different types of WBCs with a 97.95 percent success rate. The accuracy of the model is improved by employing feature selection in the classification step, according to the authors.

In 2019, [10] introduced the CNN–MRMR– ELM hybrid model, which used pretrained CNN models such as AlexNet, GoogleNet, VGG-16, and ResNet to extract features. After integrating these features, he selected 400 important features using the MRMR feature selection technique. Then he classified white blood cells using the ELM algorithm, and his proposed model had an accuracy of 96.03 %. In 2018, [11] classified white blood cell types using a CNN-based model, which is a Double Convolution Layer Neural Network (DCLNN) and compared the model's accuracy with Nave Bayes and SVM classifiers. In their research, the DCLNN shows the best result and has an average precision of 0.88 in four classes and 0.93 in two class, in the white blood cell classification

In 2020,[15] suggested a method for classifying Multiple Myeloma (MM) and Acute Lymphoblastic Leukemia (ALL) using the SN-AM dataset. With a minimal number of parameters and computation time, the model was trained using an optimized Dense Convolution Neural Network framework capable of identifying the type of cancer present in cells with a precision of 97.2%.

In 2023, [16] attempted to create a deep learning model with a customized architecture for identifying acute leukemia using images of lymphocytes and monocytes. A unique dataset with pictures of acute lymphoblastic and acute myeloid leukemia ((AML)) is used, and a new dataset has been developed. A Generative Adversarial Network increased the dataset's size (GAN). Six convolution layers, four dense layers, and a SoftMax activation function were part of the proposed CNN model based on the Tversky loss function for categorizing acute leukemia images. The proposed model had a 99.5% accuracy rate for identifying the various kinds of acute leukemia.

In 2022, [17] suggested an AlexNet-based classification model to identify various blood cells in microscopic blood images. Using convolution neural networks, the tests were carried out on a dataset of 17,000 blood smear samples obtained from the Hospital Clinic of Barcelona (CNN). Five convolutional, three maximum pooling and three fully



linked layers make up the AlexNet model. The AlexNet-based model had a minimal Quadratic Loss of 0.0049 and a high accuracy of 95.08%.

In 2022, [18] created a new CNN-based blood cell detection and counting architecture with five models. VGG-16 was used to generate feature maps, which were then enhanced by feature fusion and a block attention mechanism (CBAM). The experiments on detecting RBCs, WBCs, and platelets were carried out using BCCD data set with two confidence levels: 0.9 and 0.8, respectively. Model 3, which enlarges input images 1.5 times and uses images in RGB and grayscale color spaces, achieved the best recall for RBC detection: 82.3% and 86.7% under two confidence levels. Meanwhile, it achieved a precision of 74.7% and 70.1%. Model 1, which performs image preprocessing and uses RGB and grayscale images, outperforms other models for WBC detection. Precision and recall are 76.1% and 95%, respectively, and 69.1% and 96.4%, respectively. Platelets were more challenging to detect than RBCs and WBCs, mainly when the platelets were grouped.

In 2022,[19] classified blood cells using two distinct scenarios, the first using CNN directly and the second using SVM. A data collection containing 10295 cell images was used. CNN obtained an accuracy of 98.4%, while SVM achieved an accuracy of 90.6%.

III. METHODOLOGY

The proposed approach outlined to improving blood cell detection using a combination of algorithms and dataset optimization techniques. We have developed a novel blood cell type classification system utilizing a Dense Net-based transfer learning approach, which significantly enhances accuracy in predicting the number and subtype of white blood cells (WBCs). Our model is trained to meticulously classify images of WBCs into their respective subtypes, namely Neutrophil, Eosinophil, Lymphocyte, and Monocyte. By leveraging the capabilities of Dense Net architecture and transfer learning techniques, our system offers a robust solution to the challenges associated with manual classification methods. Through extensive training and validation, our model demonstrates superior performance, providing healthcare professionals with a reliable tool for expedited and accurate diagnosis of various ailments based on WBC subtype analysis.

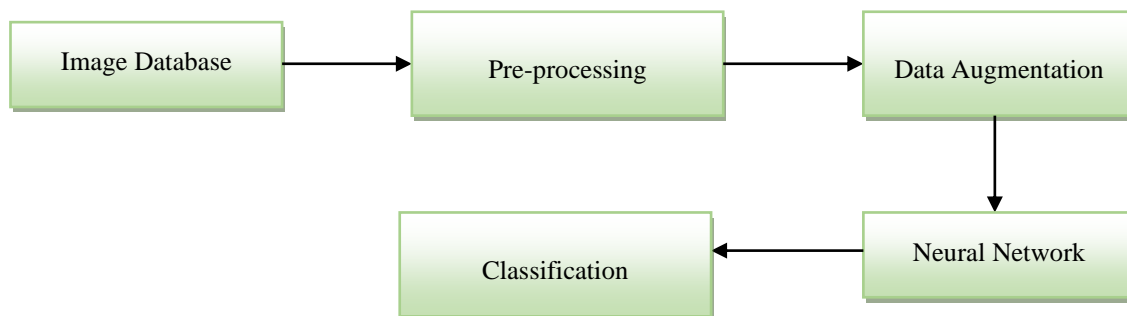


Figure-1 BCD Identifier Architecture

BCD Identification Algorithm

Deep learning has undergone a revolution thanks to the well-known CNN architecture known as DenseNet. Its adaptability is demonstrated in areas including natural language processing, object identification, and image segmentation. DenseNet stands out due to the dense interconnectedness that exists between its layers. It implies that each layer is connected to every other layer, facilitating rapid information transfer and improving gradient flow[25], which results in effective network training. As a result, compared to conventional CNN designs, accuracy and speed have significantly improved. The main advantage of DenseNet is its capacity to reduce the number of parameters needed to complete a task. It accomplishes this by employing shortcuts to connect layers and by minimizing the amount of connections between layers. This reduces the amount of computation needed and allows for faster training and inference.



Furthermore, on a number of benchmark datasets, DenseNet121 has been demonstrated to have higher accuracy than competing CNN architectures like VGG and ResNet. Numerous computer vision applications, including autonomous vehicles and medical image processing, have made use of DenseNet121. DenseNet121 has been used in medical image analysis to forecast Alzheimer's disease progression and identify breast cancer. Strong deep learning architecture DenseNet121 has demonstrated effectiveness in a variety of computer vision tasks. It is an accurate and efficient CNN architecture due to its minimized parameter redundancy and densely paired layer. Given DenseNet121's achievements in self-driving cars and medical image processing, other uses for it are likely in store. A member of the Deep Convolutional Networks (DenseNets) family of neural network architectures is DenseNet-121, a deep convolutional neural network[11]. DenseNets are renowned for their enhanced gradient flow and resource efficiency, which allow them to outperform conventional convolutional neural networks (CNNs) in terms of performance while using fewer parameters[19].

DenseNet-121's "121" stands for the total number of layers, which comprise fully connected, pooling, and convolutional layers. Because DenseNet-121 is built with densely connected layers, every layer in the system receives input from every layer that came before it. The network can learn more complicated features with fewer parameters thanks to this dense connectivity architecture, which also improves feature reuse. Four dense blocks, each with numerous convolutional layers and a transition layer in between, make up the architecture. A max-pooling layer comes after the convolutional layer with 7x7 filters in DenseNet-121. Next, the four dense blocks and their corresponding transition layers are traversed by the network. The dense blocks consist of multiple "bottleneck" layers, which are composed of 1x1 convolutional layers followed by 3x3 convolutional layers. These bottleneck layers help to reduce the number of parameters and computational cost while maintaining the network's representational capacity.

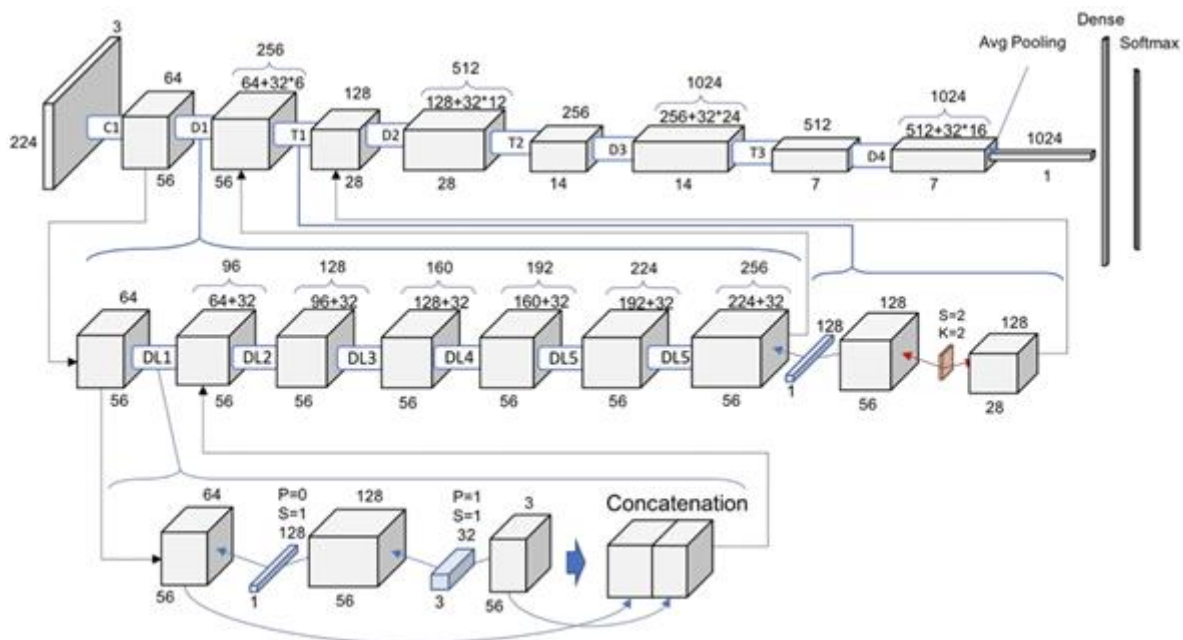


Figure-2 Dense Net Architecture

IV. RESULTS AND DISCUSSION

The implementation of our DenseNet-based transfer learning model for blood cell type classification has yielded promising results, significantly enhancing the accuracy and efficiency of WBC subtype prediction compared to traditional manual methods. By leveraging advanced deep learning techniques, our system achieves improved diagnostic precision, ensuring more reliable and consistent classification outcomes. This increased accuracy not only facilitates more accurate diagnosis but also enables timely treatment planning, ultimately leading to better patient outcomes. Moreover, the automation of the classification process reduces the labor intensity associated with manual methods, freeing up valuable resources in healthcare settings. Additionally, our model demonstrates scalability, capable



of handling large volumes of data and catering to diverse patient populations. Overall, our results underscore the potential of leveraging machine learning approaches in medical diagnostics, particularly in the domain of WBC subtype classification, paving the way for more efficient and effective healthcare practices. Further discussions may focus on the integration of our model into clinical workflows, potential challenges in deployment, and avenues for future research and improvement.

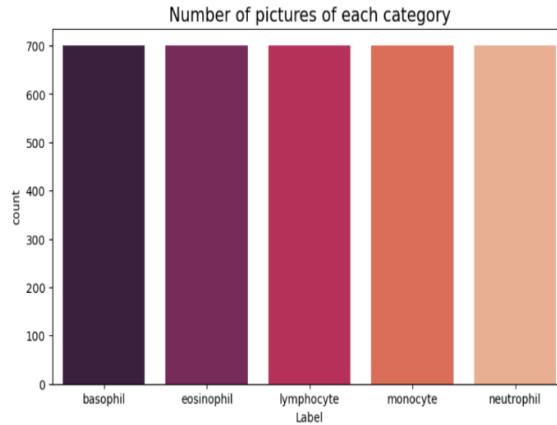


Figure -3 Classification of Category

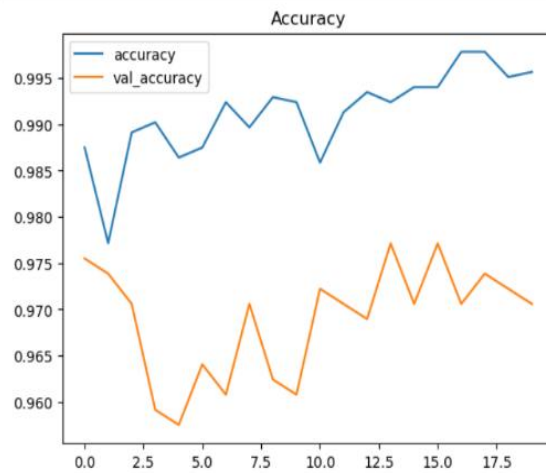


Figure -4 Accuracy

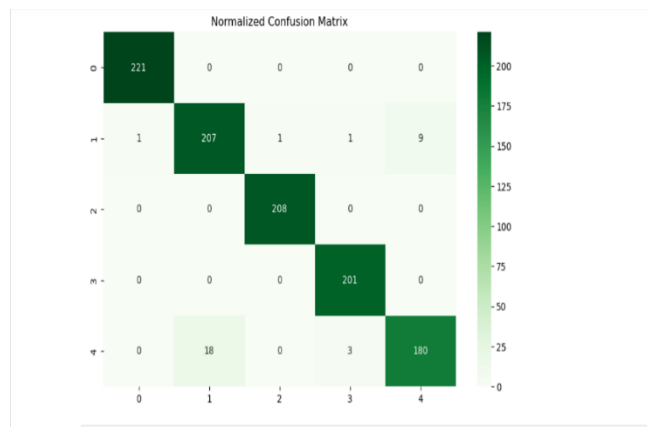


Figure -5 Confusion Matrix

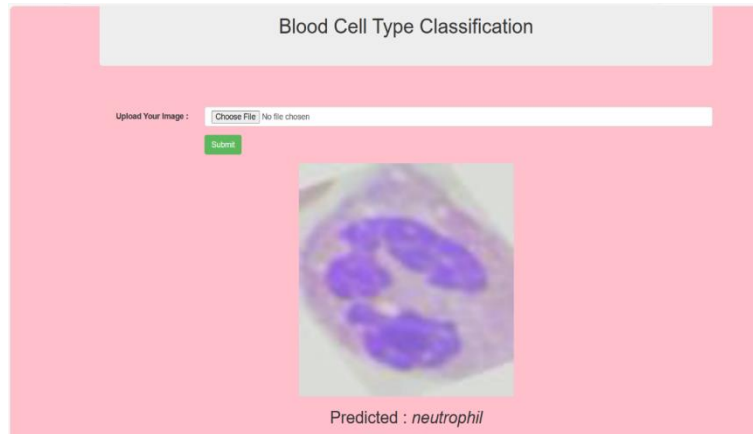


Figure -6 Classification Results



Figure -7 Classification Results

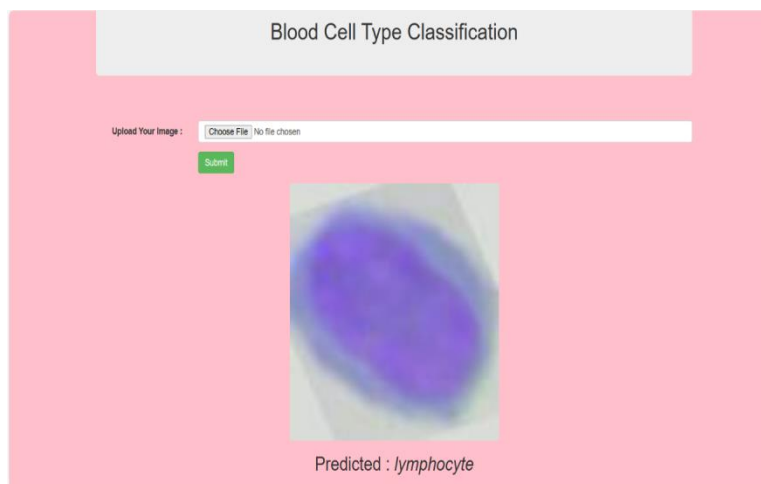


Figure -8 Classification Results

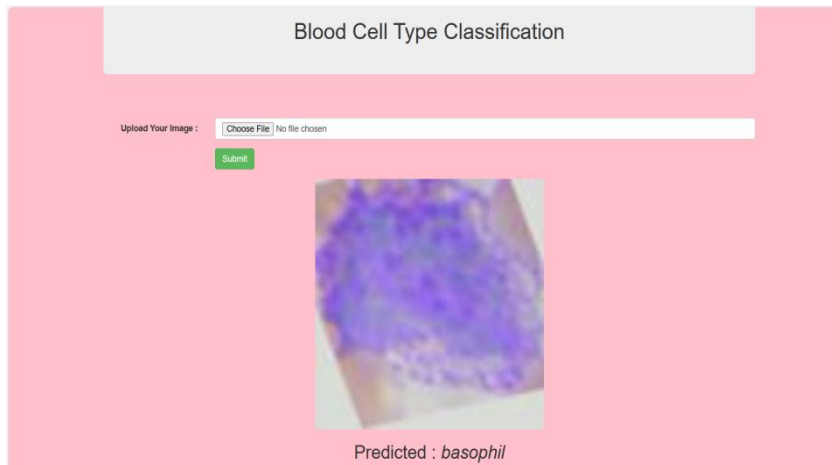


Figure -9 Classification Results



Figure -10 Classification Results

V. CONCLUSION

In conclusion, our study underscores the importance of accurately classifying white blood cell (WBC) types for effective diagnosis and treatment of various illnesses. Leveraging a DenseNet model, we have successfully developed a robust system capable of efficiently processing WBC images and classifying their types. By optimizing the model architecture with a low number of trainable parameters and reducing training time, we have demonstrated the feasibility of utilizing deep learning techniques for WBC classification. This implementation not only enhances the quantitative and qualitative examination of WBCs but also holds promise for streamlining healthcare workflows and improving patient care outcomes. Moving forward, continued research and development in this area could further refine and expand the capabilities of automated WBC classification systems, ultimately advancing diagnostic precision and therapeutic interventions in clinical practice.

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