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Deep Categorization of Blood Cells using Depthwise Convolutions

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Abstract*: Modern-day computation has become indispensable in the healthcare industry. From medical image processing to cost reduction, Artificial Intelligence has proved its significance in solving complex healthcare problems. One of the primary areas in which it can be of greater use in hematology. Categorization of white-blood cells is imperative to pre-identify abnormalities. Through this paper, we collected image samples for 4 major White Blood cell groups, which are Neutrophils, Lymphocytes, Monocytes, and Eosinophils. The aim of this research is to put forward an intelligent system that efficiently alleviates the stringent requirement of a cytological study. The proposed system classifies 4 white-blood-cell types based on their morphological variation. With the experimental modulations that we chose to integrate, the presented model attained an accuracy of 97%.

Keywords: Artificial Intelligence, Cytology, Hematology.

I. INTRODUCTION

Blood cells play a significant role in establishing how the human body is conditioned in numerous ways. WBCs, in particular, are important indicators of a defense mechanism's/immune system's effectiveness. These cells work in accordance with their instructions to eliminate foreign organisms by eliminating them. White blood cells come in a variety of forms, each with its own set of functions. To assess the blood cell metabolism, it is necessary to identify and numerically quantify these cells. As illustrated in Figure 1, each of these cells is generally recognized based on their morphology. The potential to introduce an intelligent system to properly identify/detect them is enabled by the morphological distinction.

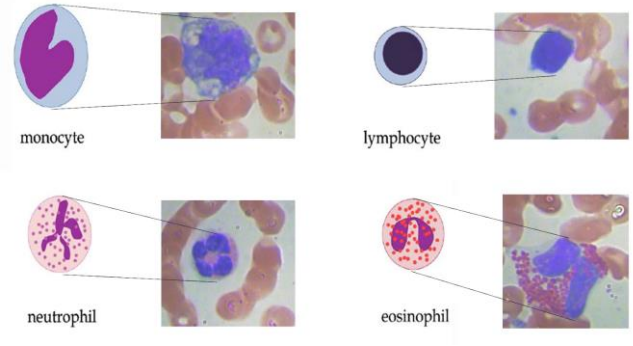

Fig.1. Morphological Differentiation of White Blood Cells

For image categorization, we used convolutional neural networks (CNN) to consider all the 2D pixel data effectively without having to cope with the parameter explosion that usually occurs when using feed-forward networks with image data [3]. A *convolutional neural network* is an architecture used to interpret image data in deep learning. It is well-known for its tolerance to minor input variations, low pre-processing requirements, and lack of a need for a specialized feature extractor [1]. The network is made up of a set of layers, each with one or more planes. At the input layer, images are roughly centered and normalized. Each unit in a plane gets the input from a local neighborhood in the previous layer's planes. At all places in the plane, the weights forming the receptive field are compelled to be equal. Each plane can be thought of as a feature map with a fixed feature detector combined with a local window scanned across the preceding layer's planes. Each layer usually has many planes so that multiple features can be detected. Convolutional layers are the same for these layers. The precise placement of a feature is less crucial once it has been identified. As a result, the convolutional layers are usually followed by a layer that performs local averaging and subsampling [2]. The standard backpropagation method is used to train the network.

II. RELATED WORK

In [4] by Mayank Sharma, Aishwarya Bhave, and Rekh Ram Janghel, a deep learning methodology using DCNN to automate the complete process of classifying WBC images for a binary class classification with an accuracy of 96% and multi-class classification with an accuracy of 87% is presented. Paper by M. Samir Abou El-Seoud, Muaad Hammuda Siala, and Gerard McKee [5] focuses on classifying white blood cells into five different categories using a CNN-based architecture. It is also stated that the proposed model has performed with accuracy up to 96.78% on a dataset consisting of 10,000 samples of blood cell images.

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Publication by A. Malkawi, R. Al-Assi, T. Salameh, B. Sheyab, H. Alquran and A. M. Alqudah [6] concentrates on the classification of Microscopic WBC images using a hybrid approach in which a Convolutional Neural Network (CNN) was employed as a feature extractor and various machine learning methods were used as classifiers. The model that turned out to be the most accurate one is Random Forest Classifier, with an accuracy of 98.7%.

The research by Khaled Almezhghwi and Sertan Serte [7] looks into operations of image processing and generative adversarial networks (GAN) for data augmentation, as well as the pre-trained CNN based architectures such as VGG-16, ResNet, and DenseNet for classifying WBC into five types. DenseNet-169, the top-performing DNN model, has performed with a validation accuracy of 98.8%.

III. PROPOSED SYSTEM

A. Data Overview

Data was gathered from an open-sourced repository hosted on Kaggle. It is made up of microscopic images of blood cells, with four different types of white blood cells (WBCs) being the primary focus. *Monocytes, Neutrophils, Eosinophils, and Lymphocytes* are the four types of White blood cells. There are a total of 12,515 Images samples in the repository. We developed a pipeline script to yield randomly sampled distributions, with The Train Set receiving 80% of the data and Validation and Test Sets receiving 20% each. We noticed that the picture sizes were not uniform. Therefore, we implemented a transformation functionality in the script to resize the images to 150x150, ensuring that the image sizes are homogeneous.

B. Proposed Architecture

The Image Classification problems typically come along with massive parameters to take into account. Considering the recursive nature of training, a Normal Artificial Neural network architecture is not an efficient option when it comes to image data with discrete feature patterns. On the other hand, Convolutional neural networks tend to capture and generalize well with multiple patterns within the Images through their filter matrices which are modified and upgraded with each iteration of training [8]. With all these layers set up in a cascading manner, Deeper layers tend to retain complex features and ultimately store a lot more information to accurately aggregate that knowledge gained to classify at the end. The feature extraction of an initial image after going through 5 convolution stages is represented in Figure 2.

Fig. 2. Illustration of Feature Extraction

Unlike the conventional architecture, we used 2D separable convolutions, an integral function from the *tensorflow.keras* framework library. This Depthwise spatial convolution is directly inspired by the DenseNet Architecture, which first introduced this ground-logic [9]. The initial layer of our network is a standard convolution module with "*same" padding* and *Max Pooling of 2x2*. Then for the following network architecture, we fabricated depthwise convolution blocks with variable kernels sizes in each module. The final portion of the network includes functionality to *flatten* the weight matrices and is followed by three layers of densely connected layers perceptrons with intermediate *Dropouts* placed in between with varying probabilities, and this ensures that the model doesn't overfit to the data and increases the overall complexity of learning. Each spatial separable convolution modules have *Batch Normalisation* as an integral part. With Batch Normalisation, intermediate activation vectors are normalized to a standard range of each mini-batch and, in turn, accentuates learning. *Rectified Linear Unit Activation (relu) [10]* is used as the default activation for all the layers except for the final layer, which has *Softmax Activation* to classify the targets. The system presented in this research gave us the optimal results out of all the empirically tried out network architectures. Figure 3 describes the architecture of the proposed system.

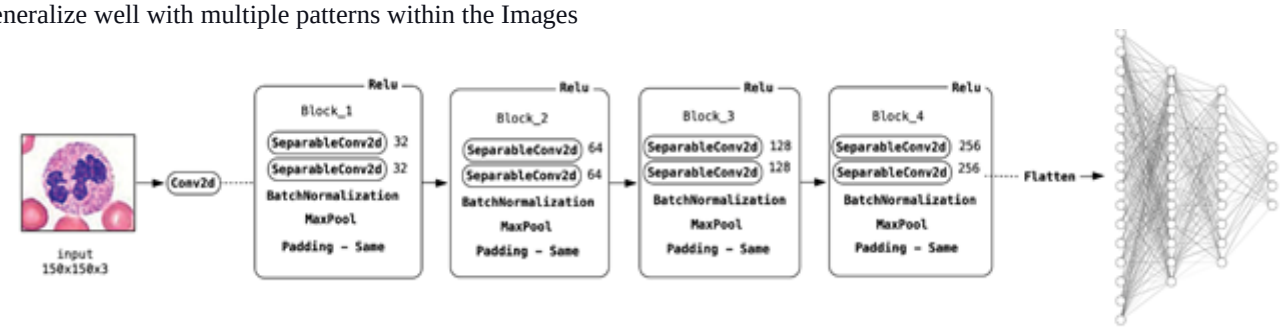

Fig. 3. Illustration of Proposed Convolutional Neural Network Architecture

C. Hyperparameters and Callbacks

This project's empirical nature and its Accuracy lie on the correct set of hyperparameters we choose to parameterize. The *batch-size was set to* 32 with 32 epochs for training. For backpropagation, *Adam* has been used as the default gradient descent algorithm. To avoid stalling at the Local Minima during training, we used a callback functionality called *ReduceLROnPlateau [11]*. This evidently helped to significantly reduce the bias-variance difference between the Training and Validation set Accuracy. The callback was set to monitor *Validation Accuracy* with the patience of 3 epochs.

The factor of Learning rate reduction was set to 0.3, which indicates that at every activation of the callback, the learning rate will be reduced by 0.3 (reduced_lr = lr * factor). From the train cycle plots in the Figures [4, 5], it is evident that the callbacks changed the learning accuracy during the epochs 5, 11, and 16, eventually establishing a constant and minute difference between Train and Validation set Accuracy. The model appears to stall between epochs 15 and 20, maintaining a consistent accuracy for the rest of the training period, yielding a 98 percent accuracy at the end.

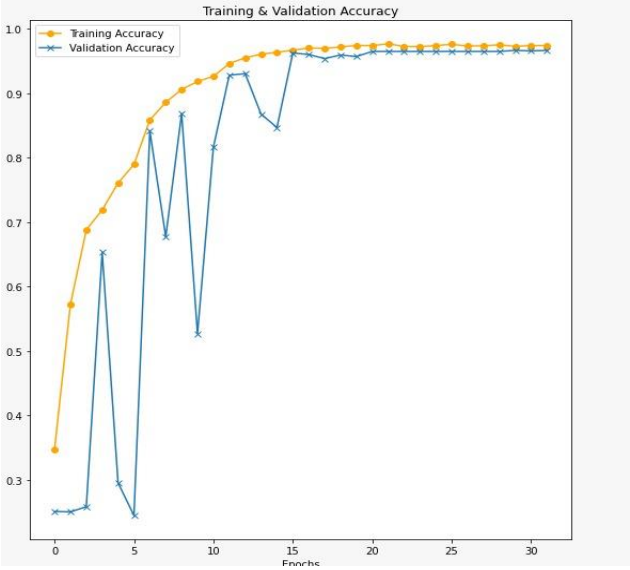

Fig. 4. Training and Validation Accuracy

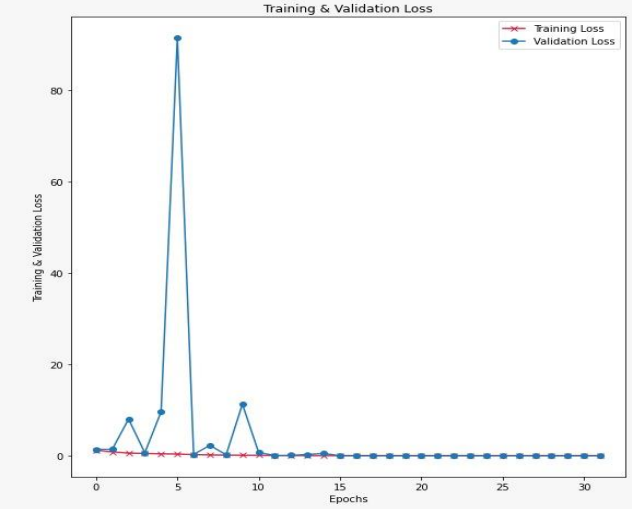

Fig. 5. Training and Validation Loss

IV. RESULTS AND DISCUSSION

In this section, we evaluate our model's performance criteria with different metrics to concrete the idea of our proposed system to be an efficient solution to the problem statement. Even though the model has minute scope to reach the optimal accuracy, there are still misclassifications that are apparent in our case. These misclassifications can be effectively pointed out with a confusion matrix. A Confusion Matrix includes a cross-tabulation of all the target classes of a problem statement, each column, and row value intersection, or simply the diagonal of the matrix represents the number of True Positives, and all the other intersections of a row represent the misclassifications. Figure 6 shows the confusion matrix of the 4 White blood cells as targets. There's an obvious misclassification between *Neutrophils* and *Eosinophils. The* reason for this can be associated to their fairly similar morphologies. The same pattern appears in the metric table as well. Table 1 shows the metric evaluation of each class. We chose to consider the metrics Precision, Recall, F1-Score, and Support to assess our model's performance.

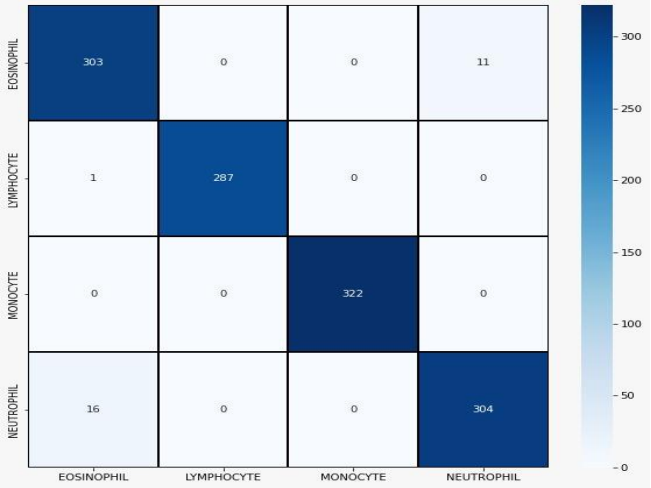

Fig. 6. Confusion Matrix

Precision and Recall are mathematically defined as the following

$$\text{Precision} = \frac{True\ Positives}{True\ Positives + False\ Positives}$$

$$\text{Recall} = \frac{True\ Positives}{True\ Positives + False\ Negatives}$$

F1-Score is defined as the Harmonic Mean of Precision and Recall combined.

$$F1 = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$$

Where,

- TP - Total Number of True Positives
- FP - Total Number of False Positives
- FN - Total Number of False Negatives

Table I: Metric Evaluation of the Proposed System

Target Class	F1-Score	Precision	Recall	Support
Eosinophil	0.95	0.96	0.96	314
Lymphocyte	1.00	1.00	1.00	288
Monocyte	1.00	1.00	1.00	322
Neutrophil	0.97	0.95	0.96	320

V. CONCLUSION

In the modern era of computational intelligence, it is essential to acknowledge the necessities of A.I in industries of utmost importance, such as healthcare.

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In this paper, we used a dataset split into four classes meant for a cytological evaluation. This paper proposed a custom Convolutional Neural Network Architecture that categorizes White blood cells into four different categories. The presented system is based on The DenseNet architecture, replacing standard convolutions with depthwise spatial convolutions and a dynamic callback system to manipulate the Learning Rate to avoid stalling at local minima. The architectural differences and the hyperparameters used resulted in an apparent efficiency boost, ultimately obtaining an F1-Score of 98% on all the target classes. Our research can be extended into developing multiple kinds of intelligent systems. For instance, in a cytological examination of blood samples, it is crucial to do a numerical evaluation of the number of WBCs. This procedure can be automated with an object recognition system whose conceptual basis is a Convolutional Neural Network.

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