Classification of WBC for Blood Cancer Diagnosis using Deep Convolutional Neural Networks

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Abstract. Classification of Leukocytes (WBCs) is widely used in the medical field for the diagnosis of various blood cancers such as Leukemia, Myeloma etc. The traditional methods of manual counting currently being used are slow and susceptible to errors. Furthermore, the instruments in use are not affordable by every hospital and clinic, and even then the results are not reliable and cannot detect morphological abnormalities. In this paper, we have implemented a model to automate the diagnosis of blood related diseases by classifying WBCs- Neutrophils, Lymphocytes, Eosinophils, and Monocytes from blood samples images, which provides a time-effective and accurate diagnostic system. Using Deep CNN we extracted minor intricacies in the structure of the cells and exhausted the dataset by generating multiple variations of the existing images, which resulted in improved accuracies. The image dataset consisted of 410 original images and 12,500 augmented images of blood cells paired with corresponding subtype labels. Our Deep CNN approach generated improved results and reduced the error rate compared to other models.

Keywords: Deep Convolutional Neural Networks, Leukocytes, WBCs, blood cancer, data augmentation, CNN

1 Introduction

The evaluation of Leukocytes (white blood cells) is the primary step to diagnose many blood related diseases. The evaluation of the 5 major subtypes of Leukocytes, namely- Neutrophils, Lymphocytes, Eosinophils, Monocytes, and Basophils, can help in identification of various diseases including AIDS (Acquired Immune Deficiency Syndrome) [1] and blood cancers, such as Leukemia, Lymphoma, and Myeloma. Approximately 174,250 people in the United States (US) are expected to be diagnosed with blood cancer in 2018 [2]. Moreover, the death tolls related to blood cancer is estimated at 58,100 in the US alone, in 2018.

Currently, the medical diagnosis of such diseases is done mainly using hematology analyzer and manual counting [1]. The manual counting

involves the counting of white blood cells (WBC) that is done primarily by medical operators, the accuracy of which is highly dependent on the operator's skills [3]. Although, the impedance-based hematology analyzer has its advantages it can wrongly classify the cell types as white blood cells as their primary parameters for classification are limited to size and the number of particles [4,5]. Therefore, there is a need to introduce precise, time-saving diagnostic systems to accurately classify the WBC count to determine various diseases. This can be made possible with the advances of Machine Learning in medical diagnosis [6], where techniques like clustering, thresholding, and support vector machine (SVM) [7] have been put to test.

In this paper, we have implemented a Deep Convolutional Neural Network to classify the 4 blood subtypes- Neutrophils, Lymphocytes, Eosinophils, and Monocytes. Convolutional Neural Network (CNN) is the widely used technique for image classification where the weights are learned with back-propagation [8]. We have implemented a CNN model based on deep Learning, where deep learning enhances the feature extraction ability and smooth scaling in case of increased parameters [9]. We consequently achieve a precision of 83% in classifying the WBCs.

This paper is organized as follows: section 2 gives the data research, including the data exploration, augmentation, and pre-processing, section 3 provides our proposed approach of Deep Convolutional Neural Networks as well as the feature extraction and model representation. In section 4, we have provided the results of our experiment. Section V gives the conclusion of this research, where we summarize the paper.

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2 Data Research

The dataset consists of 12500 images (JPEG) of blood cells along with their corresponding cell type labels. Eosinophil, Lymphocyte, Monocyte, and Neutrophil are the four blood cell types. There are around 3000 images of each type which are augmented. About 410 images are original, pre-augmented. The original images are used to find the count of blood type cells. It is found that there is a severe imbalance class

size. Augmented images are used as they no longer have class imbalance. Images of the four different blood types taken from the dataset are plotted.

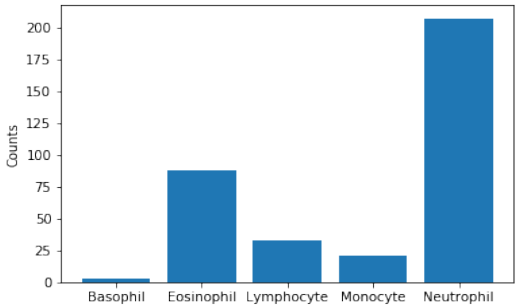

Figure 1: Cell count in original images dataset

Load Augmented Dataset: The blood cell types are labelled as integer values. These integer values can be transformed to bit values using One Hot Encoding. The four labelled classes undergo this transformation making it easier for classification algorithms.

Histogram of RGB Pixel Intensities: In a grayscale image, the intensity value of the pixel is stored from 0-255 where typically 0 is taken as black and 255 is taken as white. This range leads to 256 possible values for pixel intensity [13]. Separate red, green and blue value components need to be specified for color images. In short, color images are represented by a vector of three numbers. The three 'color planes' are usually stored separately and recombined when they are to be displayed or processed. A Histogram [11] in image processing is a graph of number of pixel values at a particular intensity value. The intensity value span from 0-255. Histogram for color images includes the intensity values for red, green and blue at each pixel. Histogram for the training dataset is carried out

Preprocess data: The images in the dataset undergo RGB Normalization [12] to remove distortions. To carry out RGB Normalization, the individual RGB pixel value is divided by 255. This transforms the component value range from 0-255 to 0.0-1.0.

$$R' = \frac{R}{R+G+B} \quad (1)$$

$$R' = \frac{G}{R+G+B} \tag{2}$$

$$R' = \frac{B}{R+G+B} \tag{3}$$

Only the values of R' and G' need to be stored as the value of B' can be calculated from the other two. This loss in information in terms of B' contributes to the removal of lighting information in the image.

2.1 Deep Learning Algorithm

CNN is extensively used for image classification because it uses neighboring pixel information to down sample the image effectively and then perform predictions, which resulted in high accuracies [10,19]. Additionally, they work using neural networks which are scalable for large datasets. It comprises of a complex feed forward neural network involving convolutions, pooling and classification. The term convolution refers to calculation of similarities between two functions when one function passes (or convolutes) over other. Pooling is used to reduce the number of parameters when the image is too large, followed by classification based on training and improvement by backpropagation. An image according to the computer is perceived as a collection of numbers or pixels organized in three dimensions viz. width, height and depth [15]. Thus, matrix multiplications are the core operations of CNN. The functioning of CNN can be divided into two parts, the feature extraction and classification.

Feature Extraction: Convolution is performed by sliding a filter (feature vector) over input data to produce a feature map. This is obtained by performing matrix multiplication between the two at every location to extract different parts of the image and sum up the result onto a feature map. This operation is performed multiple times using different values of filters to obtain multiple feature maps [14]. This is the output of the convolution layer. The output in the real world is non-negative and non-linear thus, an activation function is applied on it. In our case, we use Rectifier Activation function to introduce non-linearity. In order to prevent the feature map from shrinking we perform padding which is done by appending zeros surrounding the input. It is common to add a

pooling layer between the convolution layers to reduce the number of computations in the network by reducing the dimensionality [15]. Various types of pooling like, max pooling (taking the maximum of neighboring pixels after convoluting), average pooling (taking the average of neighboring pixels after convoluting) and sum pooling (considering all neighboring pixel values) [16].

Classification: This part is made up of fully connected layers which accept data in 1 dimension. Thus, we convert our 3D data to 1D by applying the flatten layer to the output of feature extraction. The neurons in this layer have connections to activations of the previous layers. The fully connected layer is followed by the dense layer which form the hidden layer of neurons where backpropagation (using the principle of gradient descent) is applied, followed by the softmax layer which provides a binary output of whether the input image belongs to a particular class or not.

Model Representation.

After testing multiple values for hyper parameters, we obtained the best accuracies with 32 filter, each filter size of 3 X 3, ReLU activation function for imposing non-linearity. A dropout of 25% is also applied to handle overfitting. We pad the feature maps so that the input size is equal to output size to avoid feature map shrinking. The dense is composed of 128 neurons. In order to obtain high accuracies, we consider the orientations of cell location in each image. For this, we use the ImageDataGenerator in python which generates a batch of tensor images with real-time data augmentation. We apply rotations, height and width shifting, normalizations, and flipping on original image to create a set of images containing the white blood cell type with different orientations. This will ensure that our model will take care of same cells positioned in different angles are classified correctly. The sequence of layers in our model is as shown in figure 1. We run the model for 30 epochs, i.e. we update the weights 30 times by performing backpropagation to obtain an accuracy of 83%.

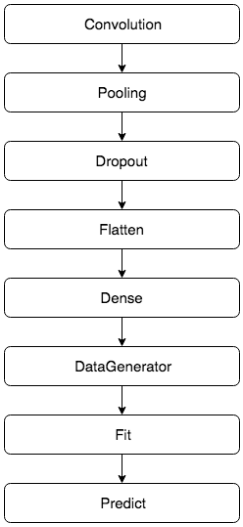

Figure 2: Layers in our model

3 Results

As seen in figure 2, with increasing number of epochs, the model obtains improved accuracies. This is because improved understanding of image features as model adjusts weights using back-propagation. The validation set accuracy remained near constant after 30 epochs.

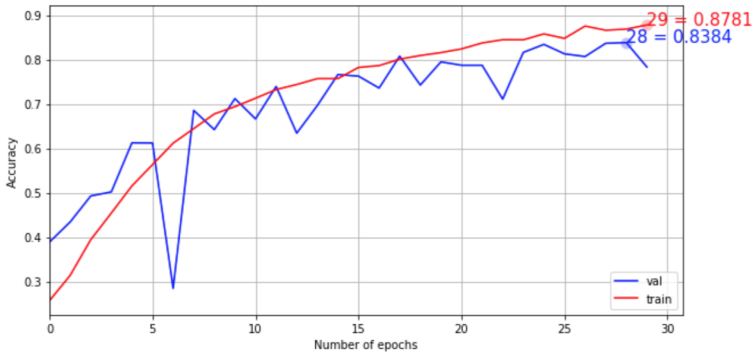

Figure 3: change in accuracy with increasing epochs

We measure metrics in equations 1, 2, 3 in order to evaluate the model.

$$\text{Precision} = \frac{True\ Positive}{True\ Positive + False\ Positive} \quad (4)$$

$$\text{Recall} = \frac{False\ Positive}{True\ Positive + False\ Positive} \quad (5)$$

$$\text{F1-score} = \frac{2 * precision * recall}{Precision + Recall} \quad (6)$$

F1 score conveys the balance between precision and recall.

Table 1. Model Accuracies on validation data.

	Precision	**Recall**	**F1-Score**
Neutrophil	0.57	0.88	0.69
Eosinophil	0.96	0.53	0.68
Monocyte	0.84	0.81	0.83
Lymphocyte	0.97	0.92	0.94
AVG/TOTAL	0.83	0.78	0.78

As shown in table 1, we obtain a value of 83% for precision, which indicates that 83% of positive tuples were correctly classified.

4 Conclusion

In this paper, we have implemented a classification model using Convolutional Neural Network based on deep learning [18], to classify the image dataset into four WBCs- Neutrophils, Lymphocytes, Eosinophils, and Monocytes. Our model achieved a precision of 83% on the testing dataset. Deep learning proves significantly better than the traditional approach as it is able to identify the minute intricacies within the image to classify them accurately. The original image dataset had imbalanced class sizes. Using augmented images restored the class balance and also created greater variation in the images, improving the quality of data for training the model. Deep learning also provides enhanced feature extraction, and is able to learn complex non-linear relations between dependent and independent variables. This implementation of deep learning provides a scalable approach [17] and results in

enhanced performance with the increase in the image dataset. This model can be implemented as a diagnostic system in clinics to determine the WBC count, and thus, determine the anomalies and various blood related diseases.

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