

Blood Cell Classification using Neural Network Models

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Abstract— Blood cells classification is a crucial aspect in medical diagnosis. Several machine learning models have been proposed under various researches for classification of blood cells in recent years. However, the traditional machine learning algorithms are limited in the accurate detection of abnormal cells. In this study, we propose deep learning based approach for blood cell classification and evaluate the efficiency of multi-layer neural network model built for the classification of the various types of White Blood Cells using Convolutional Neural Networks (CNN) and Recurrent Neural Networks (RNN) in combination. The proposed method leverages the strengths of both CNN and RNN and gives better results.

Keywords — White Blood Cells (WBCs), Blood Cell Classification, Convolutional Neural Network (CNN), Recurrent Neural Network (RNN), Long Short-Term Memory (LSTM).

I. INTRODUCTION

White Blood Cells (WBCs) are an important constituent of human blood. Sometimes called leukocytes, they play a critical function in the immunological system of the human body. Their production occurs in the bone marrow, and can be classified into several types, including lymphocytes, monocytes, neutrophils and eosinophils. One crucial component of medical diagnostics is how these blood cells are classified. The detection of abnormal cells can provide crucial information for the early diagnosis of various diseases, including cancer. The proposed method aims to categorize the WBCs using the hidden characteristics of their images. Each type of WBCs has distinct features, including variations in texture, color, size, and shape. By utilizing these underlying features of their images, the proposed approach aims to accurately classify the various classes of WBCs.

II. RELATED WORK

Characterizing and identifying a patient's blood sample is crucial for the diagnosis of blood-related disorders. In [1], Deep CNNs are implemented for separating the subclasses of WBCs. In [2], Pierre et. al. implemented multi-scale CNNs acting at different resolutions for vision based cell classification. Region-Based CNN (R-CNN) is used to classify WBCs in [3,4]. These approaches do not focus on utilizing the long-term dependency between key features. Recurrent Neural Networks are considered excellent in mapping input and output sentences in recognition/prediction

problems. Although, difficulties are reported when sequence spans over long intervals. The storing information over extended time interval involves the problem of decaying error backflow, to resolve this a gradient-based method is Long Short Term Memory (LSTM) [5,6].

Besides neural network, statistical pattern analysis analysis has been utilised [7] for classification of WBCs. It is based on controlled watershed algorithm to segment the nuclei from its microscopic image. Then their discriminating potentiality has been calculated using kernel density function. Morphological characteristics of cells have also been utilised for classification as in [8]. It was tested over gray scale images with outline feature being the outer contour of the cell. Architectures with combination of CNN and RNN are unable to produce results in case of multiple overlap cells. A Canonical Correlation Analysis (CCA) process was proposed in [9] which solved the above problem.

Segmentation algorithms are used for segmentation of WBCs in [10] using multiple features of including geometrical features, LDP features and color features using three different neural network based classifiers. Classification of Red Blood Cells (RBCs) helps in diagnosing many diseases. CNNs are used in [11], to classify various types of RBCs. Some works have combined CNN and RNN to classify WBCs [12, 13, 14].

III. METHODOLOGY USED

A. Convolutional Neural Network (CNN)

CNNs are based on shared weight architecture of convolutional kernels which slide upon features to generate feature maps. They are generalized multi-layer perceptrons CNNs are very popular for vision imagery tasks. CNN has the following layers:

1. Convolutional layer: This is responsible for creation of the activation map, simply it convolves the input and passes it on very similar to the neuron in visual cortex.
2. Pooling layer: Dimensionality is reduced by pooling layers by clustering outputs at next layer. These mainly is max pooling or can be average pooling.
3. Dropout: It is primarily utilized as a regularisation method. Since these are prone to overfitting, it is essential to be taken care of. At this layer some cells

are dropped/ignored to reduce the network complexity.

B. Recurrent Neural Network (RNN)

RNNs are the artificial neural networks where sequential data is utilized, a cycle is created allowing outputs from node to affect subsequent inputs on same node, thus inducing temporally dynamic behaviour. Developed on feedforward networks, parameter is shared across each layer of network. There are following variants of RNNs:

1. Long Short Term Memory (LSTM): LSTMs are invented in 1997. LSTMs solve the problem when the previous state influences the current prediction and leads to inaccuracy. To control the flow, LSTM has three gates: an input gate, an output gate and a forget gate. The Forget gate allows some information to be removed from current state
2. Bidirectional LSTM: In this variant, as the name suggests, the information from both sides is utilized. A finite sequence is used to predict based on elements' future as well as past context by concatenating opposite working layers.

RNN is mainly used for sequential data. Although, the blood cells do not have any sequential information in general but [12, 13, 14] have shown the applicability of RNN for WBCs classification. Therefore, we have also implemented RNN in this work.

C. Proposed Approach

The proposed model is an ensemble model of RNN and CNN.

The CNN model has the following architecture as shown in Figure 1.

1. Input layer: The input image is changes by this layer into 3-dimensional tensor.
2. Convolutional layer: An initial convolutional layer with 32 kernel filters is used for producing output of dimension $58*78*32$. On top of this, two convolutional layers with 64 kernel filters are used along with max pooling layers embedded in between to reduce the number of features.
3. Dropout layer: This layer is added for reducing the dimensionality and overfitting.
4. Flatten layer: This layer is required to feed the output to the fully connected layer.

A dropout layer is sandwiched between the dense layers for ensuring the features are learned without overfitting. Adadelata optimizer is used. The architecture is shown in Figure 1.

The RNN model layers are described as follows:

1. Input layer: This layer converts the input image into 3-dimensional tensor.
2. Lambda layer: This layer is used to implement the customized functions. Here, it converts the tensor into single channel of dimension $60*80$.
3. Bidirectional LSTM: This layer connects two opposite layers to common output, thus allowing the receiving of information from both past and future

states. Two Bidirectional LSTM layers with 64 units are used.

4. Dropout layer: Dropout layer is added to avoid the issue of overfitting and to speed up the process.
5. Dense layer: The last layer is a fully-connected dense layer which produces the final output.

Adadelata optimizer is used to avoid the continuous decay of learning rate. The architecture displayed in Figure 2.

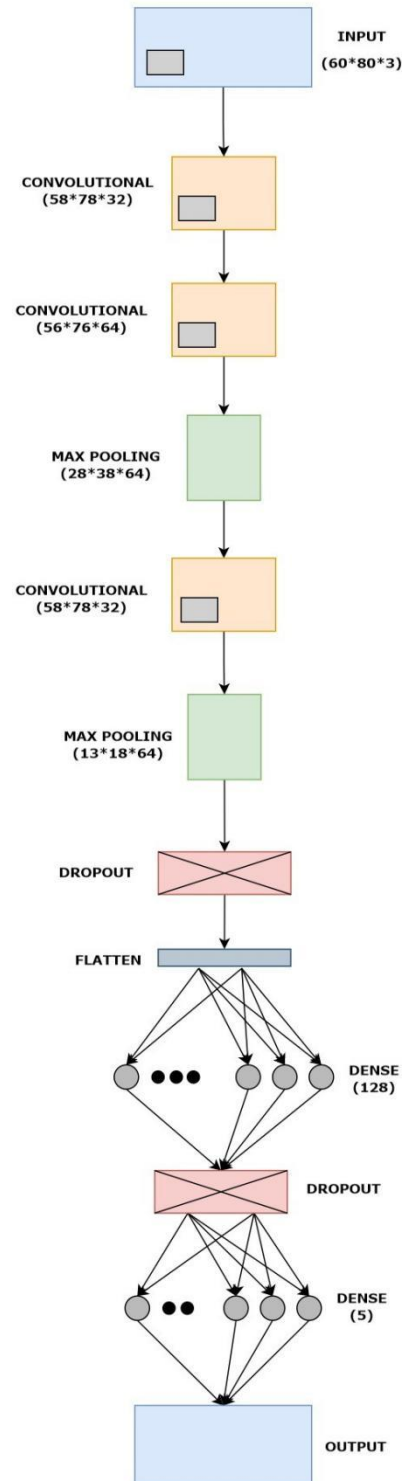


Figure 1. CNN Architecture

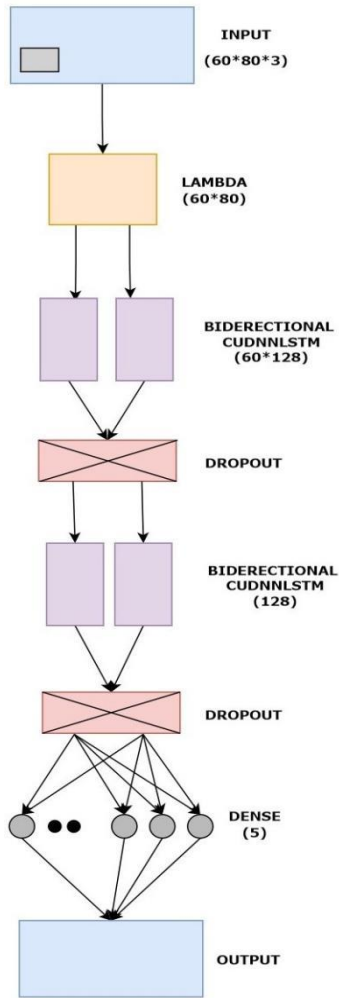


Figure 2. RNN Architecture

The concatenated ensemble model consists of the following layers:

1. Input layer: This layer converts the input image into 3-dimensional tensor, which is then fed into CNN and RNN units.
2. CNN Unit: CNN unit is the sequential model which comprises of a convolutional layer initially of 32 units and kernel size of 3*3. This was followed by two more convolutional layers along with corresponding max-pooling layers. Following that, a fully- connected layer receives the output and results are later flattened.
3. RNN Unit: This unit starts with a Lambda layer for reducing the dimensionality followed by two Bi-directional LSTMs with their corresponding dropout layers.
4. Fully-connected layer: The results from two individually working units: CNN and RNN, are concatenated and provided for this fully-connected layer's input.
5. Output layer: For obtaining the final output, two another fully-connected layers are used with reduced dimensions along with dropout layer to avoid overfitting.

The architecture is shown in Figure 3.

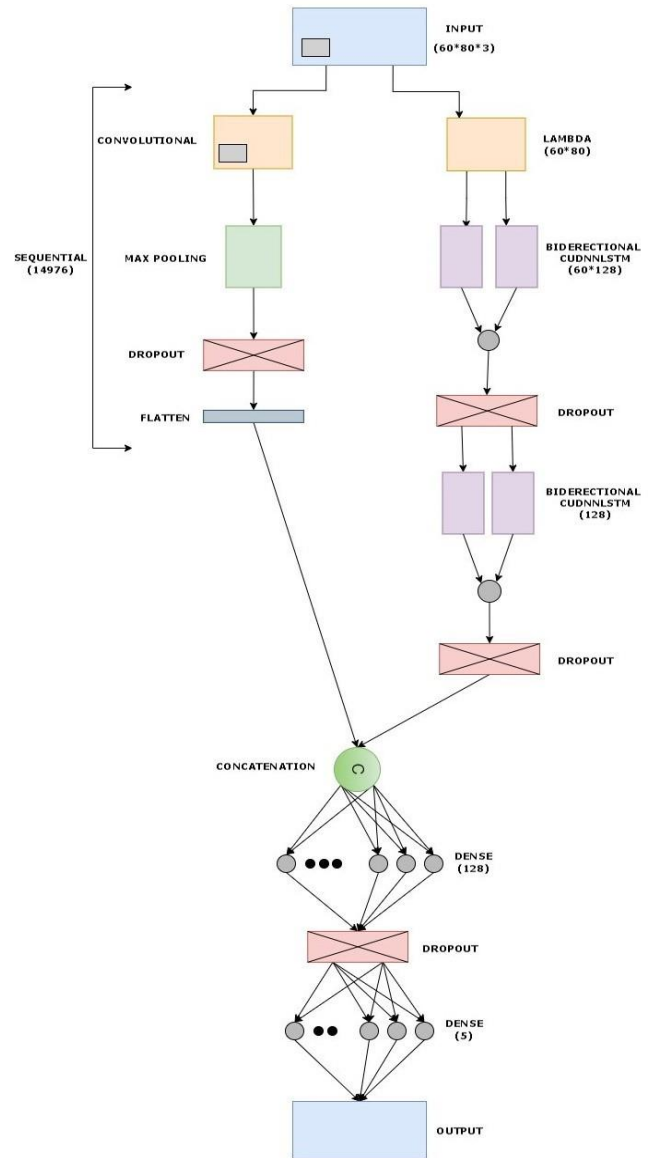


Figure 3. CNN+RNN Ensemble Model

IV. IMPLEMENTATION

A. Dataset

It is frequently necessary to identify and characterize blood cell samples for diagnosis of blood-based illness. The original raw data is available as BCCD Dataset. The processed blood cell dataset publicly available on Kaggle [15] consists of 12500 JPEG images of size 480*640*3 with their labels. There are four classes namely Lymphocyte, Monocyte, Eosinophil, Neutrophil. The entire dataset includes approximately 3000 sample images of each class. Besides we have 410 images with sub-type labels and corresponding bounding boxes (JPEG + XML). Four-way classification classifies cells among the four classes of WBCs namely Lymphocyte, Monocyte, Eosinophil, and Neutrophil. This classification is based upon the actions that the cells conduct against pathogens in the body, they do also possess differences in physical structures. On the other hand, two-way classification classifies WBCs in two broader categories i.e. Mono-nuclear and Poly-nuclear. Monocytes and

Lymphocytes are major mono-nuclear cells while Eosinophil and Neutrophil fall into the category of poly-nuclear cells.

B. Data Pre-Processing

One-hot encoding is used to normalize the cell types into four dimensional vectors. This allows utilizing the Softmax loss function for evaluation. The input images have been downscaled to 80*60 for reducing the computation time without significantly losing the accuracy. This is done without scaling transformations as size of nuclei is important for classification. A sample blood cell image with labels is shown in Figure 4.

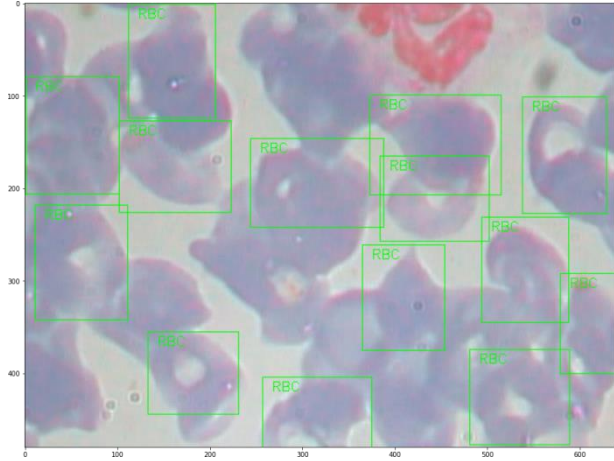


Figure 4. Blood Cell Image with Labels

V. RESULTS

The ensemble model is tested with CNN-only and RNN-only models under same conditions. Furthermore, we improved upon the models by making changes to the hidden layers and number of epoch values, referred to as Modified CNN and Modified CNN+RNN. Table 1 and Table 2 shows the results of two-way classification and four-way classification respectively.

The accuracy plots of Modified CNN for two-way classification and four-way classification are shown in Figure 5 and 6 respectively. The accuracy plots of Modified ensemble CNN+RNN model for two-way classification and four-way classification are shown in Figure 7 and 8 respectively.

Table 1: Results: Two-way Classification

Models	Two-Way Classification			
	Precision	Recall	F1-Score	Accuracy
RNN only	0.51	0.48	0.49	49.65%
CNN only	0.95	0.94	0.94	93.76%
RNN+CNN	0.95	0.94	0.95	94.53%
Modified CNN	0.96	0.95	0.95	95.13%
Modified RNN+CNN	0.99	0.97	0.96	96.05%

Table 2: Results: Four-way Classification

Models	Four-Way Classification			
	Precision	Recall	F1-Score	Accuracy
RNN only	0.30	0.25	0.27	25.13%
CNN only	0.90	0.87	0.88	86.81%
RNN+CNN	0.89	0.87	0.88	87.05%
Modified CNN	0.90	0.88	0.89	87.85%
Modified RNN+CNN	0.90	0.88	0.88	87.57%

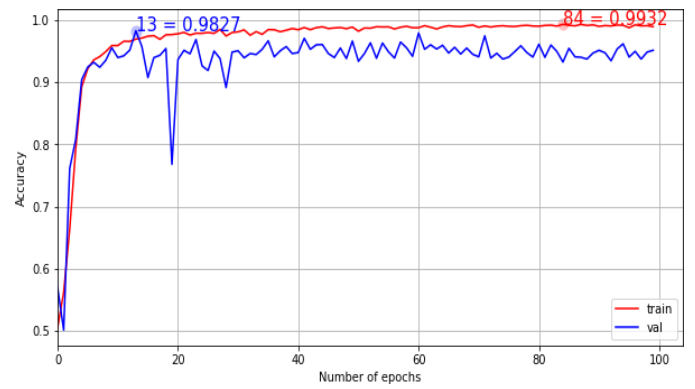


Figure 5. Accuracy Plot of Modified CNN for Two-way Classification

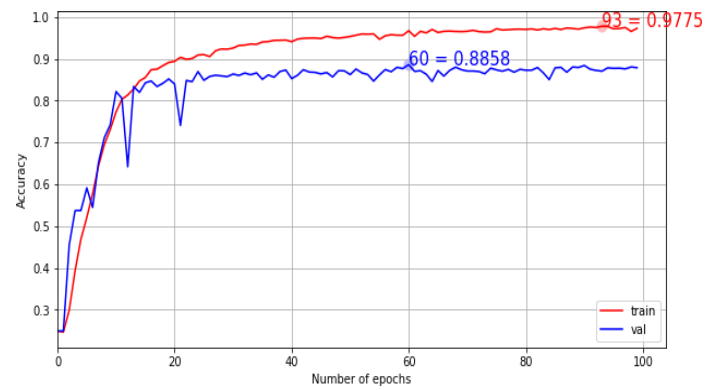


Figure 6. Accuracy Plot of Modified CNN for Four-way Classification

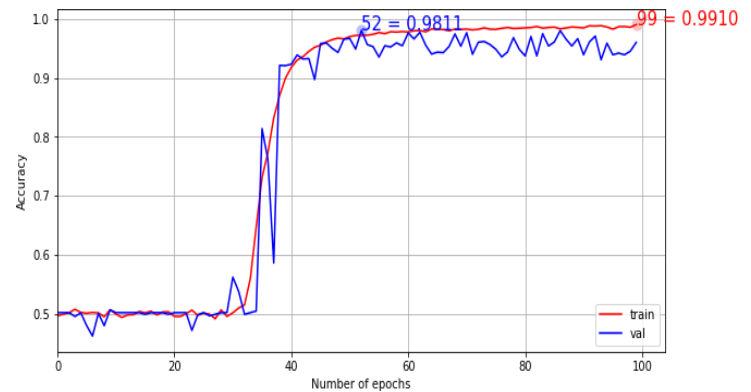


Figure 7. Accuracy Plot of Modified Ensemble CNN+RNN Model for Two-way Classification

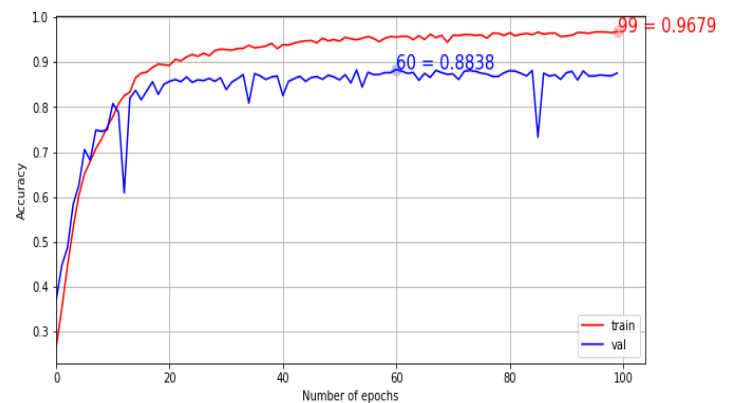


Figure 8. Accuracy Plot of Modified Ensemble CNN+RNN Model for Four-way Classification

VI. CONCLUSION

In this paper, we have implemented an ensemble model combining CNN and RNN for WBCs classification. The results show that the ensemble model of CNN+RNN achieves better accuracy as compared to the traditional CNN only and RNN only models under both the cases of two-way and four-way classification. We can also notice an increase of approximately 1% across both the CNN only and the ensemble model after tuning the number of epochs and the total number of hidden layers. The modified ensemble model outperforms the rest of the models.

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