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Deep learning approach to identify abnormalities in blood cell images

Dr. F. Mary Magdalene Jane
Professor and Head, Department of Computer Science with Data Analytics, Dr. NGP Arts and Science College Coimbatore
Email: marymagdalenejane@drngpasc.ac.in

Dr. V. Pream Sudha
Professor, Department of Computer Science with Data Analytics, Dr. NGP Arts and Science College, Coimbatore
Email: preamsudha@drngpasc.ac.in

Dr. A.C. Soundarraj
Professor, Department of Computer Science with Data Analytics, Dr. NGP Arts and Science College, Coimbatore
Email: sountharraj@drngpasc.ac.in

***Abstract*---**Blood cell imaging provides crucial diagnostic information about a person's atypical problems. Due to their multi-level structures, Deep Learning models aid in extracting complicated insights from input images. The power of automatic feature extraction makes Convolutional Neural Networks (CNN) the most widely used deep learning approach for blood cell categorization. Blood cells are classified using a recurrent neural network (RNN), which captures long-term relationships between elements. The possibility of CNN-RNN-based models for blood cell image classification is investigated in this work. The results prove that CNN-LSTM based model outperforms in classifying the blood cell images with an accuracy of 92.1%.

***Keywords*---**Deep learning, Blood cell, Convolutional Neural Networks (CNN), Recurrent Neural Network (RNN).

1 Introduction

Blood circulates in the body of the average adult in the range of 1.3 to 1.5 gallons. A person's blood makes up about 10% of their total weight. The red blood cells, white blood cells, platelets, and plasma are the four primary components of blood. The bone marrow produces the majority of blood cells. The circulatory system transports blood and performs a variety of functions. Blood cells transport nutrients, electrolytes, hormones, vitamins, antibodies, heat, oxygen, and immune cells to various body regions in order to combat illness. Hematology tests and medical imaging can reveal abnormalities in blood cell count and body tissue behaviour, which suggest the presence of an infection or disease. Medical imaging is the process of using technology to observe the human body in order to diagnose, monitor, and treat medical problems. Because diseases are most treatable when identified early, medical imaging allows doctors to diagnose diseases in their early stages.

Construction of compound rule-based systems was used to do medical imaging and analysis from the 1970s through the 1990s. Systems based on supervised learning were in use by the late 1990s. These pattern learning systems were advantageous because they made statistical classifiers and feature selection methods easier to deploy. By learning the influential properties of the input data, these machine learning systems evolved into models with multiple layers that transform input data such as photos into output data such as determining the presence of disease or not. Convolutional Neural Networks have been the most successful multi-layer model in medical imaging since 1990. CNN extracts task-specific features automatically. As a result, CNN is the method of choice for detecting abnormalities in blood cells. Over the last decade, CNN has been the most widely employed deep learning approach for blood cancer diagnosis by researchers. The individual elements in the blood cell image can be used to train a Recurrent Neural Network (RNN) to learn long-term dependencies.For better performance and to analyse blood cell images over time, recent research in blood cell classification involves a combination of CNN and RNN models [4,9,20]. The goal of this work is to investigate CNN and CNN RNN-based models for blood cell classification.

2 Convolutional Neural Networks (CNN) – RNN Models

CNN is a Deep Learning Algorithm that is based on the visual brain of animals. Through the reduction of a targeted loss function, CNN extracts task-specific characteristics from images. Convolution layers, pooling layers, and fully connected layers make up CNN, which uses a backpropagation method to automatically learn aspects of spatial hierarchies. The CNN is built using a hierarchical model, which is then used to produce a fully-connected layer in which all of the neurons are coupled to one another and the output is generated via linear propagation. Because of its excellent accuracy and automatic feature extraction, CNN is recommended for medical imaging, analysis, and diagnosis.

It has been shown in previous researches that during overlapping settings, CNN-based systems do a good job of detecting partially visible cells. Clinical inquiry and early therapy are aided by classification of corpuses utilising attributes retrieved from the CNN model. [14] proposes a new CNN model for WBC categorization that combines the properties of the first and last convolutional layers. Only the first layer of CNN is connected directly to the input image. There's a good possibility that the other convolutional layers will lose the information's originality. As a result, the layers' features are fused to ensure that original information flows to the rest of the convolutional layers, and a dropout layer is added to prevent overfitting of the classification model. On BCCD dataset, the model has a 96 percent accuracy rate.

2.1 CNN – RNN

Due to its high accuracy and ability to learn spatial temporal data, various researchers have suggested CNN-RNN model in blood cell categorization in recent years.With the help of filters, CNN retrieves the images' local and deep properties, whereas RNNs learn temporal and context aspects, as well as long-term connections between entities.RNN, unlike CNN, learns to detect picture features over time, and 2D medical images are perceived as sequential patterns. RNN is utilised in medical imaging to calculate the continuity characteristics of the CNN model's intermediate layer output, and the features are integrated into a fully connected network for blood cell classification, resulting in high classification accuracy. The comparative research of CNN-RNN models is shown in Table I. Salman Shah et al. [17] established a model to distinguish between immature lymphoblasts and normal cells, which had an accuracy of 86.6 percent. The Xception-LSTM model got the highest classification accuracy of 90.79 percent among the five models for blood cell classification. A single blood cell image takes an average of 3.8 seconds to test. At the patient level, the model developed by Lichy Han et al. [6] showed precision and recall of 0.67 and accuracy of 61 percent. Tumors with less clearly defined borders are likewise more likely to be classified as positive by the classifier.

Table I Comparative Study of CNN-RNN models

Model	Experiment	Classification Accuracy
CNN-RNN	Immature lymphoblast and normal cell Classification[17]	86.6%
	Classification of blood cell[3]	90.79%
	Methylation status prediction in glioblastoma patients [6]	61%

The literature survey shows that CNN-RNN model have performed efficiently in classification of blood cells and immature lymphoblasts. Hence it is proposed to implement the CNN-RNN models to classify the types of white blood cells.

3 Methodology

3.1 Dataset creation

The BCCD data set, which contains 410 pictures of white blood cells with cell-type identifiers, was used as the starting point for this investigation (CSV).The four blood cell types taken for study are Eosinophil, Lymphocyte, Monocyte and Neutrophil. The dataset must be improved to combat over-fitting and increase the accuracy of a model.The methylation status and tumour location are preserved by image rotation on an MRI scan, which is important during medical intervention [6]. In the classification of blood cells, a similar approach is used. Using the Xception-LSTM model, picture rotation-based augmentation has been shown to improve the accuracy of cell image categorization. Because the size and intensity of the nucleus are key characteristics that separate blood cells, some augmentation techniques, such as scale transformation and colour transformation, are not commonly used in blood cell imaging. The quantity of blood cell pictures has been balanced in order to obtain sample equalisation, which enhances the model's accuracy and convergence time [3,8]. By twisting and flipping the WBC photos, augmentation is used to generate extra images for the training set in this study. Following the method, the training set consists of 500 photos of each type of WBC image.

3.2 Model building

For blood cell image classification, a model combining CNN and RNN was proposed by Gaobo Liang et al [1,5]. A CNN model that has been pre-trained on the ImageNet dataset is used to compute the initial weight values. Multiple feature maps are produced using convolution windows of various sizes [15,16].

Long Short-Term Memory (LSTM) and Gated Recurrent Units (GRU) RNN models are integrated with CNN in the proposed architecture to create CNN-LSTM and CNN-GRU models. The internal structure of an LSTM is more sophisticated than that of a standard RNN. The input, forget, and output gates of an LSTM are utilised to discern between relevant and inconsistent data. In the model design, a merge layer is used to combine the features obtained from CNN with the features collected from RNN. Attentional neural network approaches are used in the feature mapping classification model, which are aided by appropriate element-wise multiplication procedures. A Softmax layer is applied to the merged features, revealing the class probability distribution.

This work utilises a special type of RNN known as GRU to learn long-term dependence information. As combining CNN and RNN architectures can successfully examine volumetric objects and image frames, a network with one input layer, two hidden layers with eight memory units, a masking layer, and an output layer that is a fully connected layer with four neurons for each of the four classes is designed. The output layer's softmax activation function allows the network to learn and output the distribution over all potential output values. Both models have convolutional and pooling layers, with the rectified linear unit (Relu) serving as the activation function. The inputs for each mini-batch are standardised using batch normalisation. To prevent overfitting, L2 regularisation is used to drop out layers. The RNN layer is followed by an additional fully linked layer, which is a bi-directional RNN with (GRU) with a state size of 256. The pool layer reduces the convolutional weights by a significant amount, allowing the neural network to become more adaptive. By feeding each output into the next layer, RNN decreases the complexity of growing parameters.

4. Experiment and Results

Experiments were carried out using Keras, a high-level API for neural networks, to implement CNN-LSTM and CNN-GRU algorithms. During training and testing, data is split into 32-segment mini-batches. The network had a 0.3 dropout rate and a 0.01 learning rate. During training, the network used the efficient Adam optimization approach and the sparse categorical cross entropy loss function, which is ideal for multiclass classification issues. The dataset is used to train the four deep classifiers with the specified parameter settings, and the blood cell identification models are created. To establish a successful mapping of inputs to outputs, network training is required to update the model weights. The model of blood classification is separated into two branches. The weights in the CNN branch use the parameters that have been pre-trained on the ImageNet dataset, while the RNN branch uses random parameter initialization. The cross-entropy loss function gradient is used to update the model weights throughout the training phase. To calculate training samples, the Adam optimizer is introduced throughout the network. After a predetermined number of periods, the training process is completed, and the model with the lowest verification loss is chosen.

Model Evaluation aids in finding the best model that represents the data and provides the performance estimation of the chosen model in the future with varying data. The prediction performance of the models was estimated using the usual 10-fold cross-validation technique. Prediction accuracy, logarithmic loss, precision, recall, and F-measure were used to assess the four separate models' performance.

Table II Performance Results of Deep Models

Metrics	CNN-LSTM	CNN-GRU
Precision	0.92	0.89
Recall	0.90	0.90
F- Measure	0.91	0.90
Accuracy	92.1%	90.4%

The CNN-LSTM model performs well in predicting blood cell types, according to the results. With a precision of 0.92, recall of 0.90, and F-measure of 0.91, it is successful at predicting WBC type. The Recall of the CNN-LSTM and CNN-GRU classifiers are nearly identical at 0.90, however the accuracy of the CNN-LSTM classifier is somewhat higher at 92.1 percent.

Table III Epochwise Accuracy and Logloss of Deep Models

Epochs	Accuracy		Log Loss	
	CNN-LSTM	CNN-GRU	CNN-LSTM	CNN-GRU
100	79.6%	80.3%	0.7514	0.8466
200	80.6%	80.8%	0.7501	0.8230
300	81.7%	81.6%	0.7418	0.7423
400	82.4%	83.1%	0.7322	0.7345
500	82.9%	84.3%	0.6150	0.7104

The results show that as the number of epochs increases, the log loss decreases, and the models improve their performance by reducing misclassifications. When it comes to classifying blood cell types, the CNN-LSTM model has a log loss of 0.6150, which is lower than the CNN-GRU model's log loss of 0.7104. The deep models' experimental findings are depicted in Fig.1 through Fig.3.

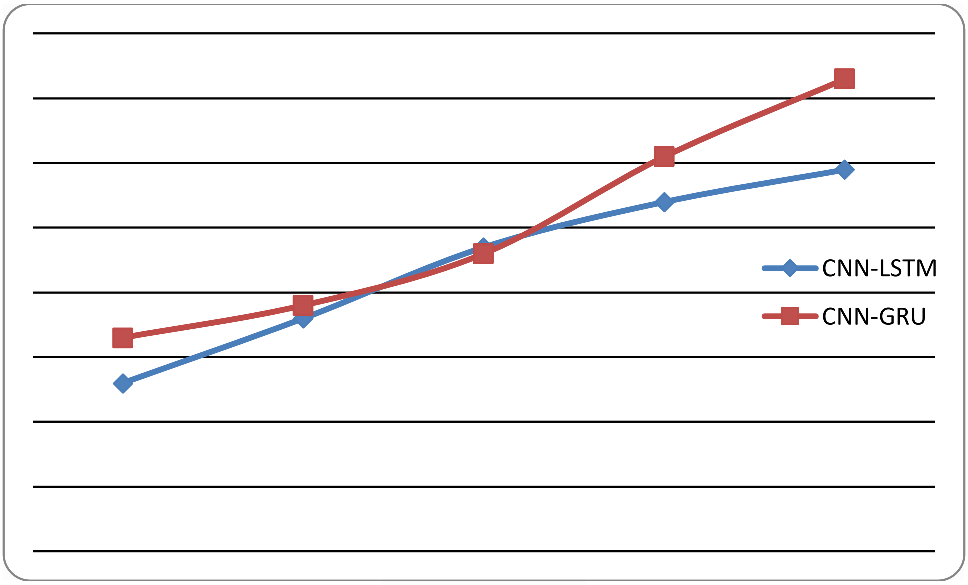

Fig.1. Accuracy

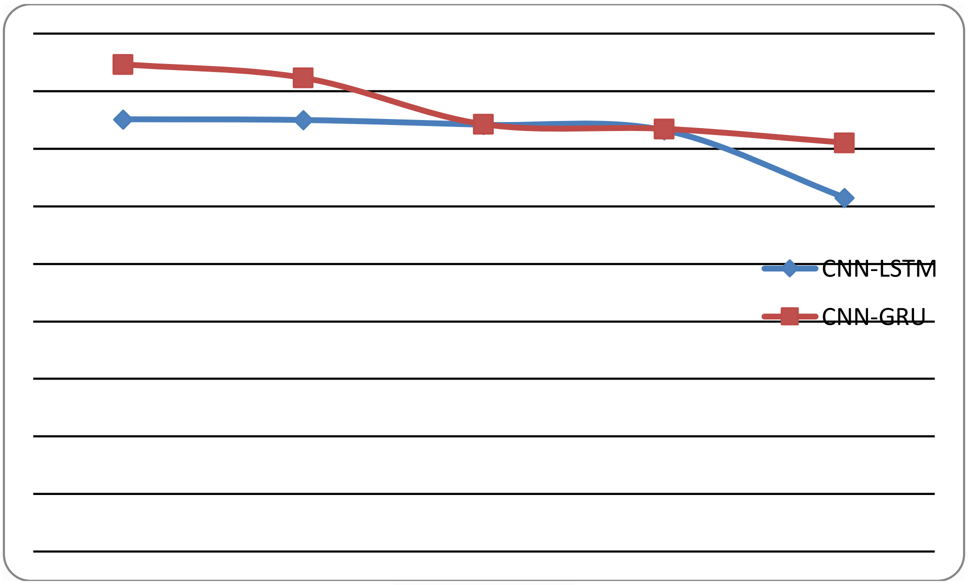

Fig.2. Logloss

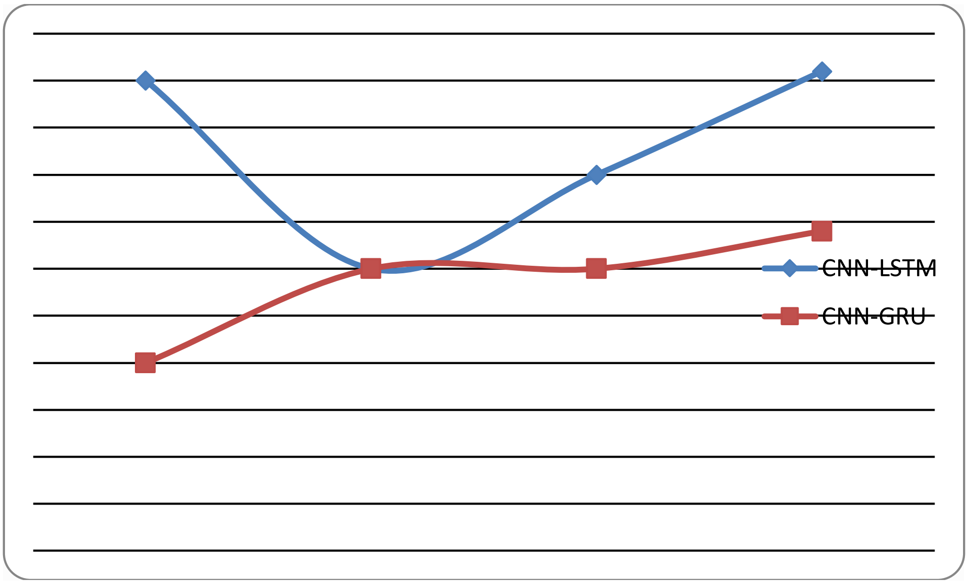

Fig.3 Performance of the Models

The epochwise accuracy values for the CNN-LSTM based blood cell prediction model are constantly growing, as shown in Fig.1. The logloss in recognising blood cell types decreases as the number of epochs increases, and the CNN-LSTM model, as shown in Fig.2, has the lowest logloss. Figure 3 shows the CNN-GRU and CNN-LSTM models' performance. While the precision of the CNN-LSTM model's blood cell type prediction is higher than the CNN-GRU model, the recall remains constant. In terms of predicting blood cell type, the CNN-LSTM model has a greater accuracy (92.1%) than the other model.

5 Conclusion

The existing CNN and CNN-RNN based models for blood cell categorization have been thoroughly investigated in this research. Due to its high accuracy and capacity to extract features automatically, CNN has become the most used deep learning approach for leukaemia detection over the last decade. For blood cell categorization, various researchers have recently integrated CNN and RNN architectures. The hybrid CNN-RNN models have been discovered to assist conserve the sequential and spatial information of blood cell imaging features while also providing insight into the structured data. When it comes to categorising blood cell types, the CNN-LSTM model has a very high accuracy rate.

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