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SENSING OF WHITE BLOOD CELLS USING RESIDUAL NETWORK AND A COMPARISON STUDY USING VARIOUS PRE-TRAINED NETWORK

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Abstract - White Blood Cells(WBCs) play a significant role in defending our body from diseases. Leukemia also called blood cancer is normally identified by testing the blood smear using a microscope by the pathologist. Both traditional methods and automated techniques are used for blood counting. In traditional methods better accuracy is achieved by the skills of technicians who are involved in diagnostic procedures. Automated techniques which are very expensive are not affordable by most of the hospitals or laboratories. Therefore, to overcome these difficulties, and for speedy diagnosis deep learning systems are employed. In this paper identification of leukemic cells whether normal or cancerous is detected through ResNet50 where an accuracy of 99.61% is achieved. A performance analysis through GoogLeNet, ResNet152, ResNet101, VGG16and VGG19 is also performed. The classification is done through the softmax layer.

Keywords - Leukemia, Deep Learning, Convolutional Neural Network(CNN), Residual Networkfirst, second, and thirdlevel headings

I. INTRODUCTION

Medical associates and medical fields are facing many problems in diagnosing diseases which are increasing day by day. For identification of diseases deep neural network has taken an important position [1]. Leukemia is a blood cancer that is caused due to the abnormal growth of immature leukocytes and also with the reduced blood count. Blood consists of Red blood cells (RBCs or Erythrocytes) that carry oxygen from lungs into other parts of the body. WBCs (Leukocytes) are white Blood cells that protect the body against sickness [2]. WBCs are classified as Granulocytes which contains Basophils (<1%), Eosinophils(<5%), Neutrophils(50-70%) and Agranulocytes contains Lymphocytes(25-30%) and Monocytes(4-10%)[2]. The life span of WBCs are short and an increase in number of WBCs the number of immature cells also increases. The infected Leukemia cells are categorized as Lymphoid and Myeloid cells. The Lymphoid types are Acute Lymphoblastic Leukemia (ALL) and Chronic Lymphoblastic Leukemia (CLL). Myeloid types are Acute Myeloid Leukemia (AML) and Chronic Myeloid Leukemia (CML)[2].

II. RELATED WORK ON CONVENTIONAL METHODS AND DEEP LEARNING (DL)

1. Conventional Methods:

S.Rezatofighi et.al[3] automatically recognizes 5 types of WBCs in peripheral blood. Snake Algorithm and Sequential Forward Selection (SFS) algorithm are used. A Comparison of two classifiers ANN and SVM is done. Anita et.al [4] designed an artificial electric field algorithm (AEFA-C) which detects WBCs in an optimization problem where the ellipses are efficiently mapped. S.Nazlibilek[5] the counting of the white blood cells are done and accurately determines their size and categorizes them according to different types of leukocytes.

2. Deep Learning

Deep Learning is an expansion of Artificial Network (ANN) proposed by LeCun [6]. Now CNN has become a powerful tool to segment, detect, recognize and retrieve images[7]. The advantages of DL are: (a) DL ignores image quality. (b) Segmentation and extraction of features are unnecessary as they are derived from convolutional concept. (c) In DL system classification is simple.

Spampinato et al [8], an assessment of automated skeletal bone age was built with 1391 images. L.H.S.Vogado et al [9] CNNs transfer learning method is used to diagnose leukemia. For feature extraction AlexNet, VGG Net, CaffeNet was used. Feiwei et al [10] using the deep residual network, classification of WBCs was performed. It used 40 leukocyte categories obtained from microscopic image dataset.

III. MATERIALS AND METHODS USED

A. Datasets

The data sets are from ALL-IDB which contains 260 blood images which are having a resolution of

257x257 in .jpg format. In this dataset 130 images are normal and 130 images are cancerous.[11]

B. CNNs used in the proposed work

Using the CNN a comparative study is conducted to calculate accuracy, sensitivity, specificity, Positive Predictive Value(PPV), Negative Predictive Value(NPV).

1. VGG Net-VGG16 and VGG19[12]

VGG Net based on CNN which was proposed by Karen Simonyan and Andrew Zisserman. VGG16 consists of a convolutional layer, a Max pooling layers, and a fully connected layer. The Total layer is 16 , each layer of 5 blocks each with a max pooling layer. The VGG19 has 19 layers, where in the last 3 blocks it contains extra convolutional layers. Compared to VGG16, VGG19 utilizes more memory.

2. GoogLeNet[12]

GoogLeNet contains 22 layers with inception networks are added[13]. It uses 1x1, 3x3, 5x5 convolutional filters, 1x1 convolutional kernels to reduce computation.

3. ResNet (Residual Network)- ResNet101,ResNet152, ResNet50[12]

Deep neural networks take a lot of time to train and are exposed to over fitting. While training with deep neural networks, there is a problem of “degradation”. This problem is placed in ResNet using “residual mapping”.

C. ResNet50

The CNN used in the proposed work is ResNet50. The architecture of ResNet50 is shown in Figure 1[14].

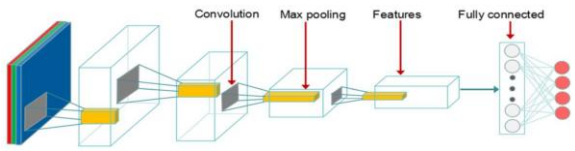

Fig 1. Architecture of ResNet50

ResNet50 is composed of residual blocks, each residual block consist of a convolutional layer, a stack normalization layer and a rectified linear unit (RELU). RELU speeds up the convergence of stochastic degradations with sigmoid functions. Batch normalization initiates the activations within a network to take a Gaussian distribution at the start of the training. ResNet50 is made up of 49 convolutional layers and a fully connected layer at the bottom. The first Convolutional Layer (CL) has a kernel size of 7*7, 64 different kernels, and with a stride of 2 in the first CL. The max pooling layer comes next with size of 3*3 and a stride of 2. The kernel size for the second CL are 1*1, 64 kernels, 3*3, 64 kernels and 1*1,256 kernels. These 3 layers are repeated 3 times in total. As a result, there are a total of 9 layers. The third CL consists of 1*1,128 kernel, 3*3,128 kernel and 1*1, 512 kernel. These 3 layers are repeated 4 times in total. In total, there are 12 layers. The fourth layer has 1*1,256 kernel, 3*3,256 kernel and 1*1, 1024 kernel. These 3 layers are repeated a total of 6 times. There are 18 layers in total. 1*1, 512 kernels, 3*3,512 kernels and 1*1, 2048 kernels make up the fifth layer. These 3 layers are repeated 3 times in total. As a result, there are a total of 9 layers. Finally, there is an average pool with 1000 nodes in a fully connected layer. Finally, the Softmax function yields 1 layer.

IV. PROPOSED WORK

The input image is in RGB format. Each image is scaled to a fixed 224x224 format. A pre-trained ResNet50 model is fine-tuned. ResNet50 is used for training phase and testing phase.

In training phase each image is trained and the fully connected layer (FC1000) is used to extract features which are known as the trained features. Then save the extracted features. In testing phase the input image is selected. The features collected from fully connected layer(FC10000) for testing, known as test features, are also extracted during this phase. These features are taken for classification which is done in softmax layer. For this process the softmax layer is trained for classification on the train features and the targets. Finally, classify the test features into one of the two classes (Normal or Cancer) using the trained softmax layer. Figure 1 depicts the proposed methodology’s flow diagram.

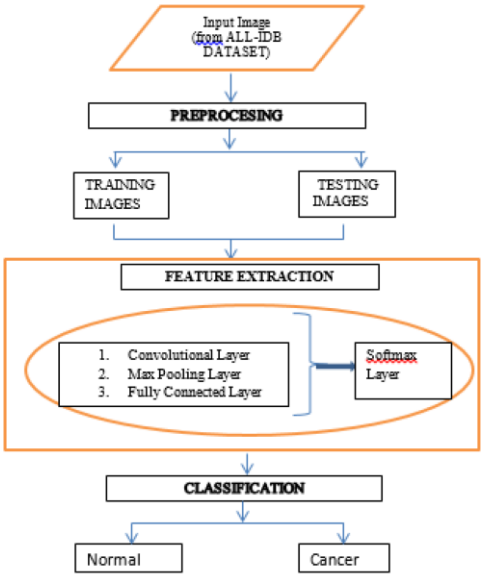

Fig. 2 Proposed Methodology

V. RESULTS

The convolutional neural network ResNet50 is used for training the datasets. The input image which is in

RGB format is selected (Fig.2). Here deep activation features are used for feature extraction. In preprocessing stage, the image is resized, that is, either down sampling or up sampling is done. Processing is performed in fully connected layers which convert the feature values into a single vector, and using this value the final probability for each label is predicted. After that features are loaded and trained in the softmax layer for classification (Fig.2). Finally, a performance analysis of GoogLeNet, ResNet101, ResNet152, ResNet50, VGG16, and VGG19 are shown in Table 1. Using ResNet50 an accuracy of 99.61% is achieved which interprets better performance.

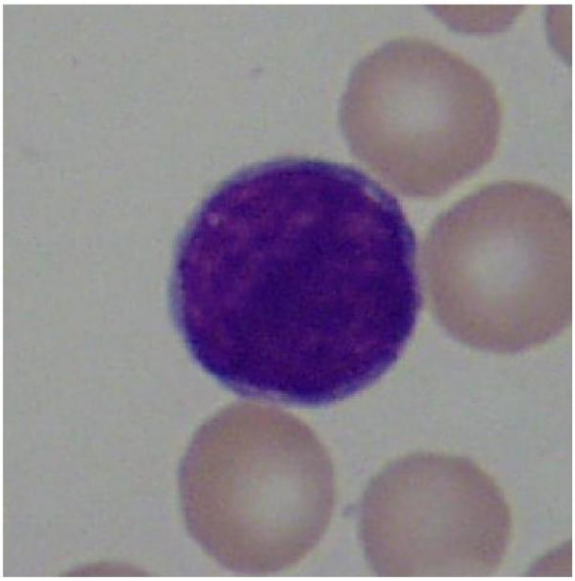

Fig.3 Input image

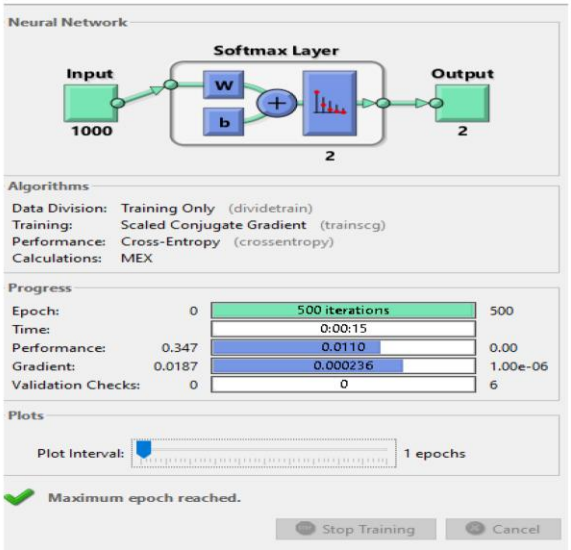

Fig.4 Neural Network

The following metrics are compared: accurate rate(acc), sensitivity(Sen), specificity(Spc), Positive Predictive Value(ppv), and Negative Predictive Value(npv). True Positive(TP) indicates that cancer has been correctly detected, False Negative(FN) indicates that cancer has been incorrectly identified as normal, False Positive(FP) indicates that normal has been incorrectly identified as cancer, True Negative(TN) indicates that normal has been correctly identified as normal.

acc = ((TN/TP)/(TN+TP+FN+FP)) (1)
Sen = (TP/(TP+FN)) (2)
Spc = (TN/(TN/FP)) (3)
Ppv = (TP/(TP+FP)) (4)
Npv = (TN/(TN+FN)) (5)

Class Performance Metrics	Googlenet	Resnet101	Resnet152	**Resnet50**	Vgg16	Vgg19
CorrectRate	95.3846	96.9231	97.3077	**99.6154**	98.0769	98.8462
Sensitivity	96.1538	95.3846	96.9231	**100**	100	98.4615
Specificity	94.6154	98.4615	97.6923	**99.2308**	96.1538	99.2308
PositivePredictiveValue	94.697	98.4127	97.6744	**99.2366**	96.2963	99.2248
NegativePredictiveValue	96.0938	95.5224	96.9466	**100**	100	98.4733

TABLE 1 –Class Performance Metrics

VI. CONCLUSION

In this paper deep learning networks are employed for the detection of WBCs. Different pre-trained networks like GoogLeNet, VGG16, VGG19, ResNet101, ResNet152, and ResNet50 are used for training the RGB image. A better performance was achieved in ResNet50 with an accuracy of 99.61%. This demonstrates that, as compared to traditional methods, deep learning networks may be utilized to detect WBCs automatically in less time and with more accuracy.

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