Applying Residual Convolutional Neural Networks (**ResNet**) For Automated Detection of Leukaemia

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Abstract- The present work proposes a technique for blood cancer (leukemia) classification based on machine learning. Manual classification of blood cancer is very challenging and prone to errors and therefore machine learning approaches are employed to perform the task. Out of machine learning algorithms, deep learning has emerged as the suitable candidate for analyzing such large and complex datasets with enormous divergences. The proposed work presents a feature selection and training algorithm based on the RESNET-50 Deep Neural Network for image classification. The RESNET employs the skip connection among the hidden layers so as to reduce chances of overfitting and vanishing gradient. The performance of the proposed system has been evaluated in terms of the error and accuracy. It is found that the proposed technique achieves almost 97.9% classification accuracy which is better than previous work for same dataset (91.84%).

Keywords- Blood Cancer Detection, Deep Learning, Convolutional Neural Networks, ResNet-50, Classification Accuracy.

I. INTRODUCTION

Artificial Neural Network (ANN) has recently emerged as one of the most powerful tools for contemporary computation. Its design is based on the fact that the human brain is a:

Highly Non Linear Structure Highly Parallel Structure

On extremely important attribute of the neural model is its ability in following trends in the input fed to it. No matter how complex or abruptly the output for a corresponding input may change, the network maps the input and output in the form of experiences called weights. The parallel structure enables data or inputs X from various paths design the weights W. The design of the network culminates in the decision making according to some function θ called the bias. The structure can be mathematically modelled as:

$$\mathbf{Y} = \sum_{i=1}^{n} \mathbf{X} \mathbf{i} \mathbf{W} \mathbf{i} + \mathbf{\Theta} \tag{1}$$

Here X represents the signal W represents the weight Θ represents the bias.





The above figure is pretty generic in nature. The task of following a trend in the given input data can be accomplished accurately using a particular architecture of a neural network. [3] The network continuously leans and adapts according to the provided input data and its corresponding data. Thus it can be thought of working as the human brain that also adapts itself according to experiences. The experiences themselves have counterparts in the mathematical ANN structure called weights. If the correspondance between the input X and a target Y is given to the network to design and adapt its weights, then the deviation of the expected output and the actual output is given by an error E which can be mathematically defined as:

$$\mathbf{E} = \mathbf{Y}_{\mathbf{a}} - \mathbf{Y}_{\mathbf{p}}(2)$$

 Y_a is the actual output Y_p is the predicted output E is the error.

II. LITERATURE REVIEW

Some salient features of the existing work in the domain has been cited in this secion.

Denny et al. proposed approach uses imaging processing techniques to detect irregular blood cells in the microscopic images of the blood. Using the training data collection, the program is trained using DCNN and is uploaded into HDFS Hadoop framework. The learned method classifies when a new image is inserted into the program whether the collected picture includes cancerous leukemia cells or irregular cells. This way the process of detection of leukemia is automated and can be accessed by any of the hospitals with connected to the cloud system.

Tuba et al. proposed a method for automatic detection of one type of leukemia, acute lymphoblastic leukemia, by classifying white blood cells into normal cells and blasts. The proposed method uses shape and texture features as input vector for support vector machine optimized by bare bones fireworks algorithm. Based on the results obtained on the standard benchmark set, ALL-IDB, the proposed method shows a competitive accuracy of classification comparing to other state-of-the-art method.

Kumar et al. proposed that leukemia is kind of blood cancer in which white blood cells are triggered to grow uncontrollably and also in an immature way. It is a leading cause of loss of lives. The detection of this illness is done using the microscope images of the affected blood samples. The pathologists carryout analysis of the samples and bring out conclusions of the diagnosis. The medical technology field has seen a huge boom and also a lot of advancement in terms of accurate diagnosis. This approach focused on use of the clustering method of K mean type.

Rawat et al. did their study on the computer based classification methods that have been employed for the accurate classification of the different forms of serious blood cancer that is leukemia. The CAD system is an efficient mechanism using which the forecasting and classification of the illness can be smoothened and made effective. As the disease is of a complex form and also shows very intricate symptoms. It is important to detect is correctly as the treatment depends on it. The microscopic samples need to have great clarity and this diagnostic assessment must be free of any errors or glitches. Several sort of morphological characteristics are used for the same. They include the shape, size, change in color, texture etc. The computer assistance has greatly improved the accuracy and effectiveness of the system and the overall approach towards the better diagnosis of the illness.

Mao et al. used DCNN approach and methodology to train samples for the cancer detection. The CTC in the blood can play a significant role in evaluating the cancer detection procedure. These markers are very necessary as they can signal the tumor response in the blood. The deep convolutional neural network is an advanced methodology that can help with training with the input data set very swiftly. This is a streamlined course of action that can help in the overall progress of the process. The microscopic image of the blood has to have a lot of clarity and precision so that the medical expert can detect any tiny variation in the sample of the blood. This detection and evaluation phase is immensely important and has to be performed without any dint of error otherwise the entire thing could go wrong including the treatment. Henceforth this technique was a good method to increase the quotient of accuracy.

Shankar et al. showed that the field of image processing has seen a lot of advancement and progress over the last few years. The application of image processing in the field of disease detection and medical diagnosis is immense. As the medical images form the basis of clinical resource for the disease evaluation. These images need to be very accurate and free from any kind of error. The microscopic image of the blood has to have a lot of clarity and precision so that the medical expert can detect any tiny variation in the sample of the blood. This detection and evaluation phase is immensely important and has to be performed without any dint of error otherwise the entire thing could go wrong including the treatment. So this process very robust and effective with good accuracy.

Rawat et al. proposed that automated technical classification methods were studied under this paper. The blood smar method becomes very easy and the identification task also becomes less tedious for the pathologist when such technology allied methods are utilized. In this microscopic analysis, the review of classification of the leukocytes is carried out very efficiently. However, the nonspecific nature of white cell with symptoms of Acute Lymphoblastic Leukemia (ALL) often leads to erroneous identification. It is important to detect is correctly as the treatment depends on it. The microscopic samples need to have great clarity and this diagnostic assessment must be free of any errors or glitches.

III. PROPOSED METHODOLOGY

Prior to feature extraction and classification, data preprocessing is done to achieve train the ANN accurately and obtain high sensitivity and accuracy of classification.[5]-[6]

Segmentation:

The division of an image into meaningful structures, image segmentation, is often an essential step in image

analysis, object representation, visualization, and many other image processing tasks. A disjunct categorization does not seem to be possible though, because even two very different segmentation approaches may share properties that defy singular categorization1. [5] The categorization presented in this chapter is therefore rather a categorization regarding the emphasis of an approach than a strict division. The following categories are used:

Threshold based segmentation: Histogram thresholding and slicing techniques are used to segment the image. They may be applied directly to an image, but can also be combined with pre- and post-processing techniques.

Edge based segmentation: With this technique, detected edges in an image are assumed to represent object boundaries, and used to identify these objects.

Region based segmentation: Where an edge based technique may attempt to find the object boundaries and then locate the object itself by filling them in, a region based technique takes the opposite approach, by (e.g.) starting in the middle of an object and then "growing" outward until it meets the object boundaries [6]

Segmentation plays a crucial role in the feature extraction and classification.Segmentation allows to separate the region of interest from the composite image.

Considering the image under interest to have an area 'A' with a central reference ' C_0 ', the radial gradient is computed as:

$$g_r = max(r, C_0,) |G_{\sigma}(r) \frac{\partial}{\partial r} \oint_{r, C_0}^{R} \frac{I(x, y)}{2\pi r} dA|$$
(3)

Here,

 g_r denotes the radial gradient

I(x, y) denotes the image under interest

*C*⁰ denotes the central reference

 G_{σ} denotes the Gaussian kernel

r denotes the radial distance from the central reference

R denotes the maximum radial distance from the central reference

max denotes the operation to find the maxima

dA denotes the differential area

The image can be separated by computing the entropy corresponding to the grayscale histogram. The entropy

of an image of $m \times n$ pixels with a histogram h_n corresponding to n grayscale levels can be expressed as [7]-[8]:

$$h_l = \frac{1}{1-l} \log_2 \sum_{i=1}^n p_{i(4)}^l$$

Here,

l denotes the order of entropy, and l > 1.

 p_i^l denotes a discrete probability distribution corresponding to the histogram h

As $\lim_{l\to 1} h_l$ approaches the Shannon's entropy. The segmentation of the image into n levels would yield an additive entropy given by:

$$E_l(t) = \operatorname{Arg\,max}\{\sum_{i=1}^n h_i c_i\}\tag{5}$$

Here,

 $E_l(t)$ denotes the additive entropy

 c_i denotes the number of categories of segmentation corresponding to the value of n

In case the image is contrast enhanced, the segmentation becomes more effective [8]

Classification using Deep Nets

The most common deep learning approach used for image classification happens to be the convolutional neural network (CNN). The CNN is an extremely effective deep learning based classifier which performs pattern recognition in each of its layers based on stochastic computing. The fundamental operation in the CNN hidden layers is the convolution operation mathematically given by [9]:

$$x(t) * h(t) = \int_{-\infty}^{\infty} x(\tau) h(t-\tau) d\tau$$
(6)

Here,

x(t) is the input

h(t) is the system

y is the output

*is the convolution operation in continuous domain

For a discrete or digital counterpart of the data sequence, the convolution is computed as [10]:

$$\mathbf{y}(\mathbf{n}) = \sum_{-\infty}^{\infty} \mathbf{x}(\mathbf{k}) \mathbf{h}(\mathbf{n} - \mathbf{k}) \tag{7}$$

Here x(n) is the input

h(n) is the system

y is the output

*is the convolution operation in discrete domain

A CNN has the following salient features:

Strided convolution: While conventional convolution is an overlap between the system and the data, strided convolutions help in covering all the data samples rather than just the internal samples of the data matrix. The stride over is just a hop in convolution [11]. Mathematically, for an (n x n) and (f x f) convolution, if 'p' is the number of strides, then the number of samples in the output are [12]:

$$Y_{Samples} = \left(\frac{n+2p-f}{s} + 1\right) \left(\frac{n+2p-f}{s} - 1\right)$$
(8)

Here,

n is the input sample matrix dimension f is the system sample matrix dimension p is the stride length

- 2) Pooling and Max Pooling: The pooling is an operation to make the features more robust and reduce the dimensionality. Typically, max-pooling is employed [13].
- **3) Employing Weighted Gradient Descent:** The gradient descent is used as the most common and effective cost function optimization based CNN training algorithm. It is given by [14]:

$$w_{k+1} = w_k - \alpha \frac{\partial e}{\partial w} \tag{9}$$

Here,

 W_{k+1} is the weight of the next iteration

 W_k is the weight of the present iteration e is the error α is the learning rate

The typical structure of a CNN is depicted in figure 2.



Another classifier employed in this work is the Residual Network which a modified version of the ubiquitous convolutional neural network (CNN) [16]. The ResNet has multiple convolution layers, but unlike typical convolutional networks, it has with skip connections between the layers. The architecture of the ResNet doesn't allow the direct cascade of the weights in the hidden layer. This serves two important purposes:

- 1) Reduces the chances of overfitting the network.
- 2) Avoiding the chances of vanishing gradient commonly encountered in conventional CNNs.

The number of convolution layers in the network are 48, with one Max-Pool layer. The activation function used is the ReLU, with a stride of 2 [17]. The addition of more hidden layers in conventional CNNs often leads to saturation in the performance with high chances of performance saturation, which is mitigated by the ResNet architecture with the skip connections and addition of identity layers [18].



Fig.3 The ResNet Architetcure

The performance of the two training algorithms are evaluated subsequently in terms of classification accuracy. The concept of skip connections in the ResNet is depicted in figure 3 [19]. The ResNet architecture used in the proposed work has an input size of 243x243x3 for the separate R,G and B channels of the image. A max pooling of 2x2 with a stride of 2 has been used. The feature layer of *Fc*1000 was employed with 1000 feature vectors.

Evaluation Parameters:

The various parameters for the classification are [20]:

- **1. True Positive (TP):** It is the case when a sample belongs to category and the test also predicts its belongingness.
- 2. True Negative (TN): It is the case when a sample does not belong to category and the test also predicts its non-belongingness.
- **3.** False Positive (FP): It is the case when a sample does not belong to category and the test predicts its belongingness.
- 4. False Negative (FN): It is the case when a sample belongs to category and the test predicts its non-belongingness.

Accuracy (Ac): It is mathematically defined as:



Fig.4 Proposed Flow Chart

VI. RESULTS

The results have been simulated on MATLAB 2020a. The data has been collected from: ALL-DB

Acute Lymphoblastic Leukemia Image Database for Image Processing

http://www.dti.unimi.it/fscotti/all



Fig.5 : Original Image



Fig.6 : Histogram of Original Image



Fig.7 : Contrast Enhanced Image



Fig.8 : Histogram of Contrast Enhanced Image



Fig.9 : Image after Segmentation with radial gradient and Shannon Entropy

Command Window	O
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ImageInputLayer with properties:	
Name: 'input_1'	
InputSize: [224 224 3]	
Hyperparameters	
DataAugmentation: 'none'	
Normalization: 'zerocenter'	
ans =	
ClassificationOutputLayer with properties:	
Name: 'ClassificationLayer_fc1000'	
ClassNames: {1000×1 cell}	
OutputSize: 1000	
Hyperparameters	
LossFunction: 'crossentropyex'	
Fig.11 :ResNet Properties	



L	 Image Input	28x28x1 images with 'zerocenter' normalization
2	 Convolution	20 5x5 convolutions with stride [1 1] and padding [0
3	 ReLU	ReLU
1	 Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0
5	 Fully Connected	10 fully connected layer
5	 Softmax	softmax
7	 Classification Output	crossentropyex





Fig.13 : Training Parameters





Fig.14 : Classification as Healthy and Leukemia



Fig.15 Confusion Matrix

$$Ac = \frac{TP+TN}{TP+TN+FP+FN} = \frac{Correct Decisions}{Total Decisions}$$
(10)

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0 0 0]

0 0]

$$Ac = \frac{491+488}{491+488+9+12} = \frac{979}{1000} = 97.9\%$$
(11)

S.No.	Parameter	Value
1.	Dataset	ALL-DB
		Acute Lymphoblastic Leukemia
		Image Database for Image
		Processing
		http://www.dti.unimi.it/fscotti/all
2.	Architecture	RESNET-50
3.	Training	Gradient Descent
4.	Iterations	4
5.	Classification	2.1%
	Error	
6.	Accuracy	97.9%
7.	Accuracy of	91.84%
	Previous	
	Work [1]	





VII. CONCLUSION

It can be concluded form the previous discussions that the proposed system achieves high values of accuracy in the detection and classification of Microscopic Blood images. This work will act as supportive tool for radiologists and will help doctor for fast and reliable diagnosis based on which the course of treatment plan can be decided. The proposed work uses segmentation and ResNet 50 convolutional neural network for classification The ResNet 50 avoids the chances of overfitting and vanishing gradient. The training approach used is the gradient descent with the objective function being root mean square error. The system trains in 4 iterations. The accuracy achieved by the proposed technique is 97.9% which is significantly higher than the existing approach. Thus the proposed technique can be used as an effective tool for blood cancer detection. Future scope as an enhancement of present work can be: Future enhancements of the proposed work can be:

- Using ensemble neural networks
- Employing Transfer Learning

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