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Deep Learning for Classifying of White Blood Cancer

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***Abstract*—Automated classification of cells is an essential but challenging task for computer vision with significant biomedical advantages. Numerous studies have attempted to construct a cell classifier based on artificial intelligence using label-free cellular images obtained from an optical microscope in recent years. While these studies showed promising results, different cell types' biological complexity could not be represented by such classifiers. However, it is well-known that intracellular actin filaments are significantly modified in terms of the malignant cell. This is believed to be closely linked to tumor cells' distinctive growth characteristics, their tendency to invade tissues around them, and metastasize. It is also more beneficial to identify various cell types based on their biological activities using an automated technique. This paper shows the differentiation between normal White Blood Cells and cancer, which can provide new knowledge on malignant changes and be used as an additional diagnostic marker. Since human eyes can not observe the features, we proposed the application of a convolutional neural network (CNN) based on malignant and normal WBCs classification. The Inception-V3 CNN model was validated on various WBCs normal and malignant cell images on regular normal and blood cancer cell lines with differing aggression levels. The study showed that CNN performed better in accuracy and efficiency than a human expert in the cell classification system**

Keywords—CNN,ANN,Transper learning,inception v3,WBCs

I. INTRODUCTION

In recent years, image recognition applications have become extremely widespread. They have become tremendously important in several life sectors such as medicine, engineering, and science. Vision is the most advanced sense of man's life. However, computerized systems, using the idea of digital image processing, computer vision and machine learning (ML), provide the capability to obtain the information about the problem under study in such a difficult way for human beings to get. In other words, this information could sometimes be indistinguishable by human vision[1]. The contribution of DIP and machine learning algorithms in medicine has been made through the digitized medical images were many phenomena can be analyzed and studied with the aid of the computer [2].Exponential progress in research and development in image analysis has contributed significantly to the area of medicine[3]. Medical images are considered a vital tool utilized to diagnose and analyze many diseases, for instance, breast, chest, abdominal illnesses, a blood disorder, etc. The digital format of the medical images provides an opportunity for further analysis that may lead to a more accurate diagnosis and hence, optimized patient management (See Fig. 1.). Such images can also be used for research and teaching purposes. The digital medical images that are used in this work are microscopic Peripheral Blood (PB) smear images[4] . The analysis of blood components and their changes is one of the regular diagnostic tests in routine clinical practice. This research is an attempt to apply digital image processing and ML techniques in the area of medical image analysis and recognition, in particular, Hematology.

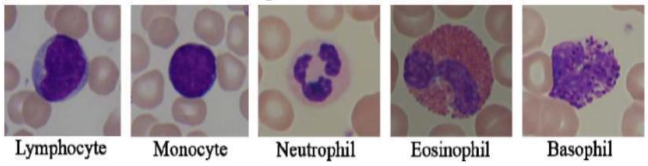

Figure 1: five types of leukocytes [4]

This project aims to do a comparative analysis study on cancer detection models that applies deep learning to address the topic of automated diagnosis. The project also uses two different models used for leukemia detection. This project aims to select two models that apply deep learning to detect leukemia and compare them to discuss their use of AI. The idea is to highlight, inform, and discuss a few selected applications on cancer predictive AI methods and the benefits and challenges in cancer detection models

II. LITRATURE REVIEW

In the proposed work [5], a new benchmark dataset consisting of 2000 microscopic blood smear images of 5 different types of WBCs is gathered/collected for classifier training and validating. The part of the data that consists of the patients' personal information is removed by applying data masks. Half image dataset is used for CNN training whereas the remaining image data is used for testing. Transfer learning based deep learning models i.e.Googlenet,VGG-16, densenet, alexnet and Xception are utilized for features extraction and classification. The proposed system achieved a satisfactory accuracy of 88%.

The proposed work [6], consist of two phases (1) segmentation and (2) classification segmentation of WBCs from blood smear images is consists of few stages. Detection of background, The region, RBCs Region and WBCs region, the segmentation of cytoplasm and

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nucleus are done separately which are then fused to make a complete image. Color statistical features are extracted and a state-of-the-art classifier i.e. SVM is trained and tested on the segmented WBCs for the recognition of type of WBC, the proposed model achieved is 93.5%.

In the presented cloud computing based resource awareness system [7], for the analysis of blood smear a benchmark image dataset is developed, the image dataset consist of 1030 images of high resolution. In the first phase WBCs are segmented from the images using color k-means clustering algorithm, various image features are detected/extracted from WBCs region i.e. geometrical, Statistical and texture, these features are quantized using PCA algorithm. Multiclass SVM that uses popular Error-correction-output-codes frame is used to create an ensemble classifier that can classify 5 types of WBCs, the proposed system achieved an average of 84.3 % accuracy.

Automated detection of blood cancer diseases (i.e. Leukemia and Myeloma) [8], using a computer aided diagnosis system is presented. Blood cancer detection is challenging and time consuming procedure in biomedical sciences and engineering .The presented work detect two types (1) Leukemia and (2), Myeloma that is used as an application for assisting medical doctors in disease diagnosis using blood smear images. The statistical morphological and texture features are extracted which are used by random forest classifier of training and predication of blood cancer. The developed system achieves higher accuracy of 94.3 in detection of types of blood cancer.

The purpose of the performed research work [9] is to develop a classification system for blood cells. The classification results obtained by classifying the validation set, an accuracy of 97.9% is achieved. The precision of the classifier for lymphocytes is 93.4, 97.37%, monocytes, 79% eosinophils and basophils 100%.

Detailed experimental work illustrate the efficacy and accuracy of the presented work. The images dataset used in experimental work consists of 12515 augmented images of blood cell which is portioned into trainset and test set. SSL algorithm is used to the classification of four WBCs types from images[10].

In the presented paper [11], a novel method for WBC segmentation and classification is developed. The method of WBC segmentation is to first find a suitable area of WBC susing HSI color space. Color of pixels that lay in a region defined by a quadric surface area will be called as nucleus/granule in cytoplasm region. Various kinds of features (i.e., shape, texture and color)are detected/extracted from the segmented ROI region. Artificial Neural network classifier is incorporated to recognize the type of WBC. The proposed system achieved 99.11% accuracy.

In the proposed work [12], a detailed survey about image acquisition, enhancement, segmentation, feature extraction, classification are discussed. Firstly the types and sub–types of WBC are discussed i.e. shape/size/color of nuclei. In this survey, the state-of-the-art techniques for segmentation, signal processing and deep learning are also discussed. The proposed research article is a quick and easy start for new researchers in the medical image processing domain.

In the proposed work [13], a novel method is develop for the segmentation of different types of WBC stypes from blood smear microscopic images incorporating HSV color models used for segmenting WBCs. [14]Classification types of WBCs and counting is done using modified deep learning alexnet, googlenet and resnet models.

III. RESEARCH METHDOLODY

Our proposed system aims to establish a methodology capable of classifying normal and malignant WBCs. Robust and time-efficient features that improve computer vision implementations' precision are known to be CNN features (i.e., object detection, biometrics, and video summarization). First of all, with the assistance of a hematologist, a benchmark dataset will be created.

A. Datasets

The data consist of two classes that is malignant and Normal Wbcs .The Images are Collected of North from the Phytology Department West Hospital Hayatabad(See Fig. 2).Each images is Cropped and save as 450x450 pixel RGB images which Consist of Single WBC.The Images are labeled by expertise (Microbiologist and technologist),so this data also consist of ground truth. The images are collected from 200 patients data.is The Total Number of Images are 1066 I in which 7272 are Normal Wbcs While 3389 are Malignant WBC. The dataset will splitted into trainset and testset using holdout cross validation method with a percentage of 70/30%, the 70% training images along with their labels will be used for model training while the trained model will be validated using 30% testing data and the model performance evaluation will be performed (See Fig. 2).

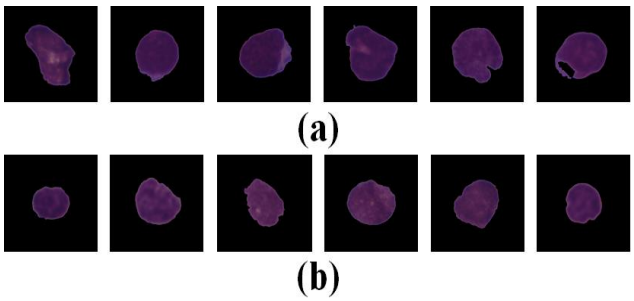

Figure 2: Sample images from the developed dataset,
(a) Some of malignant images from the dataset,
(b) Normal images from the dataset.

B. Convlution Neural Network

Convolutional Neural Networks (CNN) is a type of neural network that primarily focuses on image data, text, and times-series. CNN has different levels of dependence, one based on spatial distances. It works in grid-structures, which are data with dimensional images and

spatial dependencies in the local region, related to each pixel's color values in an image. With 3D structured input enables it to capture colour. With CNN, it shows a different level of translation and interpretations, which could process an augmented image which is an image that is upside down or shifted in different directions. This is not usual with other grid-structure data.CNN is considered to be an easy neural network to train and is composed of at least one convolutional later but can have more layers. In a standard multiple-layer network, the convolutional layer is followed by a fully connected layer(s)[14]. An image that process through the convolutional layer extract feature from an input that goes through different kernels. The pooling layer downsamples an input by reducing its dimensions but retain essential information in the input. The fully connected layer ties the output from the previous layers to the next layer neurons. CNN has many hyper parameters which are the variables that determine the structure of the network[15].

C. *Transfer Learning*

Training a large neural network can take large amounts of time, and many have trained for several weeks on expensive hardware to achieve state-of-the-art results. For projects that do not have those kind of resources in terms of time, equipment, or training data, common techniques to employ is Transfer Learning or fine-tuning. Transfer learning is a technique that means that an existing neural network model is used, with all its weights initialized to the values that are a result of previous training (See Fig. 3). Many such pre-trained models exists and are available, and they are often the result of very rigorous training[16]. What then is done is that the last few layers of the model is stripped away and replaced with layers that correspond with the problem space that is being addressed. This almost always include at least a new output layer with the new classes, and the last full connected layer that precedes the output layer. In practice, this means that the original model extracts features from the data, as it is trained to do so, and these features are then used as an input to a new network built on top which is trained using only the high level features as inputs. Even if the original model is not trained to identify the same classes as intended for the new model, it is often still better at finding high level features such as shapes or edges than a novel model would be[17].

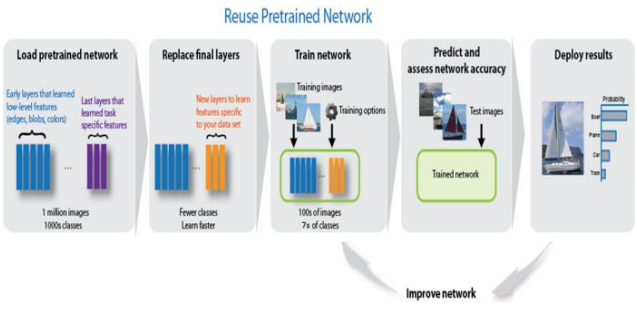

Figure 3: Transfer Learning in a Pre-Train Network for WBC classification[17]

IV. EXPERIMENTS AND RESULT

A. *Introduction*

In this chapter, a state-of-the-art WBC images dataset consisting of 2 classes is incorporated to evaluate the proposed methodology for computer aided diagnosis application. The dataset consists of malignant and Normal WBC is acquired from local medical teaching institute. The WBC digital images are taken using digital microscope, the aim of our proposed method is to develop a cancer cell recognition system that automatic recognizes a detect cancer using WBC cell images. This dataset is partitioned into train and test-set using the holdout cross-validation method for the performance evaluation.

B. *Optimizer Result*

The proposed method is implemented in MATLAB package; it has a deep learning framework that allows us to perform experiments by developing new algorithms or testing existing algorithms.

Experiment 1 Model training and validation accuracy plot with 10 Epochs BatchSize 8, learning Rate 0.0001.

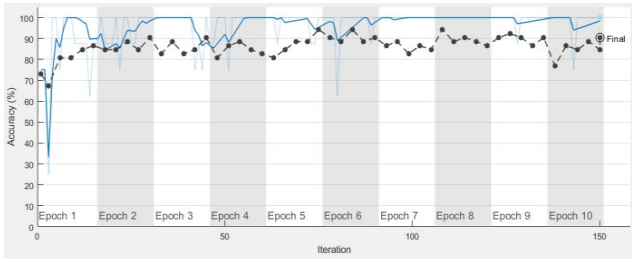

Figure 4(a): Model training and validation accuracy plot with 10 Epochs BatchSize 8, learning Rate 0.0001.

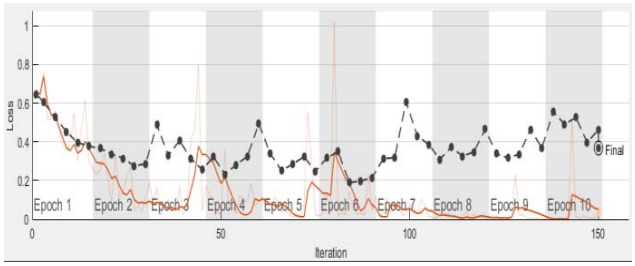

Figure 4(b): Model training and validation loss plot with 10 Epochs BatchSize 8, learning Rate 0.0001.

In the table 1(a)(b) the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of the matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform

experimentation work using deep learning, the data must be split into a train-set and test-set. There are various approaches used to validate the model and select the best model, some state-of-the-art cross-validation methods exist. In our proposed work, we have incorporated the 'Hold-Out' cross-validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 10 and Batch size 8. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2887 which give an average accuracy of 90.30% and F-Measure of 93.15%.

Table 1(a): Classification Results for 10 Epoch, Batch Size 8 and Adam Optimizer.

	Malignant	**Normal**
Malignant	**2017**	**177**
Normal	**133**	**870**

Table 1(b): Details Accuracy by Class.

Correctly Classified	2887
Incorrectly Classified	310
Accuracy	90.30%
Recall	91.88%
Precision	94.44%
F-Measure	93.15%

Experiment 2 Model training and validation accuracy plot with 10 Epochs BatchSize 16, learning Rate 0.0001.

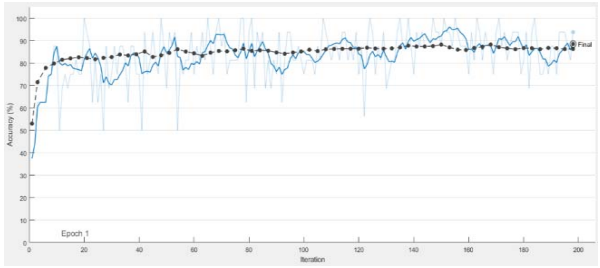

Figure 5(a): Model training and validation accuracy plot with 10 Epochs BatchSize 16, learning Rate 0.0001.

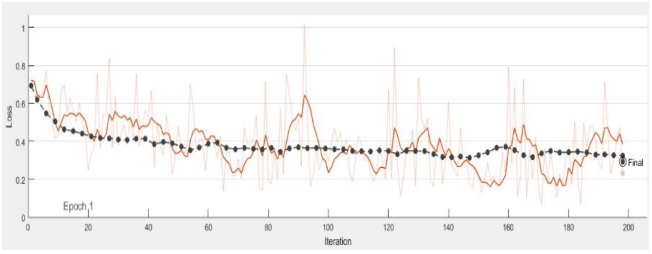

Figure 5(b): Model training and validation loss plot with 10 Epochs BatchSize 16, learning Rate 0.0001.

In table 2(a)(b) the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 10, Batch size 16 and Adam Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2830 which give an average accuracy of 88.44% and F-Measure of 91.56%.

Table 2(a): Classification Results for 10 Epoch, BatchSize 16 and Adam Optimizer.

	Malignant	**Normal**
Malignant	**2004**	**191**
Normal	**178**	**826**

Table 2(b): Details Accuracy by Class.

Correctly Classified	2830
Incorrectly Classified	369
Accuracy	88.46%
Recall	91.29%
Precision	91.84%
F-Measure	91.56%

Experiment 3 Model training and validation accuracy plot with 10 Epochs BatchSize 32, learning Rate 0.0001.

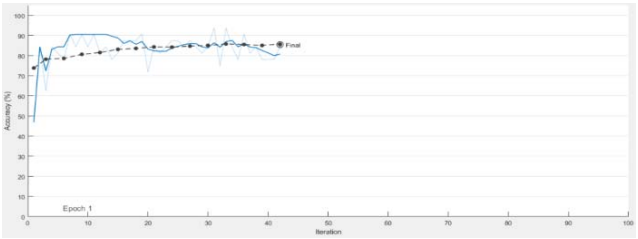

Figure 6(a): Model training and validation accuracy plot with 10 Epochs BatchSize 32, learning Rate 0.0001.

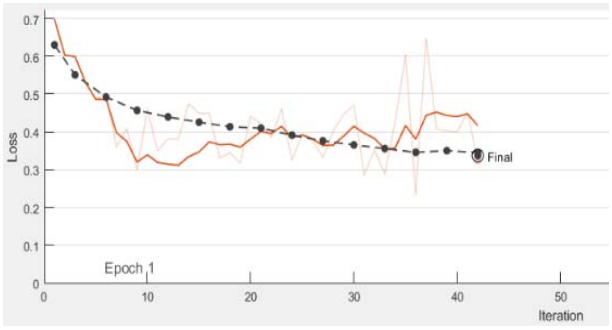

Figure 6(b): Model training and validation loss plot with 10 Epochs BatchSize 32 and learning Rate 0.0001.

In table 3(a)(b) the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 10, Batch size 32 and Adam Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2735 which give an average accuracy of 85.49% and F-Measure of 90.06%.

Table 3(a): Classification Results for 10 Epoch, BatchSize 32 and Adam Optimizer.

	Malignant	**Normal**
Malignant	**2102**	**384**
Normal	**80**	**633**

Table 3(b): Details Accuracy by Class.

Correctly Classified	2735
Incorrectly Classified	464
Accuracy	85.49%
Recall	84.55%
Precision	96.33%
F-Measure	90.06%

Experiment 4 Model training and validation accuracy plot with20 Epochs BatchSize 8, learning Rate 0.0001.

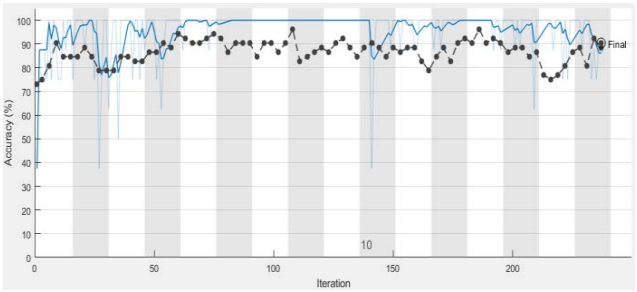

Figure 7(a): Model training and validation accuracy plot with 20 Epochs BatchSize 8, learning Rate 0.0001.

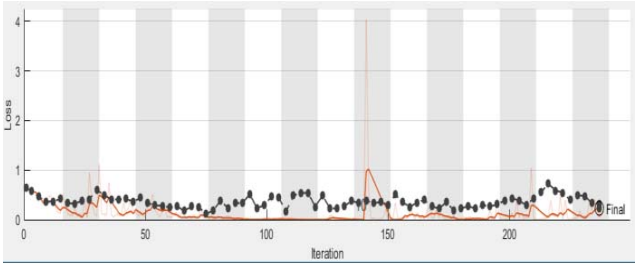

Figure 7(b): Model training and validation loss plot with 20 Epochs BatchSize 8 and learning Rate 0.0001.

In table 4(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 20, Batch size 8 and Adam Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2824 which give an average accuracy of 84.46% and F-Measure of 91.89%.

Table 4(a): Classification Results for 20 Epoch, BatchSize 8 and Adam Optimizer.

	Malignant	**Normal**
Malignant	**1964**	**231**
Normal	**144**	**860**

Table 4(b): Details Accuracy by Class.

Correctly Classified	2824
Incorrectly Classified	375
Accuracy	88.46%
Recall	89.47%
Precision	94.44%
F-Measure	91.89%

Experiment 5 Model training and validation accuracy plot with 20 Epochs BatchSize 16, learning Rate 0.0001

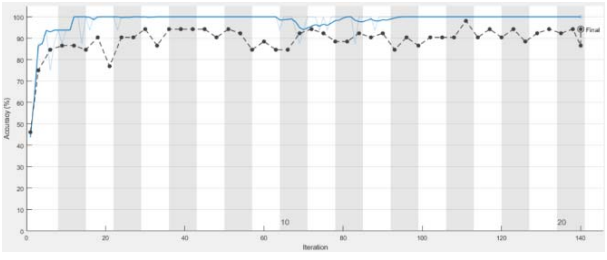

Figure 8(a): Model training and validation accuracy plot with 20 Epochs BatchSize 16, learning Rate 0.0001

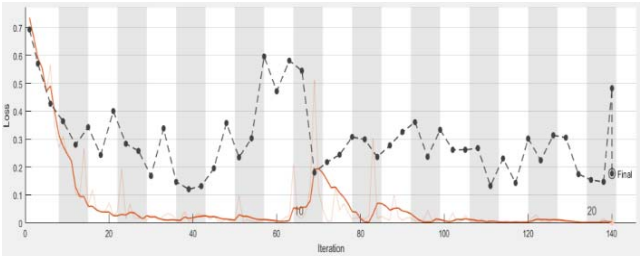

Figure 8(b): Model training and validation loss plot with 20 Epochs BatchSize 16 and learning Rate 0.0001

In table 5(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 20, Batch size 16 and Adam Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 3012 which give an average accuracy of 94.23.49% and F-Measure of 95.89%.

Table 5(a): Classification Results for 20 Epoch, BatchSize 16 and Adam Optimizer.

	Malignant	**Normal**
Malignant	**2076**	**119**
Normal	**68**	**936**

Table 5(b): Details Accuracy by Class.

Correctly Classified	3012
Incorrectly Classified	187
Accuracy	94.23%
Recall	94.59%
Precision	97.32%
F-Measure	95.89%

Experiment 6 Model training and validation accuracy plot with 20 Epochs BatchSize 32, learning Rate 0.0001

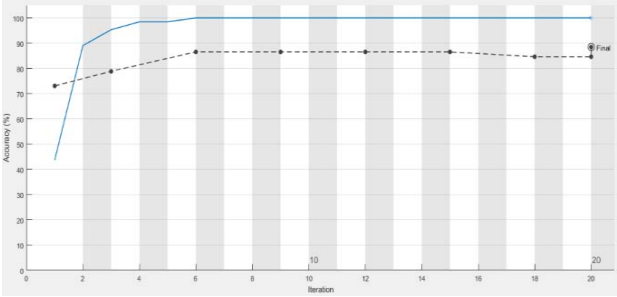

Figure 9(a): Model training and validation accuracy plot with 20 Epochs BatchSize 32, learning Rate 0.0001

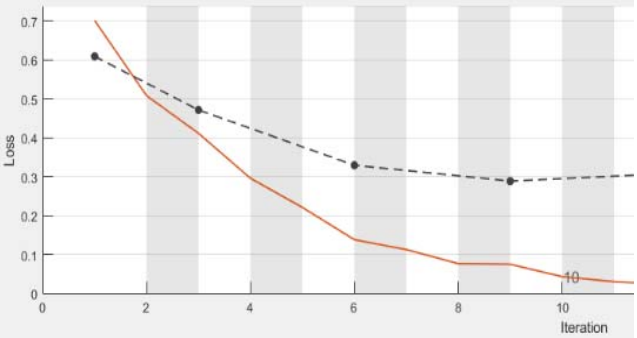

Figure 9(b): Model training and validation loss plot with 20 Epochs BatchSize 32 and learning Rate 0.0001.

In table 6(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 20, Batch size 32 and Adam Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2887 which give an average accuracy of 90.38% and F-Measure of 93.15%.

Table 6(a): Classification Results for 20 Epoch, BatchSize 32 and Adam Optimizer.

	Malignant	**Normal**
Malignant	**2017**	**178**
Normal	**134**	**870**

Table 6(b): Details Accuracy by Class.

Correctly Classified	2887
Incorrectly Classified	312
Accuracy	90.38%
Recall	91.89%
Precision	94.44%
F-Measure	93.15%

Experiment 7 Model training and validation accuracy plot with 10 Epochs BatchSize 8, learning Rate 0.0001.

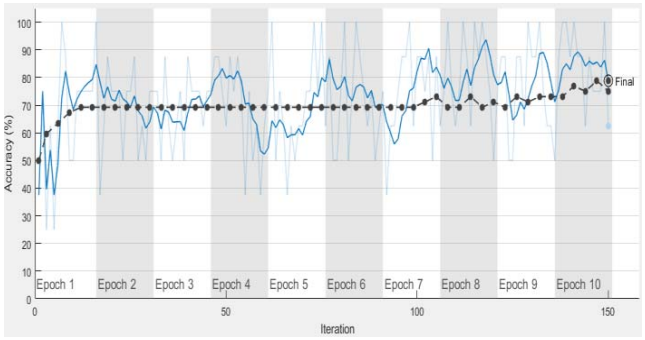

Figure 10(a): Model training and validation accuracy plot with 10 Epochs BatchSize 8, learning Rate 0.0001.

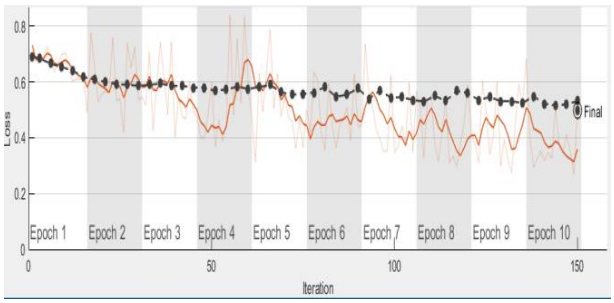

Figure 10(b): Model training and validation loss plot with 10 Epochs BatchSize 8 and learning Rate 0.0001.

In table 7(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 10, Batch size 8 and SGDM Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2685 which give an average accuracy of 78.884% and F-Measure of 86.74%.

Table 7(a): Classification Results for 10 Epoch, BatchSize 8 and SGDM Optimizer.

	Malignant	**Normal**
Malignant	**1681**	**514**
Normal	**0**	**1004**

Table 7(b): Details Accuracy by Class.

Correctly Classified	2685
Incorrectly Classified	514
Accuracy	78.84%
Recall	76.59%
Precision	100%
F-Measure	86.74%

Experiment 8 Model training and validation accuracy plot with 10 Epochs BatchSize 16, learning Rate 0.0001.

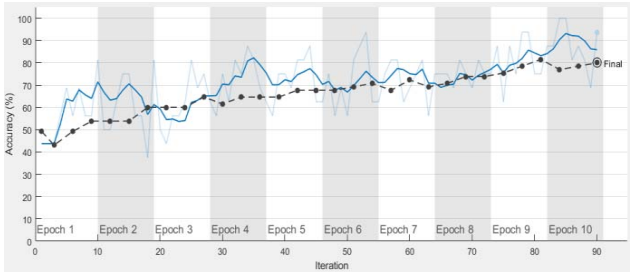

Figure 11(a): Model training and validation accuracy plot with 10 Epochs BatchSize 16, learning Rate 0.0001.

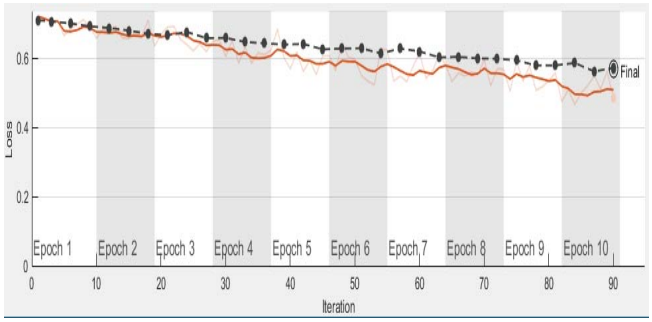

Figure 11(b): Model training and validation loss plot with 10 Epochs BatchSize 16 and learning Rate 0.0001.

In table 8(a)(b) the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 10, Batch size 16 and SGDM Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2582 which give an average accuracy of 69.23% and F-Measure of 81.81%.

Table 8(a): Classification Results for 10 Epoch, BatchSize 16 and SGDM Optimizer.

	Malignant	**Normal**
Malignant	**1635**	**560**

Normal	**57**	**947**

Table 8(b): Details Accuracy by Class.

Correctly Classified	2582
Incorrectly Classified	617
Accuracy	69.23%
Recall	69.23%
Precision	100%
F-Measure	81.81%

Experiment 9 Model training and validation accuracy plot with 10 Epochs BatchSize 32, learning Rate 0.0001.

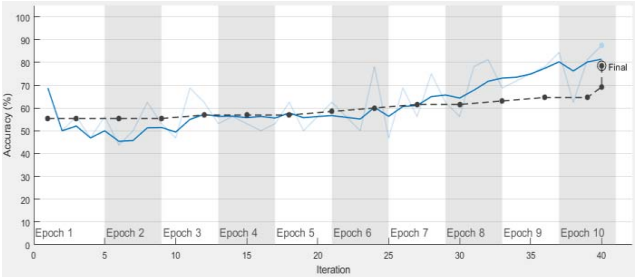

Figure 12(a): Model training and validation accuracy plot with 10 Epochs BatchSize 32, learning Rate 0.0001.

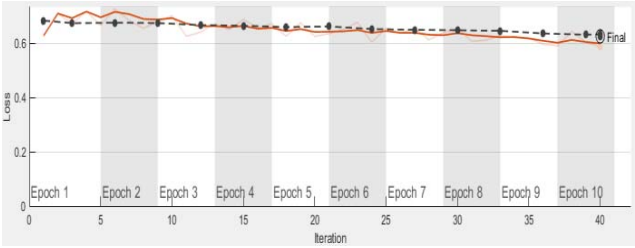

Figure 12(b): Model training and validation loss plot with 10 Epochs BatchSize 32 and learning Rate 0.0001.

In table 9(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 10, Batch size 32 and SGDM Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2520 which give an average accuracy of 78.46% and F-Measure of 82.92%.

Table 9(a): Classification Results for 10 Epoch, BatchSize 32 and SGDM Optimizer.

	Malignant	**Normal**
Malignant	**1622**	**573**
Normal	**106**	**898**

Table 9(b): Details Accuracy by Class.

Correctly Classified	2520
Incorrectly Classified	679
Accuracy	78.46%
Recall	73.91%
Precision	94.44%
F-Measure	82.92%

Experiment 10 Model training and validation accuracy plot with 20 Epochs BatchSize 8, learning Rate 0.0001.

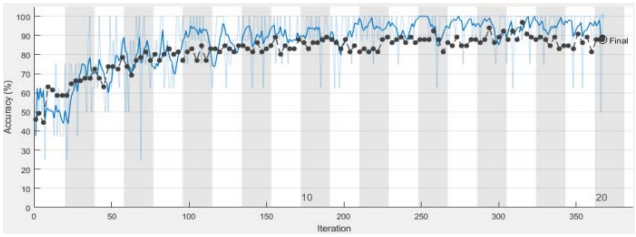

Figure 13(a): Model training and validation accuracy plot with 20 Epochs BatchSize 8, learning Rate 0.0001.

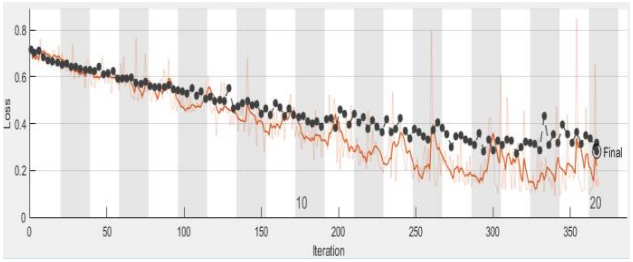

Figure 14(b): Model training and validation loss plot with 20 Epochs BatchSize 8 and learning Rate 0.0001.

In table 10(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 20, Batch size 8 and SGDM Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2788 which give an average accuracy of 87.63% and F-Measure of 89.47%.

Table 10(a): Classification Results for 20 Epoch, BatchSize 8 and SGDM Optimizer**.**

	Malignant	**Normal**
Malignant	**1865**	**320**
Normal	**81**	**923**

Table 10(b): Details Accuracy by Class.

Correctly Classified	2788
Incorrectly Classified	401
Accuracy	87.63%
Recall	85%
Precision	94.44%
F-Measure	89.47%

Experiment 11 Model training and validation accuracy plot with 20 Epochs BatchSize 16, learning Rate 0.0001

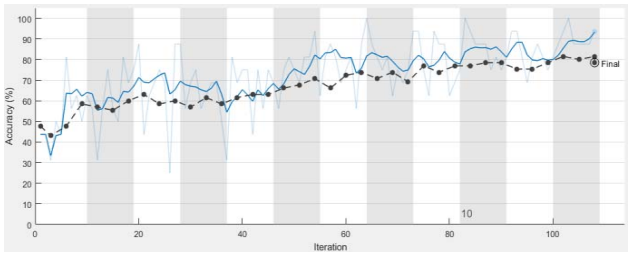

Figure 15(a): Model training and validation accuracy plot with 20 Epochs BatchSize 16, learning Rate 0.0001.

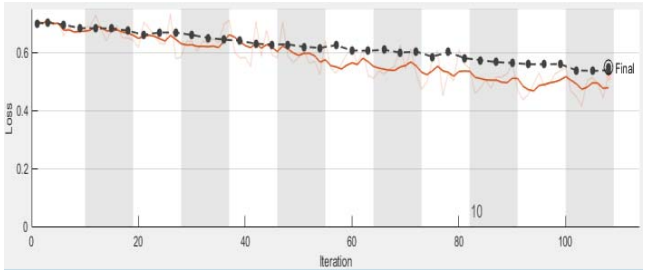

Figure 15(b): Model training and validation loss plot with 20 Epochs BatchSize 16 and learning Rate 0.0001.

In table 11(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, where each class consists of an individual image. To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 20, Batch size 16 and SGDM Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2501 which give an average accuracy of 78.46%and F-Measure of 82.05%

Table 11(a): Classification Results for 20 Epoch, BatchSize 16 and SGDM Optimizer.

	Malignant	**Normal**

Malignant	**1672**	**523**
Normal	**175**	**829**

Table 11(b): Details Accuracy by Class**.**

Correctly Classified	2501
Incorrectly Classified	698
Accuracy	78.46%
Recall	76.19%
Precision	88.88%
F-Measure	82.05%

Experiment 12 Model training and validation accuracy plot with 20 Epochs BatchSize 32, learning Rate 0.0001.

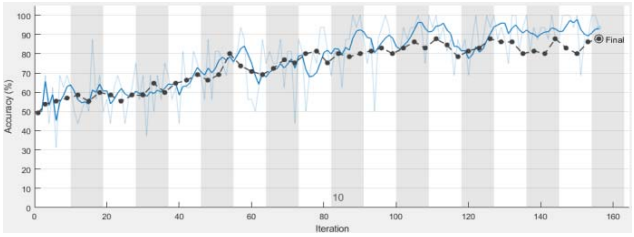

Figure 16(a): Model training and validation accuracy plot with 20 Epochs BatchSize 32, learning Rate 0.0001.

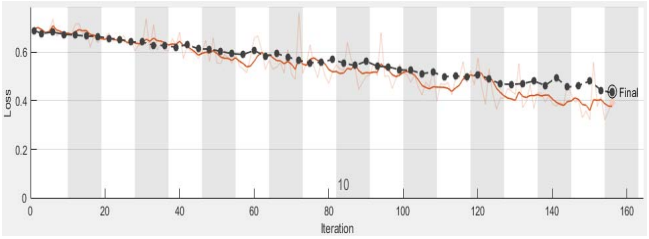

Figure 16(b): Model training and validation loss plot with 20 Epochs BatchSize 32 and learning Rate 0.0001.

In table 12(a)(b), the confusion matrix is displayed, this matrix shows the correctly classified and incorrectly images. On the Y-axis of matrix we have the actual values and the predicated values are on the X-axis. In this model we have used a dataset of 2 classes, whereeach class consists of an individual image.To perform experimentation work using deep learning, the data must be split into a train-set and test-set, there are various approach used to validate the model and to select the best model, some state-of-the-arts methods of cross validation exits. In our proposed work, we have incorporated the 'Hold-Out' cross validation scheme. In this scheme, data is partitioned randomly by the percentage specified by the user; the percentage used in our method is 70/30% where 70% (7465 images) of data is selected for training and 30% (3199 images) for validation. The hyper-parameters selected for this model are: Epoch = 20, Batch size 32 and SGDM Optimizer. The performance of the CNN model is evaluated using accuracy which is a supervised learning classification evaluation parameter. The correctly classified images are 2788 which give an average accuracy of 87.69% and F-Measure of 89.47%

Table 12(a): Classification Results for 20 Epoch, BatchSize 32 and SGDM Optimizer.

	Malignant	**Normal**
Malignant	**1865**	**330**
Normal	**81**	**923**

Table 12(b): Details Accuracy by Class**.**

Correctly Classified	2788
Incorrectly Classified	411
Accuracy	87.69%
Recall	85%
Precision	94.44%
F-Measure	89.47%

V. THE COMPARISONS OF CLASSIFICATION RESULTS

This Paper proposed a solution of two classifier of Normal and Malignant Wbcs using Deep learning model. The inception v3 model best for image recognition that has been shown to attain greater than accuracy on the Image Net dataset. We train a model using Classification of Adam and SGDM optimizer. Classification Results in table 6(b) accuracy of class have outstanding result as compared SGDM Optimizer. The correctly classified images adam are 3012 which give an average accuracy of 94.23% and F-Measure of 95.89%.SGDM Optimizer table 12(b)The correctly classified images SGDM are 2788 which give an average accuracy of 87.69% and F-Measure of 89.47%

CONCLUSION

White Blood Cell (WBC) Leukaemia is caused by excessive production of leukocytes in the bone marrow, and image-based detection of malignant WBCs is important for its detection. Convolutional Neural Networks (CNNs) presents the current state-of-the-art for this type of image classification, but their computational cost for training and deployment can be high. Transfer learning in Inception-v3 Convolutional neural network-based approach for efficient classification of malignant and normal WBCs is followed. First of all, the dataset is resized to the size of the CNN image input

size; the resized images dataset is partitioned with a percentage of 70/30%. Two state-of-the-art optimizers (Adam and SGDM) are used for optimal learning rate selection, which helps calculate optimal weights for the image features for training purposes. The results are among the best achieved on the locally developed dataset and outperform several convolutional network models. We expect that the inception-v3 is the best for the classification of WBC images by achieving higher accuracy and very efficient time.

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