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Automatic Detection of White Blood Cancer From Bone Marrow Microscopic Images Using Convolutional Neural Networks

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ABSTRACT Leukocytes, produced in the bone marrow, make up around one percent of all blood cells. Uncontrolled growth of these white blood cells leads to the birth of blood cancer. Out of the three different types of cancers, the proposed study provides a robust mechanism for the classification of Acute Lymphoblastic Leukemia (ALL) and Multiple Myeloma (MM) using the SN-AM dataset. Acute lymphoblastic leukemia (ALL) is a type of cancer where the bone marrow forms too many lymphocytes. On the other hand, Multiple myeloma (MM), a different kind of cancer, causes cancer cells to accumulate in the bone marrow rather than releasing them into the bloodstream. Therefore, they crowd out and prevent the production of healthy blood cells. Conventionally, the process was carried out manually by a skilled professional in a considerable amount of time. The proposed model eradicates the probability of errors in the manual process by employing deep learning techniques, namely convolutional neural networks. The model, trained on cells' images, first pre-processes the images and extracts the best features. This is followed by training the model with the optimized Dense Convolutional neural network framework (termed DCNN here) and finally predicting the type of cancer present in the cells. The model was able to reproduce all the measurements correctly while it recollected the samples exactly 94 times out of 100. The overall accuracy was recorded to be 97.2%, which is better than the conventional machine learning methods like Support Vector Machine (SVMs), Decision Trees, Random Forests, Naive Bayes, etc. This study indicates that the DCNN model's performance is close to that of the established CNN architectures with far fewer parameters and computation time tested on the retrieved dataset. Thus, the model can be used effectively as a tool for determining the type of cancer in the bone marrow.

INDEX TERMS Acute lymphoblastic leukemia, classification algorithms, deep learning, convolutional neural networks, image processing, multiple myeloma.

I. INTRODUCTION

Cells Cells that comprise the blood are three types: platelets, red blood cells, and white blood cells. Each of them is made continuously in the bone marrow and released timely in the bloodstream. The normal blood cell growth, hampered by the exponential growth of abnormal blood cells, is the main cause of blood cancer. There are three main types of blood cancers: leukemia, myeloma, and lymphoma. Bone marrow is the infected area for a white blood cancer type cancer called Acute Lymphocytic Leukemia (ALL). "Acute" indicates the fast progress of the disease, and if it does not get treated in the early stages, it might prove to be fatal within a short span [1], [2]. ALL is classified into L1, L2, and L3 [3]. Multiple Myeloma (MM) is an immature teratoma of cells called plasma, which helps to scrape off the infection [4]. It is thrice as common as ALL. The blood count remains normal in this case, unlike leukemia, but the infected one is found

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to have anemia (low red blood count) because the space for RBCs is occupied by the unhealthy cells. Multiple myeloma is responsible for low platelet count in the blood, which is called thrombocytopenia [5]. It also causes erosion of bones called bone lesions diagnosed in CT scans [6]. Approximately 1500 people who died due to this disease contribute to 0.2% of the total deaths caused by cancer alone in 2019 [7]. There are nearly 20,000 people diagnosed with myeloma every year in the US. Treatment for blood cancer depends on the age of the patient, type, how fast the cancer is progressing, infected areas, etc. [8]. The blood count is one of the prime factors for the distinction for categorizing the type of blood cancer. The counting can be done manually and automatically. The manual method gives a 100% recognition rate if done by a skilled person but is also a time-consuming process [9].

On the other hand, automatic counting is a faster process but has got higher risks of the count being wrong. Thus, both methods have their pros and cons. This article gives an outline of the automatic approach to determine the type of white blood cancer. The automated method of classification is cost-effective and can be deployed quickly in both rural and urban areas. The problems that are invaded through the proposed system include the inconsistencies caused due to labor work of manual classification, the requirement of a skilled professional, the errors due to cells being indistinguishable when observed under a microscope, etc.

Deep learning-based methods can help in resolving all the enlisted challenges because they derive desirable features from the raw data themselves [10]. Deep Learning is known to demonstrate better functioning than accustomed Machine Learning for processing a large number of images [11]. Convolution Neural Networks (CNNs) combine various multi-layer perceptron and display efficient results with a little pre-processing [12]. CNN's themselves act as a feature extractor as each convolution layer of the network learns a new feature that is present in the images and hence produces a high activation. In the proposed study, a robust and vigorous automated classification method for the type of white blood cancer, i.e., ALL and MM using Convolution Neural Networks is presented. The article consequently evaluates the performance of the proposed deep learning model using accuracy, precision, recall, sensitivity, and specificity as comparison parameters.

The key contributions of this article are:

- The proposed model follows a generic approach to predict the type of cancer on a small dataset. For generalization, data augmentation has been used.
- A comparative analysis has shown that the proposed DCNN out-performs specific state-of-art CNN models on the dataset hence retrieved and prepared.
- With less computation time need and trainable parameters, the proposed model outperforms existing machine learning and pre-trained deep learning models in identifying the type of cancer.

This article was structured as follows: Section II describes the related work. Section III outlines the proposed technique for classifying blood cancer, learning measures, an overview of the dataset, and assessment strategy. Extensive experiments on the proposed model were conducted in Section IV, and the final results were compared with traditional algorithms for machine learning.

II. RELATED WORK

The infected blood cell image analysis is typically divided into three stages: preprocessing of images, extraction, selection of features, and classification. There has been extensive research on different types of cancer, namely leukemia, lymphoma, and myeloma. Zhang *et al.* proposed a convolutional neural network model for direct classification of cervical cells into infected and uninfected cells without segmenting them [13]. Zhao *et al.* proposed machine learning algorithms like CNN, SVM, Random Forests, etc. for classifying various types of white blood cells(WBCs) present in the body [12]. Stain Deconvolution Layer (SD Layer) was proposed for determining cancer as well as healthy cells in which instead of training the images in RGB space, the classifier learned from the images in the Optical Density (OD) space [14]. FORAN *et al.* developed an administered clinical decision support prototype for differentiating among various hematologic malignancies based on image processing. The system allowed the analysis of images based on the ''gold standard'' dataset and suggested treatment based on the collected cases' plurality rationale [15]. The paper exhibits a structure for classification of Human Epithelial Type 2 cell IIF images by first enhancing, then augmenting, and finally processing the training data and then feeding it into a convolutional neural network (CNN) framework for image classification [16]. For classifying acute myeloid leukemia, the ALL-IDB dataset is initially augmented by applying several alterations like histogram equalization, reflection, translation, rotation, blurring, etc. Finally, a 7-layer convolutional neural network is used [17]. Shrutika Mahajan *et al.* proposed an SVM-based system with changes in texture, geometry, and histogram as the classifier's inputs to distinguish Acute Lymphocytic Leukemia (ALL) by microscopic blood sample images [18]. One of the papers contemplated a green plane extraction image preprocessing followed by a reinforcement algorithm for feature extraction. Finally, it used SVM and Nearest Neighbor Network as tools for classifying leukemia efficiently [19]. Markiewicz, Tomasz *et al.* put forward a system for the classification of 17 types of blood cells of myelogenous leukemia using the images of bone marrow. This system first categorized and extracted only the best out of all the available features and then used the Gaussian Kernel Support Vector Machine (SVM) for final grouping [20]. N.H.A. Halim *et al.* proposed an automatic method for counting of infected cells of Acute Lymphoblastic Leukemia (ALL) and Acute Myelogenous Leukemia (AML) in a leukemia image slide. Their approach included HSV-based segmentation (Hue, Saturation, and Value) to get rid of white blood cells located in the background, followed by morphological erosion operation for overlapping cells [21]. The authors

have discussed the segmentation of color smear microscopic images based on the fact that in HSI (Hue, Saturation, intensity) color space, the H component consists of white blood cell information. At the same time, the S component contains information about the nucleus of these cells using iterative Otsu's approach [22]. The authors of the paper provided a solution for manual counting problems using image processing techniques. Here, the image preprocessed for eliminating the chance of error provides the ratio of white blood cells to red blood cells after specific calculations to determine if the image is normal or abnormal in terms of leukemia detection [23]. Horie *et al.* [24] demonstrated the diagnostic capability of deep learning techniques like CNN for esophageal cancer, which included squamous cell carcinoma and adenocarcinoma with a sensitivity of 98%. Saba *et al.* [25] proposed an automated cascaded design for skin lesion detection, which consisted of three significant steps, namely, contrast stretching and boundary extraction using CNN, and finally extracting depth features using transferred learning. Sekaran *et al.* [26] proposed a model deployed using a convolutional neural network to isolate infected images from healthy ones. Further, the Gaussian Mixture Model with EM algorithm is used to get the statistics regarding the percentage of cancer spread so far. Zuluaga-Gomez *et al.* [27] proposed computer-aided diagnosis systems having a fine-tuned hyperparameter CNN optimization algorithm with a tree parent estimator for classification of thermal images [28]. The authors proposed a distinction of the breast cancer images by extracting features using CNN and then using a fully connected network for classification.

III. PROPOSED METHODOLOGY

The model, containing three types of layers, namely convolution layer, max pool, and fully connected layer, is trained on the training set, and then it is used for prediction on the testing set. The flow of the proposed methodology is shown in Figure 1.

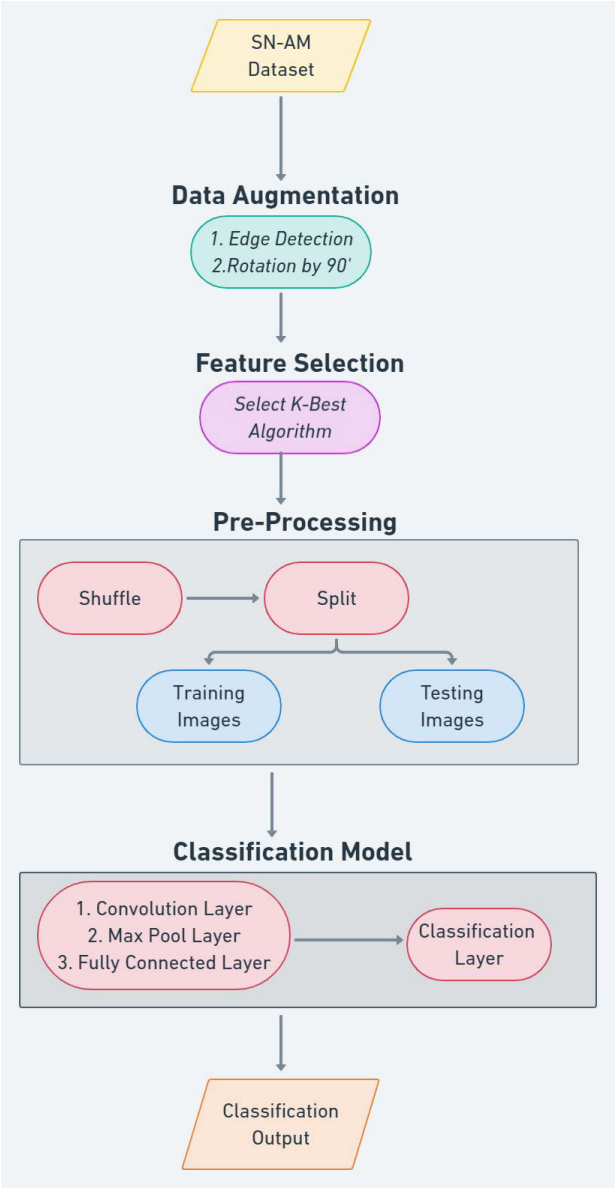

FIGURE 1. Proposed methodology.

A. DATASET DESCRIPTION

In the proposed study, the dataset is acquired from two different subsets of a dataset collection [29]. The first part of the dataset consists of images of patients having B-ALL, i.e., B-Lineage Acute Lymphoblastic Leukemia having 90 images in total. Figure 2 shows the background mask and the nucleus mask of the corresponding ALL image. On the other hand, the second part of the dataset consists of images of patients diagnosed with Multiple Myeloma, i.e., MM having 100 images.

Figure 3 shows the background mask, nucleus mask and the mask for the cytoplasm of the plasma cells for the corresponding MM image. Images of size 2560 × 1920 pixels in BMP format constitute the dataset. The combined form is used for training the proposed CNN model to determine the type of cancer cell, i.e., ALL and MM.

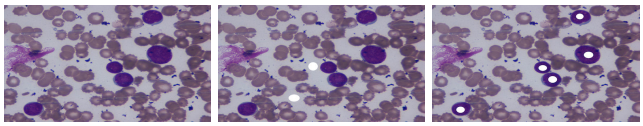

FIGURE 2. Sample images of ALL Dataset. (a) ALL sample image, (b) ALL background mask, (c) ALL nucleus mask. ALL indicates acute lymphoblastic leukemia.

B. DATA AUGMENTATION

The SN-AM dataset is first augmented by rotating the image and extracting edges. The shuffled images are divided into training and testing sets. There should be a considerable amount of data available as the object of interest must be present in varying sizes, poses, and lighting conditions for the model to generalize well during the evaluation(testing) phase.

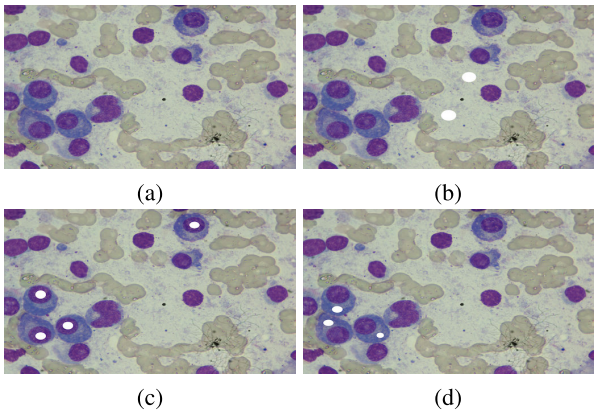

FIGURE 3. Sample images of MM Dataset. (a) MM sample image, (b) MM background mask, (c) MM nucleus mask, (d) MM cytoplasm mask. MM indicates multiple myeloma.

Data can be manufactured from existing data by manipulating images through various techniques. Figure 4 shows the resulting images after data augmentation. The first technique used is the rotation of images by 90 degrees [30]. All the images are rotated by an angle of 90 degrees as our model should be able to recognize the object present in any orientation, as shown in Figure 4(b) and 4(e). The next technique filters the image and returns an image containing only edges or the boundaries of the original image, as shown in Figure 4(c) and 4(f). Without data augmentation, over-fitting takes place, and hence it becomes difficult for the model to generalize to new examples that were not in the training set.

C. FEATURE SELECTION

Feature Selection plays a crucial role in Deep Learning and massively affects the performance of the model. A large number of features degrade the performance of a model. Therefore, the features affecting the output are selected, called Feature Selection. The key advantages of this process include: Reduction in over-fitting as less redundant data eliminates the probability of predictions based on noise, Reduction in training time due to availability of fewer data to train upon, Improvement in the accuracy as the misleading data and outliers are removed.

In the proposed study, Univariate feature selection has been used. Univariate feature selection evaluates each feature individually to assess the intensity of the feature's relationship with the target factor.

With several different statistical tests, the SelectKBest class can be used to select K specific features. The proposed model uses the Chi-square (chi^2) test. In statistics, a chi-square test is used to check the independence of two events. We can get observed count O and predicted count E given the data of two variables. Chi-square tests whether each other deviates from predicted count E and observed count O. In selecting features, we aim to select the features that are highly dependent on the output variable. The observed count is close to the expected count when two features are independent; thus, we get smaller Chi-square value. So,

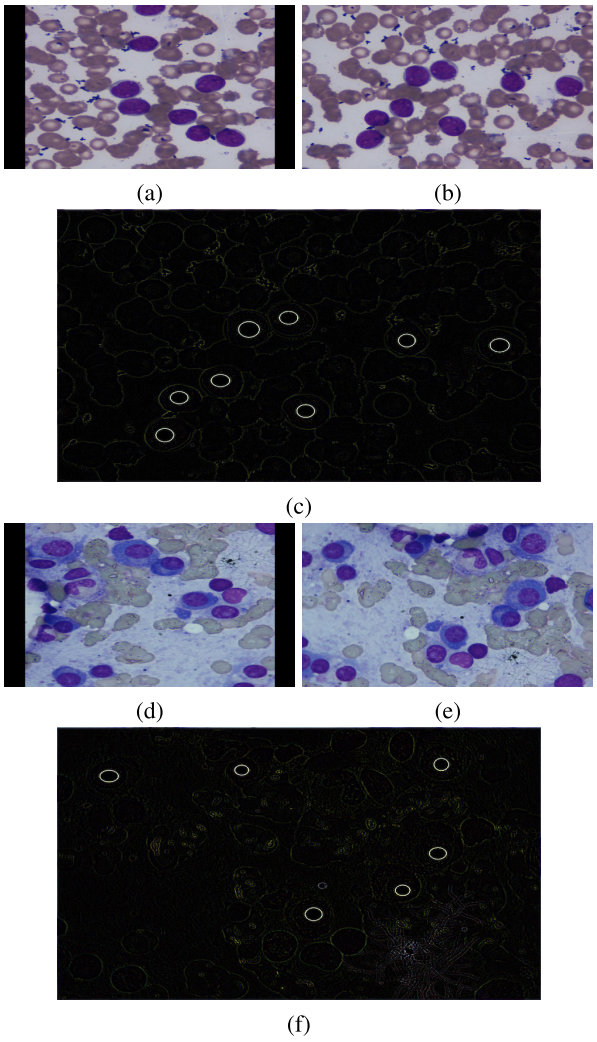

FIGURE 4. Data augmentation of microscopic images. (a) ALL original image. (b) ALL original image rotated by 90 degrees anticlockwise. (c) Detected Edges of the original ALL image, (d) MM original image. (e) MM original image rotated by 90 degrees anticlockwise. (f) Detected Edges of the original MM image. (ALL indicates acute lymphoblastic leukemia; MM indicates multiple myeloma).

the high Chi-square value indicates that the hypothesis of independence is not correct. Hence, the higher the value of Chi-square, the feature is more dependent on the response and can be selected for model training. In simple words, SelectKBest calculates the scores for each feature and then removes all the features except the K best features with the highest scores. Equation (1) shows the formula used by the chi-squared statistical test.

$$\chi^2 = \frac{(O-E)^2}{E} \tag{1}$$

where O is the number of observations of the class, E is the number of expected observations of class if there was no relation between the feature and the output.

D. PRE-PROCESSING OF IMAGES

Pre-processing includes handling null values, one-hot encoding, normalization, multi-collinearity, scaling the data,

TABLE 1. Network architecture.

S.No	Layer Name	Frequency	No. Of Units	Activation Function
1	Convolutional Layer	2	32	Softmax
2	Max Pool Layer	2	32	–
3	Fully Connected Layer	4	528	Softmax
4	Output Layer	1	–	Sigmoid

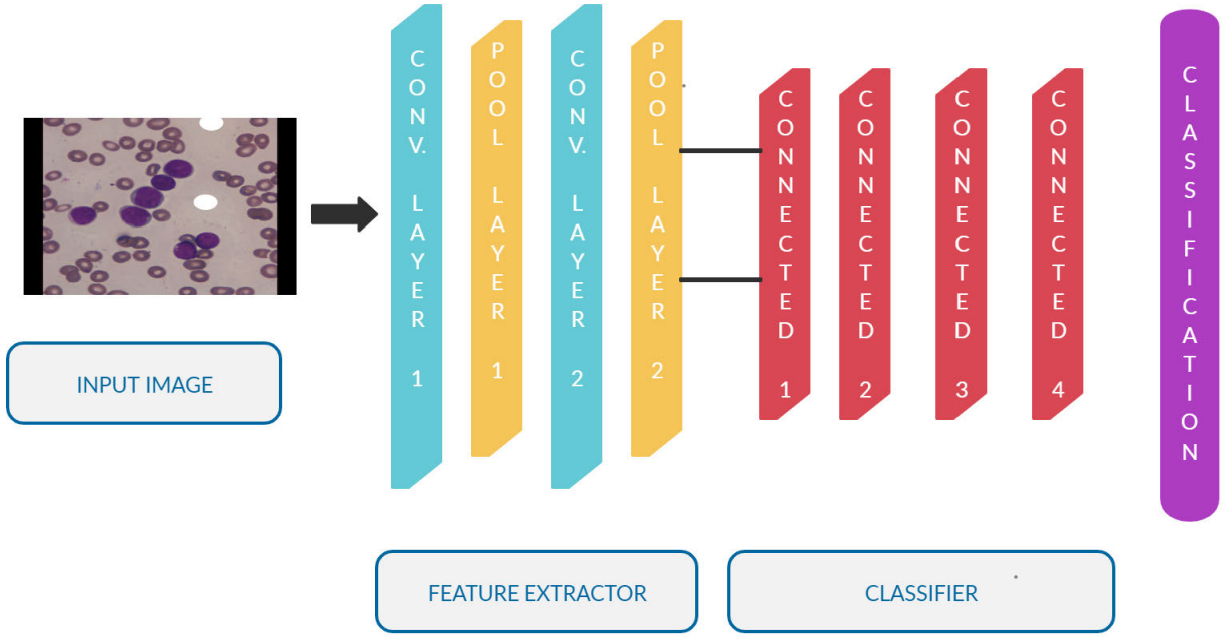

FIGURE 5. Proposed CNN model architecture.

shuffling and splitting data, etc. In the proposed study, the transformed data obtained after feature selection is first normalized and then divided into training and testing sets after shuffling them. The dataset is divided into 75% for training and 25% for testing the model.

E. PROPOSED CONVOLUTION NEURAL NETWORK AND ARCHITECTURE

In the proposed research, an optimized CNN model for classification of the type of cancer, i.e., ALL or MM, has been deployed. The network used for our deep learning model is shown in Figure 5. Convolution Neural Networks (CNNs) are majorly used for analyzing visual imagery. CNN's are the heart of image classification algorithms. They work fast and efficient for image classification.

In comparison to other image classification algorithms, they use a little pre-processing. A CNN model is comprised of an input layer, an output layer, and multiple hidden layers. In this article, the proposed model takes an image as input and returns the type of cancer as output i.e., ALL or MM. Table 1 shows the basic CNN framework used in the paper.

1) CONVOLUTIONAL LAYER

Convolution layer, the first layer where the image is fed, comprises of neurons which act as feature extracting units. A filter, $k \times k$ matrix, is convolved with the input image to produce an activation map. The fixed amount by which the filter moves along the image is termed as stride. Convolution operation for an input image of size $a \times b$ with a kernel of size k, padding p, and stride s produces an output of size $(a - k + 2p)/s + 1 \times (b - k + 2p)/s + 1$.

Also, the depth of the filter is dependent on the type of images used for training. In the proposed model, two convolution layers are present with softmax as their activation functions, and a pooling layer follows them. The standard softmax function $\sigma : \Re^K \rightarrow \Re^K$ is defined by equation (2). Equation (3) gives the activation map obtained after performing the convolution operation on the input image with the kernel function.

$$\sigma(z)_i = \frac{e^{z_i}}{\sum_{j=1}^{K} e^{z_j}} \tag{2}$$

for $i = 1, \ldots, K$ and $z = (z_1, \ldots, z_K) \in \Re^K$, where K is the total number of elements of the input vector z and z_i represents each element of the input vector z.

$$\begin{aligned} A[x, y] &= (I * f)[x, y] \\ &= \sum_i \sum_j I[i, j] f[x - i, y - i] \end{aligned} \tag{3}$$

where I is the input image, f is the kernel function, x and y are the numbers of rows and columns of the output matrix

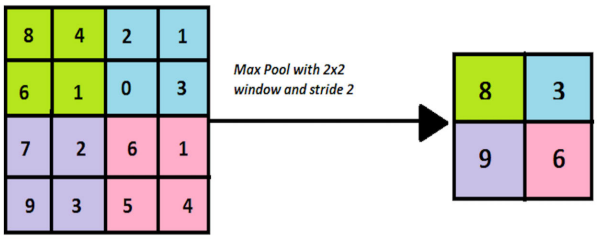

FIGURE 6. Maxpool function.

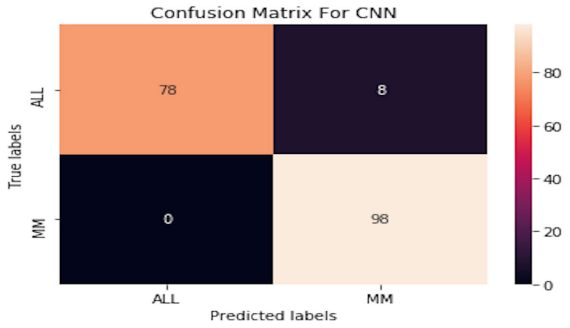

FIGURE 7. Confusion matrix – proposed DCNN model.

respectively, i and j are the number of rows and columns of the input image matrix, respectively.

2) POOLING LAYER

Another important concept of CNNs is the pooling layer, which forms a non-linear down-sampling layer. This model uses the max-pooling non-linear function, which partitions the image into non-overlapping regions and, for each such region, outputs the maximum value. The pooling layer's primary purpose is to reduce the number of parameters and the amount of computation in the network and minimize overfitting. Max-pooling extracts the maximum value in a given region on an image of size $a \times b$, specified by a kernel of size k and stride size s. The operation produces an output of size $(a-k)/(s+1) \times (b-k)/(s+1)$. Figure 6 illustrates how a max-pooling layer downsamples the given image.

3) FULLY CONNECTED LAYER

A fully connected layer is a Multi-Layer Perceptron. A dense layer is added at the end of the network of convolution layers and. As the name suggests, a fully connected layer connects each neuron in one layer to every neuron in another layer. They work as standard neural networks to classify images based on the features extracted by the convolutions. At this step, the error is calculated and then back-propagated. The proposed model consists of five fully connected layers, including the final output layer. The softmax activation function is used in all the four fully connected layers. The output layer contains the sigmoid activation function, which, for each of the classification labels that the model is trying to predict, outputs a probability value of 0 to 1. The sigmoid function is defined by equation (4).

$$Sig(z) = \frac{1}{1+e^{-z}} = \frac{e^{z}}{e^{z}+1} \tag{4}$$

Here, z is the input vector.

The algorithm used to classify the images using the deep learning approach is shown in pseudo-code Algorithm 1.

IV. RESULTS AND ANALYSIS

The classification model is built using TensorFlow, an end-to-end open-source platform. A binary classification model was trained on 424 images in 1000 iterations. Each iteration optimizes the loss function using Adam Optimizer yielding minimum loss at the last iteration. The trained model was then used for predicting the type of cancer in the images. K80 GPU is used for training the model.

The subsequent section initially describes the proposed model results. Comparison and analysis of the proposed model with state-of-art machine learning and deep learning models are also explained.

A. DEEP LEARNING APPROACH

In the CNN section, our network is trained using Adam Optimizer with a learning rate of 0.01 by updating the weights using equation (5). The loss function used is the sigmoid cross-entropy loss function, which is optimized by the Adam optimizer. Figure 8 illustrates the subsidence of loss as the number of iterations increases. As shown in the figure, the training loss acquires a constant value after 800 iterations. Thus, the minimum value, i.e., 0.5034, is obtained at the end of 1000 iterations. Figure 7 shows the confusion matrix for the binary classification of malignant white blood cancer using the CNN model. Using CNN's specificity of 95.19% and an accuracy of 97.25% is achieved, as shown in Table 2.

$$w(n) = w(n-1) - \alpha * m(t) / \left(\sqrt{v(t)} + \epsilon\right) \tag{5}$$

where w is the weight matrix, α is the learning rate, $m(t)$, and $v(t)$ are the first and second moments' bias-corrected estimators. Figure 8 depicts a plot of loss during the training period. Figure 9 shows the ROC (Receiver Operating Characteristic) curve for the proposed model. The ROC curve is formed by plotting the true positive rate (TPR) at different threshold settings against the false positive rate (FPR). Precision - recall curves are usually zig-zag curves that tend to cross each other very frequently. Due to this, a comparison between curves becomes very difficult. Thus we define a perfect test case that says that the curves passing or inclined more towards the upper right corner is the perfect case of precision and recall curves. For the proposed model, precision and recall are 1 and 0.93, respectively. Figure 10 shows the relationship between precision and recall for every possible cutoff. From Figure 10, we can observe that our classification results tend towards the perfect case of the precision-recall curve.

Algorithm 1 Proposed CNN Model

procedure CreateTraining(Images)
  for each I in Images **do**
    $Image\_new1 = filter(I.find\_edges)$
    $Image\_new2 = filter(I.rotate90)$
  end for
  $Image\_NT = Image\_new1 + Image\_new2$
  return *Image_NT*
end procedure
procedure FindLabel(Image_Name)
  if 'ALL' in Image_Name **then**
    return 0
  else if 'MM' in Image_Name **then**
    return 1
  end if
end procedure
procedure SelectKFeatures(K,Image_NT,Y_train)
  $test = selectkfeature(chi2, K)$
  $x\_transformed = test.fit(Image\_NT, Y\_train)$
  return *x_transformed*
end procedure
procedure Normalize(Image_NT)
  return $Image\_NT.pixelvalues/255$
end procedure
The proposed CNN architecture is Defined
$cost = tf.nn.sigmoid\_cross\_entropy(logits = pred, labels = Y\_Train)$
$optimizer = tf.train.AdamOptimizer(learning\_rate = 0.01)$
$optimize = optimizer.minimize(cost)$
procedure CalculateLoss(Image_NT, Y_Train)
  for iteration in range(1000) **do**
    $loss = session.run([cost, optimize], x : Image\_NT, y : Y\_Train)$
  end for
end procedure
procedure Predict(Image_TEST, Y_Test)
  $p = session.run(pred, x : Image\_Test)$
  for each *prediction* in *p* **do**
    if $prediction < 0.5$ **then**
      $prediction = 0$
    else if $prediction \geq 0.5$ **then**
      $prediction = 1$
    end if
  end for
end procedure

B. ANALYSIS USING MACHINE LEARNING

In the next subsection, we have performed a comparative analysis to show that deep learning works well in terms of performance as the scale of data increases. Machine learning provides various algorithms for image classification that we have used as a basis to analyze the proposed deep learning approach. For applying all the machine learning algorithms, two features, namely histogram and Discrete Fourier Transform (DFT), are extracted from the images. Then all the classifiers are trained on these features. SVM, a supervised learning algorithm, built the classification model on 'RBF' kernel [31]. Naive Bayes, a probabilistic classifier, uses the Gaussian form for classifying between both types of cancer [32]. The decision tree classifier model focuses on predicting the value of a variable based on an input sequence of the feature vector obtained [33]. Random forests, an ensemble learning algorithm, gives the output as the mean prediction of individual decision trees formed at the back end, giving the final distinction [34].

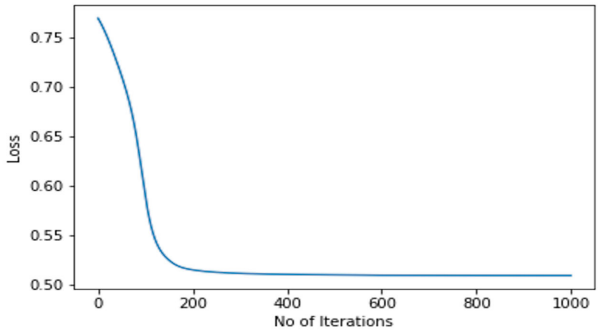

FIGURE 8. Plot of loss versus Iterations during training period.

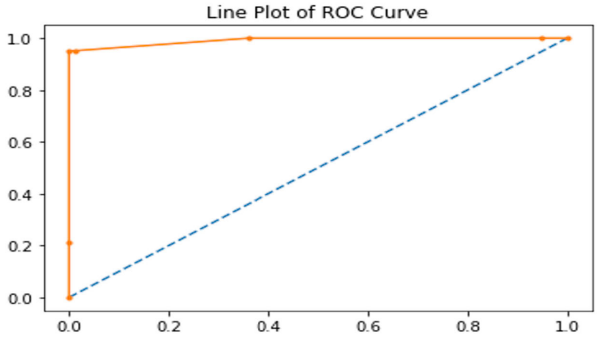

FIGURE 9. ROC curve for proposed CNN model.

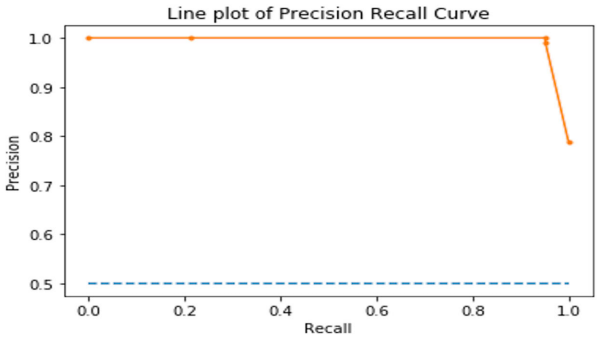

FIGURE 10. Precision-Recall for proposed CNN model.

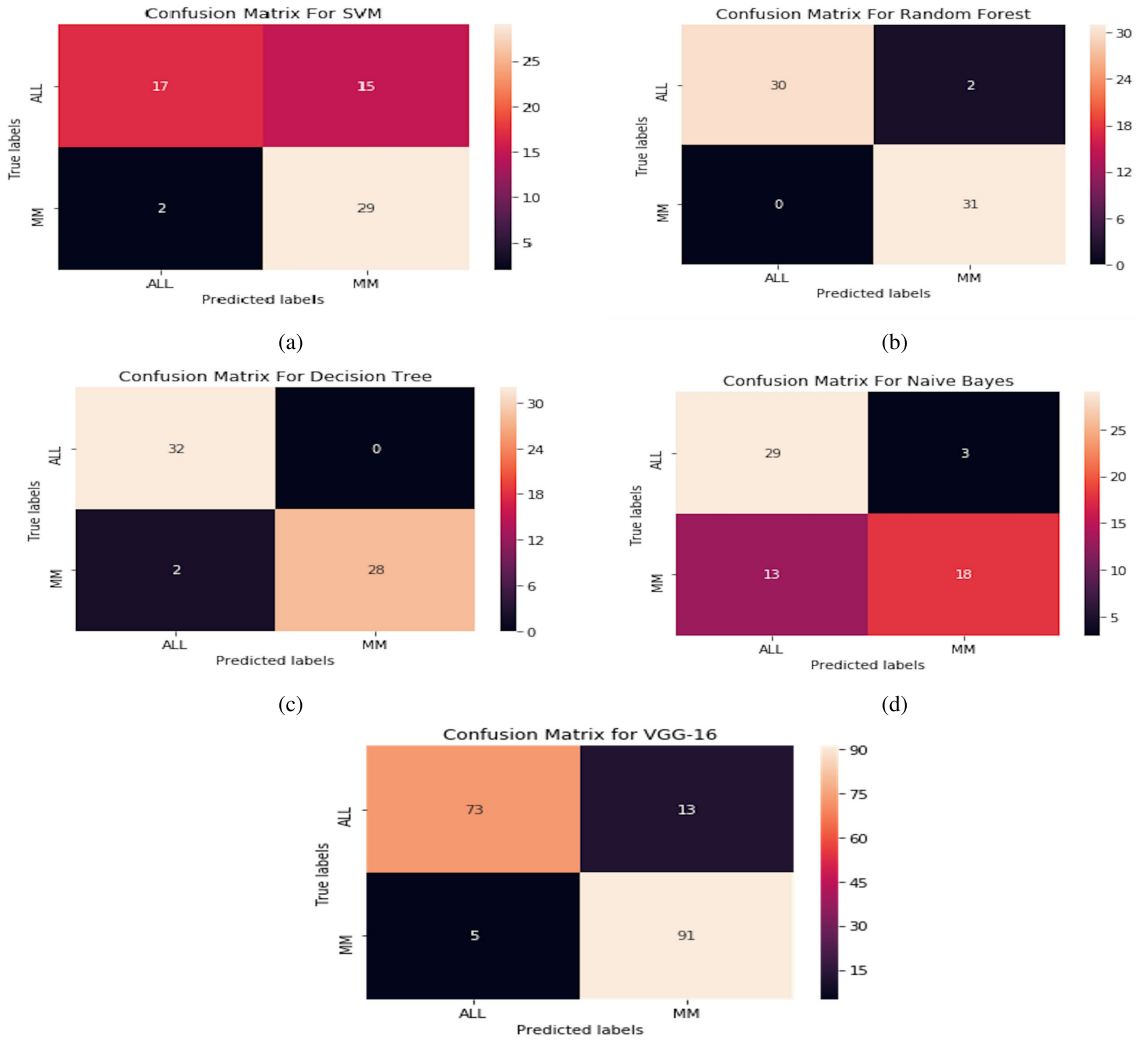

FIGURE 11. Confusion matrices for machine learning algorithms. (a) Support Vector Machines(SVM), (b) Random Forests, (c) Decision Trees, (d) Naive Bayes, and (d) VGG-16.

C. ANALYSIS USING TRANSFER LEARNING

Here, we have shown the performance superiority of the proposed model over transferred learning models like VGG-16, aiming to save the computation cost for similar problems. VGG-16 is a convolutional neural network model consisting of only 3 × 3 layers stacked on the top of each other. Two fully connected layers having 4096 nodes each constitute the model followed by the use of softmax for classification [35].

The comparison has been made on the following parameters: Accuracy, Precision, Recall, Specificity, and F1 Score. TP is defined as the number of samples correctly classified as the positive class. On the other hand, TN is defined as the number of samples correctly classified as the negative class. FP is the number of samples identified as belonging to the positive class, but actually, they don't, and FN is the number of samples when the model incorrectly predicts the negative class. Figure 12 provides a representation of Table 2.

$$AC = (TP + TN)/(TP + TN + FP + FN) \quad (6)$$
$$P = TP/(TP + FP) \quad (7)$$
$$R = TP/(TP + FN) \quad (8)$$
$$S = TN/(TN + FP) \quad (9)$$
$$F = (2 * P * R)/(P + R) \quad (10)$$

Table 2 shows the results obtained by applying different machine learning models.

Figure 11 illustrates the confusion matrices for SVM, Random forests, Decision trees, and Naive Bayes Algorithms for the binary classification of images. Confusion matrices indicate four different types of data viz True Positive (TP), False Positive (FP), True Negative (TN), and False Negative (FN).

TABLE 2. Baseline comparison table.

S.No.	Algorithm	Accuracy	Precision	Recall	Specificity	F1 Score
1	SVM	73.02	89.47	53.12	65.9	66.66
2	Random Forest	96.83	100	93.75	93.93	96.77
3	Decision Trees	96.77	94.11	100	100	96.96
4	Naive Bayes	74.6	69.05	90.65	85.71	78.37
5	VGG-16	90.1	84.88	93.58	87.5	89.01
6	CNN	97.25	100	93.97	95.19	96.89

TABLE 3. Proposed model comparison for different datasets.

Datasets	Pollinating Bees		H&E Blood Cancer Cells		Retinal OCT Images	
	Rodriguez, Ivan F., et al. [36]	Proposed Model	Hatipoglu, N., & Bilgin, G. [37]	Proposed Model	Prahs,Philipp, et al [38]	Proposed Model
Accuracy	60	82	71.5	87	85	87
Percentage of training samples	70	75	33	75	90	75
Percentage of testing samples	30	25	67	25	10	25

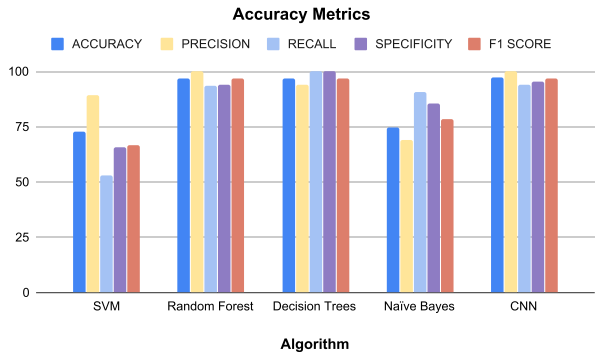

FIGURE 12. Precision-recall for proposed CNN model.

Our classification considers ALL cancer cell images to be a positive class and MM cancer cell images to be the negative class. Random Forests has shown outstanding performance and has classified MM and ALL images well with an accuracy of 96.83%. Almost no input preparation is needed, and it can handle binary or categorical features well.

Another comparative analysis is done by applying the proposed model on different datasets, as shown in Table 3. The first dataset is a pollinating bees' dataset [36]. The dataset has been created from videos captured at the entrance of a bee colony in June 2017. The proposed model classified bees into their two subtypes, namely pollinating and non-pollinating bees with an accuracy of 82%. The next dataset is Hematoxylin and eosin (H&E) blood cancer cells [37]. The dataset consists of 116 stained normalized images. The proposed model classifies the data into benign and malignant with an accuracy of 87%. Lastly, retinal OCT images dataset consisting of 84,495 X-Ray images is used for comparison [38]. The proposed model achieved an accuracy of 87% in classifying the retinal images into an infected and healthy state.

V. CONCLUSION

The proposed model annihilates the likelihood of blunders in the manual procedure by utilizing a profound learning strategy in particular convolutional neural systems. The model is first pre-forms the pictures and concentrates the best highlights out of them followed via preparing the model with the changed Convolutional neural system structure. In the end, it predicts the type of cancer in the given image. The model accuracy evaluated to 97.2%. A baseline comparison with some state of art methods like Support Vector Machine (SVMs), Decision Trees, Random Forests, Naive Bayes, etc. was also performed and presented. The proposed model performed better than these baseline methods. A clear comparison between the model and some existing proposed models is also shown over three discrete datasets where the former performed better in terms of accuracy. Therefore, the model can be utilized viably as an apparatus for deciding the sort of malignant growth in the bone marrow. However, we have to admit that a broader experimental study considering the dependence on the size of the databases has not been performed and presented here.

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