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RESEARCH ARTICLE

LEUKEMIA CLASSIFICATION USING A FUSION OF TRANSFER LEARNING AND SUPPORT VECTOR MACHINE

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Abstract – Leukemia is a malignancy that originates in the bone marrows and it is characterised by aberrant white blood cell growth. Artificial intelligence has flourished in recent years across all scientific disciplines. The accuracy of predicting the initial severity of this infection using artificial intelligence in medical research has increased. The proposed model uses transfer leaning approach with VGG-19, and ResNet-50. The input images are pre-processed by weighted distribution and gamma correction techniques; from this the edges are detected by the Sobel edge detector. The structural features are extracted by the deep neural networks and acquired as feature sets. These feature sets are fused by least absolute shrinkage and selection operator (LASSO) and the support vector machine (SVM) is utilized to categorize the four types of leukemia and healthy. When compared to the results produced by the existing deep neural networks, the proposed approach produces the most precise and effective outcomes. This model yields the accuracy rate of 99.08% and 99.02% for the classification of leukemia.

Keywords *– Leukemia, Weighted distribution, Transfer learning, Feature fusion, Classification*

1. INTRODUCTION

Leukemia is the frequently known cancer that begins in white blood cells (WBCs), although it can also spread in other types of blood cells and bone marrows [1]. The major categorization of leukaemia is performed in terms of whether it is acute (quickly increasing) or chronic (slowly growing). Similarly, it also begins in myeloid or lymphoid cells affects the blood cells of an individual. In the recent scenario nearly 9,500 peoples were affected by leukemia, according to the survey of GLOBOCAN. The major symptoms of leukemia [5,7] are fatigue, recurrent infections, weight loss, and easy bleeding or bruising are all signs of quickly developing kinds of leukaemia. The leukemia is classified as acute or chronic based on the cell immature growth and the types of the cancer. The first type is acute lymphocytic leukemia (ALL), it commonly affects the children than the other [10]. The second type is acute myeloid leukemia (AML), it commonly affects the people younger than 20 years. The next categories are chronic lymphocytic leukemia (CLL) and chronic myelogenous leukemia (CML), both affects the older adults. The figure.1 depicts the forms of leukemia.

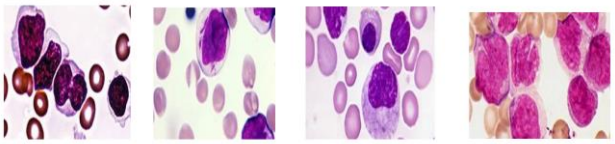


Figure 1. Microscopic view of leukemia types (a) ALL (b) AML (c) CLL and (d) CML

The early detection and diagnosis could help patients minimize expense on therapy, enhance their chances of recovery, and then even survive longer. One of most common tests for detecting leukemia is the smear test [11]. Blood samples are obtained and subjected to various tests in order to predict leukemia. Furthermore, manual diagnoses are inherently incorrect since they require more time and are susceptible to the inter-observer discrepancies. [13-15]. The development of low-cost and autonomous systems that can distinguishes the normal and abnormal blood cells without any human intervention. Several classic computer-aided technologies employ image processing with machine learning and deep learning approaches, [16-20] which often include numerous phases namely pre-processing, segmenting, extracting the features, and classifications. Both machine learning and deep learning approach is more time consuming to overwhelm this issue [21-23] the proposed model uses transfer learning [24-27]. As a consequence, rather of designing deep neural networks from the scratch, employ the principle of transfer learning [28], in which the neural networks that has been successful in addressing one

issue is optimized to resolve others. In this paper transfer learning is used that combines with two deep neural networks namely VGG-19, and ResNet-50 is used for feature extraction. The relevant features are selected by LASSO (Least absolute shrinkage and selection operator) and then the features are fused. SVM (support vector machine) is used to classify the four types of leukemia with high accuracy rate and low cost of computation [29-32].

The rest of the work is spilted into the five sections. The linked works are succinctly explained in Section II. In Section III, the suggested methodology is described. The performance results and their analysis are reported in section IV. The conclusion is provided in Section V.

2. LITERATURE SURVEY

Researchers recently proposed a number of deep learning algorithms, mostly to increase the categorization accuracy of blood cell images. In 2021 Shaheen M. *et al*. [1] had devised the prediction of Acute Myeloid Leukemia (AML) by deep learning algorithms like AlexNet and Lenet-5 models and compared the performance of these both models. The datasets were derived from Acevedo et al. publicly available microscopic peripheral blood samples. When compare both performance Lenet-5 model reaches low accuracy. But, AlexNet reaches high accuracy and detect only AML.

In 2020 Das, *et al*. [2] had developed a GLCM (gray level co-occurrence matrix) and GLRLM (gray level run length matrix) approaches are employed for extracting the characteristics of cells and detect ALL. The datasets were taken by ALL Image Database. SVM is used to classify the WBCs. CLAHE (contrast-limited adaptive histogram equalization) is employ to upgrade the sample qualities. But, SVM takes more time for training the large datasets.

In 2020 Kumar D *et al.,* [3] had proposed a DCNN (dense convolutional neural network) framework to categorize the two types of leukemia namely ALL (acute lymphoblastic leukemia) and MM (multiple myeloma). The datasets had been collected from SMS Spam research. Here, data augmentation introduced two processes, first one is rotating the images corresponding to certain degrees and second one is upgrading only the edges or boundaries of the original image. Uni-variate feature selection had been introduced and selects the features based on univariate statistical tests and its computational rate is high.

In 2019, Tammina, S.,[4] suggested a technique of transfer learning for repurposing previously learned model information for a new task. Classification, regression, and clustering issues can all benefit from transfer learning. Pre-trained InceptionV1, InceptionV2, VGG-16 was trained on ImageNet, that have wide range of image classes. The result illustrates that the introduced model acquires high accuracy than the other models.

In 2018, Cao, G., *et al.,* [5] suggested a technique where the gamma correction controlled by shortened CDF is utilised to improve the dimmed images, while the unique method of negative samples was used to realise CE of the bright ones. The proposed method's algorithm complexity is assessed. Extensive qualitative and quantitative testing demonstrates that suggested strategy provides better or comparable enhancing benefits than earlier strategies.

In 2016, Rahman, S., *et a*l., [6] had proposed an AGC technique (adaptive gamma correction) to properly increase the quality of the images, with the attributes of AGC being modified dynamic information based on the input images. An extensive trial, as well as qualitative and quantitative assessments, reveals that the concert of AGC is high than other existing approaches. AGC offers the most satisfactory contrast increases in diverse lighting circumstances when compared to other existing enhancement algorithms.

In 2019, Veluchamy, M. and Subramani, B., [7] presented an Adaptive Gamma Correction with Weighted Histogram Distribution (AGCWHD) approach to increase contrast while keeping original colour and deeper information of the input images. To assess the performance of the suggested technique, experiments are carried out and assessed on 500 TID 2008 benchmark photos. When compared to the existing procedures, experimental findings showed that the suggested methodology created extraordinarily high-quality images.

In 2020, Loey, M., *et al.,* [8] had proposed a method that employs transfer learning technique to diagnosis leukaemia, that includes two automatic classification algorithms based on the blood microscopic examination images, instead of using earlier strategies that have severe disadvantages. Blood microscopic pictures are denoised in the primary technique, and then characteristics are extracted via deep CNN. The result shows that the proposed model recognizes leukaemia in more efficient manner than other models.

In 2019 Ahmed N. *et al.* [9] had proposed CNN is used to classify the subtypes of leukemia like ALL, AML, CLL, and CML. The datasets are picking up by the two publicly available leukemia datasets are ALL image database and ASH image bank. There are various image transformation techniques are applied. The feature extraction phase is carried out in convolution and pooling layer. SGD and Adam optimizers are applied. But, Stochastic Gradient Descent (GCD) makes continuous informs with a huge change, causing the objective function to differ significantly.

In 2018 Shafique.S. and Tehsin.S., [10] had proposed a AlexNet to ALL in an automatic manner and classify its subtypes. The images were taken by public available datasets and four datasets had been selected as different colours. In data augmentation technique, image rotation and mirroring had been feed to increase the training data. For the total datasets, ALL detection accuracy was good but, the classification of subtype's accuracy was lower than the RGB image datasets.

From this study various deep learning and machine learning methods are comfortable to get high accuracy. In this proposed system, transfer learning that integrates VGG-19 and ResNet-50 for extracting the features and the classification of leukemia is performed by support vector machine (SVM) to acquire better accuracy and with low computational rate.

3. PROPOSED METHOD

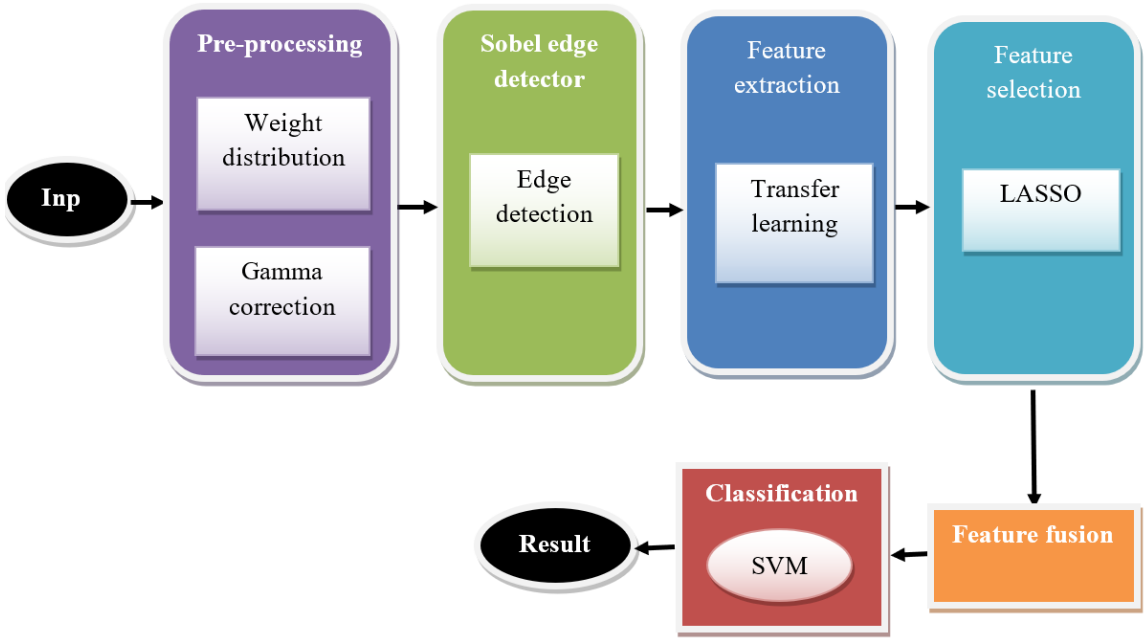


Figure 2. Visualization of the proposed approach

3.1. Dataset acquisition

In this study the blood sample images are taken from the commonly available two dataset library namely ASH image bank and ALL-IDB. Four types of leukemia images with size of 2560x1920 in BMP forms constitute this dataset. The collective formats are intended to tune the proposed method to decide the types of leukemia acute and chronic. The acute categories are acute lymphocytic leukemia (ALL) and acute myeloid leukemia (AML). The chronic categories are chronic lymphocytic leukemia (CLL) and chronic myelogenous leukemia (CML),

3.2. Image pre-processing

Pre-processing is an initial step for lessening the noise and improving the subtle variations of medical images. The microscopic blood images are first changed into an RGB colour as input to the model, and then a variety of processes are performed in this stage. To compensate the loss of the datasets, data augmentation is used. The inputs are rotated along the X and Y axes, the interval randomly selecting values. The indication process reflects images all along the vertical axis. At last, with randomly rotating the values that are limited by the intervals, the inputs are twisted right or left during the rotation procedure.

3.3. Weighted Distribution

A weighted distribution is used to ensure that image regions with a high probability do not become highly enhanced, and image regions with a lower probability do not become under-enhanced, with no loss of critical visual features. This input image is altered such that less frequent levels have higher probability or weights. The formula for calculating weighted input is:

$$pdf_w(l) = pdf_{max}(pdf(l) - \frac{pdf_{min}}{pdf_{max}} - pdf_{min})^a \quad (1)$$

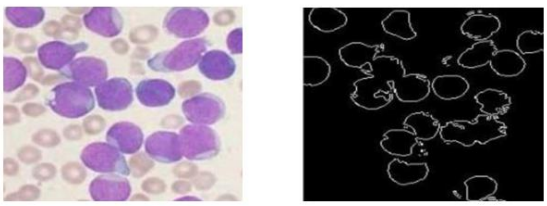
Then modified cumulative density function is derived as,

$$cdf_w(l) = \sum_{l=0}^{lmax} pdf_w(l) / \sum pdf_w \quad (2)$$

Where,

$$\sum pdf_w = \sum_{l=0}^{lmax} pdf_w(l) \quad (3)$$

Where α is the adjusted factor, $pdf_{max}$is the largest probability distribution function and pdf_{min} is the smallest probability distribution function of statistical histogram.



(a) (b)

Figure 3. Samples of (a) pre-processed image and (b) after edge detection image

3.4. Gamma Correction

The gamma correction is applied after the weighted distribution is mapped. The normalised cumulative density function (cdf) is used to apply gamma correction in this approach and it is carried out as follows,

$$T(l) = l_{max}(l/l_{max})^{\gamma} = l_{max}(l/l_{max})^{l-cdf(l)} \quad (4)$$

Where, the gamma equation is calculated as:

$$\gamma = l - cdf_w(l) \quad (5)$$

where the distribution function is indicated as cdf_w, the max signifies the exploiting operator and l defines the pixel intensity. The limited distribution function lowers the image

contrast of brightness pixels while increasing the contrast of low contrast pixels.

3.5. Edge Detection

A group of connected pixels situated between the edges of two regions in an image is referred to as an edge. Edges in binary images are black pixels that have one white neighbour. Sobel edge detection is the technique for identifying and extracting edges from digital images in order to get critical image analysis details. The result of the leukaemia and red blood cell edge detection technique are provided. There is a substantial variation in the size, shape, quantity, and location of leukaemia cells and red blood cells. The edge detection images are depicted in fig.3

3.6. Feature extraction

The feature extraction is a crucial stage that utilized for removing the irrelevant features present in the input images to diagnose leukemia. The pre-tuned models such as ResNet-50 and VGG-19 was trained on ImageNet, which contains a variety of image classifications

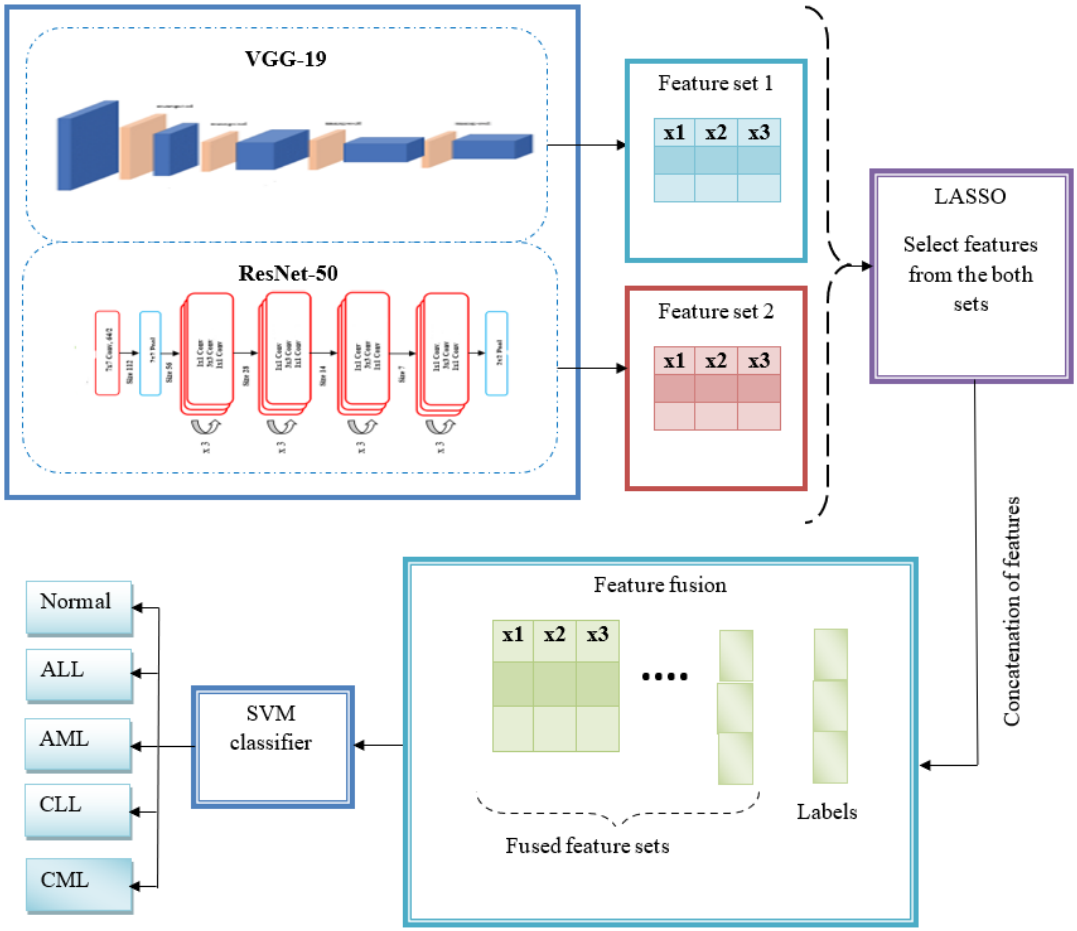


Figure 4. Architecture of the proposed transfer learning model

These models are trained on various set of images divided into various set of categories. Because the model was tuned on such a large dataset, it has built a better representation of minimal level characteristics including spatially, boundaries, rotational, brightness, and structures that can be used across dissimilar computer vision issues to allow information flow and operate as a feature extractor for the input images.

VGG-19 is used to analyse the effect of the convolutional neural networks depth by extracting the structural features. Using a 3x3 convolution filter size and 11x11 convolutional filter size, this model acquires one of the best results in the ILSVRC 2014, with improved feature extraction. Small filters improve the network's depth rather than its width in this architecture, which is crucial for achieving greater performance. Initially, the model was trained on the datasets to retrieve deep features using the transfer learning approach. This model is loaded by the dataset paths for randomly selects the input images, 70% for tuning, and 30% for testing. The function of cross-entropy is used to activate the average pooling layers and FC layers of the system. The extracted features are considered as feature set 1.

ResNet-50 is based on the principle of generating deep CNN than existing simpler networks while also establishing out the numerous layers to eliminate the over-fitting issue. Using the transfer learning approach, the model was initially trained on the datasets to extract deep features. In this model the dataset paths are loaded for arbitrary takes the input images, 70% for training, and 30% for testing. The cross-entropy function is used to activate the average pooling

layers and FC layers of the architecture and the extracted features are considered as feature set 2.

3.7. Feature selection

The feature selection reduces the dimensions of the image by selecting a set of features by using LASSO. It is commonly known technique; here it performs feature selection and regression simultaneously while imposing standard constraints l_1 on the coefficients of regression. The non-differentiability of the normativel_1, on either, prevents from evaluating the objective of gradient function. Then LASSO algorithm learns sparse regression coefficients as,

$$\beta_0 = argmin_\beta \, ||x - Y\beta||^2 + \alpha||\beta||\, l_1 \qquad (6)$$

Where response vector $= x_1, x_2 \ldots\ldots x_n$, the feature matrix $y = y_1, y_2 \ldots\ldots y_n$ and α is a trade-off parameter in determining comparative fitting efficiency and sparsity of β_0.

3.8. Feature fusion

In the field of disease recognition, the feature concatenation is an important step. To create a finished mono feature vector for illness diagnosis, the individual feature vectors are gradually fused. The key justification for carrying out this phase is to combine all descriptor data into a single feature vectors column, which can be useful in lowering the error rates. By removing the unnecessary characteristics from the input image as feature sets 1 and 2, the VGG-19 and ResNet-50 extract the structural and geometric features. The relevant or specific features are subsequently selected from the retrieved features using the fusion selection approach, and these features are combined to classify leukemia.

3.9. Classification

SVM locates and uses a hyperplane class border that maximizes the space in the training dataset to identify binary classes. The training data samples that follow the class boundary hyperplanes form the support vectors, and the margins are the spaces between the support vectors and the class border hyperplanes. It is based on the notion of decision planes, which set decision boundaries. A decision plane makes a distinction between the features of images that belong to several classes.

The training and testing data for this classification procedure frequently contains a variety of data examples. The training set has several features and class labels for each instance. The dynamically dividing hyperplane with the greatest margin and filter count is then found by the SVM. Using the gathered support vectors, the kernel is changed in a data-dependent manner to obtain the outcomes. Depending on these findings, it may be determined whether the patient have leukemia or healthy.

4. RESULTS AND DISCUSSIONS

The proposed method consists of two networks such as ResNet-50 and VGG-19 for predicting and classifying the types of leukemia with high accuracy and minimal computational cost. These networks perform on the basis of transfer learning, since the performance analysis and comparative analysis was discussed in this section.

4.1. Performance analysis

In this study the performance assessment is considered on the basis of specificity, accuracy, precision, recall and F1 score.

$$s = \frac{Tp}{Tn + Fp} \qquad (7)$$

$$r = \frac{Tp}{Tp + Fn} \qquad (8)$$

$$p = \frac{Tp}{Tp + Fp} \qquad (9)$$

$$a = \frac{Tp + Tn}{Total\ no.of\ samples} \qquad (10)$$

$$F1 = \frac{2 * p * r}{p + r} \qquad (11)$$

The performance analysis is shown below table 4.3based on the datasets namely ALL-IDB for ALL and normal and Ash dataset for CLL, CML and AML

Table 1. Performance analysis of the proposed model

Datasets	Classes	Specificity	Precision	Recall	F1 score	Accuracy
ALL-IDB	Normal	99.2	99.4	99.5	98.3	99.8
	ALL	99.8	98.5	97.1	98.6	99.5
ASH dataset	AML	97.5	95.3	95.0	94.2	97.0
	CLL	95.3	95.8	94.2	93.1	95.1
	CML	96.4	93.6	92.5	97.5	93.5

From the table1, the proposed model yields the accuracy range for dataset-1 is 99.08% and 99.02% for dataset-2 that is illustrated in fig.5.

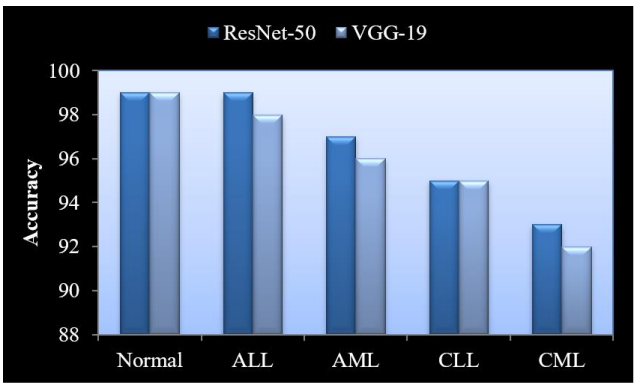


Figure 5. Accuracy acquired by ResNet-50 and VGG-19 based on datsets

From the fig.6 that traditional methods namely Resnet-50 andVGG-16 obtain high accuracy in both dataset by fusing these networks through transfer learning it scores high accuracy rate.

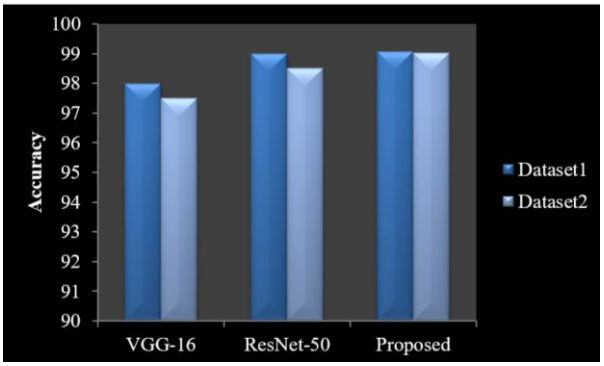


Figure.6. Accuracy acquired by the fusion of proposed method

4.2 Comparative analysis

In this proposed study, the testing methodology is used to detect the leukemia in early stages. The transfer learning with the neural networks such as ResNet-50 and VGG-19 were compared with previous techniques. From that the proposed technique reaches high accuracy than the other deep learning techniques. The accuracy obtained by the proposed model is 99.02%, which is greater than the existing techniques. The comparative analysis is performed between the proposed model and the existing models such as AlexNet+Lenet [1], DCNN [3], CNN+SGD [9] and AlexNet [10] is illustrated in table2,

Table 2. Comparative analysis of five existing models

Networks	Accuracy	Precision	Recall	Specificity	F1 score
DCNN [3]	97.02	92.4	8.3	87.5	89.1
AlexNet [10]	96.06	92.1	96.74	99.3	98.2
AlexNet+Lenet [1]	98.58	87.4	88.5	92.7	91.5
CNN+SGD [9]	88.74	87.3	86.4	85.6	87.3
Proposed method TL+SVM	99.08	98.5	97.1	99.5	97.5

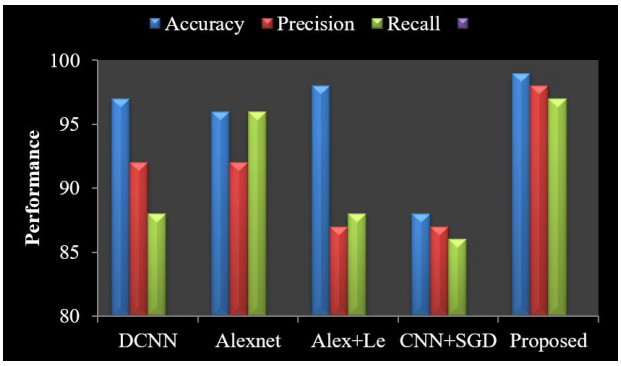


Figure 7. Graphical comparison between five deep neural networks

The outcomes of each network were compared to establish that the suggested method's result is more efficient. The range of accuracy obtained by the proposed network is 99.08% and 99.02% for both datasets. The computational cost drastically reduced compared to other networks. Then, comparison is made between the machine learning classifiers namely Random Forest (RF), Decision tree (DT), Naive Bayes (NB), k-nearest neighbour (kNN), and Support vector machine (SVM). The table.3 depicts the comparison between the machine learning classifiers and the graphical comparison is shown in figure 7. From this analysis SVM is outperformed than the other classifiers while preserving the accuracy.

Table 3. Comparison of different machine learning classifiers

Models	Accuracy	Precision	Recall	Specificity	F1 score
RF	96.5	95.7	92.0	90.0	91.2
DT	92.1	98.2	93.2	91.0	94.7
NB	93.4	94.2	94.1	90.5	94.2
KNN	92.4	93.7	88.0	86.0	87.2
SVM	99.2	94.9	94.0	95.1	98.6

From the table 3, the existing machine learning classifiers perform much slower than the SVM. Since the proposed methodology has the fusing the deep learning networks with SVM classifier to classify the types of leukaemia and it acquire high classification accuracy.

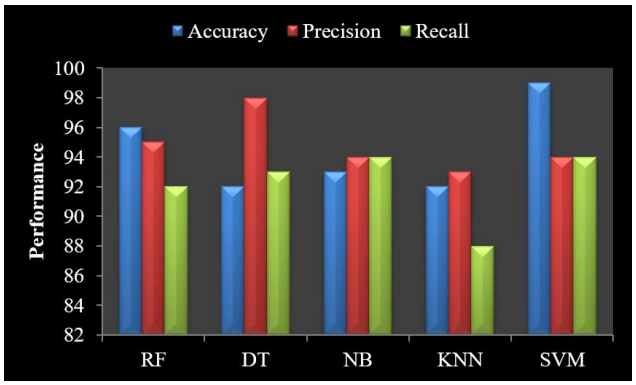


Figure 8. Graphical comparison of different ML classifiers

From the above comparisons, it is obvious that the proposed model gains better accuracy range of 99.08% and 99.02% at slight computational cost. This classification and recognition are very essential for initiation of immediate and effective therapy to the affected individuals by leukemia. However, there are some limitations by using Sobel edge detector, the gradient magnitude of the edges reduces as noise rises, subsequent in erroneous fallouts. In future the accuracy is improved by using the better and advance edge detection technique.

5. CONCLUSION

Transfer learning is a method that is currently being developed for image processing, and it is useful for resolving issues with early-stage leukemia analysis. At this firm, the proposed method uses transfer learning for extracting the features and classifies the four major types such as ALL, AML, CLL, CML and normal. The result shows that the proposed model can extract the structural features for early prediction by recognizing the changes in the blood cells. In the above results, conclude that the proposed model gains high accuracy on both training and testing datasets compared to other deep neural network. The proposed method outperforms with drastically minimum computational cost while preserving the accuracy rate of 99.08% and 99.02%. By using this method, the rate of detection can be raised and the affected patients can receive immediate and suitable clinical care. In the future, this technology may be used in hospitals to further the advancement of AI in the medical industry and to more effectively improve leukemia detection.

CONFLICT OF INTEREST

The author proclaims that there are no conflicting interests to disclose in this study.

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