AUTOMATED ACUTE LYMPHOBLASTIC LEUKEMIA CELL CLASSIFICATION USING OPTIMIZED CONVOLUTIONAL NEURAL NETWORK

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Abstract

Acute lymphoblastic leukemia (ALL) is the most common variant of paediatric cancer that creates numerous immature white blood cells affecting the bone marrow. Manual diagnosis of leukemia from microscopic evaluation of stained sample slides is an exhausting process, which is less accurate and susceptible to human errors. Additionally, identifying the leukemic blast cells under the microscope is complicated due to morphological similarity with the normal cell images. In this paper, we proposed an automated method to analyse the blood smear images using Local Binary Pattern (LBP) and classify the leukemic blast cells and normal cells. We have analysed the performance of machine learning and deep learning models such as Support Vector Machine (SVM), k-Nearest Neighbor algorithm (kNN), Artificial Neural Network (ANN), and Convolutional Neural Network (CNN). For classifying ALL and normal cell images, kNN achieved an accuracy of 94.4%, SVM, and ANN achieved an accuracy of 98.6%, and CNN achieved an accuracy of 99.6%. SVM achieved the highest sensitivity of 100%.

Keywords: Acute lymphoblastic leukemia; Blast cell; Classification; Deep learning; Machine learning

Introduction

Leukemia is a variant of cancer affecting white blood cells in blood and bone marrow. The malignant transformation of pluripotent and hematopoietic stem cells causes leukemia (Chennamadhavuni *et al*., 2023). The disease progression is relatively quick and aggressive and, therefore, requires immediate treatment. There are various types of leukemia, e.g., acute lymphoblastic leukemia, chronic lymphocytic leukemia, acute myeloid leukemia, and chronic myeloid leukemia (Dharani and Hariprasath, 2018; Chennamadhavuni *et al*., 2023).

About 80% of cases of leukemia are acute lymphoblastic leukemia (ALL). In acute leukemias, the immature malignant cells are poorly differentiated, and abnormal leukocytes or blast cells can be either lymphoblasts or myeloblasts. The peripheral blood smear can be described by more than 20% of blasts. Only the bone marrow biopsy can help to distinguish between the types of acute leukemia (Chennamadhavuni *et al*., 2023). Some of

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the risk factors of ALL are age, especially children and adults over 50 years; genetic factors such as Down syndrome, Klinefelter syndrome, Fanconi anemia, etc.; exposure to radiation as a treatment for former cancer; exposure to certain chemicals like benzene, mostly found in petroleum products and cigarette smoke; viruses, etc. Some of the symptoms include fever, excessive sweating, dizziness, fatigue, frequent bleeding, difficulty in breathing, panting, pale skin, swollen lymph nodes, pain in joints and bones, weight loss, etc.

ALL can affect both children and adults. However, it is the most common variant of cancer amongst children in the age range of 0-5 years. About 85% of ALL cases can be found in children younger than 15 (Belson, *et al*., 2007). According to the American Cancer Society (ACS), the risk of ALL reduces in the age range of the 20s and then, increases again after the age of 50 years (Siegel *et al*. 2022). Early diagnosis of ALL is crucial for the fast treatment of patients, especially children. The diagnosis of ALL is very challenging because its symptoms are common to various other diseases. The diagnostic procedures involve the microscope examination of peripheral blood to search for abnormal cancerous white cells. Generally, experienced operators perform this blood cell analysis, and they mainly perform cell classification and cell counting. However, the morphological analysis of blood cells can be performed by using a single image and does not require collecting blood samples every time. Therefore, blood cell image analysis is well suited for low-cost and remote screening systems that can provide consistent accuracy.

Acute lymphoblastic leukemia (ALL) classification is an emerging research area now due to the fact it is a fatal condition for humans, especially for children. It is difficult to get a dataset of blood smear cell images, thus, the research on classifying cancer cells at the microscopic level is still challenging. Shafique *et al*. (Shafique *et al*., 2019) proposed a method for classifying ALL and normal cell images. They segmented lymphocytes from the white blood cells and extracted features based on the color and shape of the lymphocytes. Using SVM for classification, their method achieved an accuracy of 93.7%, specificity of 91%, and sensitivity of 92% in a publicly available dataset. Muntasa *et al*. (Muntasa and Yusuf, 2019) proposed an ALL detection method based on the principal object characteristics of color images. They selected seven types of features including entropy, log energy entropy, Shanon entropy, variance, mean, energy, and correlation. These features are extracted from each color channel (red, green, and blue) and the feature values of training and testing sets are computed using distance metrics. For Euclidean Distance, their method obtained 81.54% accuracy, for Manhattan distance obtained 81.54% accuracy, using Canberra distance obtained 76.92% accuracy, and Chebyshev method obtained 82.31% accuracy. Laosai *et al*. (Laosai and Chamnongthai, 2018) used morphological operations and CD markers to categorize 3 subtypes of lymphoblastic leukemia and 8 subtypes of acute myeloid leukemia. The proposed method extracted features from the segmented images and classified the subtypes using the SVM. They evaluated the method using a set of total 200 images including 100 samples for each normal and abnormal image and obtained an accuracy of 93.89%.

Dese *et al*. (Dese *et al*., 2018) developed an automatic diagnostic method for the early detection and classification of leukemia blood cell images. The k-means algorithm was used for image segmentation and feature extraction. A multi-Class SVM achieved an accuracy of 94.62%, sensitivity of 94.17%, and specificity of 100% for the detection and classification of leukemia disease. Shafique *et al*. (Shafique and Tehsin, 2018b) used a deep CNN for automated detection of ALL and classification of its subtypes. They used transfer learning to fine-tune a pre-trained AlexNet on their data set. For ALL detection, the CNN achieved an accuracy of 99.50%, sensitivity of 100%, and specificity of 98.11%. For classifying ALL subtypes into 4 classes, viz., L1, L2, L3, and normal, CNN obtained an accuracy of 96.06%, a sensitivity of 96.74%, and a specificity of 99.03%. Bodzas *et al*. (Bodzas *et al*., 2020) proposed a three-phase filtration algorithm for ALL cell segmentation. By utilizing 16 robust features extracted from the blood cell images, the ANN achieved a sensitivity of 100% and the SVM achieved a sensitivity of 98.25%; whereas both techniques obtained a specificity of 95.31%. Rehman *et al*. (Rehman *et al*., 2018) proposed a thresholding-based segmentation and deep learning-based model to classify ALL into L1, L2, L3, or normal types. The blast cells are segmented using the thresholding method from HSV color space. They used transfer learning and used pre-trained AlexNet for classification and achieved 97.78% accuracy. Mondal *et al*. (Mondal *et al*., 2021) proposed a weighted ensemble of Convolutional Neural Networks for microscopic ALL detection. They conducted experiments on the publicly available C-NMC-2019 ALL dataset. Their proposed weighted ensemble model, using the kappa values of the ensemble candidates as their weights, obtained an F1-score of 88.6%, accuracy of 86.2%, and AUC of 0.941 in the preliminary test set. Clinton *et al*. (Clinton *et al*., 2020) presented a depth-wise separable convolutional neural network

(Xception) for detecting ALL. They tested various convolutional neural network algorithms through transfer learning. Data augmentation was done on a dataset with microscopic blood smear images and the Xception architecture obtained 91% accuracy and recall of 98% for classifying leukemic cells.

Bhattacharjee *et al*. (Bhattacharjee and Saini, 2016a, 2016b) proposed a simple segmentation method using intensity-based watershed transformation. The morphological features such as area, perimeter, the circularity of blast cells etc. were extracted for classification. They used a binary search tree and Gaussian mixture model for classification and obtained 100% sensitivity for both classifiers. The Gaussian mixture model obtained a specificity of 93.3% and the binary search tree obtained a specificity of 86.6%. Rahman *et al*. (Rahman and Hasan, 2019) used watershed transformation and clustering methods to segment white blood cells. Then extracted textural, morphological, and color features from the blood microscopic images were fed to kNN, SVM, Decision Tree, and an Ensemble classifier. With 50 features, the Ensemble classifier achieved the highest accuracy of 93.6% and sensitivity of 96% among all four classifiers. Singhal *et al*. (Singhal and Singh, 2014) used local binary pattern (LBP) and geometric pattern features from the segmented blood cell images. Then, SVM is employed to compare the classification results for both types of features. With LBP features, SVM achieved the highest accuracy of 89.7%, sensitivity of 80.43%, and specificity of 95.08%. With geometric shape features, SVM obtained the highest sensitivity of 100%.

From the existing methods, it can be observed that most of the work revolves around transfer learning and deep learning models. Whereas the performances of the deep learning models are very high, they come with the additional overhead of complexity and memory requirement. In this paper, we have focused on identifying ALL cells in blood smear images. The manual diagnostic method involves the microscopic evaluation of stained sample slides, which is time-consuming, less accurate, and prone to human errors (Shafique and Tehsin, 2018a). Therefore, automated diagnostic methods can ease up and speed up the evaluation process with higher accuracy.

In this paper, we have proposed an automated computer-aided method for classifying acute lymphoblastic leukemia cells and normal cells in microscopic images. With a statistical feature extraction method, we have compared the performance of various machine-learning algorithms such as Support Vector Machine (SVM), k-Nearest Neighbor (kNN), and Artificial Neural Network (ANN). Additionally, we exploited the deep learning model, especially the Convolutional Neural Network (CNN) for classifying ALL and normal cells. We have discussed the performance evaluation of these algorithms and pointed out the suitable approach for cancer cell detection.

Proposed Method

In this paper, we exploited various machine learning algorithms to analyze the blood smear images to classify ALL cells and normal cells. In the following subsections, we have described the proposed method for ALL classification in detail.

Image Pre-Processing:

The pre-processing of images is a crucial step for any classification task. An efficient method can enhance the performance of the consequent steps in a classification problem. However, in our case, image-enhancing methods rather highlighted unwanted features. Therefore, we only extracted the green channel of the RGB images as it was already highlighting the significant features. Figure. 1 shows the extracted green channel of the blood smear images. All the acquired images are of size 2592×1944 and are resized to 500×500 for further processing.

Feature Extraction

Here, we have used the Local Binary Pattern Histogram (LBPH) for extracting the spatial features from the images. LBP is a simple yet efficient texture descriptor that works by thresholding the neighborhood of each pixel and resulting in a binary image. It is a block-by-block process performing circular neighborhood operations (Ojala *et al*., 2002). With a sliding window of size 3×3, the circular neighborhood image pixels are compared with the center pixel.

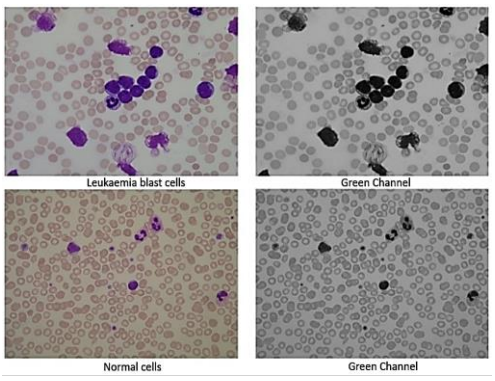

Figure 1. Green Channel Extraction of Leukaemia and Normal Cell Images

Considering the center pixel value as a threshold, the image is converted into a binary image by setting all the pixel values greater than the center pixel as 1 and 0 otherwise. For circular neighboring sample points N with radius R, if v_N and v_c represent the grey-scale values of neighboring pixels and center pixel respectively, the LBP features can be computed by the following equations (Ojala *et al*., 2002):

$$LBP_{N,R} = \sum_{N=0}^{N-1} f(v_N - v_c)2^N \quad (1)$$

Where, $f(x) = \begin{cases} 1, & x \geq 0 \\ 0, & x < 0 \end{cases}$

For the 3×3 block, the LBP operator can produce 2^8 = 256 different values. Since LBP is rotation invariant and robust against monotonic gray-scale transformations, the pixel intensity values are preserved in the local neighborhood. The computed binary values are then converted into decimal values and stored in the center pixel. The process is continued for every pixel of the image. Finally, a histogram is generated using Equation. 2 with values between 0-255, which represents the feature vector.

$$H_i = \sum_{xy} I(s(x,y) = i) \quad (2)$$

Where, i=0, 1, 2,…(n-1), n is the number of different labels computed by the LBP operator.

Now, LBPH combines the computed LBP features with the spatial information of the image. To calculate the LBP values, we can start from any neighboring pixel and go either clockwise or counter-clockwise to arrange binary values from the most significant bit (MSB) to the least significant bit (LSB). Here, we selected a counter-clockwise direction to concatenate binary bits from MSB to LSB keeping the ordering consistent for all pixels in an image. The process can be represented as shown in Figure. 2. Then, the binary value is converted into a decimal value and replaced with the center pixel. The process continues for all pixels to finally generate an LBP feature image. This image is divided into n local blocks like grids. Then, a statistical histogram of LBP features is created by concatenating the histogram of each local block.

Classification: We have exploited various machine learning algorithms to compare the performance of identifying leukemia cells. The algorithms are discussed below:

***k-Nearest Neighbors* (*kNN*)**

It is a supervised algorithm that classifies a data point to a specific class depending on the class of its neighboring k data points. Starting by selecting a suitable value of K, the distance between a given data point and all other points in the dataset is calculated using any distance metrics such as Euclidean, Manhattan, etc. Based on the computed k nearest neighbors, the given data point is classified to the class to which the majority of the neighbors belong (Weinberger and Saul, 2009; Karaca and Cattani, 2018). Here, we selected k=5 and calculated the distance using Euclidean distance.

***Support Vector Machine* (*SVM*)**

It is another popular supervised machine learning algorithm. The main goal of SVM is finding the optimal hyperplane that classifies the data points or features in an n-dimensional space distinctly into two classes. SVM selects the data points closest to the hyperplane, called support vectors, to create the hyperplane. These support vectors greatly affect the position of the hyperplane. As there can be many hyperplanes in the n-dimensional space, therefore, it computes the distance between support vectors and the hyperplane, known as the margin. The algorithm tries to find the optimal hyperplane by finding the hyperplane with the maximum margin (Cortes *et al*., 1995; Marwala, 2018).

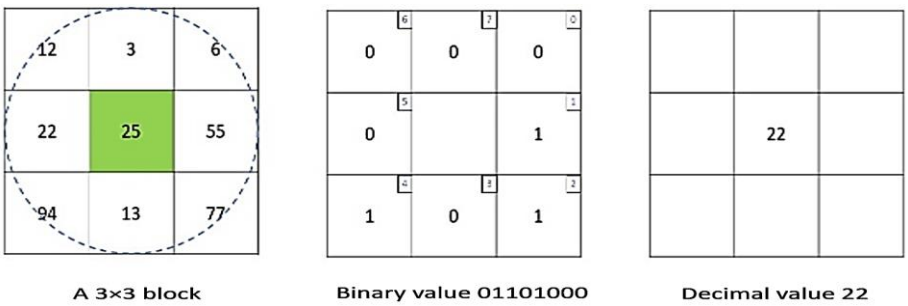

Figure 2. Processing of Local Binary Pattern Operator

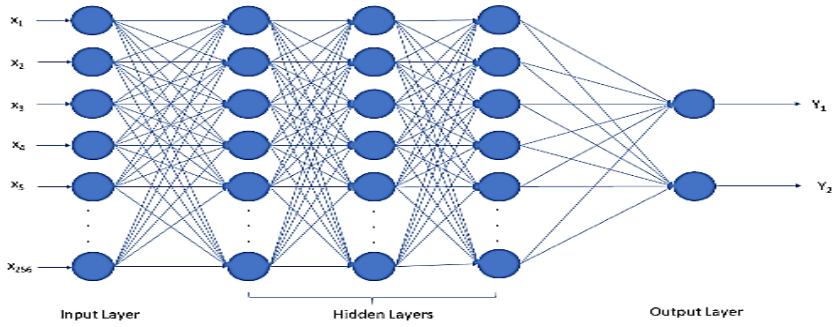

Figure 3. Architecture of ANN

In this paper, for classifying leukemia cells a linear SVM is used. For implementing the SVM model, a linear kernel is used with L2 normalization.

***Artificial Neural Network* (*ANN*)**

It mimics the working principle of the human brain. ANN is composed of multiple nodes, analogous to neurons in the human brain, arranged in a sequence of layers. The input features are processed and analyzed in each layer of ANN. The activation function helps in the learning process and the output of each layer is passed on to the next layer using the following equation (Hopfield, 1988):

$$y = \sum_{i=1}^{n} w_i x_i + b \quad (3)$$

Where y denotes the output of a neuron, w is the weight associated with each input feature x and b is the bias. The weights associated with every neuron specify the meaningful features. The overall prediction is estimated by updating the weights in every epoch during the training with the help of the Gradient Descent Algorithm.

In this paper, we have designed a sequential neural network with three hidden layers as shown in Figure. 3. The input for the neural network is the 256 LBP features. The first dense layer contains 150 neurons, the 2nd hidden dense layer contains 98 neurons, and the third hidden dense layer consists of 32 neurons. There are 2 neurons in the output layer for classifying two classes, normal and leukemia cells. For hidden layers, we have used the Rectified Linear Unit (ReLU) activation function that triggers the neurons in the hidden layers for specific features using the following equation (Glorot *et al*., 2011):

$$\mathrm{R(y)} = \max(0, y) \quad (4)$$

i.e. if y<0, R(y)=0 and if y>0, R(y)=y. The main advantages of ReLUs are sparsity and a decreased probability of vanishing gradient that we found mostly in the Sigmoid and Tanh activation function. In the output layer, the probability distribution of the input activation map over two distinct classes is predicted by the Softmax function using the following equation (Apicella *et al*., 2021):

$$\sigma(\mathrm{x})_\mathrm{i} = \frac{e^{x_i}}{\sum_{k=1}^{K} e^{x_i}} \quad (5)$$

It observes activation values of high-level features received from the preceding hidden layer and identifies the distinguishing features of leukemia cells and normal cells.

For training the ANN, all weights are initialized with 0. The model is trained with a learning rate of 0.001. Adam optimizer is used to optimize the loss during backpropagation.

***Convolutional Neural Network* (*CNN*)**

It is a popular deep-learning model used mostly for image classification. Inspired by the functioning of the visual cortex, a CNN comprises specialized components sensitive to some specific regions of the visual field, known as the receptive field. Generally, a CNN consists of two types of layers, viz. Convolution layers and pooling layers. A convolution layer extracts features from raw image pixels with the help of local filters. A filter, let's consider h(x,y), slides over the image, let's say g(x,y) and generates a new pixel as a weighted sum of the pixels in each position using the expression as follows (Smith, 2003):

$$(g * h)(x, y) = \sum_{u=-\infty}^{+\infty} \sum_{v=-\infty}^{+\infty} g(u, v).\, h(x - u, y - v) \quad (6)$$

The n-th convolution layer produces the feature maps using the following equation (LeCun *et al*., 1998):

$$y_j^n = f\left(\sum_{i \epsilon N_j} W_{ij}^n * x_i^{n-1} + b_j^n\right) \quad (7)$$

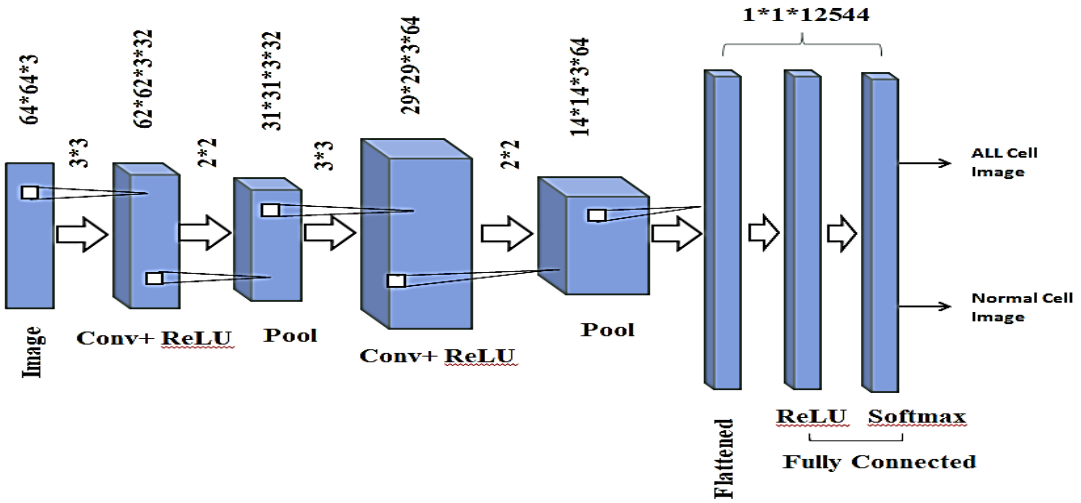

Figure 4. CNN Architecture used for ALL Classification

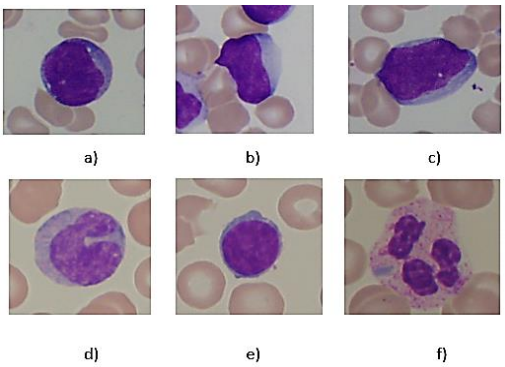

Figure 5. Sample Segmented ALL Images (a,b,c) and Normal images (d,e,f).

Where y_j^n is the output for N number of inputs, x_i^{n-1} denotes the input to a convolution layer, W_{ij}^n denotes the weight of the convolution filters of the size of $i \times j$ and b_j^n is a bias.

The outcome of the weighted sum of the input space calculated by the local filter banks is then passed through a non-linear layer or Rectified Liner Unit (ReLU) layer. It adds non-linearity to the model and activates a particular function to signal the unique identification of potential features on each hidden layer. It considers negative activation values as insignificant and, hence, turns all negative values in the feature map into positive ones using Equation. 4. This also facilitates the model to create a sparse representation of the features.

The pooling layer down-samples the features extracted after each convolution layer by significantly reducing the spatial dimension of the image. The max-pooling and average pooling are two widely used pooling layers. Here, we used max-pooling which consists of a group of filters convolving over the input feature map and selecting the maximum activation value in each sub-region using the following equation (LeCun *et al*., 1998):

$$x_j^l = f(W_j^l \max(x_i^{l-1}) + b_j^l) \quad (8)$$

Where W_j^l is weight and b_j^l is bias. The pooling layers reduce the number of parameters, which helps in cutting the computational cost and control overfitting.

Finally, the feature map generated by the hidden layers is fed to the fully connected layer that finds some high-level features strongly correlated to a distinct class. Then, the output layer provides the classification result by computing probabilities for the target classes. Here, we used a Softmax classifier to predict the probability of the input image to be the ALL or normal blood cell image using Equation. 5.

Network Architecture

Here, for ALL classification, we have used LeNet-5 architecture (LeCun *et al*., 1998) that comprises two convolution layers, two max-pooling layers, one ReLU layer, and two fully connected layers. The network architecture is shown in Figure. 4. To work with CNN, the database IDB-2 with segmented cell images of blood cells is used. Some of the segmented blood images are shown in Figure. 5. Then, to work with the raw colored microscopic blood cell image, the parameters and hyper-parameters are changed. The input images are resized to the size 64×64×3. To convolve the input image in each convolution layer, the receptive field size is kept fixed at 3×3. In the pooling layer,

the filter size is kept 2×2. In the first convolution layer, the number of filters is 32; in the second convolution layer, the number of filters is 64. In the fully connected layers, 128 filters are taken and the output layer consists of 2 filters corresponding to 2 classes of images, viz. Normal cell images and ALL cell images. The fully connected layer is nothing but the Multilayer Perceptron. Therefore, for learning and weight update Gradient Descent Algorithm and Adam optimizer has been used to calculate the cross-entropy loss. Initially, the weights are set to 0. Then, the model has been trained with 100 epochs to complete the cycle of the backpropagation for each 100 batch of the training samples. At the end of the training, the network tunes the weights of each layer and learns the features of blood cell images for classifying the ALL cell images and normal cell images.

Experimental Analysis

In this section, we will discuss the experimental setup and evaluation of the classification performance for kNN, SVM, ANN, and CNN models for leukemia cell classification.

Experimental Setup

For our experiments, we have used Python in Spyder and Google Colab along with a 16GB RAM, 8GB NVIDIA® GeForce 1560Ti graphics card for designing and training the machine learning models like k-NN, SVM, ANN, and CNN.

Database Used

The leukemia dataset has been obtained from ALL-Image Data Base (IDB) publicly available online on Kaggle (Labati, *et al*., 2011). The dataset contains images of peripheral blood samples collected by the Research Center for childhood leukemia and hematological diseases, Monza, Italy. The colorant used in the preparation of the blood tends to concentrate only on white cells. All images of peripheral blood samples have been captured with an optical laboratory microscope coupled with a Canon PowerShot G5 camera. The images are related to different magnifications of the microscope (ranging from 300 to 500). All images are 24 bits with a resolution of 2592×1944 and in JPG format (Labati, *et al*., 2011). This data set contains microscopic blood cell images and is further divided into two sub-datasets. 1) Acute lymphoblastic leukemia-IDB 1 contains 59 healthy blood cell images and 49 blood cell images affected with leukemia; 2) Acute lymphoblastic leukemia- IDB 2 consists of 130 segmented ALL blast cell images and 130 normal cell images. Since there are a smaller number of images in the dataset data augmentations are done on those images to achieve a larger number of images for training and testing purposes of the model. IDB-1 has been used for machine learning models and IDB-2 has been used for CNN. The dataset details are given in Table 1.

Table 1. Details of Images Collected from the Database

Database	No. of Normal Cell Image	No. of ALL Cell image	Total Images
IDB-1	49	59	108
IDB-2	130	130	260

For training CNN, there is a total of 780 colored segmented images of size 64×64×3. Out of that 720 images (360 images for each ALL and normal image) are selected for training and 60 images (30 from each ALL and normal cell image) are used for testing. The training set is further increased to 740 by using additional data augmentation with shear and zoom operations.

The experimental setup for kNN is set with k=5. For SVM, linear kernel is used with L2 normalization. ANN is configured with three hidden layers, ReLU activation functions in hidden layers and Softmax at the output layer, and Adam optimizer. Similar to the weight initialization of ANN, the CNN model is initialized with 0 weights. The cross-entropy loss function is used for the model and the Adam optimizer is used to optimize the loss.

Results

In this paper, we have conducted experiments on the collected images to classify leukemia images from normal images using machine learning and deep learning algorithms, viz., kNN, SVM, ANN, and CNN. We have analyzed the performance of these models for binary classification in terms of four parameters: accuracy, sensitivity, precision, and F1 value.

Accuracy measures the total number of correct predictions and can be calculated by the following equation:

$$Accuracy = \frac{True\ Positive + True\ Negative}{True\ Positive + Flase\ Positive + True\ Negative + False\ Negative} \quad (9)$$

The precision depicts how accurate the model is out of the total predicted positive and it can be computed using the following equation:

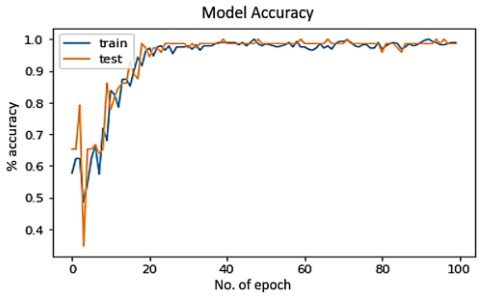

Figure 6. ANN model training and testing

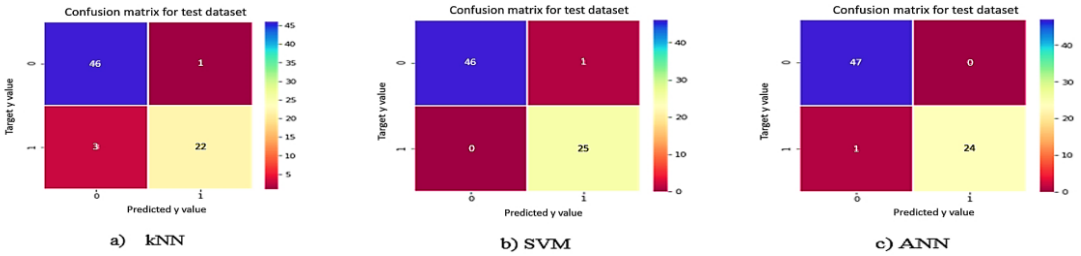

Figure 7. Confusion Matrices for Leukemia Cell detection a) kNN b) SVM c) ANN

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} \quad (10)$$

Recall or Sensitivity depicts how correctly the model can identify the true positive and it can be computed using the following equation:

$$Recall = \frac{True\ Positive}{True\ Positive + False\ Negative} \quad (11)$$

F1 score is the harmonic mean of precision and recall and can be calculated using the following equation:

$$F1\ Score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (12)$$

After pre-processing, the data augmentation is done by generating 3 extra sets of images by rotating each image into 90°, 180°, and 270° rotations. Finally, a total of 356 images (132 leukemia cell images and 224 normal cell images) are generated. The dataset is randomly divided into 8:2 ratios for training and testing, i.e. 80% of data are used for training and 20% of data are used for validation or testing. We have implemented kNN, SVM, and ANN for performance evaluation.

With k = 5, kNN achieved highest accuracy of 94.44%, precision 95.65%, recall 88%, and F1 score 0.92. With linear kernels, SVM achieved an accuracy of 98.61%, precision of 96.15%, recall of 100%, and F1 score of 0.98. The designed ANN is trained with a batch size of 100 and a learning rate of 0.001 for 100 epochs. The training and learning process of ANN is shown in Figure. 6. The ANN achieved an accuracy of 98.61%, precision of 100%, recall of 96%, and F1 score of 0.98. The performance of all three classifiers for classifying leukemia images and the normal image is summarized in Table 2. The confusion matrices are shown in Figure. 7.

Table 2. Performance Comparison

Models	Accuracy	Precision	Sensitivity	F1 Score
kNN	94.44%	95.65%	88%	0.92
SVM	98.61%	96.15%	100%	0.98
ANN	98.61%	100%	96.00%	0.98

Table 3. Performance of CNN

Classifier	Accuracy	Precision	Sensitivity
CNN	99.59%	94.68%	94.68%

Then, with a learning rate of 0.001, batch 100, and epoch 100, the CNN achieved an accuracy of 99.59%, precision of 94.68%, and Sensitivity of 94.68% as summarized in Table 3.

Discussion

From the extensive experiments with various machine learning and deep learning algorithm, it can be observed that all these algorithms are performing

quite well and more or less giving a similar performance. The LBP feature extraction method helped the algorithms like kNN, SVM, and ANN to accurately classify ALL and normal cell images. In (Singhal and Singh, 2014), LBP was used for feature extraction and SVM for classification. However, they extracted LBP features from the segmented blood cell images, whereas we extracted LBP features from the whole blood smear image without any segmentation process. Moreover, here, SVM performed better with higher accuracy of 98.61%. Here, the segmented blood smear images are used for the deep learning method. CNN extracts its features from the raw color image pixels on its own with no additional feature extraction method. While CNN achieved high accuracy of 99.59%, the sensitivity is slightly lower than that of SVM and ANN. High sensitivity is important in the medical diagnostic method for correctly identifying the patients who actually have cancer to ensure none of the cancer patients misses out on the treatment. Thus, with those criteria, SVM proved to be the best one among all with a sensitivity of 100%. There is a scope to improve the sensitivity and specificity of the CNN model. If we increase the number of epochs the sensitivity and specificity increase. However, it may also lead to overfitting with a small number of images for training and testing. With an extensive training dataset and a deep network, we can increase these values.

Conclusions

In this paper, we provided an automated method for Acute Lymphoblastic Leukemia detection from microscopic images. The automated method follows the steps such as image pre-processing, feature extraction, and classification. In this research, various machine learning and deep learning algorithms are exploited. For machine learning algorithms, the Local Binary Pattern (LBP) is used to extract features. The generated LBP histogram stores the statistical features of the image in every 256 values. The performances of kNN, SVM, and ANN are evaluated in terms of accuracy, precision, sensitivity, and F1 score. SVM and ANN equally performed well in classifying ALL cell images and normal cell images with an accuracy of 98.61%. Then, exploited the LeNet-5 architecture of CNN and evaluated the performance for classifying segmented ALL and normal cell images. For CNN, no hand-engineered feature extraction method is required as the convolution layer extracts the features from the raw image pixels. CNN achieved a high accuracy of 99.59%. In the future, with more training samples, various other deep learning models can be explored. However, an optimized model with the same level of performance is always preferable. Therefore, the proposed method for ALL detection has the potential to be applied practically in real-life data.

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