

How to Cite:

Ramya, V. J., & Lakshmi, S. (2022). Comparison of classification techniques in the diagnosis of acute myelogenous leukemia. *International Journal of Health Sciences*, 6(S1), 11248–11256. <https://doi.org/10.53730/ijhs.v6nS1.7759>

Comparison of classification techniques in the diagnosis of acute myelogenous leukemia

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Abstract--The leukemia blood cell discriminates from other blood cells by geometrical structure and cellular material by hematologist with microscope. In conventional color imaging system, the granular region in leukemia cells classify false negatively by experts due to micro geometrical and morphological changes in leukemia cell. Hence, a computer aided decision support system (CADSS) employs for automatic classification of leukemia blood cells. This paper gives the comparative study of various methods of classification of Acute Myelogenous Leukemia (AML) with improved accuracy and their results are compared. In this paper, the classification techniques such as Convolutional Neural Networks (CNN), Support Vector Machines (SVM), Fraction Black-Widow Optimized Neural Network (FB-NN), Deep CNN with Arithmetic Optimization and Hybrid Convolutional Bi-LSTM based RNN are made with blood microscopic images, in which according to measures, Deep CNN with Arithmetic Optimization has the best accuracy.

Keywords--Leukemia, Fractional Black Widow, Arithmetic Optimization, Modified DRLSE.

Introduction

Leukemia cancer cause due to abnormal cell production and normal blood cell production suppression. The abnormal cell transformation causes due to stem cell with no self-renewal. The normal blood cell elements replace by clonal expansion, diminished apoptosis and abnormal proliferation due to malignant cell transformation. The leukemia classifies based on morphologic, genetic, clinical and immunophenotype. The leukemia sub classifies as Acute or chronic based on leukemia cells present in bone marrow, myeloid or lymphoid with respect to

malignant cell lineage. The acute leukemia comprises of poor and immature cell and sub classify as acute myeloid leukemia and acute lymphoblastic leukemia. The chronic leukemia form by combination of acute and mature cells. The myeloid leukemia cause due to hematopoietic stem cell formed by immature white blood cell at DNA level. Generally, the detection of leukemia process takes more time with less accuracy and also complexity increases. Hence different classification methods are proposed for the detection of AML.

Leukemia Classification Methods

The initiative of this paper is to compare three methods of segmentation and classification techniques that differentiate between normal and leukemia cells.

Methods are:

No.	Segmentation	Classification
1	Adaptive Fuzzy Entropy (AFE) Model	Fraction Black-Widow Optimized Neural Network
2	Modified Distance Regularized Level Set Evolution (DRLSE)	Deep CNN with Arithmetic Optimization
3	Minimum Spanning Tree Algorithm	Hybrid Convolutional Bi-LSTM based RNN

First method

Initially, the blood microscopic image is pre-processed with a filter to remove the noise. Then it is segmented by the combination of Fuzzy C-Mean[1] and Active contour-based model[2].

Following segmentation, this part extracts statistical and image-level characteristics. The feature extraction process converts the supplied data into a collection of features. The performance of the classifier determines which features are chosen, and it is a crucial step in making the right choice. Statistical as well as image-level characteristics are retrieved, according to [3]. Colour, shape, texture and grey level co-occurrence matrix (GLCM) data are retrieved in particular. Because of its compactness, AML's shape properties are its most crucial attributes. The nucleus form, according to the haematologist, is a key element for haematologists to distinguish themselves. Each feature is taken from the nonzero pixels that represent the nucleus region.

The Artificial Neural Network (ANN) is used for classification. To enhance the accuracy, a variation of Black Widow algorithm[4] such as Fractional Black Widow Optimization (FBWO) is framed by adding fractional term to the Black widow algorithm[5]. The algorithm is implemented using MATLAB.

With the use of Fractional Black Widow based Neural Networks, normal and aberrant Acute Myelogenous Leukemia is classified. The Artificial Neural Network (ANN) is a crucial component of artificial intelligence in this situation. The ANN [21] is a powerful tool for solving complicated pattern recognition, system

identification, and optimization problems. In ANN, weights are present in three layers: input, output, and hidden. The common features produced via feature extraction, such as statistical and image-level properties, are fed into the ANN's input, and the neurons process the data. Each Neural Network (NN) has its own input-output and activation function, as well as its own categorization architecture. The ANN architecture is employed in this part to solve the problems. However, because to inappropriate hidden layers and weights, a traditional ANN does not produce the expected output. As a result, we applied the Fractional Black Widow Optimization (FBWO) method in tandem with ANN. As a result, the FBWO improves the performance of ANN for Acute Myelogenous Leukemia detection in terms of the hidden layer parameter and its weights. The detection performance is analysed using an ANN model, with Eqn describing the summation function (1).

$$I_R = \sum_{R=1}^N W_{nR} X_R + a_n \quad (1)$$

The entire input, or net, is I_R . The amount of inputs to the R^{th} neuron is N , according to the forward layer. The weight of the n^{th} neuron is W_{nR} connected in the forward layer.

The bias function for the R^{th} neuron in the preceding layer is a_n and the input is X_R . The activation function transforms the net input into an O_R output. The trial and error is done through the activation function. The ANN chooses different types of activation functions based on the hidden and output layers, then gives a minimum mean square error (MSE), and it frequently favours network training in connection weight computation. After using the quasi-random weights and the gradient descent approach, the FBWO algorithm optimises a few convergence values. Finally, the FBW-NN shown in figure 1 can distinguish between normal and a typical Acute Myelogenous Leukemia patients.

Steps in FBWO Algorithm

1. Initialization of Black Widow Spider Population
2. Calculate the number of reproductions depending on the procreating rate
3. Elimination based on Cannibalism
4. Calculate the mutation children depending on the mutation rate
5. Convergence and Return to the best solution

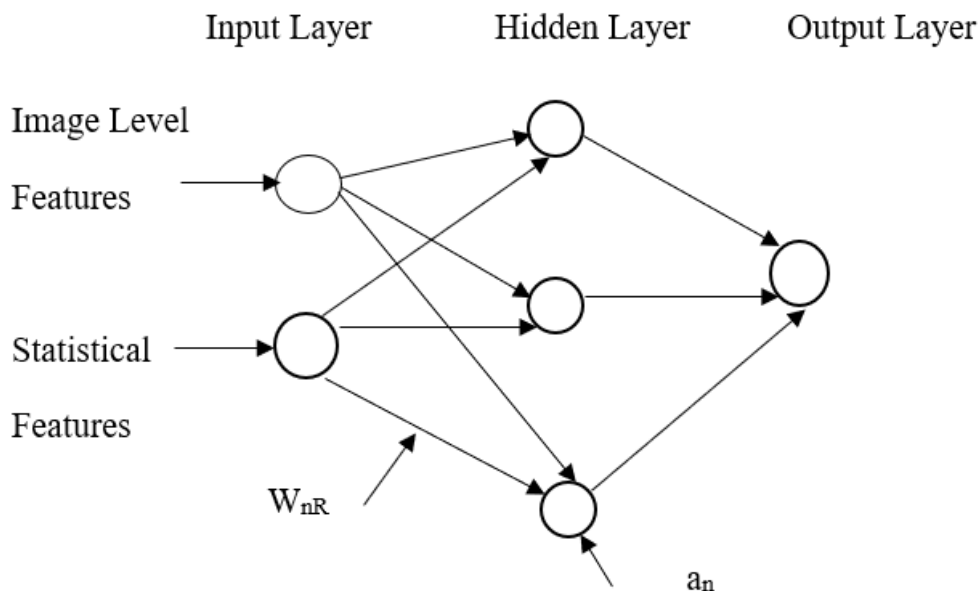


Figure 1: Detection of AML using FBW-NN

Second method:

The modified distance regularised level set evolution (DRLSE) technique is used to segment the nucleus as well as the masked cell picture. The DCNN then performs feature extraction and classification in order to recognise both normal and AML-infected pictures. The arithmetic optimization approach improves classification accuracy and performance. The analysis is done using images from the Munich AML Morphology Database and the performance is calculated using criteria like accuracy, precision, sensitivity, and specificity.

When compared to the standard level set technique in terms of initialization, the distance regularised offers various advantages. When both weak and sharp edges occur in different parts of the nucleus, it indicates that the nucleus segmentation is incomplete. When a weak boundary occurs in conjunction with minor concentration changes, the edge indicator is unable to accurately identify the boundary, resulting in erroneous segmentation. As a result, for enhanced segmentation, this study advocated including the Region scalable fitting (RSF) idea into the DRLSE [6]. Because it accounts for regional intensity information, RSF-based segmentation works in weak edges, but it suffers from the re-initialization process [8]. When RSF[7] is applied to the DRLSE, the time and computational complexity are increased [9].

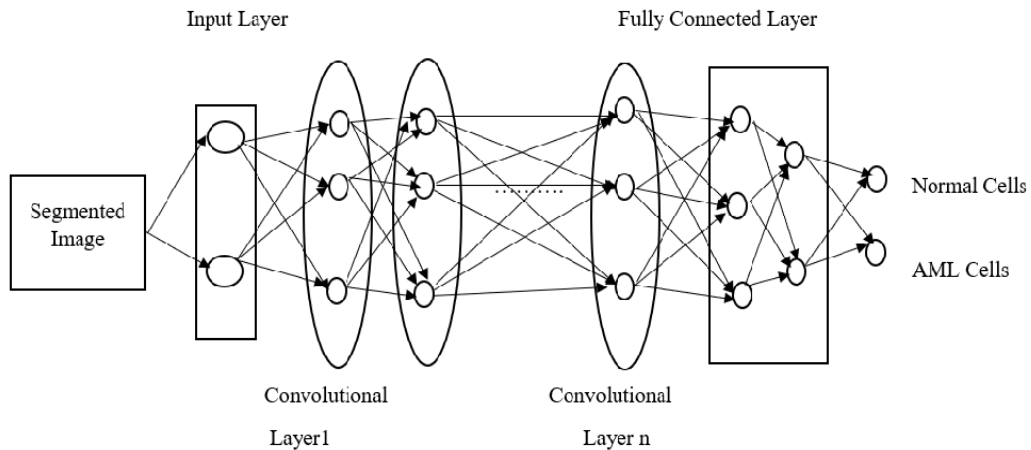


Figure 2: Detection of AML using DCNN-AOA

Figure 2 shows the topology of the AML classifier detection structure. The ideal weights are determined through optimization, resulting in accurate classification results. The DCNN's core framework is briefly outlined [10]. Deep CNN is a refined kind of CNN, and hence deep learning is fostered. Convolutional layers, fully linked layers, and pooling layers make up a deep CNN. The features are retrieved from the segmentation data and then sent to the convolutional layer. The convolutional layer aims to improve AML map's categorization. The feature map then tolerates subsampling in the pooling layer, and the fully connected layer finally performs the AML classification. The output collection is given by factors of weight-based kernel for each layer.

Deep CNN uses the arithmetic optimization approach [11] to improve its performance. This optimization approach is used to increase both the classification accuracy and the classification outcomes. Using an appropriate number of random solutions as well as optimization repetitions, the global optimal solution is found. Exploration and exploitation are the two fundamental steps of the optimization method. The exploration stage refers to the algorithm search agents' broad exposure of the search space in order to ignore local solutions. The exploitation step improves the precision of the solutions that have been acquired. Using arithmetic operations like addition (A), subtraction (S), multiplication (M), and division (D), the exploitation and exploration stages are obtained (D).

Third Method

The weight estimate guideline incorporated by the minimal spanning tree (MST) image segmentation approach[12] was proposed in this study. The FH segmentation process is merged and improved in this case by using the RGB variation formula for angular distance colour as the judge standard weight segmentation. The stability and applicability are increased by taking into account not only the variable sensitivity of human eyes based on RGB values, but also the vector connection and the spatial distance between the two pixels.

The CA-Conv-BiLSTM technique [13] includes a feature extraction portion, a class attention learning layer, and a bidirectional LSTM-based recurrent sub-network. The feature extraction strategy, in particular, makes use of an interleaved pooling stack and Convolutional layers to separate high-level features before passing them on to the class attention learning layer, which creates class-specific features. The probabilistic class dependencies are represented by a bidirectional LSTM-based recurrent sub-network.

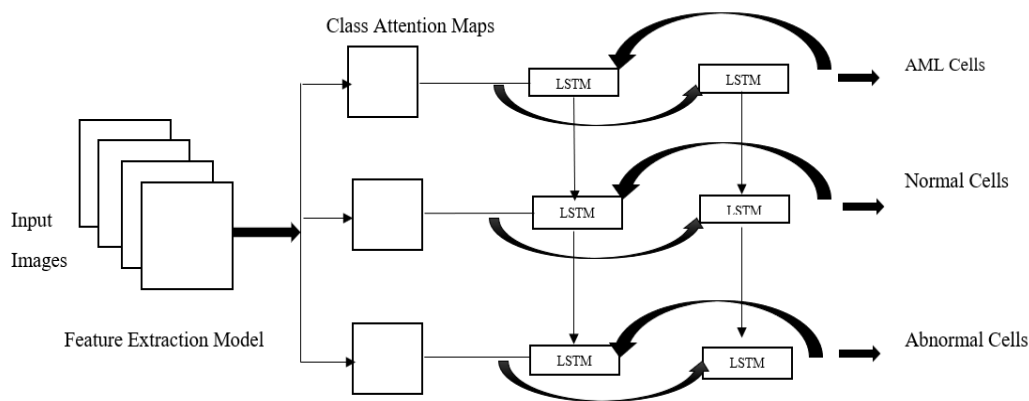


Figure 3: Detection of AML using Bi-LSTM RNN

Extraction of detailed high-level features

The categorization of photographs relies heavily on an adequate depiction of the input images. For the extraction of specific features, a typical method is to use the CNN framework [14]. As a result, the technique tweaks VGG-16 to improve its elegance and ability to extract advanced characteristics. As shown in Fig 2, the feature extraction process is made up of 5 convolutional blocks, each of which is made up of 2 or 3 convolutional layers. The filter number is the same as the convolutional block number, and it relates every pooling layer that is used to reduce the feature map spatial dimension. This model is used to simplify the feature extraction strategy in order to uncover distinct features.

The total accessible area of the convolutional filters is 3x3, which increases feature extraction non-linearities. Every convolutional layer's spatial padding is also 1 pixel. Max-pooling layers are interleaved between the convolutional blocks to reduce the feature map size while keeping the local representative maximum in the 2x2 pixel region. High-level and semantic features are learnt directly from the standard CNN. Although the spatial resolution has been reduced, this is not conducive to the creation of high-dimensional qualities in the next layer of class attention learning.

The last two convolutional blocks' max-pooling layers are removed in this technique, and convolutional filters with a dilation rate of 2 are used in the final convolutional block to preserve the unique sympathetic area. As a result, when compared to VGG-16 [15], the feature extraction approach can comprehend high-level properties with superior spatial resolution, dubbed dense. Furthermore, CNN architectures are supplied for the feature extraction process prototypes, and

therefore the research is extended to Google Net and ResNet for a thorough evaluation of CA-Conv-BiLSTM

Performance metrics used in the evaluation

The performance metric is based on the classification's possible outcomes: true negative, false positive, true positive, and false negative. Specificity, accuracy, precision, and sensitivity are examples of categorization performance metrics. The suggested technique is evaluated using the following criteria.

Accuracy: It indicates the illnesses that were correctly identified across all samples in the datasets. It describes how the technique reconstructs the high-resolution image correctly or incorrectly.

$$Accuracy = \frac{TrPo+TrNe}{TrPo+TrNe+FaPo+FaNe} \quad (2)$$

Specificity is defined as the true positive rate that the classifier reliably detects while testing. It's written like the expression below.

$$Specificity = \frac{TrNe}{TrNe+FaPo} \quad (3)$$

Precision: It is a key measure for determining exactness, and it is expressed as a positive number that corresponds to the total number of positive predicted instances as shown below.

$$Precision = \frac{TrPo}{TrPo+FaPo} \quad (4)$$

Sensitivity: It's a true positive that the classifier correctly detects during testing. The following equation expresses this.

$$Sensitivity = \frac{TrPo}{TrPo+FaNe} \quad (5)$$

Table 3 shows a comparison of the proposed classifiers with known classifiers such as SVM and CNN and Figure 4 shows the performance analysis of the given classifiers.

Table 2
Performance measures of different Classifiers

Methods	Accuracy	Specificity	Precision	Sensitivity
CNN	94.30%	83.67%	78.12%	90.34%
SVM	96.85%	97.24%	93.41%	88.75%
FBW-NN	96.56%	97.81%	96.90%	97.20%
Bi-LSTM based RNN with SMOA	97.95%	93.72%	94.64%	95.12%
DCNN-AOA	98.27%	97.91%	96.95%	98.04%

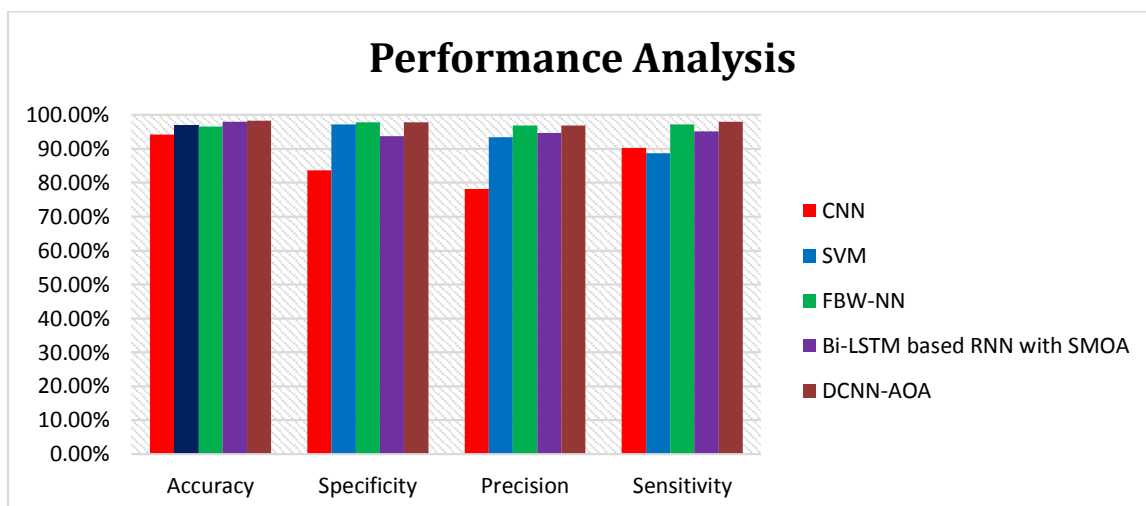


Figure 4: Performance Analysis of different Classifiers

Conclusion

This paper focuses primarily on the identification of acute myeloid leukaemia and classifies AML cells into normal and abnormal. To increase the image quality, the pre-processing procedure is used. Both the nucleus and the cell mask are segmented using the segmentation procedure. The classifier's input is comprised of the features obtained during the feature extraction method. This paper compares the three classification methods with SVM and CNN [16]. With all the results compared, the Deep CNN with Arithmetic Optimization algorithm is the best having the high accuracy. The Munich AML morphology database [17], which contains 120 photos, is used to assess the effectiveness of this strategy. Sensitivity, specificity, accuracy, and precision are some of the performance indicators that are used to estimate the detection process.

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