# **Improved Bare-Bones Artificial Bee Colony Optimization (IBB-ABC) and Enhanced Ensemble Classifier for Leukemia Diagnosis**

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#### ABSTRACT

In medical image processing, an emerging and noticeable area of research is leukaemia detection, which is a malignant neoplastic disorder. Recent works proposes an edge and ensemble classifier techniques to classify Leukaemia Diagnosis. Highly discriminative characteristics are identified using Bare-bones with Adaptive Bat Optimization (BBABO) and classification is also done by using ensemble based techniques. However, classifier accuracy is not enhanced up to the required level in the enhancing results of segmentation, the new classifiers are developed. An intelligent decision support system is proposed using microscopic images. Highly significant discriminative characteristics of blast and health cells are identified using Bare-bones with Adaptive Bat Optimization (IBB-ABC) for enabling effective ALL classification. Accelerated differential evaluation functions mechanisms of bee position update is incorporated in IBB-ABC variant for expanding search and original BBABC algorithm's premature convergence is eased. Online Learning with Enhanced Support Vector Machine (OLERSVM), RBF network (RBFNets) and Improved Convolutional Neural Network (ICNN) are used for classifying blasted and healthy cells. Various Average rule is used for combining ensemble of classifiers. Proposed classifier's experimentation results are compared with various leukaemia detection methods. On leukaemia image collections, with respect to f-measure, accuracy, recall and precision, better performance is shown by proposed method as demonstrated in qualitative and quantitative analysis.

**KEYWORDS:** Feature selection and image processing, improved bare-bones artificial bee colony optimization (IBB-ABC), Ensemble Classifier, acute lymphoblastic or lymphocytic leukaemia (ALL) diagnosis

Article Received: 18 October 2020, Revised: 3 November 2020, Accepted: 24 December 2020

#### **1. INTRODUCTION**

The bone cavity consists of marrow, which is a flexible and soft tissue, which generates, millions of blood cells in every day. Bone marrow produces three blood cell classes substantially and they are called, leukocytes, erythrocytes and platelets (white blood cells-WBC). Operation of human immune system is depends on WBC. Acute lymphocytic leukaemia is a cancer class which occurs in white blood cells. When compared with adults, children are highly affected. Chronic myeloid leukaemia (CML), chronic lymphoblastic leukaemia (CLL), acute myeloid leukaemia (AML), and acute lymphoblastic leukaemia are the most common type of leukaemia [1, 2]. Major health problem is caused by cancer frames in recent days. Major cause of death in foreign countries is cancer. Around 1:3 males and 1:3 females are suffering from cancer in their lifetime. Various examiners like chemists, biologists, malignant neoplastic disorder and grasping cancer are the major front line research area. Various diseases group defines cancer and every group has its own growth rate, treatment and cue [3,4,5].

The abnormal cells with unsuppressed growth is identified as cancer and proper treatment should be given. For leukaemia diagnosis, various techniques are proposed in past ten years. New technique using edge enhancement and detection is introduced in recent work, which enhances concerned regions visibility and perceptibility. Online Learning with Enhanced Support Vector Machine (OLERSVM), RBF network (RBFNets) and Improved Convolutional Neural Network (ICNN) are used for classifying blasted and healthy cells in proposed work.

Average rule is used for combining ensemble of classifiers [7,8]. However, classifier accuracy is not enhanced up to the level. So, for enhancing results of segmentation, new classifiers need to be developed. For acute lymphoblastic leukaemia (ALL) diagnosis, an intelligent decision support system is proposed using microscopic images [9].

Highly significant discriminative characteristics of blast and healthy cells are identified using Bare-bones with Adaptive Bat Optimization (IBB-ABC) for enabling effective

ALL classification. Accelerated differential evaluation functions mechanisms of bee position update is incorporated in IBB-ABC variant for diversifying search and original **BBABC** algorithm's premature convergence is relieved. Online Learning with Enhanced Support Vector Machine (OLERSVM), RBF network (RBFNets) and Improved Convolutional Neural Network (ICNN) are used for classifying blasted and healthy cells. Various Average rules are used for combining ensemble of classifiers.

#### **2. LITRATURE REVIEW**

Lu, et al [2014] used specifically devised trace-based separability criterion for developing genetic algorithm (GA) based novel feature selection algorithm. Independent of any specific classification, feature subset significance is measured using variable separability and class separability scores. For classification, between variables, used a mutual information matrix and it does not require any prior knowledge about feature subset cardinality. Standard lung cancer dataset is used for experimentation.

Three various classifiers like K-nearest neighbour (KNN), back-propagation neural network (BPNN) and support vector machine (SVM) are used for verifying obtained solutions and compared with those obtained by whole feature set, F-score and correlation-based feature selection techniques. Better diagnosis performance is exhibited by proposed intelligent system as shown in comparison and for diagnosing lung cancer, it can be used as a promising tool.

Negm, et al [2017] identified leukaemia cells using a decision support system which includes selection of panel, K-means clustering based segmentation, extraction of features and refinement of images. After the successful identification of cells with its internal structure by decision support system, based on morphological features, classifications of cells are performed by this system. Public dataset is used for testing this decision support system and identification of specific cell is tested. Comparison is made with various other methods. The algorithm testing this dataset demonstrated an overall using accuracy of 99.517%, the sensitivity of 99.348%,

and specificity of 99.529%. Therefore, this algorithm yielded promising results and warrants further research.

Li et al [2018] selected informative genes combining enhanced recursive feature by elimination technique and highly effective implementation of linear support vector machines. Dataset is pre-processed using a proposed simple re-sampling technique, it makes balanced information distribution of various sample types and more credible results of classification are produced. This work also studies, four common classifier's applicability. Six most frequently used microarray datasets of this field is used for conductive experimentation. Computation time is greatly reduced by this method as shown in experimentation with comparable classification performance.

et al [2014] discriminated Mohapatra, lymphoblasts (malignant) and lymphocytes (normal) of bone marrow samples and stained blood smear using a quantitative microscopic technique. ALL's computer-aided screening development is also assisted using it. Over stained films images, classification, blood feature extraction and image segmentation are performed for accomplishing automated recognition of lymphoblasts. An ensemble classifier, prominent features, enhanced segmentation techniques are used for obtaining ALL's Accurate and authentic which facilitates rapid diagnosis, patients screening. Observed the results of experimentation and around 99% of accurate results are obtained when compared with standard classifiers like support vector machines (SVM), radial basis functional network (RBFN), multilayer perceptron (MLP), K-nearest neighbour (KNN) and naive Bayesian (NB).

Mishra, et al [2017] introduced a half and half plan for distinguishing proof and order of ALL. The recommended conspire uses 2D-SWT to remove the surface highlights from the blood smear. Later on, the removed highlights are taken care of to SVM classifier to get the arrangement results. The exploratory outcomes for leukaemia grouping show that the recommended strategy beats other standard classifiers with respect to precision. The exactness is seen as 99.56% with the assistance of SVM-R classifier.

Hsieh et al [2010] introduced a technique for ordered the disease with the Leukaemia malignancy of clinical demonstrative information. Data gain has been adjusted for highlight determinations. A Leukaemia malignant growth model that uses Information Gain dependent on Support Vector Machines (IG-SVM) strategies and improvements to assess, decipher the disease characterization. The test results show that the SVM model represents the most noteworthy precision of characterizations for Leukaemia malignant growth.

Mohapatra, et al [2016] investigated the utilization of picture morphometry and design acknowledgment strategies subtyping for leukaemia lymphoblasts according to French-American–British grouping. Dependable characterization results were acquired utilizing the division strategy, conspicuous strong morphological highlights and a troupe of classifiers. To assess the presentation of the proposed strategy, relative report is a acknowledged accessible picture over the informational collection.

The characterization rates accomplished with the standard classifiers, that is guileless Bayesian, K-closest neighbour, multilayer perceptron, probabilistic neural system and bolster vector machines, were contrasted and that got utilizing a troupe of classifiers. It is seen that the characterization rate is improved with the utilization of various classifier gathering and is relied upon to help clinicians in making the indicative procedure quicker and increasingly exact.

#### 3. PROPOSED METHODOLOGY

Leukaemia detection based on proposed model is discussed in this section. Major objective of this work is to provide an effective system for leukaemia detection.

There are seven components in this model. From blood smear images, White Blood Cell (WBC) Identification based on marker-controlled watershed segmentation is performed in first stage. Identified WBC is pre-processed using an improved median filtering to remove noises in second stage, with image enhancement via Enhanced linear contrast stretching.

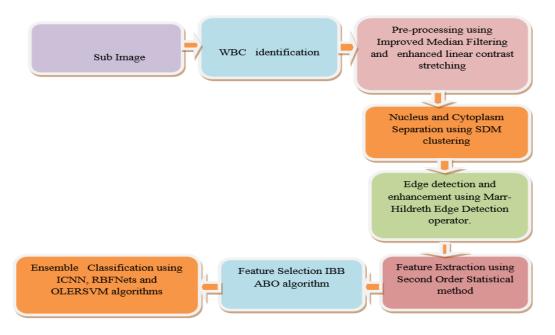


Figure: 1 Architecture of the proposed system

In pre-processing, clustering algorithm based on stimulating discriminate measure (SDM)

is used for separating cytoplasm and nucleus in third stage. Marr-Hildreth Edge Detection is used

in fourth stage for edge enhancement and detection. Second order statistical features are extracted in fifth stage. Bare-bones with Adaptive Bat Optimization (IBB-ABC) is used in sixth stage for selecting features and Online Learning with Enhanced Support Vector Machine (OLERSVM), RBF network (RBFNets) and Improved Convolutional Neural Network (ICNN) are used in seventh stage for classifying blasted and healthy cells. Average rule is used for combining ensemble of classifiers. Figure 1 shows proposed work's overall architecture.

## **3.1. White Blood Cell Identification Using Marker Controlled Watershed Segmentation**

Better performance of watershed transforms is obtained in segmentation, if background locations and foreground objects are marked. Following fundamental process is adapted in. Markercontrolled watershed Segmentation.

- 1. Computed a segmentation function for forming image, which indicates objects needs to be segmented with dark areas.
- 2. Compute foreground markers, which indicates pixel's linked blobs appears inside every objects.
- 3. Compute background markers which includes the pixels that are not included in any object segments.
- 4. Change the function of segmentation, so that, at background and foreground marker locations, it has minimum value.
- 5. Compute modified segmentation function's watershed transform.

## **3.2. Improved Median Filtering For Noise Removal**

For an effective classification, from segmented WBC, eliminated the noise after identification of WBC using improved median filtering.

#### Improvements of the median algorithm

In random noise filtering, better performance is exhibited using average filter. To a specific filtering mask size, average filter is combined with media filter. Noises can be eliminated using this novel method and in a better way, image details can be preserved.

#### **Improving ideas:**

In the mask, median value is used for substituting pixel's actual value and in next computation process, out of new pixel values, average value may reap the best advantage. An iterative process is generated using this. This results in better noise-elimination effect and reduces the complexity of time.

#### a. Contrast Stretching

#### Piecewise Linear Contrast Stretch Based On Unsharp Masking (PLCSUM)

For leather image enhancement, introduced a piecewise Linear Contrast Stretch Based on Unsharp Masking (PLCSUM) method in this paper. Unsharp masking (UM) is basic type of image manipulation technique. In enhancing detailed appearance, major role is played by Unsharp masking technique and it uses, image's edge contrast's minute enhancements. In general, image sharpening is done using Unsharp mask and in affirming image details ad image texture, this very useful. Traditional unsharp masking algorithm is expressed as,

$$z = n + \gamma(m - n) \tag{1}$$

Where, input image is represented as m, result of linear low-pas filter is represented as n, gain is represented as U and its value is >0, that means it is a real scaling factor. For maximizing sharpness, frequent amplification of signal d = m-n is done. There are image noise, details, undershoots and over-shoots in a sharp edge region, which is a result of smooth edges are there in signals.

For the enhancement of leather image, designed unsharp masking framework is presented in this work.

Generalization of unsharp masking algorithm integration with adaptive contrast stretching function forms the base for this framework on halo effect problems resolved using edge preserve filter. Another process called adaptive contrast stretching algorithm is used for sharpening and enhancement concept of this work and output is represented as w(y). With g (d) =  $\hat{U}$ (d) od, performed image details processing, where, adaptive control gain is represented as d and it is a amplitude function of d's detail signal. Algorithm's final outcome is represented as,

$$u = w(y) + [\gamma(d) + d]$$

From enhanced WBC image, it is needed for isolating nucleus-cytoplasm using clustering algorithm based on stimulating discriminate measure (SDM) after image enhancement.

#### b. Nucleus-Cytoplasm Separation Using Stimulating Discriminate Measure (SDM)-Based Clustering

### Segmentation of nucleus and cytoplasm for leucocytes

For identification of disease, cytoplasm and nucleus isolation on every detected WBC is done using a clustering algorithm based on SDM in this research work.

In this condition, in a cluster, presented data samples are indicated by every pixel and at one point of time, pixel should be a member of one cluster. Chromosome evaluation is performed after separating pixels, where, SESDM and SBSDM are used for computing chromosome fitness, F (Si), which is expressed as,

$$F(S_{i}) = \begin{cases} \frac{SW_{sdm} + \alpha}{SB_{sdm}} \\ \frac{SW_{sdm}}{SB_{SDM}}, & otherwise \end{cases}$$
 if constraints not met (3)

Major objective is to produce large SBSDM for high isolation between clusters and small SWSDM for high similarity degree for within-cluster evaluation. As mentioned before, there exist a situation where, very close pixel intensities of cytoplasm and nucleus. So, in both clusters isolation, much high degree of difficulty is indicated.

In segmentation process in this situation, two constraints are used for assistance. They are, nucleus/cytoplasm area should not be lesser than 10% of corresponding cytoplasm/nucleus region, and background area should not be greater than region enclosing entire membrane (nucleus + cytoplasm). For enhancing F (Si), used a penalty value, \_, if constraints are not satisfied.

- c. Marr-Hildreth Edge Detector Algorithms for Edge Detection :
- Gaussian is used for smoothening the image.

• Smoothed image is applied with twodimensional Laplacian (often first two steps

(2) nges are identified by looping through the result. Edge is marked, if there exist a sign change and threshold value is less than slope across sign change.

- It is possible to run Laplacian results through a hysteresis similar to Canny's edge detection for producing better results and it differs from first implementation of edge detector.
- d. Feature Selection Using Improved Bare-Bones Artificial Bee Colony Optimization (IBB-ABC)

Honey bees origin behaviour is inspired in ABC algorithm and there are three types of bees in this algorithm. They are, scout, onlooker and employed bees. Food source size is doubled to form a colony's population. Optimization problem's possible solutions positions are represented using food sources count and associated solutions quality is represented using food source's nectar amount. Food source exploitation is done using employed bees and information about food source's nectar quality which is exploited b it is passed to onlooker bees.

Count of employed bees and onlooker bees are similar. According to the information received from employed bees, an onlooker bee makes a decision about the food source to be exploited. Exhausted food sources employers become scout and they search randomly to find new food sources [17,18, 19]

According to Gauss ion distribution, location of barebone ABC search is chosen. Dimensionality term is eliminated using it and there is not D parameter. In BABC, particles new positions are generated using sampling.

A feature is allocated to every employed bee and from objective  $f_i$ , feature fitness is evaluated using below expression,

$$fit_i = 1/(1+f_i)$$
 (4)

Information is gained by onlooker bees from employed bees and feature's selection probability is computed using below mentioned expression as,

$$P_i = \frac{fit_i}{\sum_{i=1}^m fit_i} \tag{5}$$

Then onlooker bee uses, feature's predictive accuracy, which pointed by employed bee for computing new solutions and according to Gaussian sampling, selected onlooker bee features. Feature subset is pointed by employed bee, if new solution  $v_i$  is greater than  $x_i$  and neglect the newly selected feature. Below mentioned expression is used for computing new solution  $v_i$  as,

$$\mathbf{V}_{i} = \mathbf{N}\left(\frac{x_{i}+x_{j}}{2}\left|x_{i}-x_{j}\right|\right) \tag{6}$$

Were, Gaussian distribution is represented as (·) and it has  $\frac{x_i+x_j}{2}$  mean and  $x_i - x_j$  standard deviation.

Algo	rithm 1 Pseudo-code for the implemented algorithm							
1:	procedure ABC (SN;Limit;MCN)							
	Initialize							
2:	Create SN solutions							
3:	while cycle < MCN do							
4:	Employed bees phase (SN)							
Scout bees phase:								
5:	if trial i > Limit then							
6:	create random solution							
7:	end if							
8:	Onlooker bees phase (SN)							
9:	end while							
10:	end procedure							

#### Figure: 2. ABC Algortihm

In complex multimodal problems solving, premature convergence effects ABC because of intrinsic randomness. In some cases, global optimum may be near to sub optima and global optimum may be contained in trapped particles neighbourhood. In this situation, for getting better solutions, particles neighbours may be searched. Different algorithms are applied with few neighbourhood search strategies according to this concept.

Optimization problem's possible solutions positions are represented using food sources count

and associated solutions quality is represented using food source's nectar amount. In population, solutions count and employed bees count are similar. Generated positions of food sources which means initial positions of population in random distribution manner.

Repeated cycle of search process by employed, onlooker and scout bees are started after initialization. In memory of employed bees, source position modification is produced and new position of food source is discovered. New source position is memorized by bees, if new one is having high nectar amount than previous source and position of previous one is forgotten. Else, position of previous source is maintained in memory [21].

Sources position information is shared with onlooker bees via dancing after completing search process by employed bees. Nectar information is evaluated by every onlooker bees which are received from employed bees and based on sources nectar amount, food source is selected. At the same instant, employed bee modifies e position of source in its memory and computes its nectar amount. New source position is memorized by bees, if new one is having high nectar amount than previous source and position of previous one is forgotten. Compute t abandoned sources ad randomly produce new sources for replacing the abandoned ones using artificial scouts [22].

#### e. Classification Using Ensemble Classifiers

Online Learning with Support Vector Machine (OLSVM) and network (RBFNETS) are combined in this work for proposing an ensemble classifier. Online Learning with Enhanced Support Vector Machine (OLERSVM), RBF network (RBFNets) and Improved Convolutional Neural Network (ICNN) are combined to form an ensemble of classifier. Healthy and last cells are classified using an average rule.

### Improved Convolutional Neural Network (ICNN)

There are three conventional layers classes in a classifier based on CNN for classifying leukaemia as like in general convolutional neural network. They are full-connected, pooling and convolutional layers, which are shown in figure 1. These three layers are hierarchically involved in network architecture, where, learnable filters are stacked with convolutional layer and fixed stride layer by layer is stacked with pooling layer. The 8channel selected features are given as an input to network and probability vector showing predefined class of input signal is produced at the output.

For automatic feature extraction, trainable kernels are convolved with 8-channel input features using intermediate 1D convolution layer feature maps presents activation are and propagated in a forward manner. From convolution layer, feature maps are down sampled using max pooling layers and within the predefined front feature maps stride, maximum value is used for activation. In forward-propagation, significant features are highlighted using max-pooling, after doing dimensionality reduction. From input signals, derived features are classified using bottom fully-connected layers and inference is determined using probability vector produced by it [23-24].

A special type of RBF neural network is fully connected feed-forward networks. There are three layers in it, namely, output, hidden and input layer. Input vector dimensions count defines the input layer neurons count and in data, class label count defines the output layer neurons count. Network topology is determined by hidden layer neurons count and between data clusters, decision boundaries are also determined using this count. There exist an RBF activation function in every hidden neuron and between input and stored prototype in that neuron, similarity is computed using this unction.

Highly accurate results are produced by highly complex boundaries which are resulted from more prototypes. But, for evaluating network, it requires more computations. The RBF network structure is shown in figure 3. Euclidean distance between prototypes stored in hidden neurons and input layer are represented using arrows between hidden neurons and input layer in RBF network as shown in that figure. However, i hidden nodes of RBF network, activation functions are Gaussian basis functions.

#### **RBF** network (**RBFNets**):

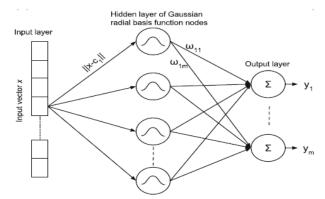


Figure: 3 Representation of ANN networks a RBF Networks

Working process of RBF ANN is given as, through an input layer, input data enters the network. Between prototype and input data, similarity is computed by every neurons in hidden layer, so called, RBF layer and nonlinear Gaussian function is used for storing it, which is expressed as,

$$\emptyset(\|\mathbf{x} - \mathbf{c}_{j}\|) = \exp - \left(\frac{\|\mathbf{x} - \mathbf{c}_{j}\|^{2}}{2\sigma_{j}^{2}}\right)$$
(7)

Where,  $||x - c_i||$  represents Euclidean norm.

Weighted average technique is used for computing RBF output as,

$$y_i = \sum_{j=1}^n \omega_{ji} \emptyset_j(x) \tag{8}$$

Where, weight between output layer and hidden layer is represented as  $\omega_{ji}$  and hidden nodes count is represented as n.

If similarity between prototype and input is large, then RBF neuron output is close to 1 else, it

(1

will be close to zero. For deciding class label, every RBF neuron output's weighted sum is taken by output layer neurons. It indicates that, in labelling the decision, contribution of every RBF neuron is considered. Huge contribution is made with RBF neuron having high similarity.

### Online Learning with Enhanced Support Vector Machine (OLERSVM):

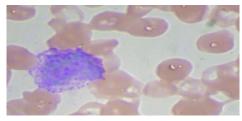
#### **Online SVM Learning Algorithm**

On flow, data is collected continuously by system as forecasted by short-term traffic flow conduction and in sequence, it returns to prediction model and then based on new collected sample, adaptive adjustment of model is done. **Hybrid GA** 

In OSVM, parameters  $\gamma$  and  $\sigma$  are optimized using GA with object value as accuracy of training.

#### **Ensemble Ling Using Averaging:**

With varied individual features or classifiers, various errors may be produced and by combining those models, overall error can be minimized via averaging. This is the basic concept behind ensemble technique. Major objective of ensemble learning is to enhance the performance of prediction or classification. In multiclass problems, these capabilities are not able to be shown by single model. In an ensemble, various methods are used combining individual networks results. for Averaging and voting are the two commonly used ensemble boosting, techniques. In better performance is shown by averaging, when compared with boosting.



**Figure 4: Input Image** 

- 1. N experts with own initial values are generated. From a distribution, these initial values are selected randomly.
- 2. Every expert is trained separately.
- 3. Experts are combined and their values are averaged.

The i<sup>th</sup> classifier computation using averaging technique as,

$$\alpha_{i} = \frac{\sum_{j} c_{ij}^{-1}}{\sum_{k} \sum_{j} c_{kj}^{-1}}$$
(9)

Where, correlation matrix c's inverse is  $C^{-1}$  is defined as,

$$C_{ij} = E\left[ (d(x) - f_i(x))^T (d(x) - f_j(x)) \right], i, j = 1, 2, ..., M,$$

Where, for a given  $inputx_i$ , desired output vector is represented as d(x) and from  $i^{th}$  network, actual output vector is represented as  $f_i(x)$ .

#### 4. RESULT AND DISCUSSION

The experimented result is carried out in proposed model. To implement the proposed work MATLAB is used. The leukemia image dataset is compared and gone through the test cases like Faccuracy, measure, recall, precision, proposedIBBABOEC(Improved **Bare-Bones** Artificial Bee Colony Optimization and Ensemble) and existing EDAEC (EDge methods and Ensemble Classifier), ESVM (Enhanced Support Machine), FNN Vector (Fuzzy Neural Network), SVM (Support Vector Machine), and NN (Neural Network) algorithm. The data set consist of 12,500 blood cell segmentation images with related with cell type labels. For every 4 various cell types, there are around 3,000 images, which are grouped with folders based on the type of a cell namely Neutrophil, Monocyte, Lymphocyte and Eosinophil.



Figure: 5: Threshold Opening and Closing Images

An additional dataset complements this dataset with 410 original images (preaugmentation) including two additional subtype labels (WBC vs WBC) with bounding boxes for every individual cell in all 410 images (JPEG + XML metadata). In specific, there are 410 blood cell images in folder 'dataset-master' including bounding boxes (JPEG + XML) and subtype labels. There are 2,500 augmented images in folder 'dataset2-master' with 4 additional subtype labels



Figure: 6: White blood cells segmented images

(JPEG + CSV). For every four classes, there are around 3000 augmented images compared with folder 'dataset-master' with 88, 33, 21, and 207 images.



Figure: 7. Colored Watershed Labelled Images

The input images are shown as Coloured labelled images using Marker Controlled Watershed is illustrated in figure 7.



Figure: 8. WBC identified image

The input image is the WBC detected images done with Marker Controlled Watershed segmentation is illustrated in figure 8.

For removing noise, input image is preprocessed using an improved median filtering and the enhanced Linear Contrast Stretching is used for

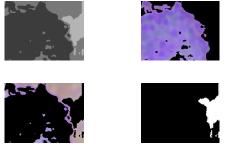
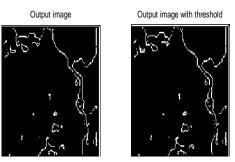


Figure: 10. Segmentation results



Figure: 9. Noise removal and enhancement result

enhancing input image, is illustrated in figure 9. In order to differentiate cytoplasm and nucleus, the pre-processed and segmentation is operated using SDM clustering model. Figure 10 illustrates the images of segmentation.



**Figure: 11 Edge Detection** 

TABLE: 2 Ferformance comparing the result values								
Method	Neural Network	SVM	FNN	ESVM	EDAEC	IBBABOEC		
Recall	54	61	63	70	75	80		
Precision	59	61	61	64	74	84		
Specificity	62	64	64	67	80	81		
F-Measure	60	62	62	65	77	82		
Accuracy	69	61	61	64	79	80		

**TABLE: 2** Performance comparing the result values

Accuracy performance metric comparison results between existing EDAEC, ESVM, SVM, NN and proposed IBBABOEC technique is shown in figure 19. Around 84% of Precision results are produced by proposed IBBABOEC technique,

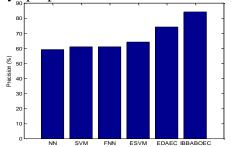


Figure: 13. Precision results of different method

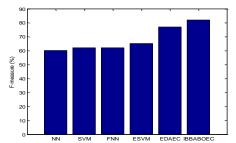


Figure: 15. F-measure results of different method

F-measure results of ESVM, 62% Fmeasure results of FNN, 62% F-measure results of SVM and 60% F-measure results of NN.

Accuracy performance metric comparison results between the existing EDAEC, ESVM, SVM, NN and proposed IBBABOEC technique is which is the greater value when compared with 74% Precision results of EDAEC, 64% Precision results of ESVM, 61% Precision results of FNN, 61% Precision results of SVM and 59% Precision results of NN.

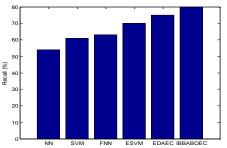


Figure: 14. Recall results of different method

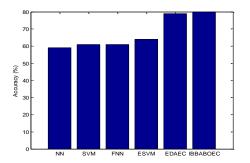


Figure: 16. Accuracy results of different method

shown in figure 21. Around 80% of accurate results are produced by proposed IBBABOEC technique, which us greater value when compared with 79% accurate results of EDAEC, 64% accurate results of ESVM, 61% accurate results of FNN, 61% accurate results of SVM and 59% accurate results of NN.

#### 5. CONCLUSION AND FUTURE WORK

To classify the type of leukaemia, an effective agenda is provided in this work. The blood smear images is taken as an input data and it is used to identify the White Blood Cell (WBC) based on work marker-controlled watershed segmentation. To perform the pre-processing technique, the image enhancement, noise removal and improved median filter is used. The stimulating discriminate measure (SDM) based on clustering algorithm is also implemented for separating nucleus and cytoplasm from input for classification.

For effective classification, the detail information is gained by selecting features using Bare-bones with Adaptive Bat Optimization (IBB-ABC). The classification is done by using Online Learning with Enhanced Support Vector Machine (OLERSVM), RBF network (RBFNets) and Improved Convolutional Neural Network (ICNN). Performance comparison is done with respect to precision, f-measure, recall and accuracy to show the better performance in exhibiting the proposed system. In order to obtain better results, more hybrid algorithms can be used in future.

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