

Acute Myelogenous Leukemia Detection using Circumventing Ant Colony Optimization based Convolutional Neural Network

B.Ramya,V.Uma Rani

Abstract: Acute Myelogenous Leukemia (AML) is a type of disease associated with acute leukemia which is getting increased in both children's and adults. AML falls under the category of cancer disease. The term acute in AML indicates rapid progression of disease in human body. The main challenge of medical field in vision of computer and multimedia is texture and color between various categories. The variation in texture and color attributes makes the classification task a tedious. Deep learning has shown its dazzling performance in various streams, which includes classification too. The objective of image classification is to differentiate the subcategories that belong to same basic-level category. The main objective of this paper is to propose bioinspired based on convolutional neural network to classify the microscopic blood images for AML. This paper has utilized bioinspired concept to extract the features more reliably. Bench mark performance metrics were chosen to evaluate the proposed classifier against the previous classifiers based on two parameters. The results indicate that the proposed classifiers has outperformed the previous works towards the classification of AML.

Keywords:AML, ACO, CNN, classification, deep learning

I. INTRODUCTION

Acute myelogenous leukemia (AML) is one among the blood cancer diseases which is getting increased among the peoples. It is also a bone marrow, where the very soft tissue were developed inside the bones. The term acute indicates the rapid development of disease in the human body. Due to continuously affecting the white blood cells (i.e., the myeloid cells), it is called myelogenous leukemia. Usually it gets developed into different types of matured blood cells, that is (i) platelets, (ii) white-blood-cells (WBC), and (iii) red-blood-cells (RBC). Some other terms used to indicate AML are (i) acute nonlymphocytic leukemia, (ii) acute granulocytic leukemia, (iii) acute myeloblastic leukemia, (iv) acute myeloid leukemia. When AML enters into the human body, its attempts to damage the DNA where the new cells get developed in the marrow of the bone. Because of happening this, production of blood cells gets entirely wrong. The heart of the bone produces the adolescent cells that result in the development of myeloblasts, which gives a way to develop leukemic WBC. These adolescent cells cannot properly function and tend to get developed. It gets build-up to affect healthy cells. In many of the cases, it is not well clear why DNA mutations lead to the development of leukemia.

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B.Ramya,Research Scholar,Department of Computer Science,Sri Ramakrishna College of Arts and Science for Women,Coimbatore-641044

Dr.V.Uma Rani,Associate Professor,Department of Computer Science,Sri Ramakrishna College of Arts and Science for Women,Coimbatore-641044B.Ramya

The drugs for AML may also lead to severe health issues in future.

Deep learning (DL) is a type of artificial intelligence (AI) enabled function which replicates the actual working methodology of the human brain to process the data and creates the patterns for making the decisions. DL is segregated from machine learning (ML) under AI. It has variety of networks having the capability of learning from the data that are unsupervised (i.e., unlabeled or unstructured). For these kinds of reasons, it some sometimes referred as deep neural network or deep neural learning. DL has seen different evolutions in this digital world, which has given a path to explore the data in various forms in different parts of the world. The data can be from different sources like social media, search engines in World Wide Web, e-commerce and m-commerce platforms, etc. This massive quantity of data is always ready to access, and finance enabled technology applications like cloud computing. The data that are found at massive level is mostly unstructured. If humans step in to analyze these means, it may take plenty of years to extract the appropriate information. With traditional programming for analyzing the massive data leads to linear approach, but DL's hierarchical function will enable to systems to progress the data in nonlinear manner approach.

The observed familiar drawback in the previous systems is just a classification of sub-images alone and not for AML. The main objective of this paper is to develop a bioinspired CNN for AML classification. The bioinspired concept is based swarm intelligence. K-fold validation method is used for evaluating the performance of proposed classifier. Further, the results are compared with existing models result.

II. LITERATURE REVIEW

Deep Classification [1] proposed by ensembling the CNN with feature reduction. Its aim was to make an investigation against the acoustic features and make DL sound classification. CNN made to attempt generalizing the features and resulted in low F1-measure. Multi-level Image Classifier [2] was proposed to diagnosis lung cancer and breast cancer. Its aim was to apply the DL to help the health

supervisors in assessing the AML. This method has reduced the massive amount of data for increasing the classification accuracy, but the classifier has discarded the benchmark details, which resulted in low accuracy.

DL based color classification [3] was proposed to segment the home images of forests. Once after applying the algorithm, it generates the binary segmentation of the image. Nevertheless, the results

indicate that the algorithm has weak performance in terms of classification accuracy over the considered dataset. DL for classification [4] proposed to classify the sperms into different categories referred by world-health-organization. The classifier has taken more time to classify the sperm. The algorithm was aimed to give more true positive, but the results came with increased false positive.

Auto Assessment DL Classifier [5] proposed to classify the human disease based on sperms. DL applied to detect false information and analysis different parts of the sperm. The method of sampling applied to fix the imbalanced data. The results with low accuracy indicate that the algorithm needs major improvement for improving the classification accuracy. Hyper-Spectral Image classification [6] was a DL based algorithm designed for small-scale data. It focuses only on main targets with limited samples. Initially, relations between different bands analysis made based on nearby pixels. It extracts the information of spatial information. It combines the relationship between spectral and spatial-spectral. Deep CNN classifier [7] proposed to classify the tissues in lung. It aimed to detect and perform classification on lung disease based on the tissue in the lung. CNN applied to make a non-parametric and deep classification, further it models the patterns in a virtual manner. The results indicate that the independent probability has lead to degradation in classification accuracy. Deep Feature Learning Classifier [8] proposed to classification based on feature extraction and fusion. Its main aim was to analyze the employability of DL for feature extraction and fusion. The algorithm was applied on 5 RGB-D datasets and it was found that the classification accuracy has gone down remarkably.

Land-use classification [9] proposed as a method for classifying the spatial images. It ensemble the sparse representation with transfer learning. It performed the classification using sparse representation. Trained images were used to perform classification and results indicates that the proposed classifier has poor classification accuracy. DL based Auto Classifier [10] proposed to detect the calcaneus fractures. The two types of CNN utilized for evaluating and comparing the performance of the proposed algorithms against the previous algorithms. The results with more false negatives indicate the algorithm performance on the considered dataset. Deep CNN [11] developed to combine the stages of feature selection and classification. Its focus was to discriminate the date fruits as healthy or unhealthy. By using the CNN concept, the classifier predicts the stage of ripening in healthy dates. The results with low

classification accuracy indicate the necessary improvement in feature engineering. Deep Topology Network Classification [12] proposed to improve the network depth and complexity computation for classifying the images. It works on the concept of iterating the feedback from DL. After the specific iteration count, the learning rate modified based on the feedback received.

Joint DL based Classification [13] incorporates the concepts of the multi-layer perceptron and CNN for classifying the land-cover and land-use. It fully utilizes the Markov method. The probability rate with actual image made to re-utilize as inputs. It attempted to give mutual complementary based information to the classification process, but results ended with low accuracy. Trichrome Image Classification Using DL [14] proposed to classify kidney diseases. In this CNN trained using cropped images and labels. Further, by utilizing the model images, it was scanned and tested for results, but classification accuracy and kappa statistics value represents the need of improvement. DL for Steganalysis [15] proposed to hide messages deeply in steganography. It establishes the new paradigm for learning the features for adjusting the characteristics, where it focuses to enhance the expression of steganalysis feature. However, the results indicate that the algorithm did not make remarkable detection due to having less classification accuracy. Automatic Screening System (ASS) [16] proposed to classify and detect the presence of AML in blood-microscopic images. It performs the classification, forms the sub-images by performing the segmentation, and detects the nucleated cells. It conducts the classification based on the presence and absence of local binary pattern. Low classification results indicate that the accuracy is not sufficient to detect the AML. Bio-inspired concepts [17], [18] with CNN proposed to lower the delay in cognitive networks, but it did not give any benchmark results. Power-Aware Multicast tree-based Methodology [19] proposed to reduce the energy, but it increased the delay and energy in heterogeneous network. Artificial-Neural-Network based genetic algorithm (ANN-GA) [20] utilized to classify the requirements of platelet transfusion for AML patients. It attempted to improve the accuracy of training by using the back-propagation methodology. Due to having no feasibility, the classification accuracy has become lower.

III. CIRCUMVENTING ANT COLONY OPTIMIZATION BASED CONVOLUTIONAL NEURAL NETWORK

3.1 Circumventing Ant Colony Optimization (CACO)

Ant-Colony-Optimization (ACO) is one among the Swarm-Intelligence (SI) algorithm. It makes a deal with the two entities, namely cooperative behavior, and uncomplicated effort. It is used in multiple domains and applications. In the year 1990s, ACO is one of the eminent meta-heuristic

algorithms under the family of SI. ACO is used and being used to resolve multiple higher-level complex issues, which are associated with data mining, networking, and other research domains. ACO is enthused by the natural food searching behavior of ants. During the food searching process, ants exchange the information concerning the trails by using the pheromone (i.e., a chemical substance) which they spread. The communication between the ants continues only by using pheromone. The other ants in the swarm follow the path that higher pheromone than lower pheromone. In short, the attractiveness of the path is entirely dependent on the concentration level of pheromone. The pheromones are expected to evaporate with a specific time, and it is necessary to add new pheromone. If pheromones are not added, then it will diminish the path. This concept embeds with ACO, and it makes ACO fall under meta-heuristic. The proposed work of this paper will be based on ACO with the subsequent significant necessities:

The proposed CACO can provide an absolute solution as an ensemble of various components. Hence, a new methodology is in need to find out the quality (i.e., the fitness) of solutions, and it should have the nature of heuristic to analyze the solution.

Consider an associated-graph $AG = (W, E)$, where W indicates the all available nodes, and E indicates the possible number of edges used for connection. By default, ACO has utilized to seek the minimum distance path between two nodes in AG , i.e., between source node ' W_s ' and a target node ' W_d '. The distance between the source and target nodes is determined by node count and calculation of cost values related to path. Every edge in AG that connects ' W_p ' and ' W_q ' has artificial pheromone (i.e. the variable) that is available to modify by the ants while they visit the nodes.

Once after an ant visits a node it searches for the next node to visit, it makes utilization of two parameters to compute the likelihood of a specific node which is (i) node distance, and (b) level of pheromone level available in connecting edge. Assume $d_{p,q}$ represents the distance connecting ' p ' and ' q ' nodes. The ant selects next node as ' q ' once after visiting the node ' p ', where the node ' q ' is available in set ' S ', and ' S ' indicate the group of nodes that are not visited by the ant. Mathematically it is expressed as

$$P_{p,j} = \frac{[\tau_{p,q}]^\alpha [\eta_{p,q}]^\beta}{\sum_{k \in S} [\tau_{p,k}]^\alpha [\eta_{p,k}]^\beta} \quad (1)$$

where $\tau_{p,q}$ represents the value of the availability of pheromone in the edge $e(p, q)$, and $\eta_{p,q}$ indicates the heuristic-based value and it computed by using $1/d_{p,q}$.

The variables α and β are the corresponding values that identify pheromone-value (PV) and heuristic-value (HV)

correspondingly. Initialization of PV gets to start with minimum values that are generated randomly. The whole route of the ant from ' p ' and ' q ' is termed as solution to the identified problem (i.e., the shortest path), where the route is evaluated by utilizing the fitness function. Not all ants have the best solution where a few ants have best solutions, where the remaining ants update their pheromone value based on the best solutions. The pheromone updation is mathematically shown as

$$\tau_{p,q} = \tau_{p,q} + \frac{Q}{L} \quad (2)$$

where ' Q ' denotes a constant value, ' L ' denotes the route length to ' q ', minimum value of ' L ' indicates the maximum value for pheromone, and it updates the previous pheromone value with this value. Meanwhile, the absorption level of pheromone gets decreased because of diffusion effect, in short evaporation. This provides the surety of never having or using the old pheromone value again in the future. The evaporation offers a chance to minimize the stuck in ACO. The evaporation of pheromone is mathematically performed as

$$\tau_{p,q} = \tau_{p,q} \cdot \rho \quad (3)$$

where the value of ' ρ ' lies between 0 and 1

The different level that constitutes the proposed work are discussed in next sub-sections.

3.1.1 Construction of Search Space and Tour

The initial stage of CACO algorithm begins with design of issue that concentrates the search space, where the ants carries out the searching process to seek the candidate solutions. The search-space is segregated into two equal parts namely hierarchy based sub-graph and construction based sub-graph, which are related with handling memories and the statistics about that is mathematically shown in Eqn (4):

$$Total_terms = \sum_{n=1}^a b_n \quad (4)$$

3.1.2 Initialization of Pheromone

The preliminary pheromone between $term_p$ and $term_q$ that belong to two diverse attributes are calculated as:

$$\tau_{p,q} (iter = 1) = \frac{1}{\sum_{n=1}^a x_n b_n} \quad (5)$$

In Eqn.(5), if $term_p$ is contained in the attribute, then x_n value is set to 0, else it is set to 1.

3.1.3 Selection of Terms

In the increasing manner, the ants will add the terms in

antecedent area of the rule, which is constructed during the visit it makes in the sub-graph. When an ant in the rule adds a term, then none of the attribute is considered further. Based on this condition, likelihood of selecting the next term to add will be given by the Eqn.(6)

$$P_{pj}(t, pter) = \frac{\tau_{pj}^\alpha(ite\text{r})\eta_{pj}^\beta(s)}{\sum_{j=1}^{\text{Total_terms}} x_p \{ \tau_{pj}^\alpha(ite\text{r})\eta_{pj}^\beta(s) \}} \quad (6)$$

3.1.4 Updation of Pheromone and Evaporation

Ant’s determination about making the next move in the available search-space is restrained with 2 main parameters in Eqn.(6). Values of the pheromone available in the edges are significant for learning the dynamicity in CACO. The quality of trails available at ants plays a major role in the effective utilization of pheromone values, where it provides the direction for the swarm to learn. The quantity of pheromone at the edges that is available between the terms during the iteration is mathematically expressed as:

$$\tau_{pq}(t+1) = (1 - \rho)\tau_{pq}(t) + \left(1 - \left(\frac{1}{q} + Q\right)\right) \tau_t \quad (7)$$

where ρ represents the evaporation rate of pheromone and Q indicates the current iteration’s quality for the trail

3.2 CACO-CNN

Convolution Layer (CL) is an arrangement of multiple filters that are of fixed-size. It permit the functions that are loaded with complexity to apply to the images that are given as input. This specific process is concentrated and continued by the trained filters that are trained locally for the images. It is estimated to have the same weight values for the image till the process gets complete, and it called as weight-sharing-mechanism. It have the capability to indicate the common feature on an individual image. Neighborhood field (i.e., the neuron) denotes the location where the neuron is linked with the preceding layer. The neighborhood field’s size is computed by the filters size.

Let $u \times v$ and $d \times d$ denote the input image size and kernel size, i indicate an image, wt and bs represents the filter weight and bias values. The estimated output $OP_{0,0}$ is possible to calculate using Eqn.(8), where af indicates the function used for activating the process. The sigmoid is utilized as activation function in CACO-CNN, and its behavior is seen in Eqn.(9)

$$OP_{0,0} = af \left(c - \sum_{t=0}^c \sum_{r=0}^c wt_{t,r^i t,r} \right) \quad (8)$$

$$af(y) = \begin{cases} y & y < 1 \\ 1 & else \end{cases} \quad (9)$$

3.2.1 Pooling Layer

The process of pooling is used to map the features that are made to pass through convolution and activation function.

It affords the generation of lesser feature maps, where it briefs the maps of input feature. Pooling method is carried out by stop and wait concept on the input to perform the chosen operation. The three common pooling methods are (a) average-pooling (AL), (b) maximum-pooling (ML), and (c) L2-pooling (L2P). The AL performs by calculating the average from the input values, ML performs by checking the maximum value, and L2P performs by calculating the norm of L2 from the inputs. The huge benefit of applying the pooling operation is the minimization of image size and independent feature extraction .

3.2.2 Layers of Fully-connected

Once after convolution and pooling layers process gets completed, the input image is passed to single-dimensional vector. This vector is the input of fully-connected network of ant swarm. Every neuron provides a evolution for connection weights that is received from the previous layers and finally it adds a bias value. The computed value gets pass through the af before it is passed to the next level of layers. The calculation operation that is made by neuron is shown in Eqn.(10).

$$af_c = af \left(bs - \sum_{q=1}^N wt_{1,r} \times o_r \right) \quad (10)$$

where af represents the function used for activation, wt represents the vector used to indicate the weight, o is denotes the input vector received from the r th neuron and bs used to represent the value of bias.

3.2.3 Softmaxing Activation Function

Softmaxing Activation Function (SAF) is a subtype of logistic regression. SAF is mostly used for classification in the output layer of CNN and it is mathematically defined as in Eqn.(11)

$$classification_k = \frac{\exp(ASF_k)}{\sum_r \exp(ASF_r)} \quad (11)$$

3.2.4 Augmentation of Data

Augmentation of Data is a sample that gets keep on increased artificially. To avoid the overfitting issues during the training process this step is carried out. Example of augmentation of data includes resizing the image, condition of lighting the image, and changing the orientation. This step is more utilized to extract the features by the ants using Eqn.(7).

3.2.5 Drop-Out

Drop-Out is an idea to avoid memorization. In drop-out, certain neuron values that are generated dynamically are assigned 0, where few selected neuron values are modified in the training process, and it increases the reliability and complexity of over-fitting is avoided.

3.2.6 Drop-Connect

This method is used to check whether overfitting exist in CACO-ANN. In this few selected neuron values are considered as 0, which is inverse in drop-out. Drop-connect maximizes the performance of the ant network, which will result in increased classification of AML.

IV. PERFORMANCE METRICS

To make sure the efficiency of proposed algorithm over the existing algorithms and to make decision this research work utilizes performance metrics (i) Sensitivity, (ii) Specificity, (iii) Precision, (iv) F-Measure, and (v) Classification Accuracy. While making an attempt to classify the specimen, it comes 4 possibilities which are:

- ✓ True Positive: It indicates the correct identification of cancer cells.
- ✓ False Positive: It indicates identification noncancer cells as cancer cells.
- ✓ True Negative: It indicates the correct identification of noncancer cells.
- ✓ False Negative: It indicates identification cancer cells as noncancer cells.

4.1 Sensitivity

It indicates the ability of the algorithms towards finding the results in a positive manner. It is mathematically expressed as

$$\text{Sensitivity} = \frac{TP}{(TP + FN)} \quad (12)$$

4.2 Specificity

It indicates the ability of the algorithms towards finding the results in a negative manner. It is mathematically expressed as

$$\text{Specificity} = \frac{TN}{(TN + FP)} \quad (13)$$

4.3 Precision

It indicates the fraction of subjects respect to results in positive manner that are accurately identified. It is mathematically expressed as

$$\text{Precision} = \frac{TP}{TP + FP} \quad (14)$$

4.4 F-Measure

It indicates the harmonic-mean of sensitivity and precision which provides the overall performance of classification. It is mathematically expressed as

$$F - \text{Measure} = \frac{2 \times \text{Precision} \times \text{Sensitivity}}{\text{Precision} + \text{Sensitivity}} \quad (15)$$

4.5 Classification Accuracy

It indicates the proportions of prediction made by the algorithms. It is mathematically expressed as

$$\text{Classification Accuracy} = \frac{TP + TN}{TP + FP + TN} \quad (16)$$

V. DATA MINING TOOL AND DATASET

5.1 About MATLAB

MATLAB is one of the language having high-performance for computing. It ensembles the programming environment, computation and visualization. By default, MATLAB contains space for editing, tools for debugging and supporting of object-oriented-programming. These kinds of factors give the feeling of excellence to the users when they use MATLAB for research and teaching. This research work uses the MATLAB R2018b for evaluating the proposed work against the base works.

5.2 About Dataset

To classify the AML, this research paper considers (i) shape feature, (ii) grey-level co-occurrence matrix feature, and (iii) color feature. The diagnostic performance of shape feature is fully utilized in this paper to classify the AML. The dataset holding 410 microscopic-blood images, 184×138 sized are used for the evaluation. Among many features, shapes are substantiated as the best measure to classify AML. In accordance with haematologists, nucleus shape is fundamental for discriminating the myeloblasts. Moreover, boundary-based and region-based shapes are obtained for analyzing the shape of nucleus. Feature extraction is made from nucleus's binary-equivalent image, where non-zero pixels indicates the region of the nucleus. The illustration [16] of variation in the values of shape features for a pair of cancer and noncancer nuclei are used in this research work to classify AML.

VI. RESULTS AND DISCUSSION

From Fig 1 to Fig 6, 10-fold and 5-fold cross validation parameters are plotted in x-axis, and y-axis is plotted with percentage indicating the result of corresponding metrics.

6.1 Sensitivity Analysis

From Fig 1 it is clear that the proposed algorithm CACO-CNN has overcome the previous algorithms namely Auto-SS [16] and ANN-GA [20], by providing the enhanced sensitivity. It is because of constructing the search-space in a clear manner before the algorithm starts.

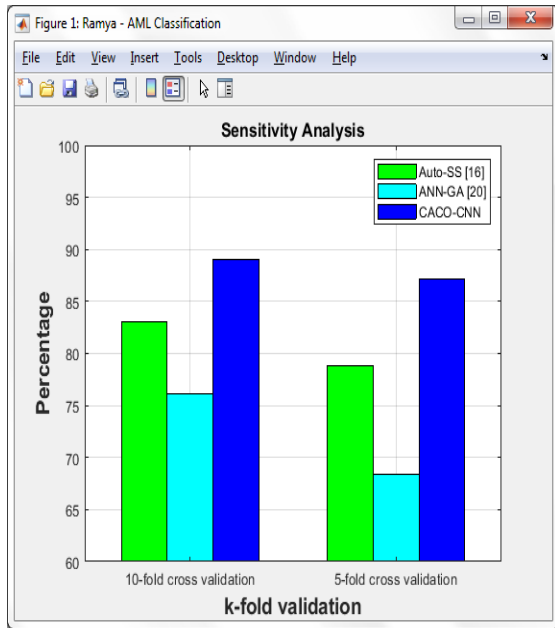


Fig 1. Sensitivity vs AML

6.2 Specificity Analysis

From Fig 2 it is obvious that the proposed algorithm CACO-CNN has classified AML more correctly than Auto-SS [16] and ANN-GA [20]. The reason for getting enhanced specificity includes the construction of search-space earlier before the algorithm starts.

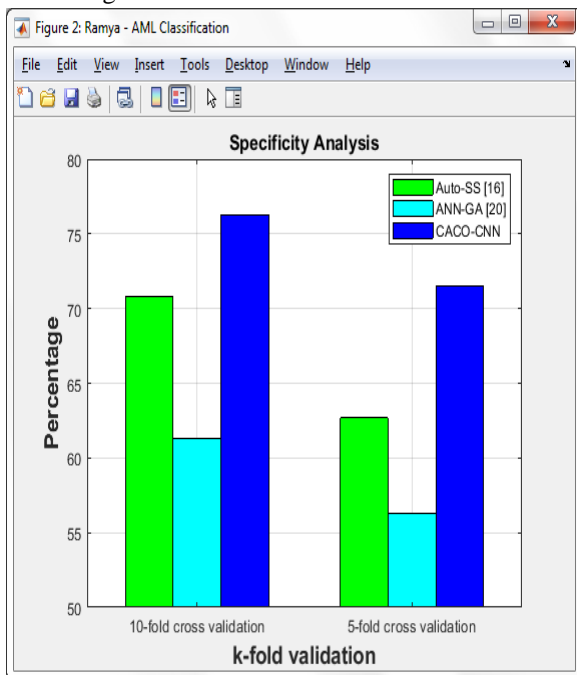


Fig 2. Specificity vs AML

6.3 Accuracy Analysis

From Fig 3 it is evident that the proposed algorithm CACO-CNN has outperformed Auto-SS [16] and ANN-GA [20], by providing the better specificity. Due to updation of pheromone and evaporation details in the swarm, CACO-CNN has correctly classified the AML than others.

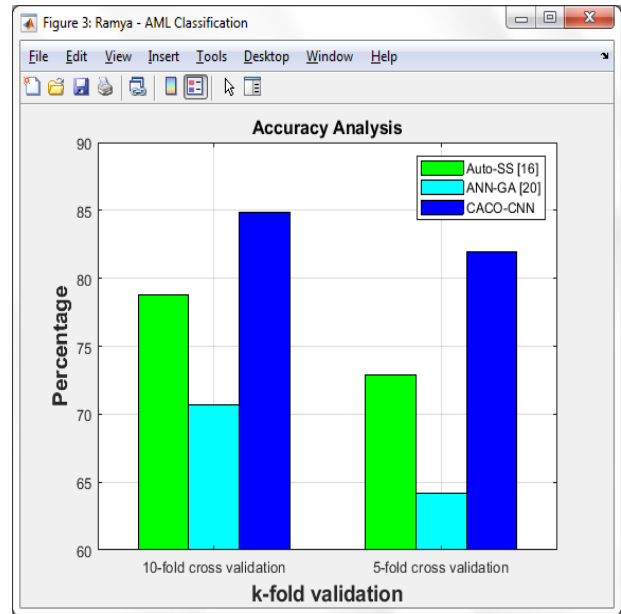


Fig 3. Accuracy vs AML

6.4 Precision Analysis

From Fig 4 it is noticeable that the proposed algorithm CACO-CNN has outperformed Auto-SS [16] and ANN-GA [20], by providing the good precision which is because of selecting the better terms at the correct stage, if the terms selection are not good means, then the precision values will go inversely.

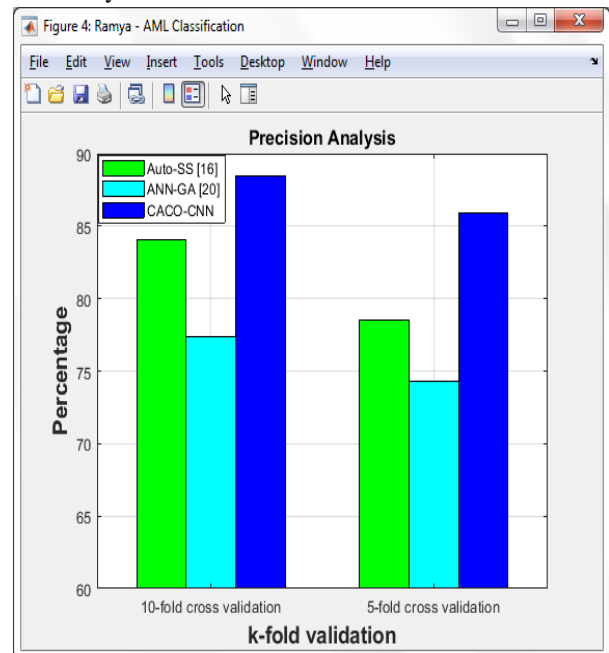


Fig 4. Precision vs AML

6.5 Recall Analysis

From Fig 5 it is visible that the proposed algorithm CACO-CNN has returned utmost the relevant results than the Auto-SS [16] and ANN-GA [20] previous algorithms. Also, Fig 5 indicates the relevant instances from the retrieved instances. The low values of Auto-SS [16] and ANN-GA [20] indicates the irrelevant instances in the retrieved instances.

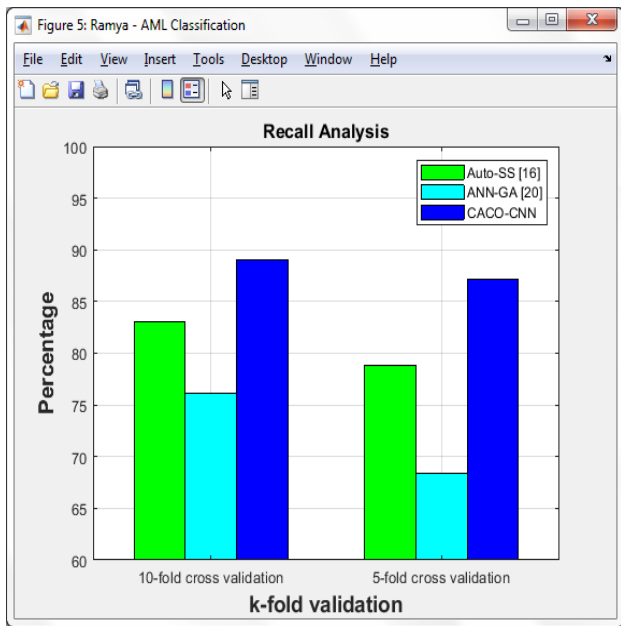


Fig 5. Recall vs AML

6.6 F-Measure Analysis

From Fig 6 it is evident that the proposed algorithm CACO-CNN has obtained the better F-Measure in 10-fold cross validation and 5-fold cross validation tests, but Auto-SS [16] and ANN-GA [20] has received very low F-Measure result. Because of using the CNN in CACO the F-Measure value has got increased more.

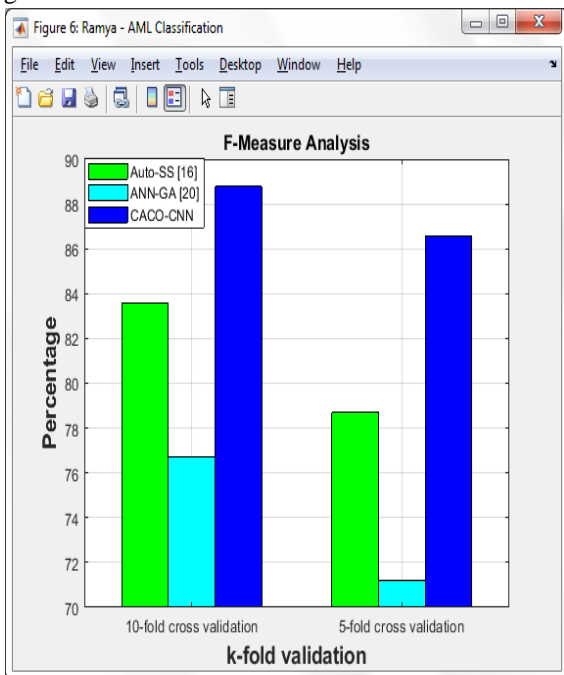


Fig 6. F-Measure vs AML

VII. CONCLUSION

This paper has proposed design and development of bioinspired based CNN for classification of AML in microscopic images of blood. The proposed classifier has performed automation based processing using the bioinspired concept resulted in better feature extraction. The feature set includes color, texture, and shape. This research work considered the shape feature for classifying the

presence and absence of AML. The results indicate that the proposed classifier is having better classification accuracy than the existing classifiers. The future dimension of this research work will focus on utilizing the advanced bioinspired concepts in CNN for increased classification accuracy.

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