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BiCNN-CML: Hybrid Deep Learning Approach for Chronic Myeloid Leukemia

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***Abstract*— chronic myeloid leukemia (CML) is an uncommon kind marked by genetic changes in early myeloid cell progenitors. The only efficient approaches for identifying leukemia are blood smear analysis, bone marrow aspiration, and biopsy. Because the tests mentioned above are time-consuming and expensive, leukemia diagnosis needs automation. Image processing is a low-cost and efficient way of identifying leukemia using stained blood microscope pictures. The major goal of this Research is to improve the accuracy of CML diagnosis. Recently, deep learning technologies have been employed in the medical business for early cancer detection and therapy prescription. Existing algorithms are exclusively concerned with image segmentation and feature extraction, and output may be provided as a consequence. In this paper proposed BiCNN-CML framework for predicting the CML. The datasets are collected and normalized using gray scale and morphological operation. The segmentation has done with FCM and PSO. The features are selected using GLCM and finally classification has done with Bi-LSTM with CNN algorithm. the experimental results has shown the classification metrics..**

Keywords—Chronic myeloid leukemia, Classification, Deep learning, Feature extraction, Segmentation

I. INTRODUCTION

Chronic myeloid leukemia (CML) is cancer that causes an excess of white blood cells (WBC) and blood deposition in the bone marrow. Because it ensures everyone's safety, blood is the most valuable component of the human body [1]. It maintains the body's metabolism by performing numerous vital functions, such as oxygen and mineral transfer [2]. Cells expand and replicate to generate new cells as the human body needs. Cells die and are replaced by new cells as they age [3]. When the body is affected by CML, this loop is rendered ineffective. CML patients are mostly between the ages of 45 and 55. However, newborns are often afflicted. CML has three stages: chronic, fast, and explosive [4]. The natural history of CML development normally lasts three to five years, from chronic to acute and fast phases. Numerous writers have studied CML from the viewpoints of clinical features, molecular genetics, leukemogenesis, treatment approaches, and medical advancement in recent years. Many image-processing algorithms for leukemia detection have been developed [5]. Accurate image segmentation is a fundamental challenge that must be met in automated haematological Research [6]. A subfield of haematological image processing science is leukemia classification algorithms [7]. The fundamental barrier to sickness identification is prediction accuracy. Certain clustering and classification approaches are used in developing models and detecting similarities in results. Data from the microarray, including leukemia BCs, were utilized as input [8]. Pre-processing processes are carried out before analyzing BC leukemia. BCs are used to determine if a cell is dangerous. Current databases include noisy or inadequate information gathered from several sources. To remove noise and missing data, preprocessing is performed [9]. Preprocessing increases the value of data. Following preprocessing, the programme will choose the final dataset [10]. A feature selection approach is used to choose a subset of BCs from a single data source. To improve prediction performance, the best BCs were picked. Following the completion of the filtering process, Clustering and classification algorithms may be used to determine whether or not a patient is disease-affected.

The main contributions of this paper as follows.

- The datasets are normalized using gray scale and morphological operation.
- The segmentation has done with FCM and PSO.
- The features are selected using GLCM
- Classification has done with Bi-LSTM with CNN algorithm.

The remaining paper is as follows: Section II discusses the existing literature survey, and Section III discusses the proposed BiCNN-CML framework model. Section IV represents the results and discussion about the BiCNN-CML method. Finally, the paper concludes in section V.

II. BACKGROUND STUDY

Ali et al. (2018) For the purpose of dental X-ray image segmentation, a novel fuzzy clustering algorithm based on neutrosophic orthogonal matrices was presented. By transforming the image data into a neutrosophic set, we were able to calculate the cutting matrix. This study used dental records from the Hanoi Medical University Hospital in Vietnam to assess the performance of the proposed system. Francis, J. et al. (2015) The overall research cohort survival rate was higher for patients who had a complete cytogenetic response at one year. Patients with CML who are taking imatinib would benefit greatly from a cutting-edge approach that includes pharmacogenetic evaluation and risk score classification. Heuser M. et al. (2017) Offer a robust risk model that consolidates the patient's demographics with information about the transplant procedure, the donor's cytogenetics, and the recipient's molecular makeup into a single predictive tool that can provide accurate, individual outcome projections. Once our technology has been independently verified, it will be able to warn doctors and patients about HCT's potential dangers while also classifying people into groups for targeted clinical trials. Ilander, M. et al. (2014) This study aims to update the current immune system dimensions of CML patients and to develop mechanisms for monitoring their immunotherapy use. Identification of multiple leukemia-specific antigens is a promising phase of CML immunotherapy. According to multiple research groups, WT1 will be targeted by other known and evolving CML-specific antigens. Iriyama, N. et al. (2018) There was no discernible difference between the molecular response rates and outcomes for patients treated with nilotinib and dasatinib, according to the literature review conducted. The author also shows that scoring methods are not useful for predicting MMR and prognosis, but that the Hasford scoring system may help in predicting DMR in patients receiving first-line 2G-TKI. Clinical research into the efficacy and safety of 2G-TKI therapy as first-line treatment is currently underway in Japan. Rundo et .al (2018) During the preliminary processing of the Prostate MRI image, stick filtering and contrast stretching were used to lower the level of background noise. In this research, the Fuzzy C-means (FCM) clustering algorithm was used to deconvolute the axial MRI components from the prostate gland image. The region of interest (ROI) in a prostate image is automatically extracted using this method. Ratna Saha et al. (2016) A novel method for segmenting Pap smear cell nuclei is proposed using digital image processing. The Circular Shape Function was used to increase the resistance of Pap cell nucleus segments with fuzzy c-means clusters. CSF imposed a type limit and strengthened the nucleus boundary after the maximum capacity of the predefined clusters was reached. The pixel generation method distinguished the spatial distributions of pixels with identical intensities.

III. PROPOSED METHODOLOGY

This article focuses on feature extraction using segmentation and fuzzy approaches. The Fuzzy/PSO optimization approach gets its name because the features are first produced using the Fuzzy system, then particle swarm optimization is utilized to find the best centroid. There are several research suggestions for CML diagnosis. Various algorithms were used in various proposals. Researchers concentrated on a variety of topics like segmentation, feature extraction, classification, and so on. This chapter describes an integrated structure for the suggested technique. Fuzzy C Means are used for Clustering, Hybrid Gray Level Co-occurrence Matrix for feature extraction, and convolutional neural network (CNN) for classification in the proposed system.

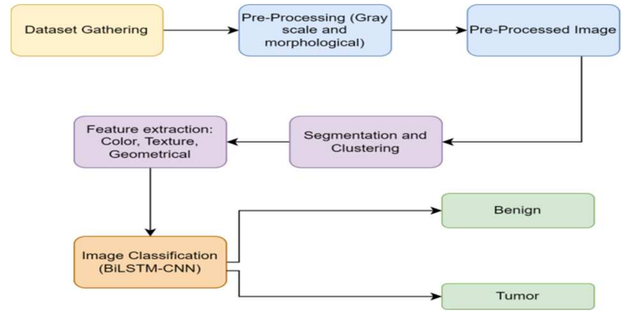

Fig. 1: BiCNN-CML framework architecture

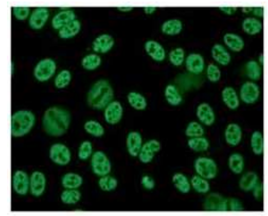

Fig. 2: blood cell image

a) Pre-Processing

Figure 3 exemplifies the BC image input. Multiple stains, such as Leishman's, Wright's, Giemsa, and others, may be used on microscopic blood smear images. Digital microscopes often produce images in RGB colour. It's repetitive and tough to section. Furthermore, the changing light, age stain, and camera settings all impact the clarity and colour of the shot and BCs. Grayscale image processing, including scaling, reshaping, and sharpening as a function of filter value, is shown in Figure 3. The Morphological outer procedure with near open dilation and erosion is shown in Figure 4. Grayscale includes monochromatic colours ranging from black to white. Because there are no colours in a grayscale picture, the image is merely varying shades of grey. In several image editing programmes, a colour picture may be converted to black and white or grayscale. Only the brightness of each pixel is preserved using this approach.

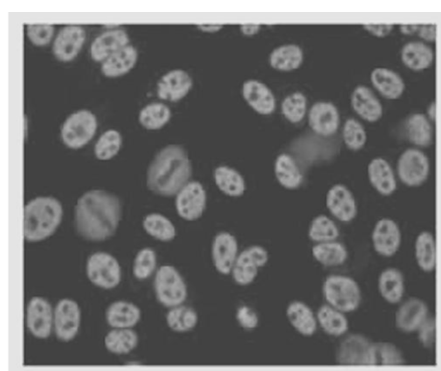

Fig. 3: Grayscale image

The max thresholding and cache thresholding to convert a grayscale image to a morphological image. If an image's pixel intensity goes below a specified threshold value (I ij T), it becomes a black pixel; if it surpasses the threshold (Iij > T), it becomes a white pixel. A specified area is the region within which an item is subdivided in region max thresholding. The pixels next to this area are examined to determine if they are inside or outside the region. Morphology employs opening and closing procedures to reduce picture noise. Upon opening, it removes small, brilliant pixels from the foreground and sets them in the background. Tiny islands in the background are replaced by small holes in the front during the closure procedure.

Image processing procedures such as erosion and dilation are crucial. The process of deleting pixels from the picture border is known as erosion. The dilation technique extends the image's border by adding pixels. A rule that considers the individual pixel and its neighbours determines whether an operation is an erosion or dilation.

The equation for erosion /dilation operation is

$A \circ B = (A \ominus B) \oplus B$

A and B are 2 sets, and $\ominus \oplus$ represents erosion and dilation operation, respectively.

Non-linear morphological procedures cover the form or morphology of picture features. In a morphological operation on a binary image, a new binary image is created in which only pixels that test positive in the input picture have a non-zero value.

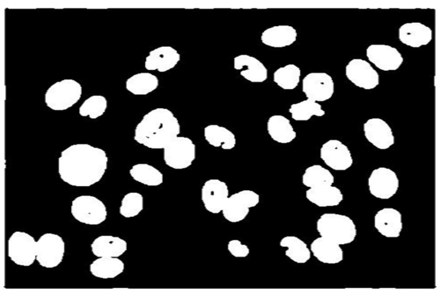

Fig. 4: Morphological operation

b) Segmentation

Segmentation is the process of dividing a picture into sections or components. The answer to the question determines the level of detail at which the subdivision is executed. The Accuracy of segmentation influences whether automated analytic procedures succeed or fail. Furthermore, precautions may be taken to increase the likelihood of correct segmentation.

Segmentation is accomplished using edge detection algorithms in this method. A region is an image field in which all pixels have the same intensity value, color, and texture. There is a significant difference between neighbouring locations. Each region has contours that set it apart from the others. This method assumes that region boundaries are distinct and allows for boundary identification based on local amplitude discontinuities.

Segmentation is required to extract important information from a given input image. For the separated image, image segmentation features are used. White blood cells (BCs) are extracted from an image using colour segmentation

c) Fuzzy C means Clustering

The fuzzy C-Means clustering approach is used in this work for Clustering. This method works well for grouping large datasets. FCM is an improved clustering approach that allows the same data point to be placed in several clusters.

Each data point's membership is determined by its closeness to the cluster core; the closer it is to the cluster core, the more members it obtains.

The FCM approach generalizes the primitive c-means algorithm such that a point may be part of many clusters. It provides a soft partition for the given dataset. The FCM clustering approach is a popular soft segmentation technique for microscopic images. Clustering algorithms provide substantial advantages, especially for photographs with many pixels. The FCM algorithm, for example, identifies less fuzzy clusters with pixels. Unlike K-means clustering, which requires pixels to be assigned to just one class, Based on their membership ratings, Fuzzy C-means encourage pixels to belong to several clusters. As a result, points near the cluster's edge will be smaller than those in the cluster's core. This clustering method produces the best results for overlapping datasets. However, the intricacy of its processing and the fact that it deteriorates drastically with increasing noise is its principal shortcomings.

Algorithmic steps for Fuzzy c-means Clustering

Let $X = \{x_1, x_2, x_3 ..., x_n\}$ be the set of data points and $V = \{v_1, v_2, v_3 ..., v_c\}$ be the set of centers.

1) Randomly select $'c'$ cluster centres.
2) Calculate the fuzzy membership $'\mu_{ij}'$ using the following:

$$\mu_{ij} = 1 / \sum_{k=1}^{c} (d_{ij}/d_{ik})^{\frac{2}{m}-1}$$

3) Compute the fuzzy centres' v_j' using:

$$\boldsymbol{v}_j = \frac{\sum_{i=1}^{n} (\mu_{ij})^m x_i}{\sum_{i=1}^{n} (\mu_{ij})^m}, \quad \vartheta_j = 1,2, \ldots c$$

4) Repeat steps (2) and (3) until the minimum $'J'$ value is achieved.

d) Particle Swarm Optimization(PSO)

The colony in Particle Swarm Optimization has a finite number of particles. For the particles, subsets of BCs are shown. Each subset's health benefit is calculated. Because the new fitness value exceeds the previous value, the fitness value is changed. This technique is done until the correct qualities are found.

The particles in the region change at each repetition to determine the total maximum. Each particle has space and velocity vectors that it can use to direct the motion of subsets of BCs. Geometric Particle Swarm Optimization (GPSO) was developed to address PSO's shortcomings and improve gene selection.

e) Feature Selection

The feature selection approach selects a subset of features from the original feature space without making any changes. It preserves the original properties and makes function feature extraction superior in terms of readability and interpretability. The dimension of relevant data has grown rapidly during the previous three decades. High-dimensional data presents a serious challenge to traditional machine learning algorithms.

The feature selection strategy is the most often used technique for lowering the dimensionality of the results. The goal of feature selection is to pick a limited subset of significant elements from the original features based on some acceptable assessment criteria, thereby increasing learning results. Feature selection improves classification learning accuracy, reduces processing costs, and improves model interpretability. Characteristics like texture and WBC count per unit of blood are calculated throughout the feature selection stage.

Feature selection approaches are classified as Controlled, Unsupervised, or Semi-supervised based on whether or not the training set is labelled. Filter, Wrapper, and Embedded models are the three types of controlled feature selection methodologies. The selection of filter model features differs from the selection of classifier learning features. The feature selection approach's bias does not influence the learning algorithm's bias. This feature selection technique is based on training data attributes such as Accuracy, dependency, detail, distance, and correlation. The most common Filter model function range forms are relief, Fischer, and information benefit strategies. The Wrapper model function selection classifies the consistency of the selected features using the anticipated Accuracy of a prediction learning approach. The Wrapper model function collection has the disadvantage of being expensive to operate data with many characteristics. In order to overcome these restrictions and drawbacks, we propose the Embedded model as a middle ground between filter and wrapper feature selection approaches. In the same way that the filter model combines statistical parameters to select a single feature, the wrapper method selects multiple candidate features until the required cardinality is reached. The subgroup with the highest classification accuracy is then chosen. As a result, the Embedded method provides precision and dependability comparable to the Wrapper and filtering models.

f) GLCM Feature Extraction

Features in a picture are visible patterns that add distinct visual information. The extraction process includes retaining vital picture information while removing extraneous data. Preprocessing a picture enhances its Accuracy but not its amount of detail. Pre-processing, which comprises removing extraneous distortion and details and optimizing the relevant and desirable picture properties of numerous processing techniques, is generally useful depending on the intended output. Before proceeding with feature extraction, the first job is to locate and pick the accessible features. Although there is no perfect approach for extracting features, the retrieved features should give enough information about the relevant picture. These characteristics may not be difficult to compute. The estimated features must be strongly relevant to human experience and accurate to be used for diversification.

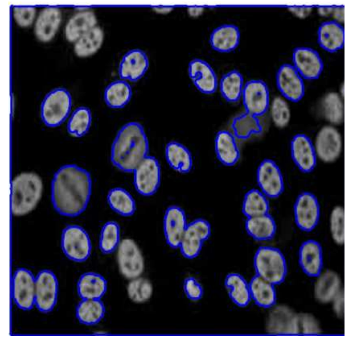

Fig. 5: Identifying the affected and normal blood cells separately

HGLCM: Texture Equations

Energy feature

$Energy = \sum_{i,j=0}^{N-1}(P_{ij})^2$

Entropy feature

$Entropy = \sum_{i,j=0}^{N-1} -ln(P_{ij})P_{ij}$

Contrast feature

$Contrast = \sum_{i,,j=0}^{N-1} P_{i,j}\,(i-j)^2$

Homogeneity feature

$Homogeneity = \sum_{i,j=0}^{N-1} P_{i,j}\,/(1+(i-j))$

Correlation feature

$Correlation = \sum_{i,j=0}^{N-1} P_{ij}\,((i-\mu)(j-\mu))/\sigma^2$

Shade feature

$Shade = sign(A)/A/^{1/3}$

Prominence feature

$Prominence = sign(B)/B/^{1/3}$

where:

Pij = Element i,j of the normalized symmetrical HGLCM

N = Set the number of grayscale levels in the picture using the Quantization option on the HGLCM texture's page of the Variable Properties dialogue box.

μ = the HGLCM average (representing a best guess of the brightness of every pixel in the associations that formed the HGLCM) :

$$\mu = \sum_{i,j=0}^{N-1} iP_{ij} \text{ ------------- (1)}$$

g) Classification with Bi-LSTM-CNN

With promising outcomes, it is heartening to see academics using CNN's potential computer vision breakthroughs for CML prediction. Consequently, we have presented a hybrid network for anticipating blood cell cancer that incorporates CNN and Bi-LSTM. CNN is one of the most important nodes in this network. Bi-LSTM recognizes and analyses the CNN output sequence after the CNN layer. To extract temporal features from CML variables, the CNN network aids the process. As a result, the Bi-LSTM network is more accurate in predicting chronic myeloid leukemia (CML). The convolutional and pooling layers are hidden layers in CNN on past training models. The Kaggle repository's "CML Data Set" is used in the proposed technique.

The network mentioned above's convolutional layers will minimize spectral dispersion. CNN's local connections and weight-sharing features allow the model to discover local patterns with fewer tuning parameters. Some translation invariance is included in CNN with Bi-LSTM to its "local and global pooling" layers.

$$h^{(s)} = f_h\left(A_{hh}h^{(s-1)} + A_{ih}x^{(s)}Wish(s) + b_h\right) \text{ --------- (2)}$$
$$y^{(s)} = f_0\left(A_{ho}h^{(s)} + bo\right) \text{ ---------------------------------- (3)}$$

Where

X^s - the input data

h^s - the hidden layer units

y^s - the output

$A_{ih'}, A_{hh}$ *and* A_{ho} - the transformation matrices between $X^{(s)}\&\ h^{(s)}, h^{(s-1)}\&h^s$ *and* $h^{(s)}\&y^s$

b_h *and* b_o - the constant bias terms

f_h *and* f_o - the no-linear activation function

Some function of this net input is the activity or state of RCL, which is given by

$$z_{ijk}(t) = f(g(X_{ijk})) \text{ ------------------------------------- (4)}$$

Where g, the rectified linear activation function is defined by $g((x_{ijk}(t)) = \max(x_{ijk}(t), 0)$ and f is the local response normalization (LRN) function defined by

$$f\left(g\left(x_{ijk}\right)\right) = \frac{g(x_{ijk}(t))}{\left(1+\frac{\alpha}{n}\sum_{k'=\max\left(0,k-\frac{n}{2}\right)}^{k'=\min\left(K,k+\frac{n}{2}\right)}(g(x_{ijk'}(t)))^2\right)\beta} \text{ --------- (5)}$$

Here k is the total number of feature maps in the current layer α, and β are constants of normalization.

IV. RESULTS AND DISCUSSION

MATLAB 2015 was used to create this proposed Hybrid Deep learning approach for CML prediction (BiCNN-CML) architecture. MATLAB is a set of functions designed to improve the programming environment. It offers a wide range of workflow and guiding techniques for encoding, analyzing, viewing, and producing pictures. A range of viewing and analyzing capabilities, as well as simulation results, are provided depending on the basic operation and inventive conditions for the successful implementation of an algorithm. This programme has some image editing and filtering tools. Photos of leukemia patients are pre-processed in the proposed technique to increase Accuracy. The WBC segmented picture is then retrieved from the rest of the image. Function extraction is performed on the segmented WBC for each image to get statistical and colour-based information. These features are sent into the neural network to identify the kind of leukemia.

Fig. 6: Confusion Matrix

180 of the 200 images of leukemia were used to train the neural network, and 90 were tested. The tests were used to determine the classification procedure's overall precision. The outcome demonstrated that the proposed method performed more precisely than other algorithms. Figure 6 depicts the confusion matrix of Training and Testing. The classifier has four potential outcomes. If cancerous images are accurately identified, they are referred to as true positives (TP). If noncancerous images are accurately identified as noncancerous, they are referred to as true negatives (TN). In contrast, false positives occur when noncancerous images are interpreted as cancerous. A false negative (FN) occurs when cancerous images are misidentified as noncancerous.

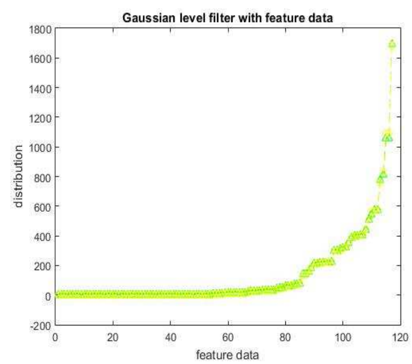

Fig. 7: Performance graph

Figure 7 represents the proposed performance graph; the X-axis denotes the feature data, and the Y-axis denotes the distribution.

TABLE 1: COMPARISON TABLE FOR PERFORMANCE METRICS

Methodology	Precision	Specificity	Recall	Sensitivity	F-Measure	G-Mean
SVM	87%	86%	6%	82%	50%	45 %
BiCNN-CML	93%	70%	8%	96%	80%	60%

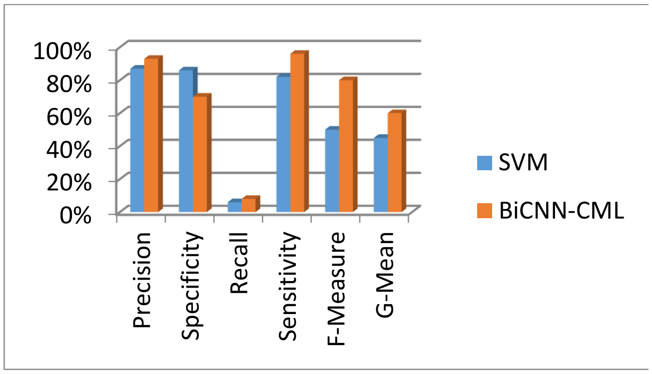

Fig. 8: Classification metrics comapricon chart

TABLE 2: ACCURACY COMPARISON TABLE

ALGORITHM	ACCURACY
K-Means	91%
SVM	95%
Random Forest	94%
Naïve Bayes	92%
BiCNN-CML	98%

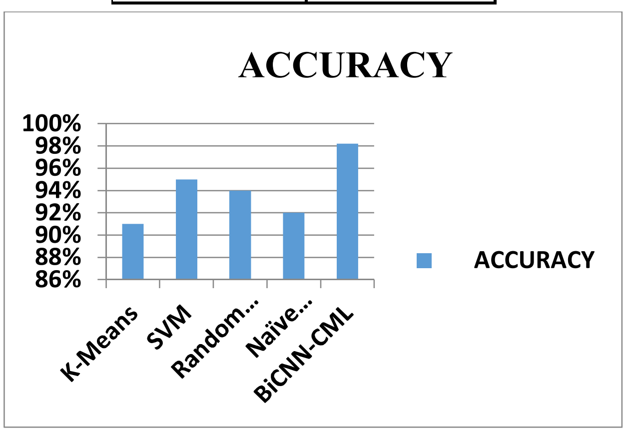

Fig. 9 Accuracy Comparison chart for Various Algorithms

Figure 8 and 9 displays a comparison chart between the Proposed technique and current algorithms. Compared to current algorithms, the suggested approach attained the highest precision. SVM delivers 95% accuracy in CML prediction, which is superior to other techniques. Random Forest gives the following degree of Accuracy, 94%. Naive Bayes yields 92% accuracy, whereas K Means provides 91%. The suggested algorithm, HLD, has an accuracy of 96%, showing that it is more efficient than other current algorithms. Table 1 and table 2 examines the precision of several methods. Precision and Accuracy are often used metrics in engineering, statistics, and other scientific disciplines. Accuracy quantifies the correctness of a value relative to its true or absolute value. This value's Accuracy indicates how closely it approaches the actual value. When a dataset is symmetric, precision is the optimal metric. Precision is the degree to which a result is exact. It is closer to consistency, dependability, etc.

V. CONCLUSION

This article proposed BiCNN-CML framework for CML prediction. Massive dimensionality data, especially microarrays of BCs, have several drug discovery diagnoses and properties. The dataset has collected and pre-processed using morphological operation. The segmentation has done using FCM with PSO algorithm. The best features are selected by using GLCM algorithm. finally the classification has done with BILSTM with CNN algorithm. the accuracy has achieved with 98%. Consequently, the proposed technique enabled the development of automated solutions for the identification and categorization of regular and irregular WBCs with a shorter computation time and a reduced error rate. In future Research, the types of cancer cells impacted by WBCs may be broadened using flexible standards. And using the transfer learning method for improving accuracy and predicted results

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