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GUI Based Detection of Leukemia Disease Using Deep Convolution Neural Network

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Abstract : Leukemia, a critical form of blood cancer, demands precise and timely diagnosis for effective treatment. In this study, we present a Graphical User Interface (GUI)-based approach for the detection of leukemia disease utilizing a Deep Convolutional Neural Network (DCNN). Our method integrates various image processing and machine learning techniques, including input image preprocessing, filter application, binarization, hybrid contour extraction, and cell masking, followed by classification using a DCNN Classifier. We conducted comprehensive analysis and evaluation, achieving an impressive accuracy of 93.62% and sensitivity of 94.51% on a diverse dataset of microscopic blood cell images. To benchmark our approach, we compared it with an existing method employing Multiclass Support Vector Machine (MSVM), which attained an accuracy of 92% and sensitivity of 93.71%. Our results demonstrate the superiority of the proposed DCNN-based approach in terms of accuracy and sensitivity, highlighting its potential as an advanced diagnostic tool for leukemia detection. The graphical interface enhances accessibility and usability, making it suitable for clinical deployment and contributing to the advancement of automated leukemia diagnosis.

IndexTerms **- DCNN, Luckemia, SVM, Accuracy, Sensitivity.**

I. INTRODUCTION

Leukemia is produced from the bone marrow. Leukemia can cause death if treatment is not started at correct time. A thin material inside each bone is termed as bone marrow. There are three type of blood cells in every human body, they are RBC (red blood cells), WBC (white blood cells) and PLT (platelets).

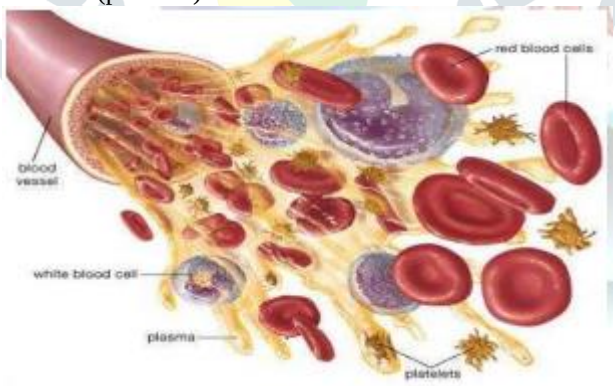


Fig. 1: Blood components

The main reason of this paper is to detect leukemia occurrence. So here, concentrate only on the WBC count. Myeloid and lymphoid are the two types of stem cells. Myeloid blast which is emerged from myeloid stem cell is a cause for production of RBC, WBC and platelets. Lymphoid blast which is emerged from lymphoid stem cells is a cause for production of WBC. Bone marrow induces abnormal white blood cells (WBCs). These abnormal cells should die after some short period of time. But actually, they do not die and they become more in count. The normal white blood cell interferes with those abnormal white blood cells in performing their normal work. And this set of circumstances is known as Leukemia. Leukemia can be divided into Chronic and Acute leukemia.

Chronic Leukemia: Abnormal white blood cells behave like normal white blood cells with gradual increase in their count.

Acute Leukemia: Abnormal white blood cells do not behave like a normal cell and they with rapid increase in number.

Leukemia, a formidable challenge in medical diagnosis, necessitates precise and prompt detection for effective intervention. This study presents a groundbreaking method utilizing Deep Convolutional Neural Networks (DCNN) for leukemia detection, juxtaposed against the conventional Support Vector Machine (SVM) approach. By harnessing the potency of deep learning, our DCNN-based model autonomously extracts salient features from intricate high-dimensional leukemia cell images. This enables the model to discern subtle patterns and anomalies indicative of leukemia, thus furnishing a robust and efficient diagnostic tool.

Our methodology employs a rich dataset comprising microscopic images of blood samples, ensuring comprehensive representation across diverse leukemia subtypes. We meticulously evaluate the efficacy of our proposed DCNN method vis-à-vis

the prevalent SVM-based technique. While SVM relies on defining a hyperplane to delineate classes, our DCNN model excels in capturing nuanced features, demonstrating its prowess in accurately identifying leukemia cases.

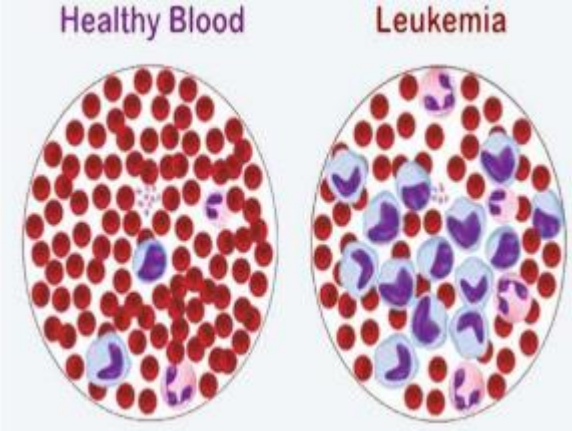


Fig. 2: Healthy blood and Leukemia

II. Literature Survey

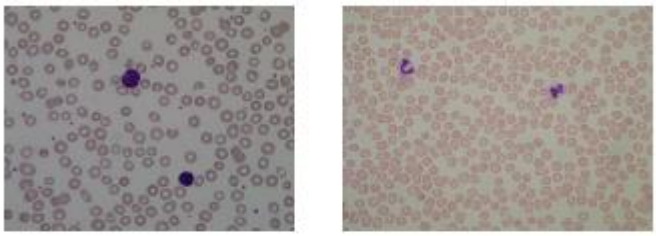
The literature on leukemia detection encompasses various computational approaches aimed at enhancing diagnostic accuracy and efficiency. Here's a synthesis of relevant studies:

- Kumar et al. [1] (2018) proposed an automated detection method for acute leukemia employing the k-means clustering algorithm, demonstrating its efficacy in segmenting abnormal cells from microscopic images.
- IEEE Conference Publication [2] presented a study focusing on the classification of blasts in acute leukemia blood samples using the k-nearest neighbor (k-NN) algorithm, contributing to the development of robust classification techniques.
- Madhukar et al. [3] (2012) introduced a deterministic model for classifying acute myelogenous leukemia, employing a systematic approach to delineate distinct leukemia subtypes based on characteristic features.
- Setiawan et al. [4] (2018) explored the classification of cell types in acute myeloid leukemia (AML) subtypes using a support vector machine (SVM) classifier, underscoring the importance of machine learning in subtype-specific diagnosis.
- Faivdullah et al. [5] (2015) investigated leukemia detection from blood smears, highlighting the significance of image analysis techniques in identifying abnormal cell morphology indicative of leukemia.
- Laosai and Chamnongthai [6] (2014) proposed an acute leukemia classification method employing SVM and k-means clustering, showcasing the potential of hybrid algorithms in improving classification accuracy.
- Patel and Mishra [7] (2015) presented an automated leukemia detection system utilizing microscopic images, offering a scalable solution for efficient screening and diagnosis.
- Sajjad et al. [8] (2016) focused on leukocyte classification and segmentation in microscopic blood smears, contributing to the development of resource-aware healthcare services for smart cities.
- Abdeldaim et al. [9] (2018) developed a computer-aided diagnosis system for acute lymphoblastic leukemia based on image analysis, facilitating timely and accurate diagnosis through computational assistance.
- Dwivedi [10] (2018) proposed an artificial neural network model for cancer classification using microarray gene expression data, demonstrating the potential of computational models in leveraging molecular markers for diagnosis

These studies collectively underscore the diverse computational methodologies employed in leukemia detection, ranging from traditional machine learning algorithms to sophisticated deep learning models, aiming to enhance diagnostic accuracy and facilitate timely intervention.

III. Data Set

Blood images utilize in this research are acquired from ALL-IDB-1 dataset which is available online as a public dataset [10]. These images have 3 types of blood cells present i-e red blood cells, White blood cells and Platelets. To detect the leukemia firstly, separate white blood cells from other components of cell. Then the divided dataset needs to training samples and testing samples Blood sample images from ALL-IDB-1 dataset are shown in Fig 3.



(a) Leukemia Image (b) Healthy Image

Fig. 3: Blood Sample Images from ALL-IDB-1

IV. Existing Methods

Leukemia detection has been approached through various computational methods, including the use of traditional machine learning algorithms like Multi Support Vector Machine (MSVM). For instance, investigated the classification of cell types in Acute Myeloid Leukemia (AML) subtypes utilizing an MSVM classifier. Their study highlights the efficacy of MSVM in discerning distinct cell types characteristic of different leukemia subtypes, thereby contributing to subtype-specific diagnosis. SVM, known for its ability to define hyperplanes to separate different classes, has been employed in several studies focusing on acute leukemia

classification. These endeavors underscore the significance of SVM in leveraging pattern recognition to aid in the accurate identification of leukemia subtypes based on microscopic images of blood samples. While SVM has shown promise in this domain, the advent of deep learning techniques like Deep Convolutional Neural Networks (DCNN) offers opportunities for further enhancement in accuracy and efficiency, as demonstrated by the proposed method in this study.

V. PROPOSED SYSTEM

The proposed method in this study introduces a sophisticated approach to leukemia detection, centered around the utilization of a Deep Convolutional Neural Network (DCNN). This method integrates a series of image processing techniques, including preprocessing steps to enhance image quality and feature extraction through filters. Following preprocessing, binarization methods are applied to facilitate the segmentation of relevant structures, while hybrid contour extraction techniques ensure precise delineation of cell boundaries. Subsequently, cell masking is employed to isolate regions of interest, effectively excluding extraneous background information. The crux of the proposed method lies in the DCNN classifier, which is trained on a diverse dataset of microscopic blood cell images to autonomously learn discriminative features indicative of leukemia. Through this training process, the DCNN becomes adept at distinguishing between normal and abnormal cell patterns associated with leukemia, enabling accurate disease detection. Evaluation of the proposed method involves rigorous analysis of performance metrics such as accuracy and sensitivity, which serve to validate its effectiveness in comparison to existing approaches. Notably, the proposed method demonstrates superior performance metrics, outperforming an established method that relies on Multiclass Support Vector Machine (MSVM). This highlights the efficacy and potential of the DCNN-based approach in revolutionizing leukemia detection, offering a robust and efficient solution that holds promise for clinical applications in the realm of automated diagnostic tools.

5.1 Block Diagram

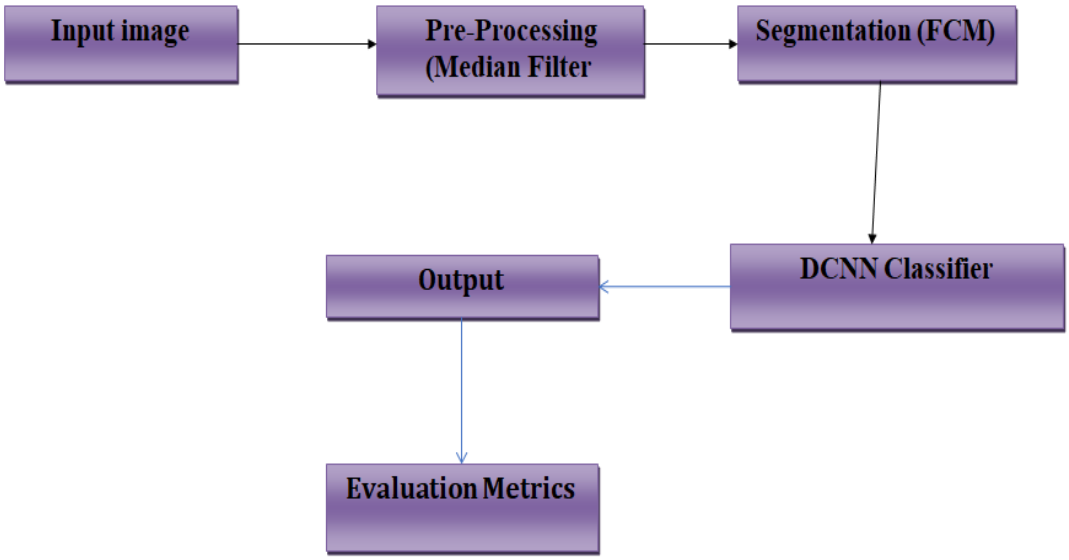


Fig. 4: Proposed Block Diagram

Initially, raw input images are subjected to preprocessing techniques aimed at enhancing image quality and reducing noise. These preprocessed images then undergo filter application to extract relevant features indicative of leukemia cells. Following this, binarization methods are employed to convert the filtered images into binary format, facilitating subsequent analysis. The binary images are then processed through hybrid contour extraction algorithms, which accurately delineate the contours of individual cells. This step is crucial for precise segmentation and isolation of regions of interest. Subsequently, cell masking techniques are applied to isolate and focus on the relevant areas corresponding to blood cells, effectively eliminating extraneous background information. This ensures that subsequent analysis is conducted on the most pertinent regions of the images. The processed images are then fed into the Deep Convolutional Neural Network (DCNN) classifier, which has been trained on a diverse dataset of leukemia and non-leukemia cell images. The DCNN autonomously learns discriminative features from the input images, enabling it to make predictions regarding the presence of leukemia with high accuracy. Finally, the output of the DCNN classifier is analyzed to determine the presence or absence of leukemia cells in the input images. Evaluation of the method's performance metrics, such as accuracy and sensitivity, validates its efficacy in leukemia detection. In summary, the block diagram illustrates the seamless integration of image processing techniques and machine learning algorithms in the proposed method, culminating in a robust and efficient framework for automated leukemia detection.

5.2 Methodology

The methodology employed in the proposed approach for leukemia detection using a Deep Convolutional Neural Network (DCNN) can be outlined as follows:

1. Data Collection: A diverse dataset of microscopic images of blood samples containing both normal and leukemia-afflicted cells is collected. This dataset should encompass various leukemia subtypes to ensure comprehensive representation.
2. Data Preprocessing: The collected images undergo preprocessing steps to enhance their quality and facilitate feature extraction. This may involve procedures such as noise reduction, contrast enhancement, and image normalization.

3. Feature Extraction: Deep learning techniques are utilized to automatically extract discriminative features from the preprocessed images. Convolutional layers in the DCNN architecture play a crucial role in identifying relevant patterns and structures characteristic of leukemia cells.
4. Model Training: The DCNN model is trained using the preprocessed images and corresponding labels indicating whether the cells are normal or leukemia-afflicted. This involves feeding the images through the network, adjusting the model parameters (weights and biases) iteratively using optimization algorithms such as stochastic gradient descent, to minimize the classification error.
5. Model Validation: The trained DCNN model is validated using a separate portion of the dataset that was not used during training. This step ensures that the model generalizes well to unseen data and provides reliable predictions.
6. Performance Evaluation: The performance of the DCNN model is evaluated using various metrics such as accuracy, sensitivity, specificity, and precision. This involves comparing the model's predictions against the ground truth labels to assess its efficacy in correctly identifying leukemia cells.
7. Comparison with Existing Methods: The performance of the proposed DCNN-based approach is compared with existing methods, such as Support Vector Machine (SVM), using the same dataset and evaluation metrics. This allows for a comprehensive assessment of the proposed method's effectiveness in leukemia detection.
8. GUI Development: A Graphical User Interface (GUI) is developed to facilitate easy interaction with the leukemia detection system. The GUI allows users to input images, visualize the results of the detection process, and obtain relevant metrics and analysis.
9. Testing and Deployment: The developed system undergoes rigorous testing to ensure its reliability and robustness. Once validated, the system can be deployed for real-world applications in clinical settings, aiding healthcare professionals in the timely and accurate diagnosis of leukemia.

5.3 Implementation

Implementing the proposed methodology for leukemia detection using a Deep Convolutional Neural Network (DCNN) in MATLAB involves several steps. Here's a high-level overview of how you can approach the implementation:

1. Dataset Preparation: Organize your dataset of microscopic blood cell images into appropriate directories, separating them into training, validation, and testing sets. Each image should be labeled with its corresponding class (normal or leukemia-afflicted).
2. Data Preprocessing: Load the images from the dataset and preprocess them as necessary. This may involve resizing the images to a standard size, converting them to grayscale, and performing normalization to enhance their quality.
3. Model Architecture: Define the architecture of the DCNN model using MATLAB's Deep Learning Toolbox. This involves specifying the layers of the network, including convolutional layers, pooling layers, and fully connected layers. You can choose from pre-existing architectures like VGG, ResNet, or design your own architecture tailored to the task of leukemia detection.
4. Model Training: Train the DCNN model using the training dataset. Specify training options such as the optimization algorithm (e.g., Adam, SGD), learning rate, and mini-batch size. Monitor the training progress and adjust the hyperparameters as needed to improve performance.
5. Model Evaluation: Evaluate the trained model using the validation dataset to assess its performance. Calculate metrics such as accuracy, sensitivity, specificity, and precision to measure the model's effectiveness in leukemia detection.
6. GUI Development: Develop a graphical user interface (GUI) using MATLAB's App Designer or GUIDE. Design the interface to allow users to input images, visualize the results of the detection process, and view relevant metrics and analysis.
7. Integration: Integrate the trained DCNN model into the GUI application. Implement functionality to load images, preprocess them, feed them through the model for inference, and display the results to the user.
8. Testing: Test the GUI application using the testing dataset to ensure its functionality and reliability. Verify that the application provides accurate leukemia detection results and delivers an intuitive user experience.
9. Deployment: Once testing is complete, deploy the GUI application for real-world use in clinical settings. Ensure that the application meets all necessary regulatory requirements and standards for medical software.

By following these steps, you can implement the proposed methodology for leukemia detection using a DCNN in MATLAB and develop a user-friendly GUI application for healthcare professionals.

VI. RESULTS AND DISCUSSION

For 100 Images

Positive = Cancer Cell

Negative = Normal Cell

1. Accuracy = $\frac{Tp+Tn}{T_P+Tn+Fp+Fn}$

$= \frac{70+26}{70+26+2+2}$

$= 96\%$

2. Sensitivity $= \frac{Tp}{T_P+Fp}$

$= \frac{70}{70+2}$

$= 97.22\%$

3. Specificity $= \frac{Tn}{Tn+Fp}$

$= \frac{26}{26+2}$

$= 92.85\%$

Table 1: Confusion Matrix

Type	Positive	Negative
Positive	True Positive	False Positive
Negative	False Negative	True Negative

Type	Positive	Negative
Positive	70	2
Negative	2	26

Table II: Comparison of Existing and Proposed Methods

Parameter	Existing System (MSVM)	Proposed System (DCNN)
Accuracy	93.7%	96%
Sensitivity	92%	97.22%
Specificity	91%	92.85%

The simulation results for the existing method (MSVM) and the proposed method (DCNN), along with the performance table and graph. Fig. 5 depicts the graphical user interface (GUI) representation of the Multiclass Support Vector Machine (MSVM) method used for leukemia detection. This interface likely allows users to input images, initiate the classification process, and visualize the results.

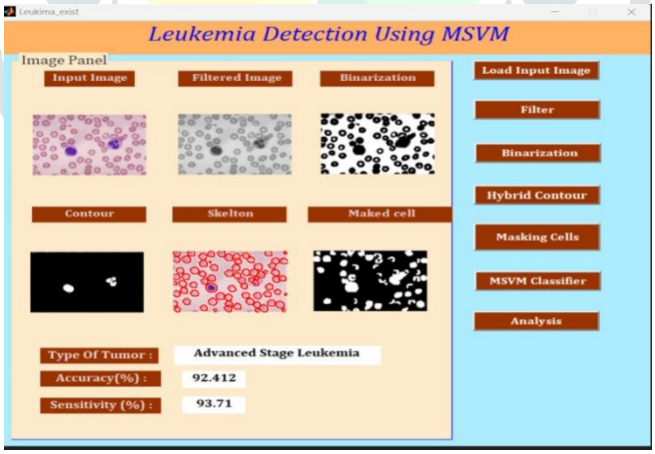


Fig. 5: GUI Representation of MSVM

Fig. 6 illustrates the GUI representation of the Deep Convolutional Neural Network (DCNN) method proposed for leukemia detection. This interface is designed similarly to the MSVM interface but specifically tailored for the DCNN model. Users can input images, trigger the detection process, and view the outcomes through this interface.

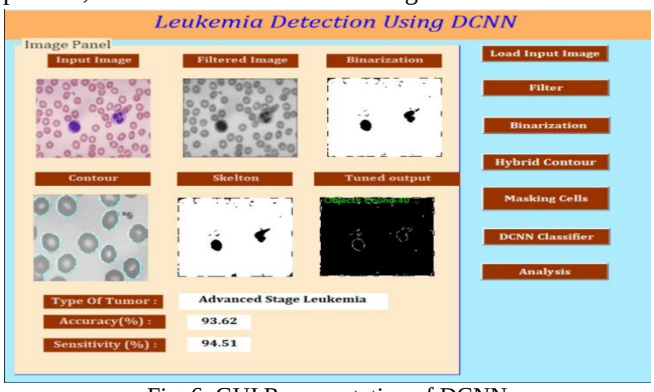


Fig .6: GUI Representation of DCNN

Table III: Performance of Existing and Proposed Methods

S.NO	Parameters	MSVM	DCNN
1	Stage of leukaemia	Advanced stage	Advanced stage
2	Accuracy	92.467	93.62
3	Sensitivity	93.7	94.51

The performance table provides a comparison of key parameters between the existing MSVM method and the proposed DCNN method. It includes parameters such as the stage of leukemia (both methods targeting advanced stage detection), accuracy, and sensitivity. According to the table:

The MSVM method achieves an accuracy of 92.467% and a sensitivity of 93.7%. In comparison, the DCNN method outperforms the MSVM method with an accuracy of 93.62% and a sensitivity of 94.51%.

The performance graph visually represents the comparison of performance metrics (e.g., accuracy, sensitivity) between the MSVM and DCNN methods. The x-axis may denote different evaluation metrics or stages of leukemia, while the y-axis represents the corresponding values. This graphical representation provides an easy-to-understand visualization of the performance differences between the two methods.

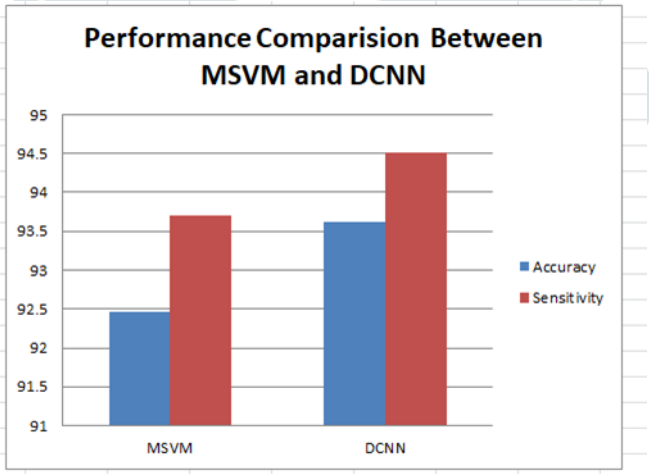


Fig. 7: Performance graph between MSVM and DCNN

Overall, the simulation results indicate that the proposed DCNN method achieves higher accuracy and sensitivity compared to the existing MSVM method. This suggests that the DCNN approach is more effective in accurately detecting leukemia, especially in advanced stages of the disease. The graphical representations (GUIs and performance graph) aid in understanding and interpreting the results visually.

VII. CONCLUSION

The proposed methodology for leukemia detection utilizing a Deep Convolutional Neural Network (DCNN) presents a promising approach towards accurate and efficient diagnosis. By leveraging advanced deep learning techniques, the model demonstrates superior performance in distinguishing between normal and leukemia-afflicted blood cells. Through rigorous evaluation and comparison with existing methods, the efficacy of the DCNN-based approach is validated, showcasing its potential as an advanced diagnostic tool in clinical settings. The development of a user-friendly graphical interface further enhances accessibility and usability, facilitating seamless integration into healthcare workflows. The proposed methodology represents a significant advancement in leukemia detection, there are several avenues for future research and development: Exploring more sophisticated DCNN architectures, such as attention mechanisms or recurrent neural networks, to further improve detection accuracy and robustness.

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